

# **TIBCO Spotfire DecisionSite 9.1.1 for Microarray Analysis - User's Manual**

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# 1 Preface

## 1.1 What is Spotfire DecisionSite?

TIBCO® Spotfire® DecisionSite® is a solution for accessing, analyzing, and reporting on data. It enables you to rapidly identify trends, anomalies, outliers and patterns in your data.

Spotfire DecisionSite can access data residing in databases, in a local or networked file system, or on the desktop. It is database independent and extracts data (several hundred thousand records or more, depending on computer performance) from commercial data sources such as Oracle, SQL-Server, Informix, and Sybase.

Spotfire DecisionSite uses the patented Spotfire DecisionSite visualization technology, allowing you to interactively query data and instantly visualize results as scatter plots, bar charts, profile charts and a number of other modes.

Spotfire DecisionSite stores data internally in a proprietary data format, allowing for rapid response times to user interaction. It has a series of built in heuristics and algorithms that helps you find interesting alternative views of data.

Spotfire DecisionSite allows you to share your work. Analyses can be easily presented as structured reports for printing or Internet publishing.

## 1.2 Third Party Components

### **SharpZipLib 0.8.4 from IC#Code**

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If you have any questions about a TIBCO Spotfire® product, please do the following:

- Use the built-in help function.
- Consult the README files which are included with the product.
- Visit the Spotfire web site, <http://support.spotfire.com>, where you can send questions to our support department.
- Get personal contact from TIBCO Spotfire Support.

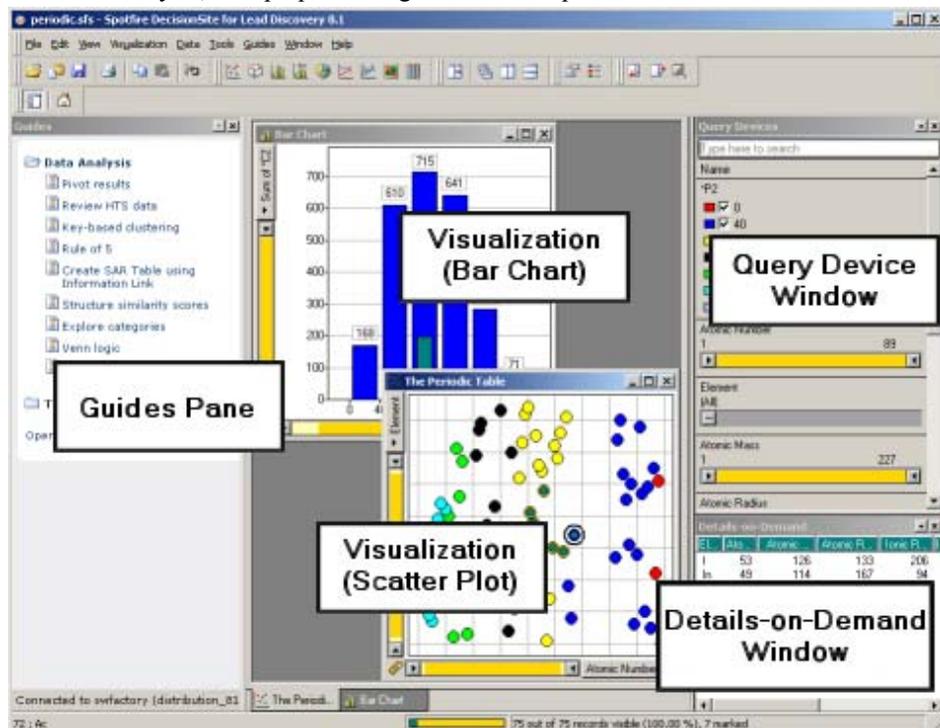
TIBCO Spotfire offers a variety of support agreements. Contact TIBCO Spotfire for more information about support, training, consulting agreements, and our Product Subscription Programs.

## 2 Introduction

### 2.1 Spotfire DecisionSite Overview

#### 2.1.1 The User Interface

The image below shows the main parts of the TIBCO® Spotfire® DecisionSite® user interface. The entire application window is referred to as Spotfire DecisionSite. It is the core of the Spotfire DecisionSite solution, which encompasses a suite of applications for database access, statistical analysis, data preprocessing and domain-specific tasks.



#### Visualizations

Visualizations are the key to analyzing data in Spotfire DecisionSite. A variety of visualization types can be used to provide the best view of the data:

- Scatter Plots
- Bar Charts
- Pie Charts
- Line Charts
- Profile Charts
- Heat Maps
- Tables

Different types of visualizations can be shown simultaneously. They are linked, and are updated dynamically when the query devices are manipulated (see below).

Visualizations can be made to reflect high-dimensional data by letting values control visual attributes such as size, color, shape, rotation and text labels.

### The Query Device window

Query devices are used to filter your data. Query devices appear in several forms, and you can easily select a type of query device that best suits your needs (e.g., check boxes, sliders, etc.). When you manipulate a query device by moving a slider or selecting a check box, all visualizations are immediately updated to reflect the new selection of data.

### The Details-on-Demand window

The Details-on-Demand window can be used to show the exact values of a record or group of records. By clicking a record in a visualization, or marking several records by drawing a rectangle around them, you can study their numerical values and textual data in a tabular form.

### The Guides pane

The Guides pane is a web browser, fully integrated into the Spotfire DecisionSite environment. This is where you can run Guides, step-by-step instructions for common workflows or tutorials, guiding you through an analysis.

## 2.1.2 Microarray Analysis Features

Spotfire delivers several different Guided Analytical applications. Which tools are present in your DecisionSite depends on which application package you are using and what licenses you have bought. Depending on the nature of the various features, you will find them under the File, Data, Tools or Guides menu.

Tools that are launched in the Guides pane (e.g., Information Builder) or in separate web windows have their own online help files. To access the online help for these applications, you must first start the application by selecting the appropriate link from the menu. Once an application has been launched, the online help is reached via the Help menu in the application window.

## 2.2 Installation and Setup

### 2.2.1 Hardware Requirements

Spotfire DecisionSite in itself does not require very high powered computers to run smoothly. However, if your data sets are large they will require both a certain amount of RAM, and will of course benefit from high processor speeds.

#### Minimal Client Hardware requirements

Processor:	Intel Pentium™ or equivalent, 500 MHz
RAM:	128 MB (256 MB or greater is recommended)
Hard Disk:	The installation footprint is approximately 30 MB
Display:	VGA or better, resolution 800x600 pixels, 256 colors (1024x768 pixels, 16 bit high colors or greater is recommended)
Others:	Network card or modem Mouse CD-ROM drive (if installation is done from a CD-ROM)

#### Graphics cards

When 3D visualizations are used for analyzing, you will find that the graphics card of the computer is an important component. OpenGL support is required and hardware acceleration

beneficial to allow the processor to devote its work to other things than presenting the display with information. Due to the great variety of graphics cards manufacturers, Spotfire DecisionSite has not been tested on all of them. If you experience difficulties or slow performance, check that the most recent drivers for your hardware are installed and that the manufacturer's recommendations are met.

## 2.2.2 Software Requirements

During the installation process the setup program checks that your computer contains all necessary operating system components. Most components are mandatory, while some may be missing without the installation being aborted. If this is the case you will be warned about the missing system component.

Please visit <http://support.spotfire.com/sr.asp> for information on which operating system and other software versions that are required to run DecisionSite Client.

### Web connection

Spotfire DecisionSite requires a Web connection to a Spotfire Analytics Server, either at <http://home.spotfire.net> or a company specific Spotfire Analytics Server.

Microsoft Internet Explorer on the client should be configured to access the Spotfire Analytics Server via the standard Web connection. The security settings in Microsoft Internet Explorer for accessing the Spotfire Analytics Server should be set to Medium Security. This includes enabling ActiveScripting, enabling cookies and enabling the download of signed ActiveX components. Downloading signed ActiveX components and scripts from the Spotfire Analytics Server must be allowed through the firewall.

### Other requirements

You must have Administrator privileges to install Spotfire DecisionSite.

Microsoft PowerPoint must be installed on the computer in order to use the PowerPoint presentation tool.

Microsoft Word must be installed on the computer in order to use the Word presentation tool.

## 2.3 Getting Started

### 2.3.1 Logging In

#### Logging In

When you start Spotfire DecisionSite a login dialog appears. First select which DecisionSite Analytics Server you want to log into by clicking on the **Server** drop-down list. Usually you will only have one server so there might not be a need to choose. You can also add a new server if you need to, by clicking on the **Server** drop-down list, selecting **Add new...** and typing in the location and name of the new server.

Then type your **User ID** and **Password**, and click on the **Login** button to start Spotfire DecisionSite.

Logging into Spotfire DecisionSite will give you access to the Guides and Tools that are specific for your profile. Pressing **Cancel** will start Spotfire DecisionSite but will not provide access to these Guides and Tools. See also **Working Offline** below.

Depending on the configuration of your DecisionSite Analytics Server, some of the following options may be available in the login dialog:

#### Remember me

If you select this check box when you log in, you will not be prompted to log in when you start Spotfire DecisionSite the next time. Your User ID and Password will be saved on your computer and will be used automatically each time you start Spotfire DecisionSite.

### Register a new user

If you are not a registered user of Spotfire DecisionSite click on the **Register a new user** link. This will display a new window in which you can register. You will then be able to access the specific features of Spotfire DecisionSite that you have a license for.

### Working Offline

If you have no network connection to the DecisionSite Analytics Server you can still use most features of Spotfire DecisionSite. Start DecisionSite as usual and log in when prompted. Even though you are working offline without any connection to the Spotfire DecisionSite Analytics Server or the internet, you will still be able to use most of the Guides and Tools if these were cached locally on your computer the last time you were connected to the server. The exceptions are those Guides and Tools that need to connect to databases, etc., which obviously cannot do so while working offline.

**Note:** Working offline requires at least one previous successful login to the Spotfire DecisionSite Analytics Server. Each time you log into the server it checks to see which Guides and Tools that should be available to you, and if there are any new updates. Spotfire DecisionSite automatically downloads these to your computer so that they are available the next time you log in, whether you are connected to the server or not.

### Unsupported Software

If your computer does not have the proper software installed (for example an Internet Explorer version that is too old) a dialog will appear. This dialog will state exactly what is wrong, and also ask you to contact your Administrator for further help.

## 2.3.2 Welcome to Spotfire DecisionSite

When you have logged in to Spotfire DecisionSite, you will be presented with a Welcome screen.



This will help you get started with the application by providing some useful options:

**Get an introduction** – This option gives you a five minute tour of Spotfire DecisionSite and of how to use its features. It is the perfect way to get the basic knowledge of how to get started with the application.

**Open a sample file** – This option presents a number of example data sets, and describes the content of each data set. You can easily open any of these data sets in DecisionSite and explore the visualizations on your own.

**Open data** – This option provides a quick way for you to access your own data. It gives you the choice to open a file, paste data from your clipboard or open data from an information link to a database.

**Switch to another DecisionSite** – Different DecisionSites have a different set of Tools and Guides. If you are missing a certain Tool or Guide that you believe should be available, you may need to switch to another DecisionSite. This option explains how to do this.

Click on **Close this window** to close the welcome screen and start using DecisionSite.

If you also select the **Don't show this window at startup** check box, the welcome screen will not appear when you start the application in the future. However, if you wish to display it again it is always available from the **View** menu, by selecting **Getting Started**.

## 2.3.3 Loading Data

### The Periodic table data set

As an example of simple, yet interesting information, the periodic table of the elements will be used. The data set holds 75 records with 9 fields each. The columns are: the name of the element, six of its properties, and finally the coordinates of each element when the periodic table is printed in the familiar layout first suggested by Dimitri Mendeleev. The text file contains the column names, column types (integer or string) and the data itself.

```
Element, Atomic Number, Atomic Mass, Atomic Radius, Ionic Radius,  
Ionization Energy, Electronegativity,*P1,*P2  
STRING, INT, INT, INT, INT, INT, INT, INT, INT  
Ac, 89, 227, 200, 126, 51, 11, 140, 0  
Ag, 47, 107, 144, 129, 75, 18, 630, 80  
Al, 13, 27, 143, 67, 60, 16, 750, 160  
.....
```

This data is stored in one of the data formats recognized by Spotfire DecisionSite. This particular example can be found in the directory named **Data/General/Periodic Table** in the Spotfire DecisionSite distribution as *periodic.csv*.

### Loading a data set

#### ► To load a data set into Spotfire DecisionSite:

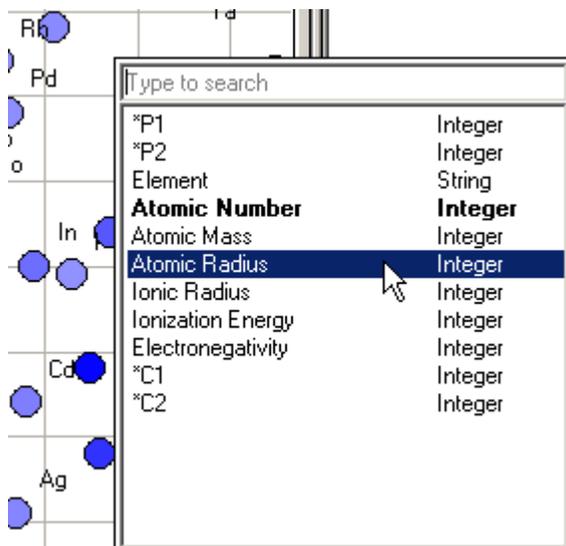
1. Start Spotfire DecisionSite by selecting **Spotfire DecisionSite** from **Programs** in the Windows **Start** menu, or by double-clicking the Spotfire DecisionSite icon on the desktop.
2. Select **File > Open** in the Spotfire DecisionSite main window. The **File** open dialog will appear.
3. The folder *Data* will be shown in the *DecisionSite* directory.
4. Browse to the folder *General/Periodic/Periodic Table*.
5. Select the file *periodic.csv* and click the **Open** button.

Spotfire DecisionSite will automatically set up an initial visualization where each record is represented by a marker, along with a number of query devices for manipulating the visualization.

**Tip:** An alternative way of loading the data is to open the file *periodic.sfs*. This may be preferable since *sfs*-files contain Spotfire-specific information on how the visualizations will be initially set up.

## 2.3.4 Changing Visualization Axes

To change the column to be mapped to each axis, click on an axis selector, and select a column name. For example, to see the Mendeleevian layout of the periodic.csv example data set, select *P1* for the X-axis and *P2* for the Y-axis.



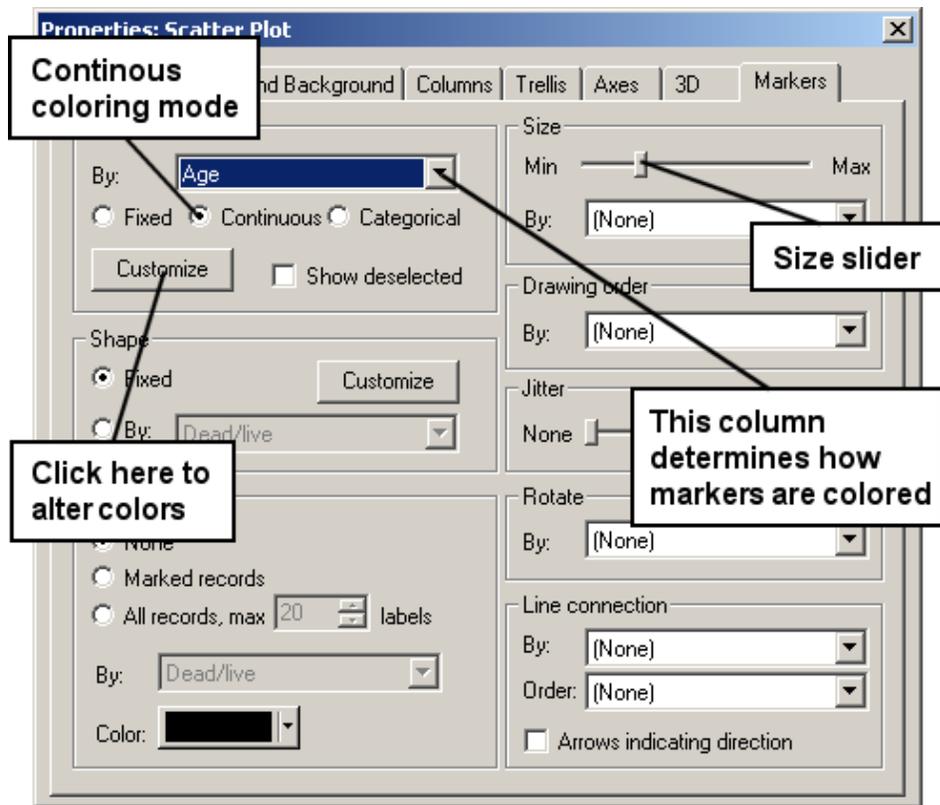
**Note:** You can also select which column to use as an X, Y or Z-axis by right-clicking on the Query Device representing that column, and selecting **Set Property > Axis** from the pop-up menu.

## 2.3.5 Setting Visualization Properties

To make a visualization more informative, activate the Properties dialog by selecting **Edit > Properties**. This dialog contains many settings which can be used to modify the visualization. The keyboard shortcut is [Alt+Enter] or [Ctrl+Enter].

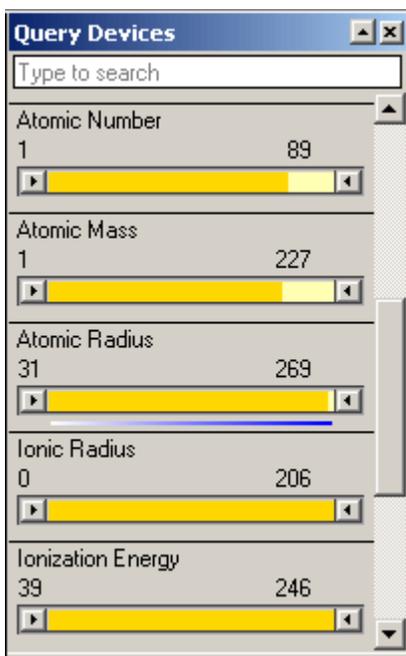
### ► To adjust the appearance of a visualization:

1. Select the **Markers** tab.
2. Move the **Size** slider towards **Max** to make the markers larger.
3. Set the **Color** control to *Continuous*, and the **By** control to *Electronegativity*. This will cause the markers to be colored according to their electronegative potential. The elements with the lowest values will be red and the highest blue. You may alter these colors with a dialog box that opens under **Customize**.



### 2.3.6 Querying the Data Set

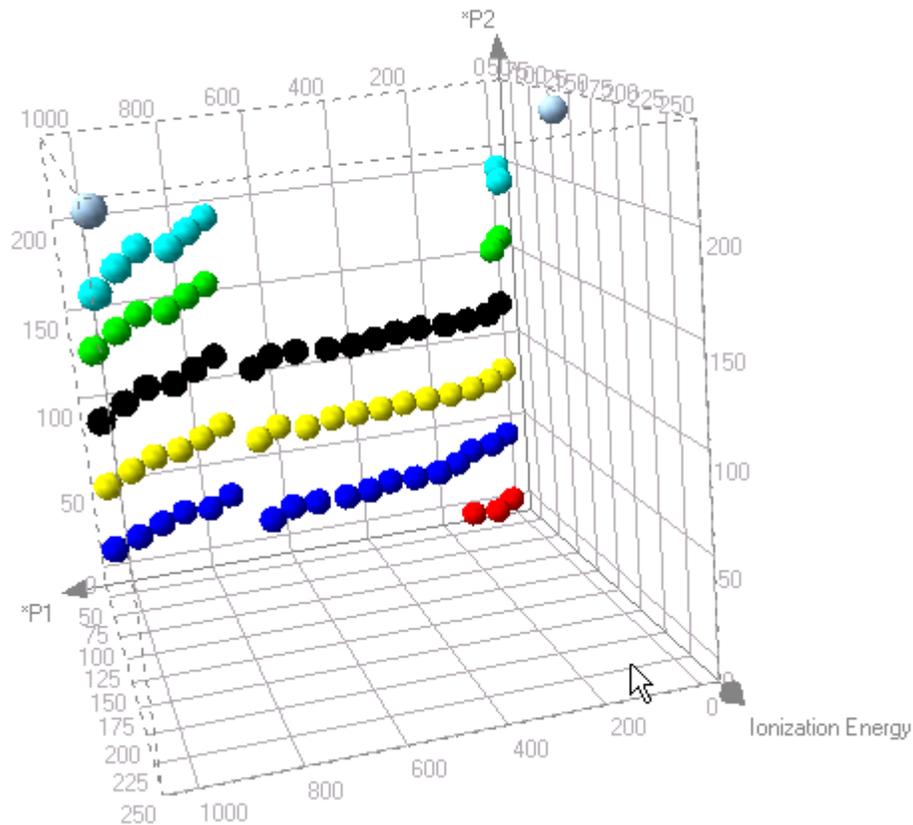
To select a subset of markers to display in the visualizations, change the settings of the query device sliders found in the area to the right. For example, using the Periodic Table data set, move the left drag box of the *Ionization Energy* slider, as shown in the image below, to select only those elements with high ionization energies. We can now see that the elements with high ionization energy are more or less the same as those with high Electronegativity since there are few markers with color representing low electronegative potential in the visualization.



## 2.3.7 Creating a New Visualization

### ► To create a new visualization:

1. Select a visualization type from the **Visualization** menu. For this example, select **New 3D Scatter Plot**.
2. Reassign the X-axis to *Electronegativity* the Y-axis to *Ionization Energy* and the Z-axis (along the top of the visualization) to *Ionic Radius*
3. View the plot from different angles by pressing Shift and/or Ctrl + dragging with the right mouse button.



The 3D plot created in this example will cover the 2D plot but you can show both plots by selecting Window > Auto Tile.

If you move your mouse pointer over one of the markers in the 2D plot, the corresponding marker will also be highlighted in the 3D view. If you activate one element in the 2D plot (by clicking on it) you can move the circle indicating the active element using the arrow keys.

## 2.3.8 Checklist for Exploring New Data

The following steps are typically helpful when exploring a new data set, especially if its content is unknown.

### ► To explore a new data set:

1. Start off by selecting different combinations of visualization axes to reveal patterns, trends, and anomalies. Use View Tip to browse through different combinations of axes. The anomalies should be scrutinized to determine if they are due to erroneous data.
2. Write down particularly interesting combinations of axes, or save the settings so that you can retrieve interesting visualizations later.
3. Color the visualization objects, first by category. Again, write down or save variables that produce interesting groupings and/or patterns.
4. Color visualization objects by continuous variables, to reveal areas where interesting features such as consistently high or low values occur.
5. Go through the range sliders to reveal markers with values occurring in a certain range and observe if they are grouped in some kind of cluster.
6. When interesting clusters are identified, these may be either zoomed in on or marked, followed by changing to another view to reveal whether the markers are clustered for a particular reason.

## 3 Loading Data

### 3.1 Loading Data

#### The Periodic table data set

As an example of simple, yet interesting information, the periodic table of the elements will be used. The data set holds 75 records with 9 fields each. The columns are: the name of the element, six of its properties, and finally the coordinates of each element when the periodic table is printed in the familiar layout first suggested by Dimitri Mendeleev. The text file contains the column names, column types (integer or string) and the data itself.

```
Element, Atomic Number, Atomic Mass, Atomic Radius, Ionic Radius,
Ionization Energy, Electronegativity,*P1,*P2
STRING, INT, INT, INT, INT, INT, INT, INT, INT
Ac, 89, 227, 200, 126, 51, 11, 140, 0
Ag, 47, 107, 144, 129, 75, 18, 630, 80
Al, 13, 27, 143, 67, 60, 16, 750, 160
.....
```

This data is stored in one of the data formats recognized by Spotfire DecisionSite. This particular example can be found in the directory named **Data/General/Periodic Table** in the Spotfire DecisionSite distribution as *periodic.csv*.

#### Loading a data set

##### ► To load a data set into Spotfire DecisionSite:

1. Start Spotfire DecisionSite by selecting **Spotfire DecisionSite** from **Programs** in the Windows **Start** menu, or by double-clicking the Spotfire DecisionSite icon on the desktop.
2. Select **File > Open** in the Spotfire DecisionSite main window. The **File** open dialog will appear.
3. The folder *Data* will be shown in the *DecisionSite* directory.
4. Browse to the folder *General/Periodic/Periodic Table*.
5. Select the file *periodic.csv* and click the **Open** button.

Spotfire DecisionSite will automatically set up an initial visualization where each record is represented by a marker, along with a number of query devices for manipulating the visualization.

**Tip:** An alternative way of loading the data is to open the file *periodic.sfs*. This may be preferable since *sfs*-files contain Spotfire-specific information on how the visualizations will be initially set up.

## 3.2 DecisionSite Library

### 3.2.1 What is DecisionSite Library?

DecisionSite Library provides publishing capabilities for all of your analysis materials, so you can share the data with your colleagues. Using the Library, you can organize your analysis material and collaborate with others in a distributed environment. The Library can be used directly from DecisionSite Client by anyone who has at least read privileges.

The DecisionSite Library is divided into Library Sections which contain all material published to the Library and where access permissions are set. With write access you can open and

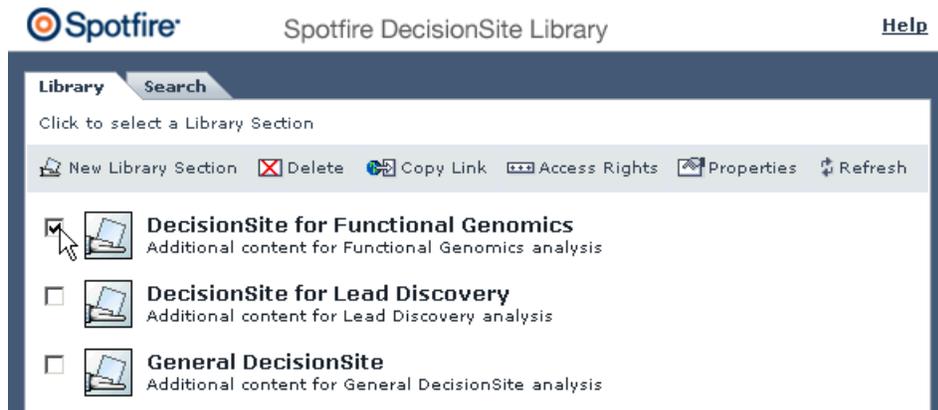
publish any type of analysis material; Analyses, Guides, or Posters. If you have read access you can open any material in the Library Section.

For more information, see the Library Help in the DecisionSite Library tool.

**Note:** The license for DecisionSite Library must be enabled if you intend to use the Library.

**Note:** You must have a license for DecisionSite Posters to use DecisionSite Posters.

Please contact your DecisionSite Administrator for information about licenses.

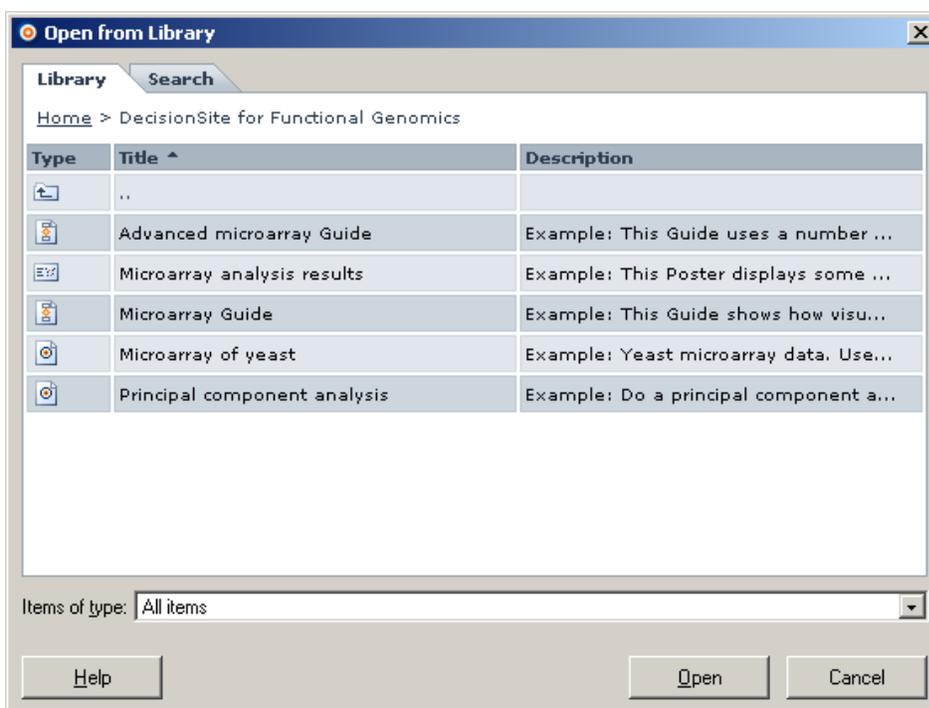


### 3.2.2 Open from Library

This dialog lets you select and open an item in the Library. Each item type, Analysis, Guide, or Poster, opens in different ways:

- Analysis: opens in the DecisionSite Client as a regular Analysis stored in a Spotfire Analysis File. The Analysis consists of your data, visualizations, annotations and everything else you use to explore your data.
- Guide: opens in the Guides pane where the Guide is run. Guides are captured analyzes made by you or your colleagues for repetitive analysis flows.
- Poster: opens in a separate Microsoft® Internet Explorer where the Poster is displayed. Posters are web based snap-shots of your Analysis, designed for easy sharing and collaboration.

To locate the item, either look in a Library Section's content on the **Library** tab, or search for it on the **Search** tab. Navigate in the Library by using double-click on Library Sections and folders.



### Library tab options

#### Library tab

### Description

All Library Sections, items, and folders are listed in the Library View under the **Library** tab. Each item is displayed with type, title and description.

To open an item, select it by clicking on it and click **Open**.

You can view your position with the flight view. The flight view is seen between the Library tab and the item table.

**Note:** Only the Library Sections that you have access to are listed.

#### Items of type:

Select the item type you want to view. This filter allows you to see only the options you are interested in. There are four alternatives:

All items  
Analyses  
Guides  
Posters

#### Open

Select the item you want and click **Open** to open it. See the top of the page about the various responses.

### Search tab options

#### Search tab

Use **Search** to search for the item you want to open.

#### Search for:

Enter the search string in the **Search for:** field and click **Search**. See Searching in the Library for information about search strings.

If you click a folder in the **Search** result, you will be redirected to the Library View under the **Library** tab.

#### Look in:

Select which Library Section you want to perform your search in. Either all Library Sections or one can be searched. Only Library Sections you have access to are listed.

<b>Items of type:</b>	Select which type of Library item you want to perform your search on. There are four alternatives: All items Analyses Guides Posters
-----------------------	--

► **To reach the Open from Library dialog:**

Click **File > Open from Library...**

## 3.2.3 Searching in the Library

### Search

Searches are performed on title, description, and keywords for a precise result. Searching works according to the following criteria:

- The search is either performed on all Library Sections or one at a time.
- The search is either performed on all Library items or on only one type at a time. (If the Open from Library dialog is reached via the Guides pane or the Guides menu, Guides are always the only items found in the search.)
- The search words are matched according to title, keywords, or description. Note that folders are also included in the search.
- The search words are separated by space.
- All words used in the search must be present in the item properties.
- To find a phrase, use quotation marks (") around it.
- The search is case sensitive.
- Wild cards, asterisks (\*), can be used inside words to find variations on that word.

### Example

Suppose that there is a Guide in the Library whose properties include:

- Title: "Wafer anomalies Guide"
- Description: "This Guide captures how we find anomalies in our wafer production data. Look closely at Temperature vs Time!"
- Keywords: "Plant A"; "Wafer"; "CODE1A".

Examples of a few search strings which can be used to find the Guide:

- **Wafer** - Finds the title and keyword.
- **anomalies** - Finds the title and description.
- **wafer** - Finds the description since "wafer" is lower case.
- **"wafer production"** - Finds the phrase part in the description.
- **"wafer production" CODE\*A** - Finds the description and keyword.

**Note:** The search will only be performed on items that you have read access to.

## 3.3 Import Data

### 3.3.1 Importing Data

Spotfire DecisionSite can access data from a variety of sources:

- Spotfire Analysis File (SFS)
- Text files (TXT, CSV, SKV)
- Microsoft Excel Workbooks (XLS)
- MDL SDFiles (SDF)
- Databases (OLE DB or ODBC)
- The Windows clipboard

SFS files, text files and SDFiles can be opened directly using the **Open** option on the **File** menu. This is the quickest way to access unambiguously formatted data from a file.

**Note:** You can also enter a URL in the File name field, and access data from a web server.

Similarly, properly formatted data on the clipboard can be pasted directly into Spotfire DecisionSite.

However, if your data resides in a database, or if it needs some kind of preprocessing before being visualized in Spotfire DecisionSite, then use **Import Data**. This dialog is designed to help you access your data, whatever the source and whatever preprocessing you require.

### ► To import data:

Select **File > Import > Import Data...**

1. Select a data source, such as a file or database.
2. Select methods for data conditioning, such as pivoting, aggregation, or normalization. You can also choose to normalize the character case, so the data is imported non-case sensitively.
3. Optionally, save all settings for data source and/or data conditioning as a favorite. This will allow you to reuse the same data without having to configure data source and data conditioning each time.

The details of each of these steps vary depending on which type of data source or data conditioning method is chosen. A sequence of dialogs will guide you through the required interaction in each case. For example, accessing a database involves setting parameters that are not required when working with a text file. The following sections will deal with each of the three steps above, describing in detail the different cases that may arise.

## 3.3.2 Data Sources

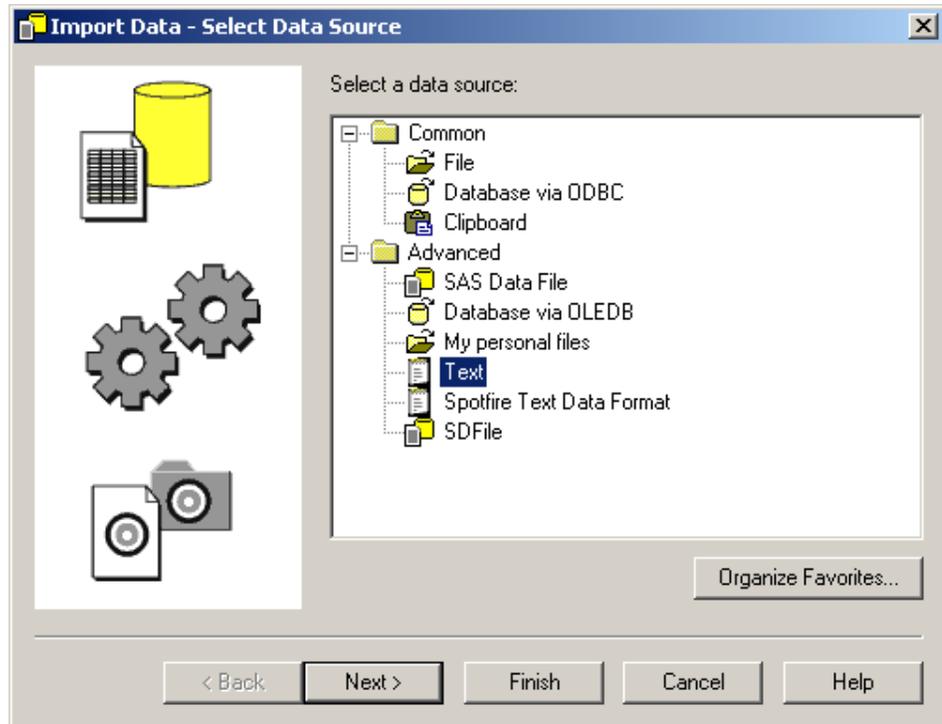
### 3.3.2.1 Selecting a Data Source

The first step in the Import Data dialog to specify a data source. A data source can be one of the following:

- A file
- The clipboard
- A database
- The Spotfire Text Data Format
- A data source defined in a previous data import session, a so called Favorite.

### ► To select a data source:

1. Select **File > Import > Import Data...**



2. Double-click a data source, or select an item and click **Next >**.

### 3.3.2.2 Importing from a File

#### ► To import data:

Select **File > Import > Import Data...** and:

#### ► To import an SFS file:

1. In the **Select Data Source** dialog, select **File**.
2. Click **Next >**.
3. In the **Open** dialog, select the file containing the data. Click **Open**.
4. Unless any conditioning is needed, click **Finish**.

#### ► To import a text file:

1. In the **Select Data Source** dialog, select **File**.
2. In the **Open** dialog, select the file containing the data. Click **Open**.
3. In the **Specify Delimiter** dialog, select a column delimiter. Click **Next >**.
4. In the **Specify Data Types** dialog, click on a data type in the table head to change the type. Click **Finish**.
5. Unless any conditioning is needed, click **Finish**.

#### ► To import an Excel file:

1. In the **Select Data Source** dialog, select **File**.
2. In the **Open** dialog, select the file containing the data. Click **Open**.
3. In the MS JET OLE DB dialog, click **OK**.
4. In the Database dialog specify which Excel worksheets and which columns to include. (An Excel file is treated as a database).
5. Click **OK**.

► **To import an SDF file:**

1. In the **Select Data Source** dialog, select **SDF file**.
2. Click **Next >**.
3. In the **Open** dialog, select the file containing the data. Click **Open**.
4. Unless any conditioning is needed, click **Finish**.

### 3.3.2.3 Importing from the Clipboard

► **To import data from the Windows clipboard:**

1. Mark a number of cells in a text window, a spreadsheet program or another program providing a tabular presentation of data, such as Statistica, Microsoft Excel, Word, etc.
2. Select **Edit > Copy** or hit [Ctrl+C] to copy them to the clipboard.
3. In Spotfire DecisionSite, select **File > Import > Import Data...**
4. From the Common folder, select **Clipboard**.
5. Click **Next >**. This triggers the same dialog as when importing text files.

**Tip:** If your clipboard data is formatted using a standard column delimiter, and if no preprocessing is required, you can paste it directly into Spotfire DecisionSite. Press [Ctrl+V].

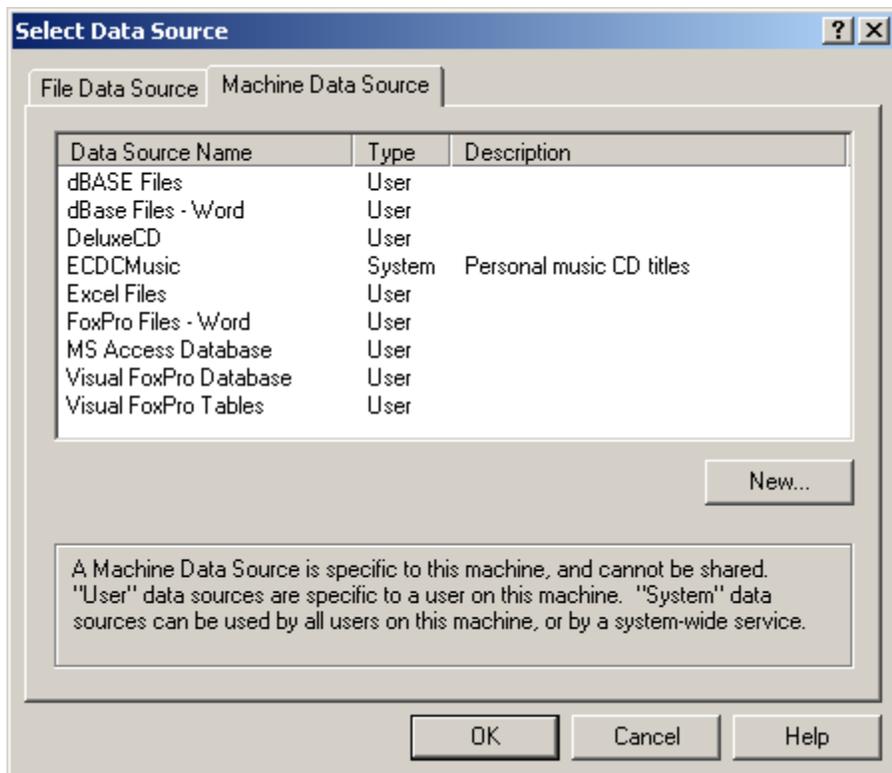
### 3.3.2.4 Importing from a Database

By default, Spotfire DecisionSite connects to external sources of data by means of ODBC (Open Database Connectivity). This allows you to import data from virtually any kind of database commercially available.

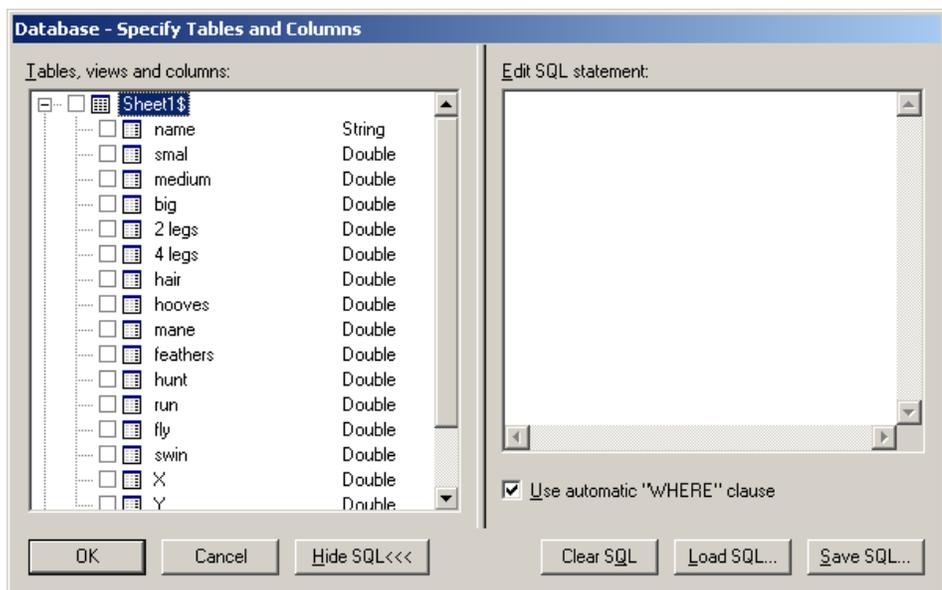
To learn how to set up an ODBC data source, please refer to the database vendor's documentation and the Windows documentation on ODBC. It might be necessary to install ODBC driver software particular to the database used before being able to utilize the ODBC option.

► **To import from a Database:**

1. Select **File > Import > Import Data...**
2. Select **Database** from the list of data sources.
3. Click **Next >**.
4. In the **Select Data Source** dialog, go to the **Machine Data Source** tab.



5. Select the source from which data should be loaded.
6. Click **OK**.
7. Enter login name and password to log on to the database.



8. Determine which database fields to import by selecting the corresponding check boxes.
9. Edit the SQL statement manually if required. This may be necessary for example when joining tables.

10. Click **OK**.

### 3.3.2.5 Importing a Spotfire Text Data File

The Spotfire Text Data format uses a method which enables quick opening of text files. The file is saved as Unicode which makes it possible to read all alphabets. This format is useful when you have data that can be imported wrongly, e.g., if you have strings that contain semicolons or tabs which would otherwise cause the imported file to be split up into the wrong number of columns.

► **To import a Spotfire Text Data File:**

1. Select **File > Import > Import Data...**
2. Select **Advanced > Spotfire Text Data Format** from the list of data sources.
3. In the **Spotfire Text Data Format** dialog, select the file containing the data. Click **Open**.
4. In the **Data Conditioning** dialog, select a conditioning method if desired.
5. Click **Next >** to save this as a Favorite, or simply click **Finish**.

### 3.3.2.6 Importing Using a Favorite

Using a Favorite requires that you have defined a data source and preprocessing methods in a previous session and have saved these settings (see Creating Favorites).

► **To use a Favorite:**

1. Select **File > Import > Import Data...**
2. Select a favorite from the list of data sources.
3. Click **Finish** to load the data set, or **Next >** to edit data conditioning before loading.

## 3.3.3 Data Conditioning

### 3.3.3.1 Data Conditioning

Once you have specified a data source, it is possible to manipulate the data in various ways. Standard methods include the "Tall/Skinny => Short/Wide" conversion (described in What is Tall/Skinny-Short/Wide Conversion?) as well as the Depivot (Short/Wide => Tall/Skinny) conversion, but custom methods designed by Professional Services or a third party may also be available.

You can also select the **Normalize case** filter. This will cause the data to be imported non-case sensitively. This means "Chrome", "chrome" and "CHROME" will be interpreted as the same string. The default when importing is to import case sensitively, thus the examples above would be interpreted as three different strings.

**Note:** When importing strings, duplicates are removed. In Spotfire DecisionSite version 7.0 and older, comparison ignored differences in case. Version 7.1 and later treats two strings as different if they contain the same sequence of characters but not the same case. Selecting the Normalize case filter will mimic the old behavior.

► **To apply a conditioning method:**

1. Select a data source.
2. Click **Next >**.
3. Select a method from the drop-down list.
4. Make the required settings.
5. Click **OK**.

### 3.3.3.2 Applying Multiple Conditioning Methods

When applying several transformations on top of each other, it is important to decide in which order the methods should be applied. Once one conversion has been applied, the next conversion will apply to the output from the previous one, and so on.

► **To apply multiple conditioning methods:**

1. Select a method from the drop-down list.
2. Configure the method and click **OK**.
3. Repeat from step 1 as many times as required.

### 3.3.3.3 Tall/Skinny-Short/Wide Conversion

#### 3.3.3.3.1 Tall/Skinny to Short/Wide Conversion

Tall/Skinny to Short/Wide conversion is a method for modifying the format of a data table during import. It can be used for pivoting and aggregating data.

**Note:** You can also reach this dialog via **Data > Pivot Data...** if you want to apply pivoting to an already opened data set. See Pivot Data for more examples.

► **To apply Tall/Skinny to Short/Wide conversion to your original data:**

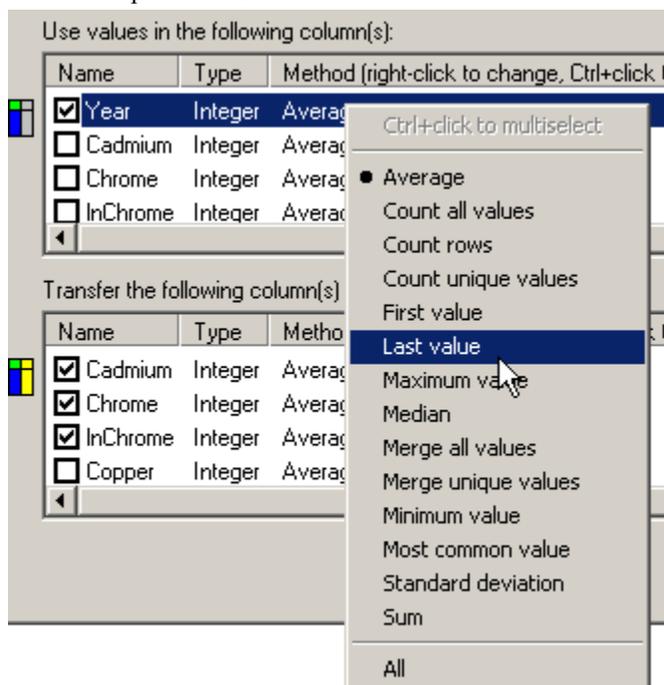
1. Select **File > Import > Import Data...**
2. Select a data source, and click **Next >**.
3. Select **Tall/Skinny -> Short/Wide** from the drop-down list.
4. Click **Configure...**
5. In the **Identity** list, select one or more columns.  
Comment: Each unique value in the chosen column produces a row in the generated table. You can choose more than one column. Doing so means that the new table will have a separate row for each unique combination of values in the chosen columns.
6. In the **Category** list, select one or more columns.  
Comment: Each unique value in the chosen column produces a new column in the generated table. Selecting more than one column means that the new table will have a separate column for each unique combination of values in the chosen columns.
7. In the **Values** list, select one or more columns.  
Comment: The column selected under Values is the column from which the data is pulled. It is possible to select more than one Value column. The values in the generated table are always computed as the average of values in the original table, unless the original values are strings. If so, values in the generated table will consist of concatenated strings. To change the way the values are calculated, right-click on the Method and select a different method from the list, or use Ctrl+click to select multiple methods.
8. In the **Other Columns** list, select one or more columns.  
Comment: This option allows you to include an overall average of a particular measurement, for each row in the generated table. For each column selected here, one new column will be created in the new table. To change the way the measurements are calculated, right-click on the Method and select a different method from the list, or use Ctrl+click to select multiple methods.
9. Click **OK**.

Option	Description
<b>Identity</b>	Each unique value in the chosen column produces a row in the generated table. You can choose more than one column. Doing so means that

<p><b>Category</b></p>	<p>the new table will have a separate row for <i>each unique combination</i> of values in the chosen columns.</p> <p>Each unique value in the chosen column produces a new column in the generated table.</p> <p>Selecting more than one column means that the new table will have a separate column for <i>each unique combination</i> of values in the chosen columns.</p>
<p><b>Values</b></p>	<p>The column selected under Values is the column from which the data is pulled. It is possible to select more than one Value column.</p> <p>The values in the generated table are always computed as the average of values in the original table, unless the original values are strings. If so, values in the generated table will consist of concatenated strings. To change the way the values are calculated, right-click on the Method and select a different method from the list, or use Ctrl+click to select multiple methods.</p>
<p><b>Other Columns</b></p>	<p>This option allows you to include an overall average of a particular measurement, for each row in the generated table. For each column selected here, one new column will be created in the new table. To change the way the measurements are calculated, right-click on the Method and select a different method from the list, or use Ctrl+click to select multiple methods.</p>

## Method Selection List

Right-click on the Method to change the method of calculation for your column. Ctrl+click to select multiple methods.



For examples of how Tall/Skinny to Short/Wide conversion can be used, see [Pivoting and Pivoting and Aggregation](#).

### 3.3.3.3.2 Pivoting

Pivoting, in its simplest form, means rotating a table. Mostly, though, it also includes performing some form of aggregation, so that the new table is more compact than the original. Pivoting a data set means changing it from a tall/skinny format to a short/wide format. Consider the following tall/skinny table, based on a series of temperature measurements:

City	Month	Temp
London	February	4
New York	February	6
London	May	16
New York	May	19
London	August	28
New York	August	26
London	November	13
New York	November	11

As we add more observations, the table grows taller, but remains three columns wide. While useful during data collection, this format may not be appropriate for certain types of calculations or visualizations. For example, the entities that interest us are the different cities, so we may want a representation with a single record for each city.

Tall/Skinny=>Short/Wide conversion lets us pivot this table, producing the following (note that avg(Temp) is the average of a single cell):

City	avg(Temp) for August	avg(Temp) for February	avg(Temp) for May	avg(Temp) for November
London	28	4	16	13
New York	26	6	19	11

Each city is now represented by a single record, which makes this format very suitable for Spotfire DecisionSite profile charts. This example demonstrates three steps:

- Creating a row for each unique value in City.
- Creating a column for each unique value in Month.
- Entering a value from Temp for each cell in the resulting grid.

In the Tall/Skinny => Short/Wide dialog, the following settings would be made:

Identity: City

Category: Month

Values: Temp

### 3.3.3.3.3 Pivoting and Aggregation

**Note:** To understand this example, it is recommended to read Pivoting first.

Apart from changing format from tall/skinny to short/wide, pivoting can be used to create a more compact table. Consider the following table, based on a series of temperature measurements:

City	Month	Day	Temp
London	February	1	5
London	February	15	8
London	May	1	15
London	May	15	22
New York	February	1	9
New York	February	15	7
New York	May	1	18
New York	May	15	24

Tall/Skinny=>Short/Wide conversion lets us pivot and aggregate this table, producing the following:

City	avg(Temp) for February	avg(Temp) for May
London	6.5	18.5
New York	8	21

A smaller table has been created, summarizing the original table. In the Tall/Skinny => Short/Wide dialog, the following settings would be made:

Identity: City

Category: Month

Values: Temp

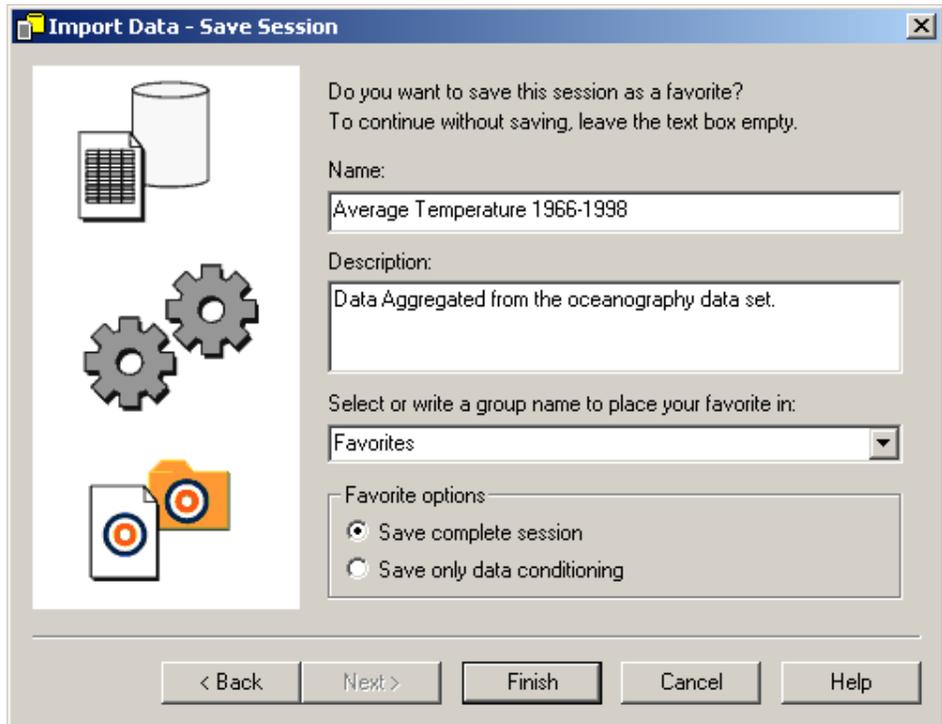
## 3.3.4 Favorites

### 3.3.4.1 Creating Favorites

Favorites are combinations of data sources and data conditioning methods. A favorite stores all settings made during a session with the Import Data dialogs. A favorite may, for example, specify a database, all the information required to log on, and a data conditioning method. Favorites can also specify just a data source, or just a preprocessing method.

#### ► To create a favorite:

1. Define a data source as described in Selecting a Data Source.
2. Define a data conditioning method as described in Data Conditioning.
3. In Save Session dialog, specify a name for your favorite, e.g., "Average temperature 1961-1991". You can also add a description.
4. Under **Favorite options**, select both **Include reference to data source** and **Include reference to data conditioning methods**

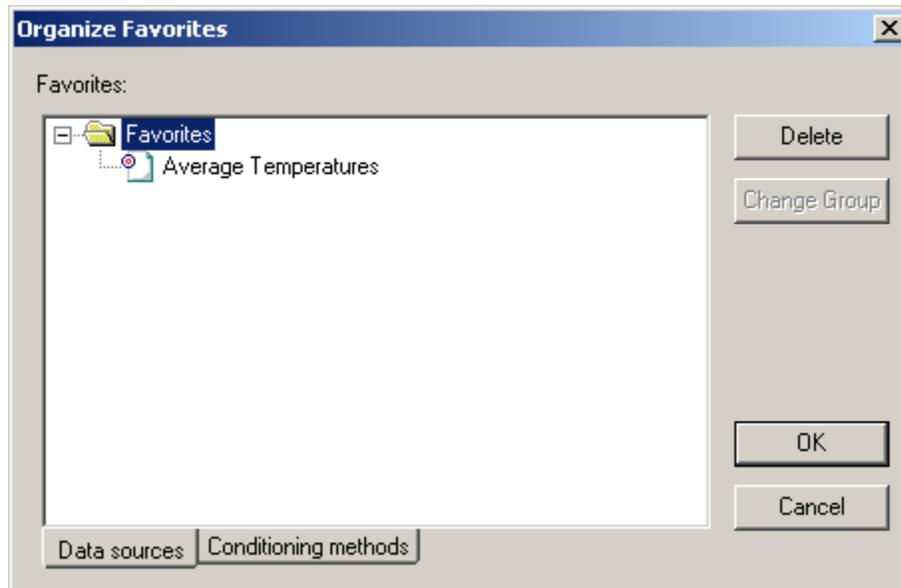


5. Click **Finish**.

**Note:** Your choice of Favorite options affects how the favorite can be used. If a data source is included, then the favorite can be opened directly from the Select Data Source dialog. If only the method is saved, then you must first select a data source, and then in the second step apply the favorite as a data conditioning method.

### 3.3.4.2 Organizing Favorites

Favorites are organized in folders. Click **Organize Favorites** in the **Select Data Source** dialog.



The **Data source** tab contains favorites that are linked to data. These can be loaded directly from the **Select Data Source** dialog.

The **Conditioning methods** tab contains favorites that are not linked to a data source. These can only be applied from the **Data Conditioning** dialog (i.e., you must specify a data source before using them).

► **To move a favorite to a different folder:**

1. Highlight a favorite.
2. Click **Change Group**.
3. Select a group from the list, or enter a new group name.

► **To remove a favorite:**

1. Highlight a favorite.
2. Click **Delete**.

## 3.3.5 Text File Formatting

### 3.3.5.1 General Text File Specifications

A data set imported into Spotfire DecisionSite consists of the following:

One line containing the name of each column (optional)

One declaration line describing the type of data in each column (optional)

The first two single lines make up the header. If the original data set has no header (i.e., it consists of raw data) Spotfire DecisionSite will name the columns Column1, Column2, ...

One line per data record

[Carriage return] followed by [Line feed] end each row

**Note:**

- The type declaration is case insensitive.
- Data sets must contain at least 3 rows to be valid. Add an empty row if you need to import a data set with 2 rows.
- The number of columns present in the first row determines the number of columns used in the entire data set. Additional columns in subsequent rows will be ignored. Therefore, make sure the first row contains the correct number of columns.
- The first row of a data set must never be empty, i.e., it should only contain a row break or similar.

The following are examples of well-formatted text files:

---

```
City,Month,Day,Temp
String,String,Integer,Integer
London,May,5,14
New York,May,5,23
London,May,10,16
New York,May,10,27
London,May,15,20
New York,May,15,24
London,November,5,7
New York,November,5,12
```

---



---

```
Location;Day;Temp
London;5;14
New York;5;23
London;10;16
```

---

```
New York;10;27
London;15;11
New York;15;29
London;20;13
New York;20;20
```

---

### 3.3.5.2 Spotfire Text Data Format Specifications

A Spotfire Text Data file imported into Spotfire DecisionSite consists of the following:

One line containing information about the format.

Two lines which explain how the file was generated.

One line containing the name of each column.

One declaration line describing the type of data in each column.

One line per data record.

[Carriage return] followed by [Line feed] end each row; each column ends with a semicolon.

**Note:** The type declarations and the column names are case sensitive.

The following is an example of a well-formatted text file:

---

```
\! filetype=Spotfire.DataFormat.Text; version=1.0;
City;Month;Day;Temp;
String;String;Integer;Integer;
London;May;5;14;
New York;May;5;23;
London;May;10;16;
New York;May;10;27;
London;May;15;20;
New York;May;15;24;
London;November;5;7;
New York;November;5;12;
```

---

### 3.3.5.3 Supported Formats

The following standardized text file formats are supported:

CSV – values are separated by the default list separator. (This is a Regional Setting property of your system. Comma is used in the US.)

TXT – values are separated by tabs

SKV – values are separated by semicolons

All these file formats are simple and text based – they do not contain any formatting or product specific information. The CSV and SKV formats can be exported from many spreadsheet and database programs. Many research tools produce output in these formats as well.

**Note:** Spotfire Text Data Format is also available see Spotfire Text Data Format Specifications for more information.

### 3.3.5.4 Column Separators

Individual fields (column names, type strings, and values) are delimited by column separators—usually commas, semicolons or tabs, but the | (pipe) symbol is also recognized.

Spotfire DecisionSite automatically decides which character is interpreted as separator. To do this, Spotfire DecisionSite checks the first line in the database for the following characters:

Separator	Name	ASCII code
[tab]	Horizontal tab (invisible on screen)	9
,	Comma	44
;	Semicolon	59
	Pipe	124

The most common character of the ones above is selected as separator (characters enclosed in quotation marks are not considered). All following lines are assumed to use this most common character as column separator.

**Note:**

- To load text data that uses a column separator different from those mentioned above, use the Import Data option. This will allow you to specify manually which character to interpret as separator.

**Dialog Box Controls for the Specify Delimiter dialog:**

Delimiter – Select one of the four common delimiter symbols, or enter a character of your choice.

Column names – Check the box if you know that the first row contains column names and not data.

Data preview – The table shows how the file will be interpreted, given the specified delimiter

- Values in a Spotfire DecisionSite data set may contain any character (including white space) except the column separator. If enclosed in double quotation marks, columns may also contain separator characters. Column headers are allowed to contain separators if double quoted and the first double quotation mark is preceded by a backslash.

### 3.3.5.5 Name and Type Strings

The first one or two lines in a text file or file may be interpreted as name and type information according to the following rules:

If the second line appears to be type information, i.e., containing columns with strings like INT, STRING, DATE etc., it is used as type information. The first line is then expected to contain name information. For example, a small database with personal data and both name and type information looks like the table below. Here, the second line is interpreted as type information and the first as name information.

Data	Spotfire DecisionSite Interpretation
Name, Age	name info
STRING, INT	type info
Peter, 26	data
John, 35	data

If the first line contains only type information, Spotfire DecisionSite will use that line for type information. The column names are automatically generated as "Column1", "Column2", etc.

**Note:** The type determined by the type declaration line has the highest priority when determining the type of each individual data line. If a value cannot be converted into the relevant type, it will be set to empty. For example, a string appearing in a column defined as integer cannot be converted and will therefore be set to empty.

Data	Spotfire DecisionSite Interpretation
STRING,INT	type info
Peter,26	data
Susan, 19	data
John,35	data

Spotfire DecisionSite tries to find type information in lines one and two. If it cannot, line one is used as name information, and the program makes a qualified guess of the types contained by analyzing the type of the following first non-empty 100 values in each column.

If more than 80% of the values can be interpreted as one and the same type other than String, the column will be set to that type. Any values not corresponding to that type will be set to null. If there are the same numbers of records for two different types among the 100 analyzed values, then the type guessing will be done according to this priority list:

1. Integer
2. Decimal
3. Date
4. Time
5. TimeStamp

If more than 80% of the values cannot be interpreted as a type other than String, then all values in the column will be set to String.

**Note:** Date format is determined in a similar way. Please see Date for more information.

The following is a small database with personal data, but no type information. Here, the first line is interpreted as name information, and the types are set to STRING and INT.

Data	Spotfire DecisionSite Interpretation
Name,Age	Type guess: STRING, STRING
Peter,26	Type guess: STRING, INT
Susan, 19	Type guess: STRING, INT
John,35	Type guess: STRING, INT

If 1,2 and 3 fail, the column names are automatically generated as "Column1", "Column2", etc. The program then makes a qualified guess of the types just as in section 3 above.

For example, for a small database with personal data with no type or name information, the type information is set to STRING and INT, and the names are set to Column1 and Column2:

Data	Spotfire DecisionSite Interpretation
Peter,26	Type guess: STRING, INT
Susan, 19	Type guess: STRING, INT
John,35	Type guess: STRING, INT

**Note:** If a column is declared as being of one type, but some values in the column are of a different type, then the incongruous values will be set to null.

## 3.3.6 Data Types

### 3.3.6.1 General Specifications for Data Types

White spaces and ASCII control characters (i.e., all code characters less than 32) are always ignored at the start of a string. Type strings (strings that declare the data type) are not case sensitive.

In the descriptions of data types, the following abbreviations are used:

[ ] (i.e., square brackets)	For any item, this indicates optional items or groups of correlated items.
YY	Year as two digits.
YY[YY]	Year as two or four digits.
MM	Month as one or two digits.
DD	Day as one or two digits.
HH	Hours as one or two digits
Mm	Minutes as one or two digits.
SS	Seconds as one or two digits.
fff	Fractions of a second, as many digits as there are.
MonthString	In English only. This may also be the abbreviated version of the month, e.g., Jan stands for January.

If you are uncertain about whether or not Spotfire DecisionSite supports a data type, or how it must be formatted to be recognized during import, use a text editor to write a short file with sample data using the types that you want to test. Copy and paste the text directly into Spotfire DecisionSite, and use Details-on-Demand to verify the results.

The following tab-separated file can be used as a template for such a file:

int_col	time_col	date_col	str_col
int	sfTime	date	string
1	11:01:32 PM	990807	"hello"
2	110132.6	08/07/99	hello
3	11:01 AM	99-08-07	""Hello!", I said"

### 3.3.6.2 Time

#### Format

Description	Fields
Colon as field separator	HH:Mm[:SS[.fff]][AM PM]
Dot as field separator	HH.Mm[.SS[.fff]][AM PM]
No field separator	HHMm[SS[.fff]][AM PM]

#### Type strings

time, sfTime

### Remarks

The format requires that hour and minute be specified. Optionally seconds and fractions of seconds can be included. The fractions must be in the range of real values, and must begin with a period or the decimal separator defined by the regional settings in Windows.

In addition to a colon separator (as above), it is also possible to use a decimal point or no character at all.

AM or PM can optionally be specified at the end of a time string.

Time must be within legal values. For example, **13:00 AM** is not supported. Negative times are not supported.

### Examples

Accepted	Not accepted
14:05:32.6	14:05:32:6
14.05	25.05
140532	140532,6
2.05.32 PM	14.05.32 PM
2.05.32 AM	14.05.32 AM
2.5.2	

The display format of a Time column can be changed in the Time Format dialog.

### 3.3.6.3 Date

#### Date

Please see the Remarks section following the formats table for more information on priority formats and other important details of the formats.

It is recommended that you use Long ISO formats, since there is no ambiguity in these.

When type guessing a text file that is being imported, DecisionSite makes a qualified guess of any dates contained by analyzing the format of the following first non-empty 100 values in each column.

DecisionSite checks to see how many matches each of the following format receives, and then chooses the one with the most matches. If several formats should receive the same amount of matches, then DecisionSite will choose the date format according to the Interpretation Priority as seen in the table below.

Dates not matching the selected format will be discarded as conversion errors.

### Formats

Name	Fields	Interpretation Priority
ISO format:	YY[YY]-MM-DD	Highest
User Locale Setting:	<MS Windows setting>	
Reverse ISO format:	DD-MM-YY[YY]	
USA & UK format:	MM/DD/YY[YY]	
European format:	DD/MM/YY[YY]	
Custom format:	YY[YY]/MM/DD	
Custom format:	YYYYMMDD	
Custom format:	YYMMDD	
Custom format:	DD.MM.YY[YY]	

Long ISO format:	DD MonthName YY[YY]	
Long ISO Internet:	DD-MonthName-YY[YY]	
Long USA & UK format:	MonthName DD, YY[YY]	Lowest

### Type strings

date, sfDate

### Remarks

The year, YY, can always be specified in two or four digits, e.g., **89** or **1989**. If only two digits are given for the year, the date is assumed to belong to the 20th century if the number representing the years is higher than the dividing year, and to the 21st century if equal to the dividing year or below. Microsoft Windows settings provide the dividing year. Windows default dividing year is 31. If alterations have been made there, they will be reflected in the way Spotfire DecisionSite calculates dates.

Months can be written using the initial three letters. If spelled out, names should be in U.S. English. Month names are not case sensitive.

Spotfire DecisionSite performs a leap year control when importing data of type *Date*.

Once date data is loaded into Spotfire DecisionSite it will be presented in localized format (set in the Regional Properties of your system).

Years may range from 100 to 9999.

The display format of a Date column can be changed in the Date Format dialog.

## 3.3.6.4

### DateTime

DateTimes are also known as TimeStamps.

### Formats

DATE TIME

DATE/TIME

Where DATE is any date as described above, and TIME is any time as described above.

Note that there must be at least one of the following between both main groups:

a single Space

a single Slash

Multiple Spaces are allowed and ignored, but multiple Slashes are illegal.

### Type strings

datetime, timedate, timestamp, sfTimeStamp

### Remarks

The DateTime format is used to combine date and time in a single data column. In previous documentation it has been referred to as TimeStamp.

A value is accepted as *DateTime* even if it lacks the *Time* component.

### Examples

DateTime	Interpreted as
99-08-07 11:01:32.6	August 7, 1999, 11:01:32.600
99-08-07 11.01.32	August 7, 1999, 11:01:32
08/07/99 11:01	August 7, 1999, 11:01:00

08/07/99 11:01:32.6 PM	August 7, 1999, 23:01:32.600
99/08/07 11:01	August 7, 1999, 11:01:00
990807 11:01:32.6	August 7, 1999, 11:01:32.600
990807 110132 AM	August 7, 1999, 11:01:32
07 aug 99 11:01	August 7, 1999, 11:01:00

The display format of a DateTime column can be changed in the Date and Time Format dialog.

### 3.3.6.5 String

#### Format

Any string of characters, with or without quotation marks

#### Type strings

string, text, str, sfString

#### Remarks

Matching pairs of quotation marks at the beginning and end of the string are removed.

Column separators appearing within outermost quotes are not interpreted as separators (see the last example below).

Columns beginning or ending with empty noise (control characters except the separator currently being used) will be stripped of that noise.

Strings are by default case sensitive, e.g., a12 is treated as different to A12.

#### Sorting

Spotfire DecisionSite handles Strings case-sensitively. Strings are sorted based on ASCII (see also Unicode and Character Encodings) which means that all uppercase characters will be sorted before any lowercase characters (A, B, C, a, b, c).

For example, strings would be sorted as seen below:

1  
1005  
34  
Arizona  
Beethoven  
Zebra  
anaconda  
bakery

Be mindful of this when using Query Devices, since setting a Range Slider to include everything between Arizona and Zebra, will not include anaconda or bakery.

The reason for handling sorting this way, and not according to the locale setting on the computer, is to insure that a Spotfire DecisionSite file looks exactly the same where ever it is opened. Therefore country-specific characters may be sorted in other ways than according to the locale setting.

#### Examples

String	Interpreted as
Hello	Hello
"Hello"	Hello
""Hello""	Hello

"Hello "there""	Hello "there"
"3" 5"	3" 5'
one, two, three	one two three (separate columns)
"one, two, three"	one, two, three (one column)
""Hello", I said"	"Hello", I said

### 3.3.6.6 Integer

#### Format

```
[#|##|###|####][[ |,]#####]*[%]
```

#### Type strings

int , integer, long, mapstring, sfInt

#### Remarks

An integer can include a grouping symbol for thousands, millions, etc. Permitted symbols are comma and white-space.

However, every value in the entire column must be a valid integer, or else the entire column will be interpreted as Decimal or even Invalid.

Optionally, the %-character can be appended at the end. The %-character will be removed during import, thus 68% will be interpreted as 68 not 0.68.

#### Examples

Accepted	Interpreted as
6843	6843
6 843	6843
6,843	6843 (see Remarks above!)
68,432,701	68432701
68%	68
Not Accepted	Interpreted as
68,43	68.43 Decimal
68,432,70	Invalid

### 3.3.6.7 Decimal (Real, Double)

An 8 byte floating point number.

#### Format

```
[#|##|###|####][[ |,]#####]*[.#*][ ][%]
```

#### Type strings

decimal, real, float, real1, real2, real3, real4, real5, dbl, num, dreal, double, dfloat, sfReal, sfDecimal

### Remarks

Written as an integer, optionally followed by a decimal part. The decimal separator can be a comma or period, but must be different from the thousands separator.

Optionally, the %-character can be appended at the end. The %-character will be removed during import, thus 0.68% will be interpreted as 0.68.

In Spotfire DecisionSite 6.1 and later versions, all Decimals are treated as Doubles. Older versions differentiate between 4 byte Reals and 8 byte Doubles.

### Examples

Accepted	Interpreted as
6,84	6.84
6,843	6.843 (see Integer description!)
6.843	6.843
6 843.27	6843.27
6 843,27	6843.27
6,843.27	6843.27
0.68%	0.68
1E17	1E+017
1d17	1E+017
Not Accepted	Interpreted as
6.843,27	Invalid
6.843.27	Invalid
6,843,27	Invalid

## 3.3.6.8 Data Type Constraints in Current 32 Bit Operating Systems

### Int

Integer 32 bits signed

Maximum (signed) int value	2147483647
Minimum (signed) int value	-2147483647

### Double

64 bits

Number of decimal digits of precision (That is the total number of digits, not to be confused with number of digits after the decimal point)	15
Smallest such that $(1.0 + \text{DBL\_EPSILON}) \neq 1.0$ The minimum difference between numbers that are to be calculated as having different values	2.2204460492503131e-016
Number of bits in mantissa	53

Maximum value	1.79769313486231e+308
Maximum decimal exponent	308
Maximum binary exponent	1024
Minimum positive value	2.22507385850720e-307
Minimum decimal exponent	(-307)
Minimum binary exponent	(-1021)
Exponent radix	2
Addition rounding: near	1

## Real

In Spotfire DecisionSite 6.1 and later versions, all Real are treated as Double. For older versions see below:

Float 32 bits

Number of decimal digits of precision (That is the total number of digits, not to be confused with number of digits after the decimal point)	6
Smallest such that $(1.0 + FLT\_EPSILON \neq 1.0)$ The minimum difference between numbers that are to be calculated as having different values	1.192092896e-07F
Number of bits in mantissa	24
Maximum value	3.402823466e+38F
Maximum decimal exponent	38
Maximum binary exponent	128
Minimum positive value	1.175494351e-38F
Minimum decimal exponent	(-37)
Minimum binary exponent	(-125)
Exponent radix	2
Addition rounding: near	1

## 3.3.7 OLE DB

### 3.3.7.1 Connecting to a Data Source Using OLE DB

An OLE DB data provider allows native access to data, such as a SQL Server or Oracle database. Using an OLE DB provider, Spotfire DecisionSite can retrieve and manipulate data from a wide variety of data sources, not just relational databases. When you create a data link, you specify the OLE DB provider that is designed to work with your data. For example, you could access a flat file system using the **CSV provider** and display the data in Spotfire DecisionSite.

You can create data links for any Microsoft or third party OLE DB provider. The following providers are included with the Microsoft data access components:

- Microsoft Jet 3.51 OLE DB Provider
- OLE DB Provider for Oracle
- OLE DB Provider for SQL Server
- OLE DB Provider for ODBC Drivers

**Note:** For more information about OLE DB providers, see the OLE DB Programmer's Reference. This documentation is available in the Microsoft Data Access SDK.

► **To import data using an OLE DB provider:**

1. Click **Open** on the **File** menu, and select **Full OLE DB Connect** from the **Files of type** drop-down list.
2. Use the **Data Link Properties** dialog box to specify initialization properties for your OLE DB provider. Data link properties may vary depending on your OLE DB provider. **Next** navigates to the **Connection** tab for the selected OLE DB provider.

Before you can access data from OLE DB, you must provide specific connection information such as:

- The type of *data* that you want to access
- The *server* on which the data resides
- The *database* in which the data is stored

Use the **Connection** tab to specify how to connect to Oracle data. Enter the server where the database you want to access is located. Click **Test Connection** to attempt a connection to the specified data source. If the connection fails, ensure that the settings are correct. For example, spelling errors and case sensitivity may be the cause of a failed connection. Click **OK** to connect.

For more information about advanced initialization properties, see the documentation provided with your OLE DB provider. Use the **All** tab to view and edit all of the OLE DB initialization properties that are available for your OLE DB provider.

### 3.3.8 Rearranging the Data by Formatting

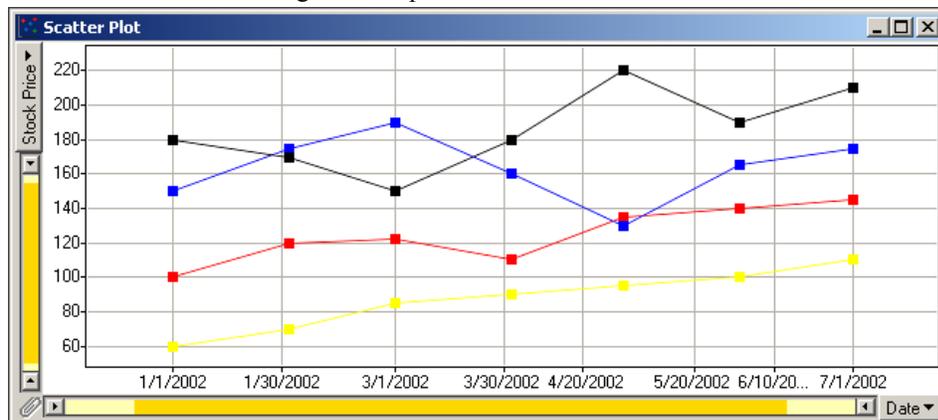
If you have a Time, Date or a DateTime (TimeStamp) column in your data set, you can change what you actually filter on with the query devices just by changing the format of the column.

**Example 1:**

You have a data set containing stock prices for a number of different stocks during a selected time period:

Date	Stock Price	Stock
1/1/2002	100.0000	Barkley Books Ltd.
1/1/2002	150.0000	Cameo Cars Inc.
1/1/2002	60.0000	Finc Foods Inc.
1/1/2002	180.0000	Machton Machinery Ltd.
2/1/2002	120.0000	Barkley Books Ltd.
2/1/2002	175.0000	Cameo Cars Inc.
2/1/2002	70.0000	Finc Foods Inc.
2/1/2002	170.0000	Machton Machinery Ltd.
3/1/2002	122.0000	Barkley Books Ltd.
3/1/2002	190.0000	Cameo Cars Inc.
3/1/2002	85.0000	Finc Foods Inc.
3/1/2002	150.0000	Machton Machinery Ltd.
4/1/2002	110.0000	Barkley Books Ltd.
4/1/2002	160.0000	Cameo Cars Inc.
4/1/2002	90.0000	Finc Foods Inc.
4/1/2002	180.0000	Machton Machinery Ltd.
5/1/2002	135.0000	Barkley Books Ltd.
5/1/2002	130.0000	Cameo Cars Inc.
5/1/2002	95.0000	Finc Foods Inc.
5/1/2002	220.0000	Machton Machinery Ltd.
6/1/2002	140.0000	Barkley Books Ltd.
6/1/2002	165.0000	Cameo Cars Inc.
6/1/2002	100.0000	Finc Foods Inc.
6/1/2002	190.0000	Machton Machinery Ltd.
7/1/2002	145.0000	Barkley Books Ltd.
7/1/2002	175.0000	Cameo Cars Inc.
7/1/2002	110.0000	Finc Foods Inc.
7/1/2002	210.0000	Machton Machinery Ltd.

Traditionally, you could plot the data in a scatter plot or a profile chart to see how the price of each stock has varied during the time period:

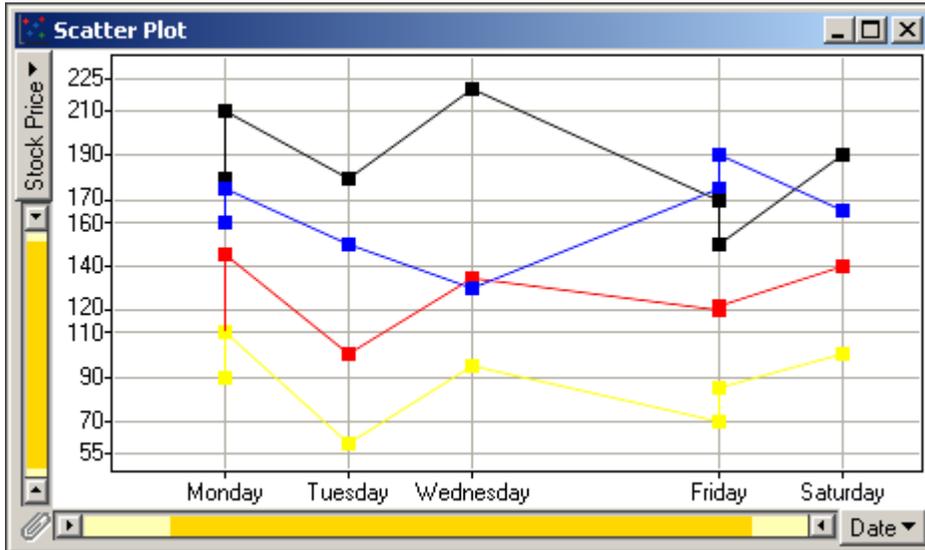


But by changing the way the date column is represented, you can obtain new views of the data. Right-click on the date column in the Query Devices panel and select **Set Property > Format > Date...** to display the Date Format dialog. Here, you can select Day of week, Monday first (day name), to show the different weekdays instead. The language is determined by your current locale.

Date

- Monday
- Tuesday
- Wednesday
- Friday
- Saturday

This way, you can get a completely different view of the data and spot whether the stock prices tend to be higher or lower on a certain day of the week:



According to this scatter plot, it looks like it would be a good idea to buy new stocks on Tuesdays. (This example does not contain any real data and the advice should therefore not be taken literally.)

### Example 2:

Another example of how the data interpretation can be changed via formatting is if you have a time column where hours, minutes and seconds are displayed, and then change the formatting to a HH:MM format.

	Data values:	Represented in a scatter plot:								
<b>Original data:</b>	<table border="1"> <thead> <tr> <th>Column 1</th> <th>Column 2</th> </tr> </thead> <tbody> <tr> <td>1</td> <td>11:59:00</td> </tr> <tr> <td>2</td> <td>11:59:30</td> </tr> <tr> <td>3</td> <td>12:00:00</td> </tr> </tbody> </table>	Column 1	Column 2	1	11:59:00	2	11:59:30	3	12:00:00	
Column 1	Column 2									
1	11:59:00									
2	11:59:30									
3	12:00:00									
<b>Formatted data:</b>	<table border="1"> <thead> <tr> <th>Column 1</th> <th>Column 2</th> </tr> </thead> <tbody> <tr> <td>1</td> <td>11:59</td> </tr> <tr> <td>2</td> <td>11:59</td> </tr> <tr> <td>3</td> <td>12:00</td> </tr> </tbody> </table>	Column 1	Column 2	1	11:59	2	11:59	3	12:00	
Column 1	Column 2									
1	11:59									
2	11:59									
3	12:00									

Hence, the number of unique values is reduced from three to two.

The following formats change the perceived data type of the column from a Date, Time or DateTime into an Integer or String:

Format	Perceived type
Year (YYYY)	Integer
Year, short (YY)	Integer
Day of week, Monday first (day name)	String
Day of week, Sunday first (day name)	String
Day of month (dd)	Integer
Day of year (ddd)	Integer
Week of year (ww)	Integer
Month of year (mm)	Integer
Month of year (short name)	String
Month of year (full name)	String
24 hour time, hour only (HH)	Integer

Resetting the formatting to the original brings back the original data type as well as any temporarily trimmed values.

## 3.4 Information Links

### 3.4.1 Introduction to Information Library

Information Library is a tool for accessing data from databases. This is done by opening *information links*. An information link is a preconfigured database query, specifying the columns to be loaded, and any filters needed to reduce the size of the data set prior to visualization in Spotfire DecisionSite.

Information Library is built on top of the *Information Model* (IM). This model resides on your server, and is a representation of one or more databases which may be geographically dispersed. It allows you to execute advanced database queries without any knowledge of the underlying database structures. The model appears as a folder structure (see Information Library Dialog).

Information Library is part of a suite of tools called *Information Services* (IS). The other tools are Information Builder and Information Designer. While Information Library is primarily designed to execute predefined queries stored in the IM, Information Builder lets you create such queries from building blocks such as columns and filters. Information Designer is the administrative tool for designing the Information Model, configuring the database connections and assigning user permissions for accessing various parts of the model.

### 3.4.2 Using Information Library

#### 3.4.2.1 Opening an Information Link

Information Library provides a set of information links (predefined queries), organized into different domains. Which domains are available to you depends on how your permissions have been set by the administrator. The information links are defined in Information Builder.

► **To open an information link:**

1. Select **File > Import > Open Information Link...**  
Response: The Information Library dialog is shown.
2. In the **Information Links** pane, select a link, .

Response: Information about the selected link is displayed in the **Information Link details** pane.

Comment: Click the + symbols to see the contents of a domain.

3. Click **Open**.

Comment: To open a link directly, double-click the link icon, .

Response: The information link is opened, and the data is shown in DecisionSite. If the information link includes run-time filters, one or more dialogs will now appear. See Filtering Data During Retrieval for details.

### 3.4.2.2 Filtering Data During Retrieval

An information link can include columns with *run-time filters*. For each such column that is loaded, you are asked to specify the values that you are interested in. Only records with the selected values will then be loaded.

**Note:** To enable run-time filtering for a column, or to set the type of control used for selecting values, use Information Builder to edit the information link.

► **To open an information link with run-time filters.**

1. Select **File > Import > Open Information Link...**

Response: The Information Library dialog is shown.

2. In the **Information Links** pane, select a link with run-time filters.

Response: Information about the selected link is displayed in the **Information Link details** pane. You will see here whether or not the link includes columns with run-time filters.

3. Click **Open**.

Comment: To open a link directly, double-click the link icon, .

Response: The first Set Filter for Column dialog appears.

4. Specify the values or range of values in which you are interested.

Comment: Information links may include more than one run-time filter. In this case each prompt will reduce the data set, such that subsequent prompts may present fewer values. See the Run-time Filter Example for more details.

5. Click **Next >** (or **Finish** if this is the last filter).

6. Repeat steps 4 and 5 for each column with a run-time filter.

### 3.4.2.3 Using Current Query Device Settings as a Filter

When opening information links with run-time filters that prompt for values or value range (see Filtering Data During Retrieval) it is possible to use the visual capabilities of Spotfire DecisionSite to set these values.

► **To use the current visualization for filter definition:**

1. Open a suitable data set in DecisionSite.

2. Choose a subset of data either by using the query devices, or by marking records.

Comment: *Marking* means clicking and dragging a rectangle around a group of markers in a visualization.

3. Open the information link.

4. When the **Set Filter for Column** dialog for the desired column appears, click **Get Values...** or **Get Range...**

Response: The Get Values from Data Set dialog is displayed.

5. From the **Matching column** drop-down list, select the column (in the visualized data set) from which you want to get the values or the range.

6. Click **Selected records** or **Marked records**, depending on which values you want to use.

7. Click **OK**.
8. In the **Set Filter for Column** dialog, click **Next >** (or **Finish** if this is the last prompted column).
9. Repeat steps 4 to 8 for each column that has a run-time filter.  
Response: The data is loaded and displayed in a visualization.

### 3.4.2.4 Using Structure Search

Users of DecisionSite for Lead Discovery can use structure search in run-time filters. This means using substructure or similarity search to limit the data set to chemical structures of a particular type.

#### ► To use a run-time filter with structure search:

1. Open an information link that contains columns with structure search run-time filters.  
Response: The system will begin to retrieve data. For each column with run-time filter the Set Filter for Column Dialog will appear, asking you to specify the filter conditions for this column.
2. Select **Substructure** or **Similarity**, depending on the type of search you want to perform.
3. Click **Edit Structure**.  
Response: ISIS/Draw is launched.
4. Draw a structure to use as search template.  
Comment: See ISIS/Draw documentation for more information on how to edit structures.
5. When you are done drawing the structure, click the  button in ISIS/Draw.  
Response: ISIS/Draw is closed and the structure appears in the Set Filter for Column dialog.
6. Click **Next >** (or **Finish** if this is the last prompted column).  
Response: The data is retrieved. If this is the last run-time filter, then the data is displayed in a visualization.

### 3.4.2.5 Run-time Filter Example

Information links may include more than one column with run-time filters (which prompt you for input during retrieval). In this case, each filter will reduce the data set, such that subsequent prompts may present fewer values. Consider the following example:

This is the data as it would look if no filters were being applied:

Name	Salary	Location
Prompt: None	Range	Check Boxes
Miller	1300	New York
King	1400	New York
Clark	700	New York
Ford	1100	Dallas
Adams	900	Dallas
Scott	1300	Dallas
Jones	1200	Dallas

James	800	Chicago
Turner	1000	Chicago

As the information link is opened, Salary will be filtered first (the order is set using Information Builder).

Lower	Upper
<input type="text" value="1100"/>	<input type="text" value="1300"/>

The user enters the limits 1100 to 1300. After the first filter, the following remains:

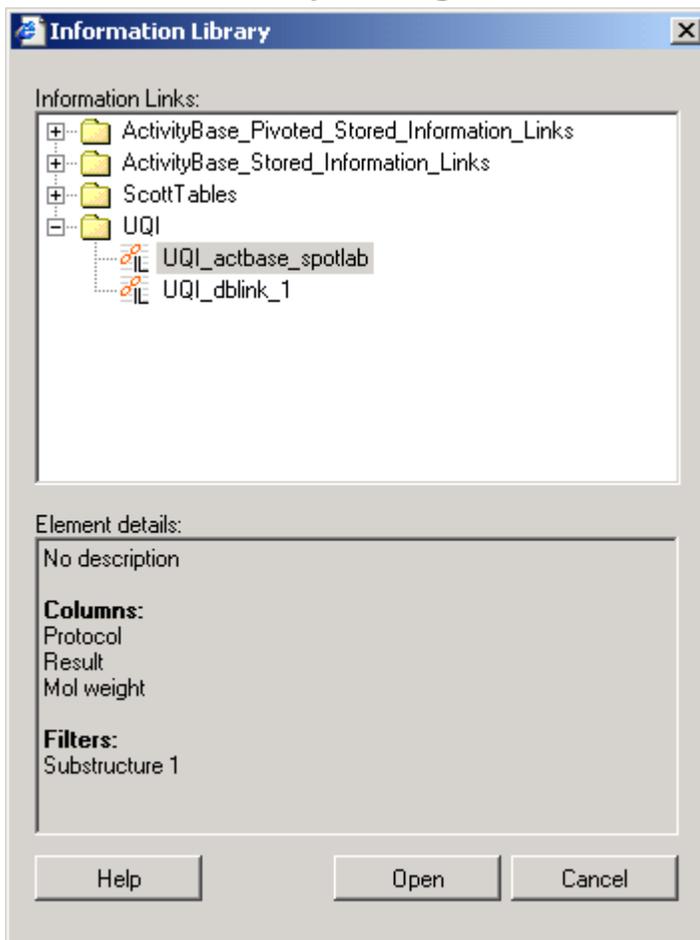
Name	Salary	Location
<b>Prompt: None</b>	<b>Range</b>	<b>Check Boxes</b>
Miller	1300	New York
Ford	1100	Dallas
Scott	1300	Dallas
Jones	1200	Dallas

Several rows, including all Chicago employees, have been filtered out. This means that when the Location filter is shown, Chicago will not be presented as an option:

<input type="checkbox"/> DALLAS
<input type="checkbox"/> NEW YORK

### 3.4.3 User Interface

#### 3.4.3.1 Information Library Dialog



Part	Description
<b>Information Links</b>	Displays the information links to which you have access organized in a folder structure.
<b>Information Link details</b>	Describes the selected information link (click an information link once to select it). The pane will show the data elements that are included and a description if one exists.

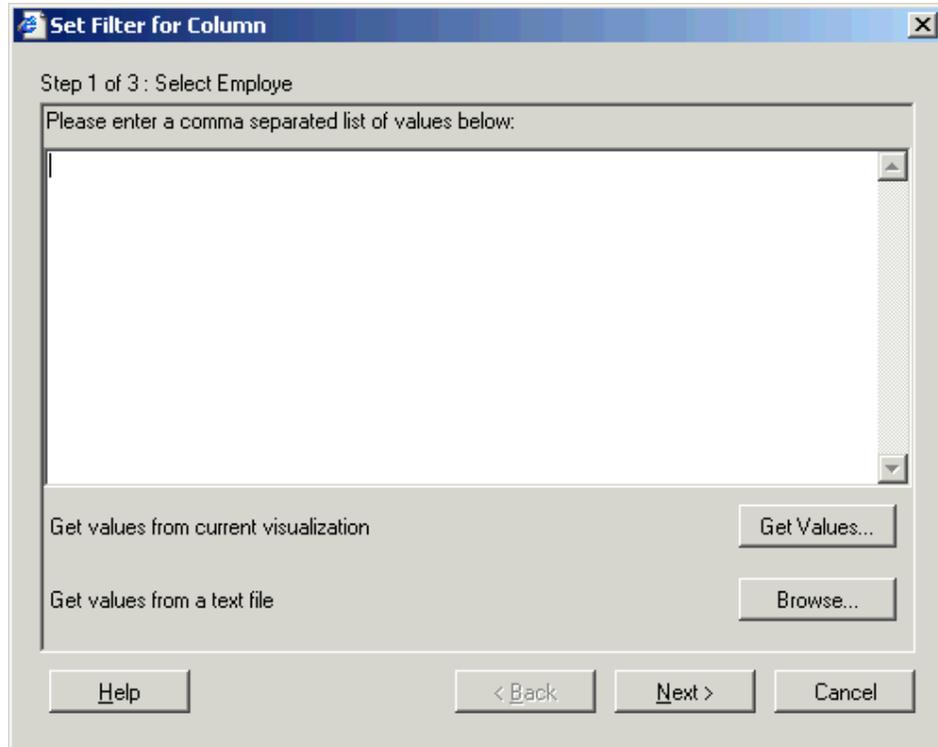
► **To reach the Information Library dialog:**

Select **File > Import > Open Information Link...**

#### 3.4.3.2 Set Filter for Column Dialog

The Set Filter for Column dialog appears when an information link is being opened, and a column is encountered that has been set up with a run-time filter. The dialog may take various forms depending on the type of prompt selected. Strings containing commas can be included both as values, as well as range limits by escaping the comma with a backslash.

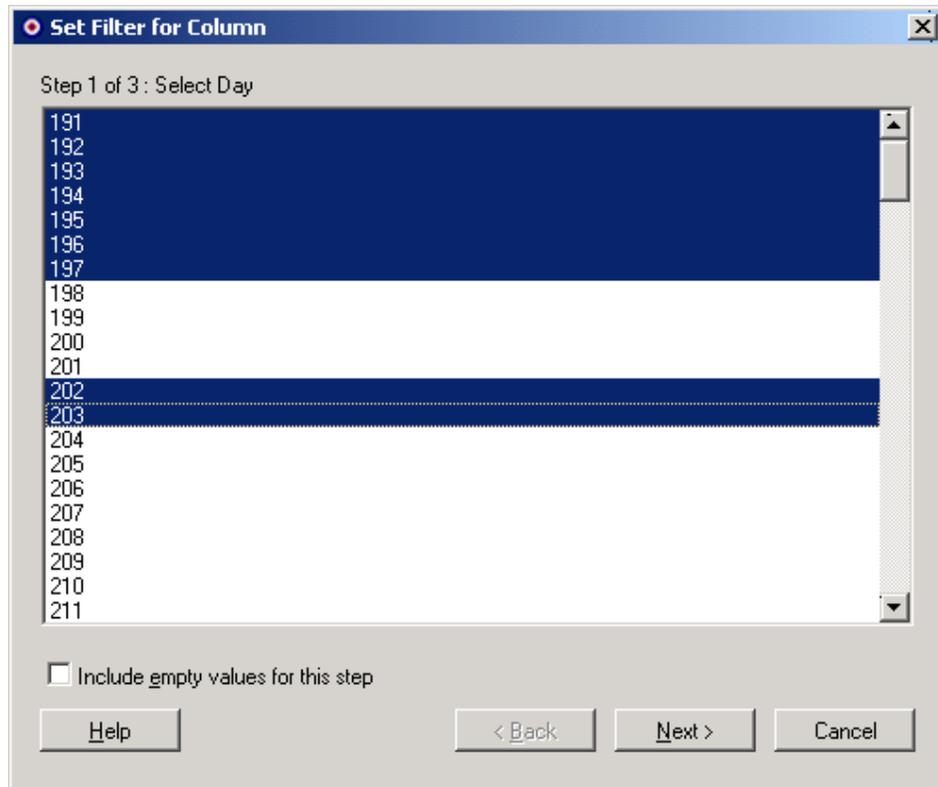
## Values



Part	Description
<b>Text field</b>	<p>Enter a comma-separated list of column values that you want to use as a constraint.</p> <p>You can also paste values of a column from a Microsoft Excel® sheet. The data will automatically be formatted in the right way.</p> <p>Enter \, to include a comma as a value.                      Enter \\ to include a backslash as a value.                      For Procedures, enter \NULL to include the null value.                      Example: apple,pear,\NULL,orange,banana</p>
<b>Get Values...</b>	Use this button to set the column filter by fetching values from the current visualization in DecisionSite. Opens the Get Values from Data Set dialog.
<b>Browse...</b>	Fetch filter values from a text file.

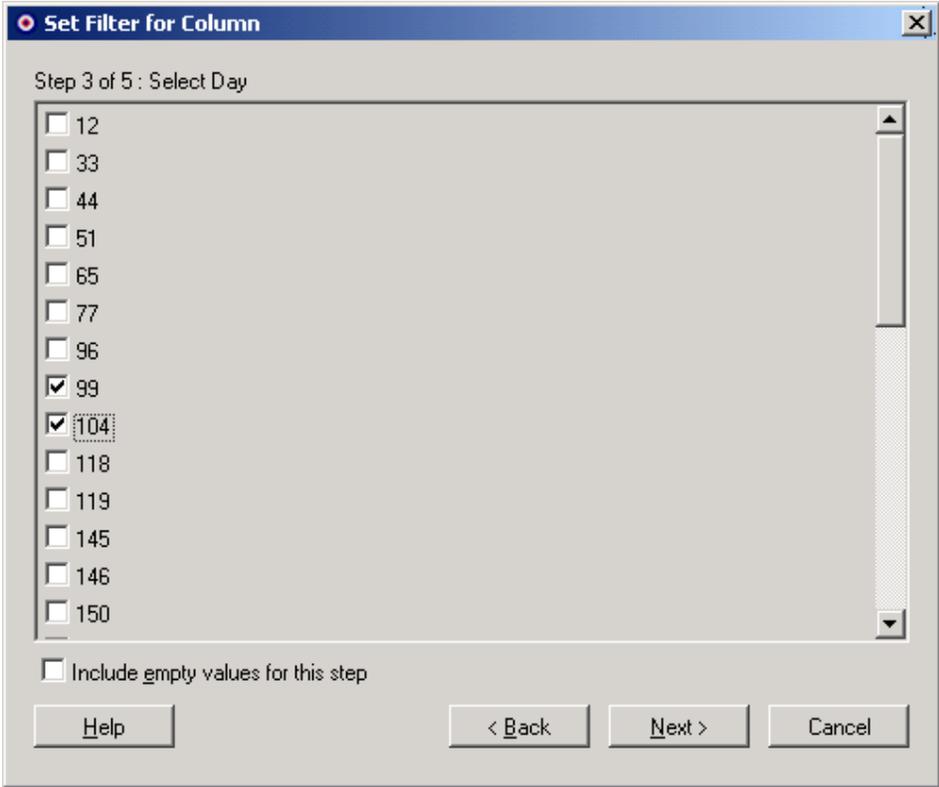


## List Box



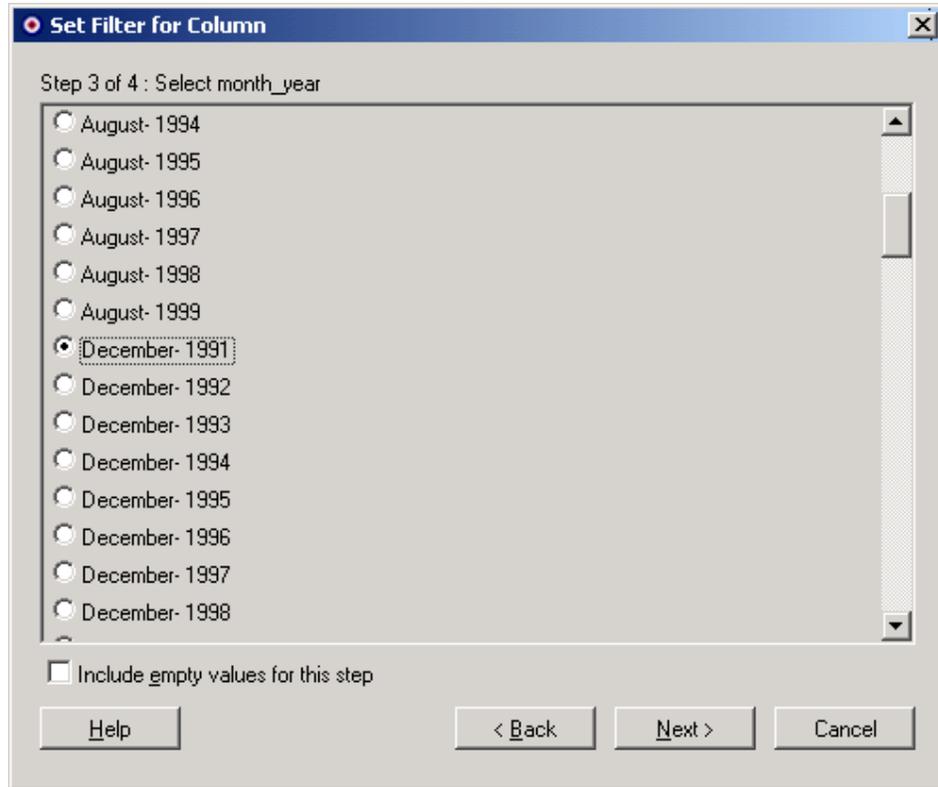
Part	Description
<b>List box</b>	Select the individual values for the column by clicking the entries in the list. To select consecutive values, click the first item, press and hold down SHIFT, and then click the last item. To select multiple entries that are not consecutive, press and hold down CTRL, and then click each item. To select all the values in the list, press CTRL+A.
<b>Include empty values for this step</b>	Select this check box to also include records that contain no data for this column (consequently not available in the list).

### Check Boxes



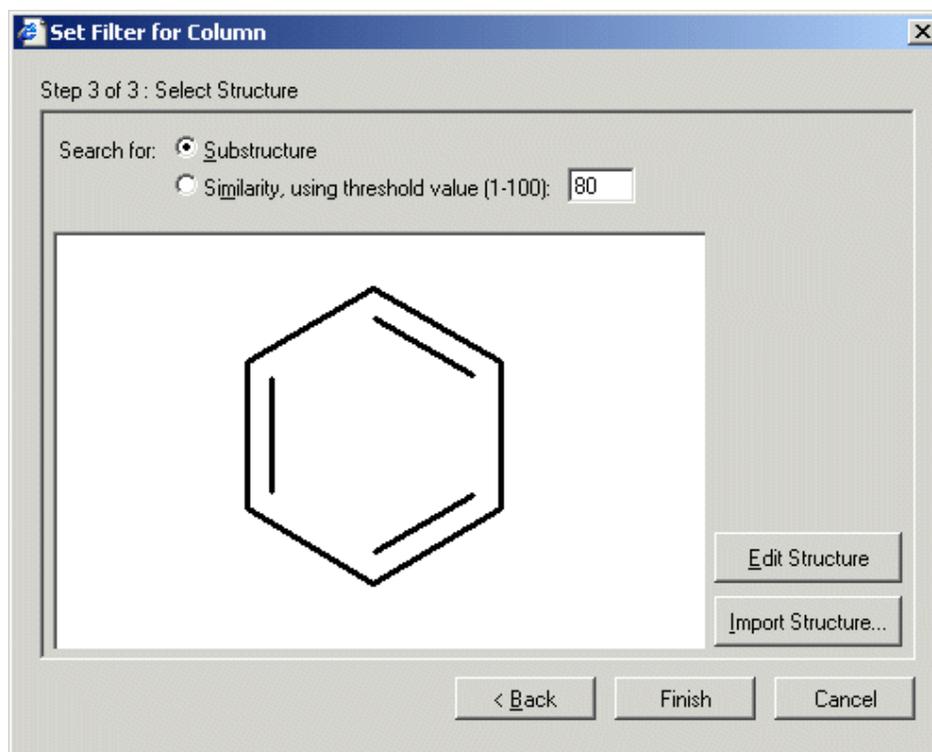
Part	Description
<b>Check boxes</b>	Select individual values for the column from the list. To select all the values in the list, press CTRL+A.
<b>Include empty values for this step</b>	Select this check box to also include records that contain no data for this column (consequently not available in the list).

## Radio Buttons



Part	Description
<b>Radio buttons</b>	Select a unique value for the column by clicking an entry in the list.
<b>Include empty values for this step</b>	Select this check box to also include records that contain no data for this column (consequently not available in the list).

## Structure Search



Option	Description
<b>Search for</b>	Select whether to search using a substructure, or to search for structures similar to a master structure. If similarity is selected, type a threshold value between 1 and 100. A high value means that only very similar records will be included in the resulting list.
<b>Edit Structure</b>	Launches ISIS/Draw, where you can edit the master structure before performing the search.
<b>Import Structure</b>	Displays the Open dialog where you can select a MOL file to use in the search.

### 3.4.3.3 Get Values from Data Set Dialog



Part	Description
<b>Matching column:</b>	Use the drop-down list to select the column in the current data set from which to get the values.
<b>Get values from:</b>	Select whether to use <b>Marked records</b> or <b>Selected records</b> as filter values (or range limits).

► **To reach the Get Values from Data Set dialog:**

1. Open an Information Link with run-time filters.
2. When the **Set Filter for Column** dialog for the desired column appears, click **Get Values...** or **Get Range...**

## 3.5 Import Affymetrix CEL/CHP Files

### 3.5.1 Affymetrix CEL/CHP File Import Overview

The import and summarization of Affymetrix microarray data files, including CHP and CEL files, can be performed in DecisionSite for Microarray Analysis. Methods used to summarize expression measures are often designed to correct for non-specific binding and background noise. In the Affymetrix system, each gene is represented by 11-20 perfect match (PM) and mismatch (MM) pairs of probes, each probing a different region of the mRNA transcript, typically within 600 base pairs of the 3' end. Cell intensity (CEL) files containing probe level PM and MM values can be summarized by robust multi-array analysis (RMA) or GC-RMA. The RMA method of Irizarry et al. (2002, 2003) models PM intensity as a sum of exponential and Gaussian distributions for signal and background, respectively. Quantile normalization (Bolstad et al., 2003) and a log-scale expression effect plus a probe effect model that is fit robustly (median polish) are used to define the RMA expression estimate for each gene. The GC-RMA method of Wu et al. (2004) describes an algorithm similar to RMA, but incorporates the MM using a model based on GC content (GC-RMA).

#### CHP files

Probe level data that has been summarized to a single intensity value per gene/transcript by the MAS5 algorithm, using the Affymetrix GCOS system, is stored within Affymetrix chip (CHP) files. CHP files can be imported by using the appropriate Affymetrix chip description file (CDF) which contains probe layout information for the specific array that is being used.

#### CEL files

Probe level data is contained within Affymetrix cell intensity (CEL) files and can be imported and summarized to generate a single intensity value per gene/transcript by alternate methods that include robust multichip analysis (RMA) or GC-RMA.

► **RMA is a procedure that completes the following steps:**

1. Probe specific correction of the perfect-match (PM) probes using a model based on observed intensity being the sum of signal and (background) noise (Irizarry et al., 2002; Irizarry et al., 2003),
2. Normalization of corrected PM probes using quantile normalization (Bolstad et al., 2003),
3. Calculation of expression measures using median polish.

GC-RMA is a robust multi-array expression measure using sequence information (Wu et al., 2004). It provides background estimates based on a model using GC content. GC-RMA is a modified version of RMA that models intensity of probe level data as a function of GC-content. The theory being that you would expect to see higher intensity values for probes that are GC

rich due to increased binding. This is seen as an improvement over RMA which does not consider the physical processes. Expression intensities returned from GC-RMA are normalized and summarized using quantile normalization and median polish summarization.

## References

- Bolstad, B. M., Irizarry, R. A., Astrand, M., and Speed, T. P. (2003). A comparison of normalization methods for high density oligonucleotide array data based on bias and variance. *Bioinformatics* 19(2): 185-193.
- Irizarry, R. A., Bolstad, B. M., Collin, F., Cope, L. M., Hobbs, B., and Speed, T. P. (2002). Summaries of Affymetrix GeneChip Probe Level Data. *Nucleic Acids Research*. Vol. 31, No. 4 e15.
- Irizarry, R. A., Hobbs, B., Collin, F., Beazer-Barclay, Y. D., Antonellis, K. J., Scherf, U., Speed, T. P. (2003). Exploration, Normalization, and Summaries of High Density Oligonucleotide Array Probe Level Data. *Biostatistics* 4:249-264.
- Wu, Z., and Irizarry, R.A. (2004) Stochastic Models Inspired by Hybridization Theory for Short Oligonucleotide Arrays . *Proceedings of RECOMB 2004*.

## Summary Reports

During CEL file import, Summary Reports can be generated containing box plots and RNA degradation plots that describe variability across experiments before and after summarization, and the quality of the starting RNA used in the experiments, respectively.

Box plots are created of logged expression before and after summarization for each sample chip. Visual inspection shows whether or not the distributions are well aligned at their centers and quartiles. Although normalization may be repeated sequentially to summarized expression intensities there is little need to apply more normalization.

RNA degradation plots display lines representing the sequence of average expression intensities at each probe location in a probe-set, averaged across all probe-sets on one array. Different colors represent different experimental conditions. Trends in the lines indicate uneven hybridization over the probe-set.

## MIAME (Minimum Information About Microarray Experiments)

Minimum information about microarray experiments (MIAME) can be entered on import allowing you to specify experimental information to be permanently stored with the Spotfire analysis file (SFS). It is used to label data and it is appended to the Summary Reports.

## 3.5.2 Importing Affymetrix CEL/CHP Data Files

The import and summarization of Affymetrix CEL and CHP files can be performed using the same tool in DecisionSite for Microarray Analysis. CHP files can also be imported using the Import Affymetrix Data Files tool.

### ► To import Affymetrix CEL/CHP files:

1. Select **Import > Affymetrix CEL/CHP Files...**  
Response: The Affymetrix Import dialog is displayed.
2. Enter the number of files to be imported by using the arrow keys to increase/decrease the number, or type a number directly in the text box. Click **Reset Grid**.  
Comment: The Reset Grid button will make sure that the selected number of rows are available for file selection in the area below.
3. Select the desired CEL or CHP files within the File column grids by typing the file path and name for each file on a row, or simply right-click in the grid and browse to the files in the resulting file open dialog. Multiple selection (SHIFT + click) allows for the addition of all files at once in sequential order.  
**Note:** You cannot import both CEL and CHP files simultaneously.

4. If desired, double-click and highlight the name in the Name column to rename an experiment. The columns of data loaded into Spotfire will inherit this naming.  
Comment: When importing CHP files you must browse to a CDF file corresponding to the Affymetrix arrays used in the experiment. These files can be downloaded as part of the GCOS library files from Affymetrix found here:  
<http://www.affymetrix.com/support/technical/libraryfilesmain.affx>.  
**Note:** File type and Array Type will automatically be assigned to CHP or CEL files depending on which files you have selected above. If an unknown Array Type is being used the Array library will need to be updated.
5. If importing CHP files, select the **MAS Variables & Filtering** tab. Within this tab you can, on import:
  - Apply Log2 transformation to the Signal values.
  - Filter on Absence Detection Call.
  - Filter on Detection P-value.
  - Filter on probe pairs used.
  - Filter control probes with a specified prefix, e.g., "AFFX".
  - Add extra variables for filtering later in DecisionSite.
6. Select the **Options** tab. This tab provides options for specifying the number of header lines to skip and the delimiter used in the data file.
7. Select the desired values and click **OK**.  
Response: If importing CEL files, the Affymetrix CEL File Import Summarization dialog is launched where you can select summarization parameters. If importing CHP files, the MIAME dialog is displayed, see comment in step 10.
8. Choose RMA or GCRMA for summarization of CEL file data and, if desired, select to generate a Summary Report.
9. Click **OK**.  
**Note:** Import of CEL files requires that you have definition library files for the selected CEL files available on your computer. You may be prompted to download missing files at this step. Library files can also be downloaded separately by using the Download Affymetrix CEL Libraries tool.  
Response: You will be prompted to save your current data set.
10. Select whether or not to save your data.  
Response: The MIAME dialog is launched.  
Comment: This information is not required, but it is used in table output and graphics, and thus it is to your advantage to complete the information in this page. Once you have entered information for any experiment, the fields are saved and are automatically filled in the next time you open this dialog. This information will be used to label the Summary Report and will be stored with the experimental data in the Spotfire analysis file (SFS).
11. Click **OK**.  
Response: If you chose to generate a summary report in step 8, you will now be prompted to select Box plots and/or RNA degradation plots. You must choose at least one option from the Affymetrix CEL Reports dialog.
12. Click **OK**.  
Response: Reports are now generated and can be printed or stored for future reference. Your registered handler for rich text format (RTF) files will be started (typically Microsoft Word or Microsoft WordPad).
13. The experimental data should now appear in DecisionSite for Microarray Analysis.

### 3.5.3 Affymetrix CEL Report Examples

The Affymetrix CEL file import allows you to obtain reports during the import. Below are two examples of the available report types.

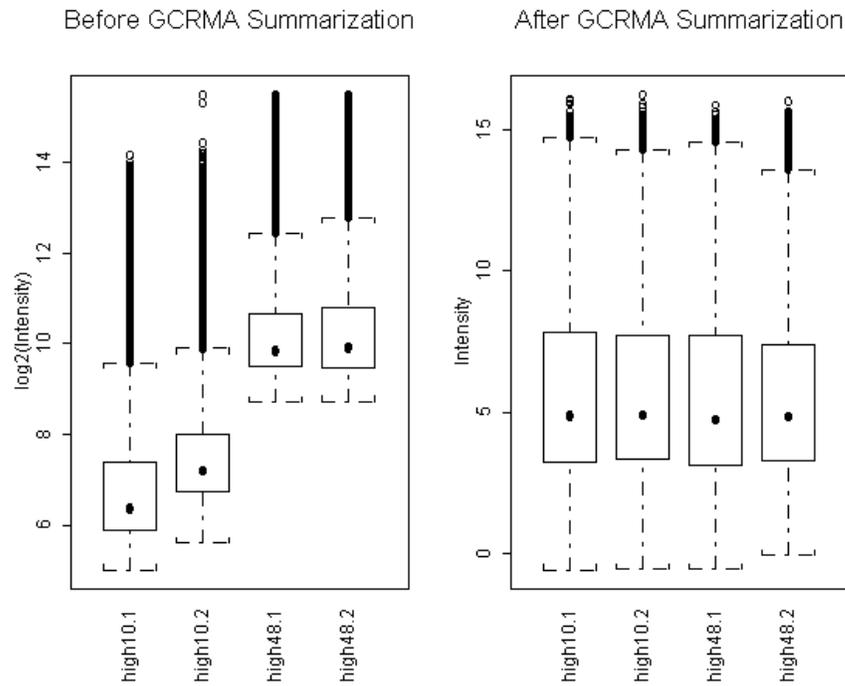
#### Box Plot Report:

##### Affymetrix Experiment Summary/QC Report

**Experiment Title:** Drosophila Experiment

**Summary Method Used:** GCRMA

**Expression Distribution Boxplots:** Comparison of expression distribution between all chips in the experiment.

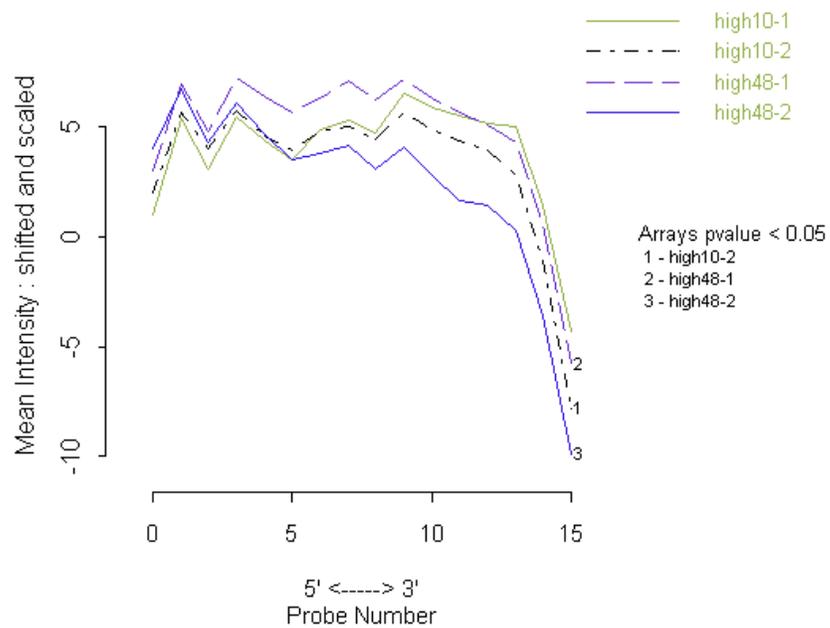


## RNA Degradation Plot Report:

### RNA Degradation Plot:

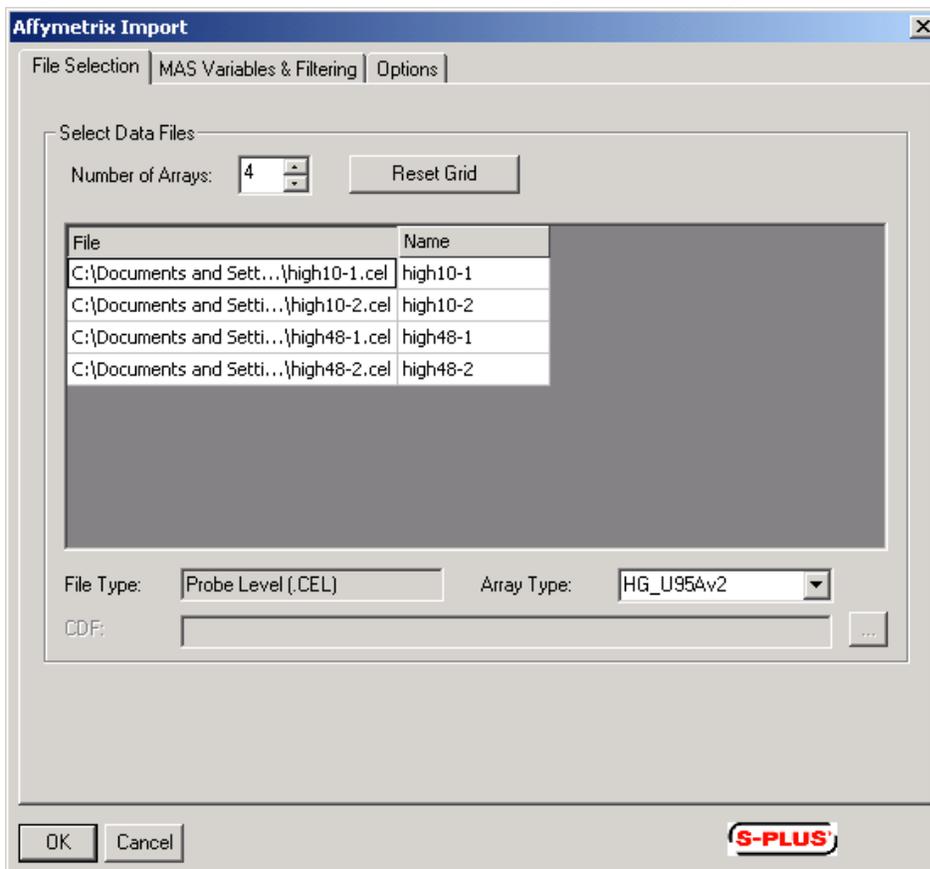
RNA Degradation Results		
	slope	pvalue
high10-1	-0.1286477	0.3937839
high10-2	-0.3812816	0.0340949
high48-1	-0.3512073	0.04636325
high48-2	-0.6673451	0.0003203799

### RNA Degradation Plot

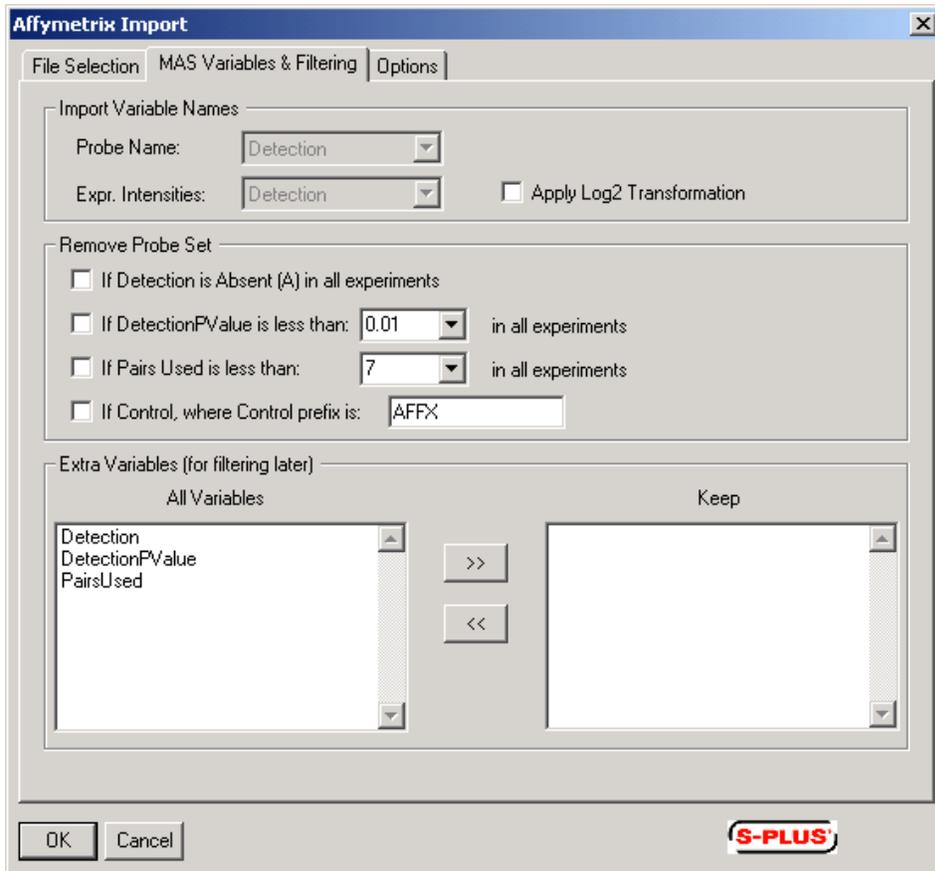


## 3.5.4 User Interface

### 3.5.4.1 Affymetrix CEL and CHP File Import Dialogs

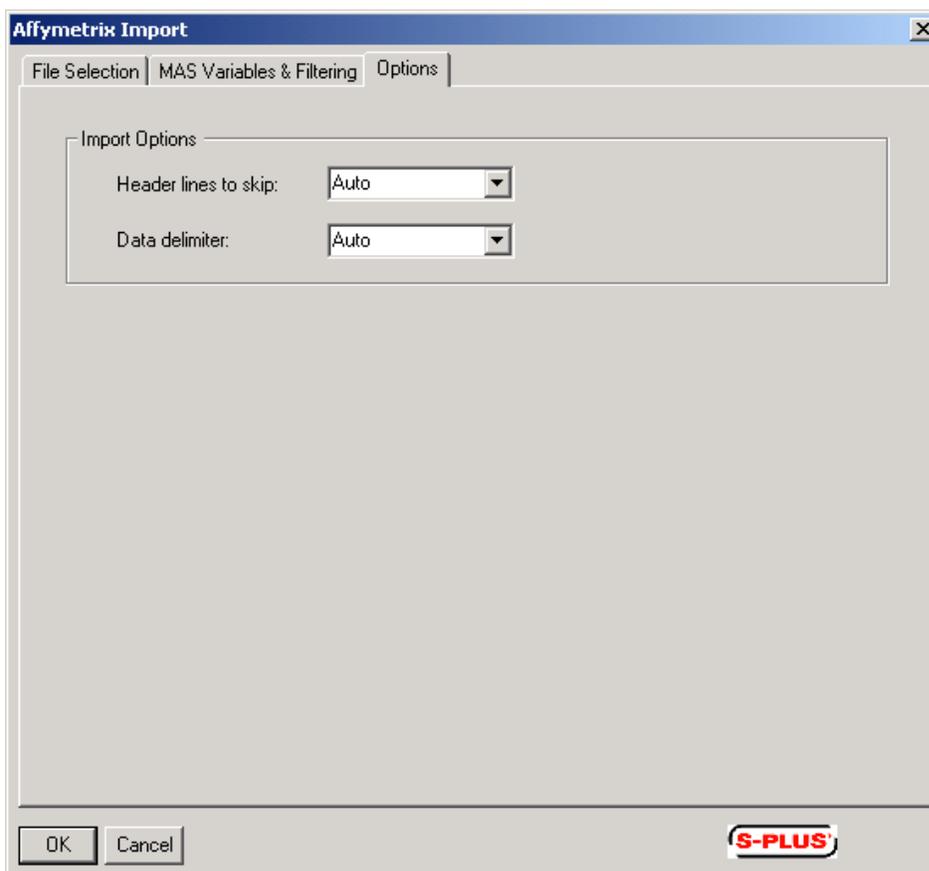


Option	Description
<b>File Selection Tab</b>	Tab for selecting and importing Affymetrix CEL or CHP files.
<b>Number of Arrays</b>	Specifies the number of arrays to be imported and scales the import grid accordingly.
<b>Reset Grid</b>	Resizes the import grid to allow room for the correct number of files, based on the number entered above.
<b>File Type</b>	Specifies the Affymetrix file type.
<b>Array Type</b>	Specifies the Affymetrix array type.
<b>CDF</b>	Specifies the location of the CDF file containing probe location information and is only required for CHP file import.



Option	Description
<b>MAS Variables &amp; Filtering tab</b>	Tab for choosing transformation, filtering, and data import options for Affymetrix CHP files.
<b>Probe Name</b>	The columns in the data files corresponding to the probe names.
<b>Expr. Intensities</b>	The columns in the data files corresponding to the expression intensities.
<b>Apply Log2 Transformation</b>	Returns the log2 of expression intensity values.
<b>If Detection is Absent (A) in all experiments</b>	Removes probes that were not detected in any sample.
<b>If DetectionPValue is less than: in all experiments</b>	Removes a probe if detection p-value is less than a specified value in all samples. Default p-value is 0.01.
<b>If Pairs Used is less than: in all experiments</b>	Removes a probe if the number of pairs used in computing the summarized expression intensities is less than a specified value in all samples. The default value is seven. The maximum is the total number of probe pairs in a set, typically 11, 16 or 20.
<b>If Control, where Control prefix is</b>	Removes control probes that have a specified prefix. Default prefix is AFFX.

<b>All Variables</b>	Additional variables that are available from the CHP file that can be selected for import. Click on a variable name in the list to select it. To select more than one column, press <b>Ctrl</b> and click on the variable names in the list. Use the >> button to send the selected variable to Keep field, see below.
>>	Moves selected variables from the All Variables field to the Keep field.
<<	Removes a variable from the Keep field and brings it back to the All Variables field.
<b>Keep</b>	The additional variables selected for import.



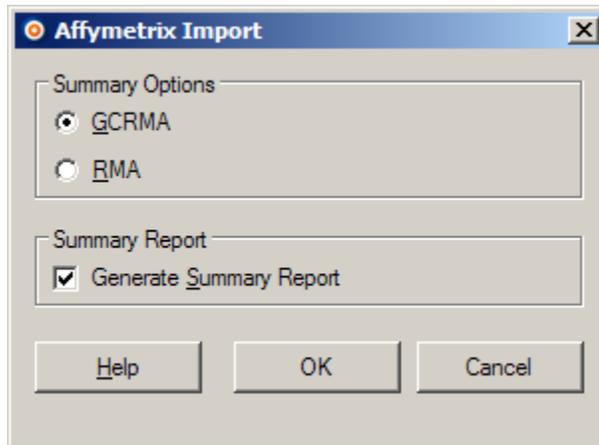
Option	Description
<b>Options tab</b>	Tab for detailed specification of parameters for the imported files.
<b>Header lines to skip</b>	The number of header lines to skip in each file before reading the data. Normally this can be detected automatically but it is provided as an option for unusual cases where auto-detection cannot find the row with column names.
<b>Data delimiter</b>	The delimiter separating the fields in each line of the data files. Normally these are tabs but alternative choices include comma, space, colon and semi-colon. Normally the delimiter can be detected automatically but this option is provided for unusual cases where auto

detection can not determine the field delimiter.

► **To reach the Affymetrix Import dialog:**

Select **Import > Affymetrix CEL/CHP Files...**

### 3.5.4.2 Affymetrix CEL File Import Summarization Dialog

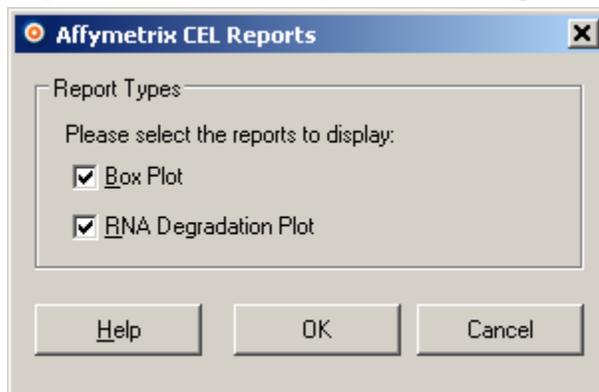


Option	Description
<b>GCRMA</b>	Robust multichip analysis that takes into account GC content of probe sets, thus hybridization efficiency.
<b>RMA</b>	Robust multichip analysis.
<b>Generate Summary Report</b>	Select whether to create a Summary Report during CEL file summarization and import or not.

► **To reach the Affymetrix CEL File Import Summarization dialog:**

1. Select **Import > Affymetrix CEL/CHP Files...**
2. Import one or more CEL files according to the steps described under Importing Affymetrix CEL/CHP Data Files.

### 3.5.4.3 Affymetrix CEL Reports Dialog



Option	Description
<b>Box Plot</b>	Box plots are created of logged expression before and after

summarization for each sample chip. Visual inspection of post summarization data shows whether or not the distributions are well aligned at their centers and quartiles.

**RNA Degradation Plot** RNA Degradation plots display lines representing the sequence of average expression intensities at each probe location in a probe-set, averaged across all probe-sets on one array. Different colors represent different experimental conditions. Trends in the lines indicate uneven hybridization over the probe-set.

► **To reach the Affymetrix CEL Reports dialog:**

1. Select **Import > Affymetrix CEL/CHP Files...**
2. Import one or more CEL files according to the steps described under Importing Affymetrix CEL/CHP Data Files.
3. In the Affymetrix CEL File Import Summarization Dialog, select the check box **Generate Summary Report**.

### 3.5.4.4 MIAME Annotation Dialog

Option	Description
<b>Experimenter's Name</b>	Name of scientist running experiment.
<b>Laboratory</b>	Name of the laboratory.
<b>Contact Information</b>	Contact information for scientist running experiment.
<b>Experiment Title</b>	Descriptive title that reflects goal of the experiment (e.g., the title from the related publication).
<b>Experiment Description</b>	A brief description of the experiment (e.g., the abstract from the related publication).
<b>Existing Notes</b>	Link or path to document containing additional information. For

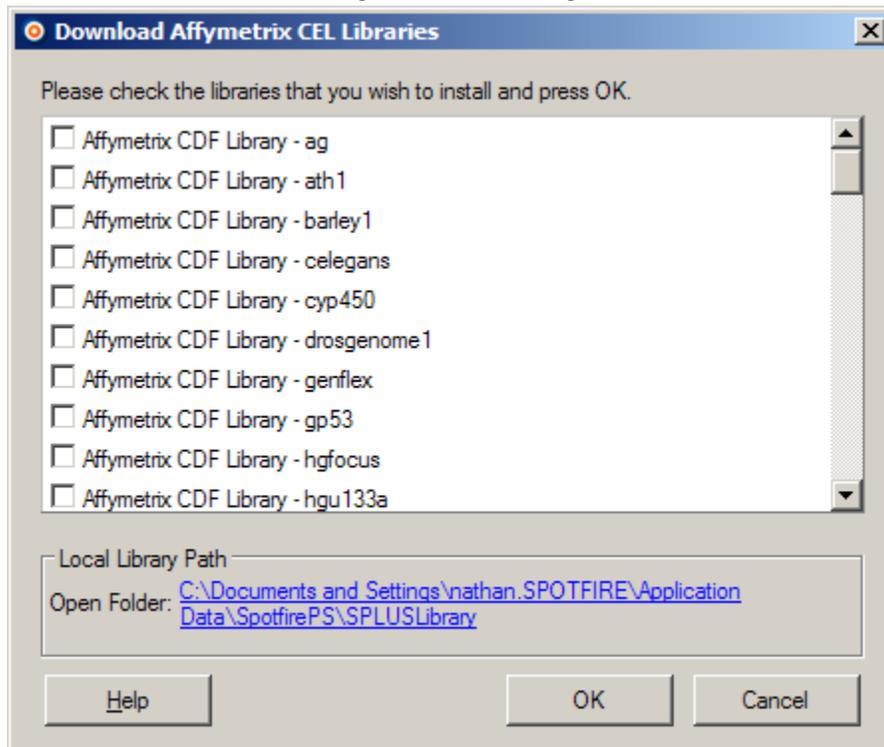
example, keywords, experimental factors, design, quality control steps, links to publications or supplemental websites, samples used, extract preparation and labeling, hybridization procedures and parameters, image scanning and data extraction details, and array design.

► **To reach the MIAME Annotation dialog:**

Select **Tools > MIAME...**

### 3.5.4.5 Download Affymetrix CEL Libraries Dialog

If you do not have the required libraries available for a set of CEL files, you can download annotation libraries from the Insightful web site using this tool.



Option	Description
<b>Please check the libraries...</b>	Select the check boxes for the libraries that you wish to install.
<b>Local Library Path</b>	This is the path to where the selected libraries are downloaded. The libraries must be located in the folder %USER_PROFILE%\Application Data\SpotfirePS\SPLUSLibrary for the tools of DecisionSite for Microarray Analysis to find them. You may click on the link to see what libraries you have currently installed.

► **To reach the Download Affymetrix CEL Libraries dialog:**

Select **Tools > Download Affymetrix CEL Libraries...**

## 3.6 Import Two Channel Array Files

### 3.6.1 Importing Two Channel Data

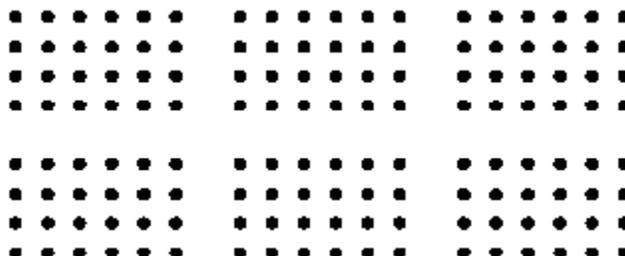
The process of analyzing expression data from custom cDNA arrays can be done using the two channel data import options in Spotfire DecisionSite for Microarray Analysis. When importing the data, one can specify background intensity columns so adjustment for background intensity levels can be made prior to normalization and further analysis. This import supports text files from GenePix, Spot, Agilent, and any text file where a header and delimiter can be identified automatically or specified in the import dialog.

#### ► To import two channel data files:

1. Select **Import > Two Channel Array Files...**  
Response: The Two Channel Import dialog is displayed.
2. Enter the number of files to be imported by using the arrow keys to increase the number or type the number and click **Reset Grid**.
3. Comment: The Reset Grid button will make sure that the selected number of rows are available for file selection in the area below.
4. Select the desired files within the File column grids by typing the file path and name for each file on a row, or simply right-click in the grid and browse to the files in the resulting file open dialog. Multiple selection (SHIFT + click) allows for the addition of all files at once in sequential order. From the file type pull down menu, be sure to select the desired file type (GPR, SPOT, CSV, etc.) or All types.
5. If desired, double-click and highlight the name in the Name column to rename an experiment. The columns of data loaded into Spotfire will inherit this naming.
6. Select the **Variable Selection & Filtering** tab.
7. Select the columns containing **Green** and **Red foreground** intensities (required). These drop-down lists are populated using the column headers in the imported data files.
8. If desired, specify a column of spot quality **Weights**.  
Comment: These weights are used in subsequent computations to down-weight poor quality spots during normalization.
9. If desired, select any **Extra Variables**, such as flags for later filtering, from the files for import into DecisionSite.
10. Select the **Create Layout** tab and choose the desired values.

**Note:** This information is required for running Print tip normalization methods selected in subsequent steps.

Comment: The schematic in the figure below represents a cDNA array. The spots are arranged in large blocks or print-tip groups. Within each print-tip group are spots where the cDNA is fixed. To specify the array layout, you must specify the size and arrangement of both the print-tip groups (the outer grid) and the spot matrix (the inner grid) within each group. You specify this layout in terms of rows and columns. In the schematic shown here there are two rows and three columns of print-tip groups, as well as four rows and six columns in the spot matrix. It is assumed that the spot matrix size is the same for each print-tip group.



**Note:** Some arrays have a single large print-tip group covering the entire array. In this special case, the outer grid has just one row and one column.

Select the **Options** tab.

Specify the number of **Header lines to skip** and the **Delimiter** used in the data file.

11. Click **OK**.

Response: The Two-Channel Normalization dialog is launched where you can select normalization parameters.

12. Select the desired normalization parameters.

Comment: Two-channel normalization within arrays by median, Print Tip Loess, Scale Print Tip MAD, Loess TwoD, Global MAD, Print Tip MAD methods can be selected. Next, the option to normalize between arrays several ways by quantiles is available. Lastly, the option to generate Summary Reports that include Box plots and MvA plots is available in the normalization dialog.

13. Click **OK**.

Response: You will be prompted to save your current data set.

14. Select whether or not to save your data.

Response: The MIAME dialog is launched.

Comment: This information is not required, but it is used in table output and graphics, and thus it is to your advantage to complete the information in this page. Once you have entered MIAME information for any experiment, the fields are saved and are filled automatically the next time you open this dialog. This information will be used to label the Summary Report and will be stored with the experimental data in the Spotfire analysis (SFS) file.

15. Click **OK**.

Response: If you chose to generate a summary report, you will now be prompted to select Box plot and/or MvA plot. You must choose at least one option from the Two Channel Reports dialog.

16. Click **OK**.

Response: Reports are now generated and can be printed or stored for future reference.

Comment: If you chose to generate reports, your registered handler for rich text format (RTF) files will be started (typically Microsoft Word or Microsoft WordPad).

17. The experimental data should now appear in DecisionSite for Microarray Analysis.

## 3.6.2 Two Channel Report Examples

The Two Channel file import allows you to obtain reports during the import. Below are two examples of the available report types.

**Box Plot Report:****[Two Channel Experiment Summary/QC Report**

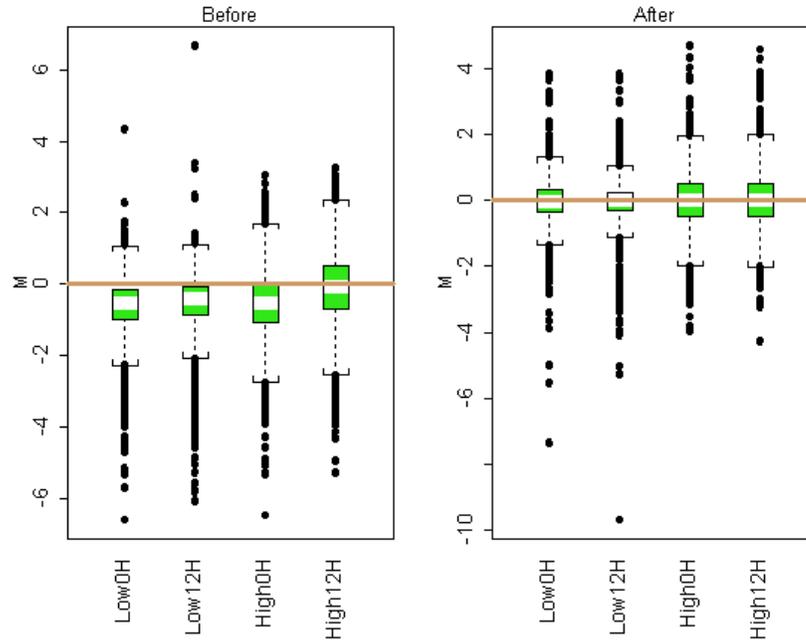
**Experiment Title:** Mouse MPRO Experiment

**Within-chip Normalization Method Used:** printTipLoess

**Between-chip Normalization Method Used:** quantiles on A

**Expression Distribution Boxplots:** Comparison of expression distribution between all chips in the experiment.

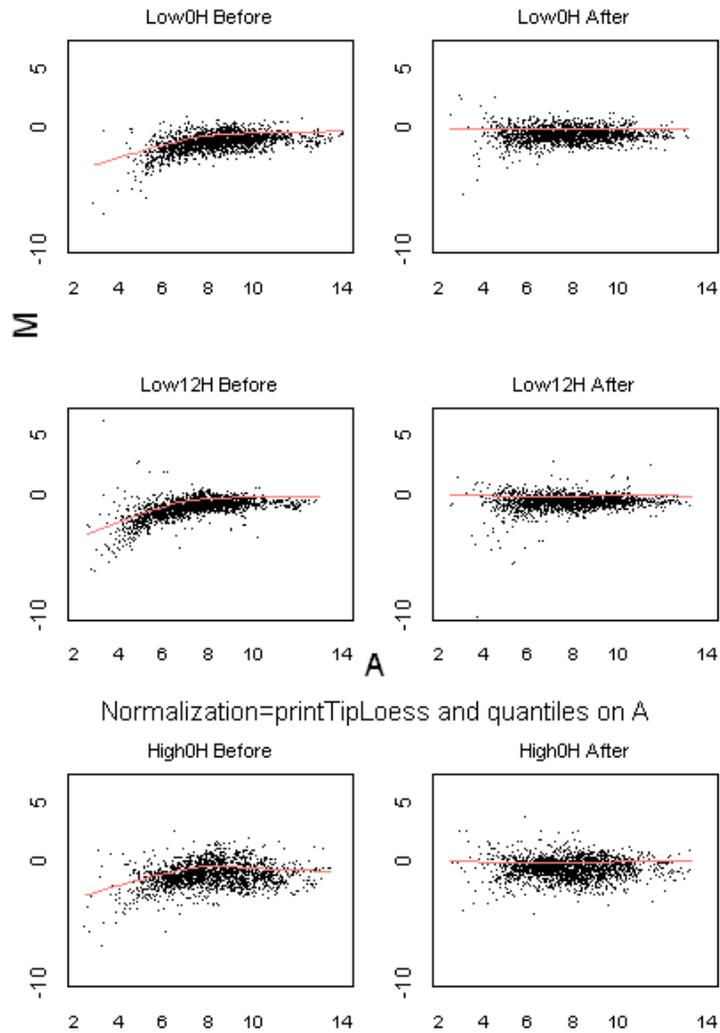
Normalization=printTipLoess and quantiles on A



Box plots of intensity log-ratio (M) before and after normalization.

**MvA Plot Report:**

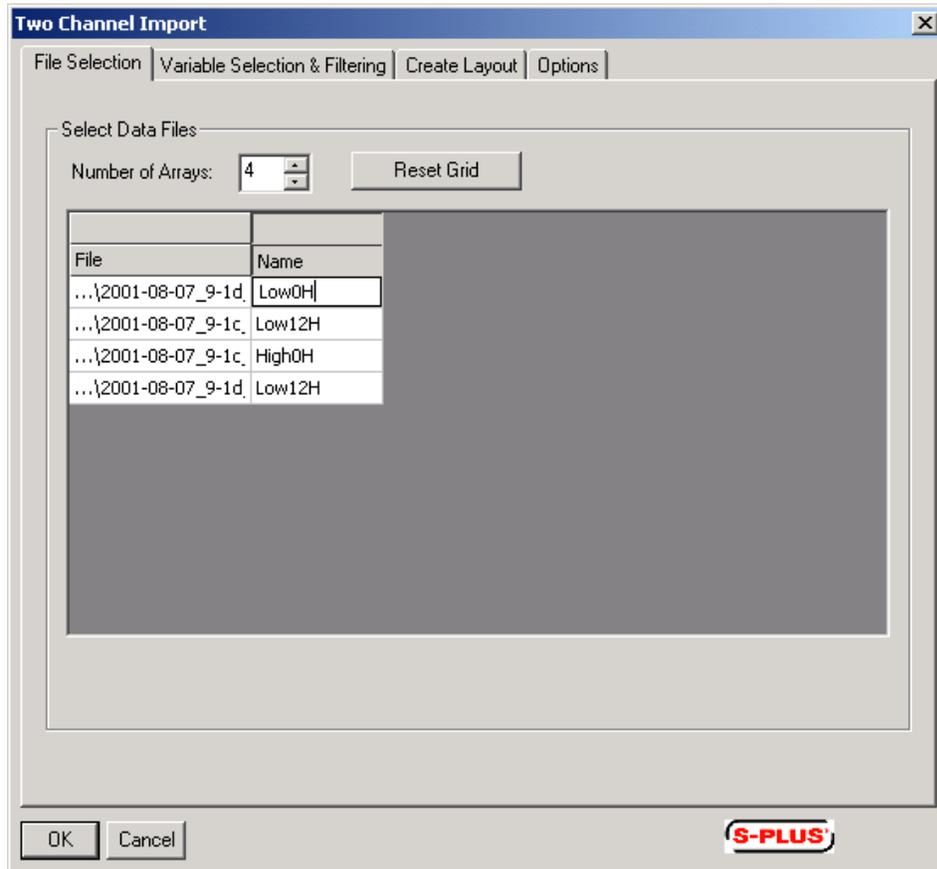
**Bland-Altman Plots:** Evaluation of expression variability within chips.  
 Normalization=printTipLoess and quantiles on A



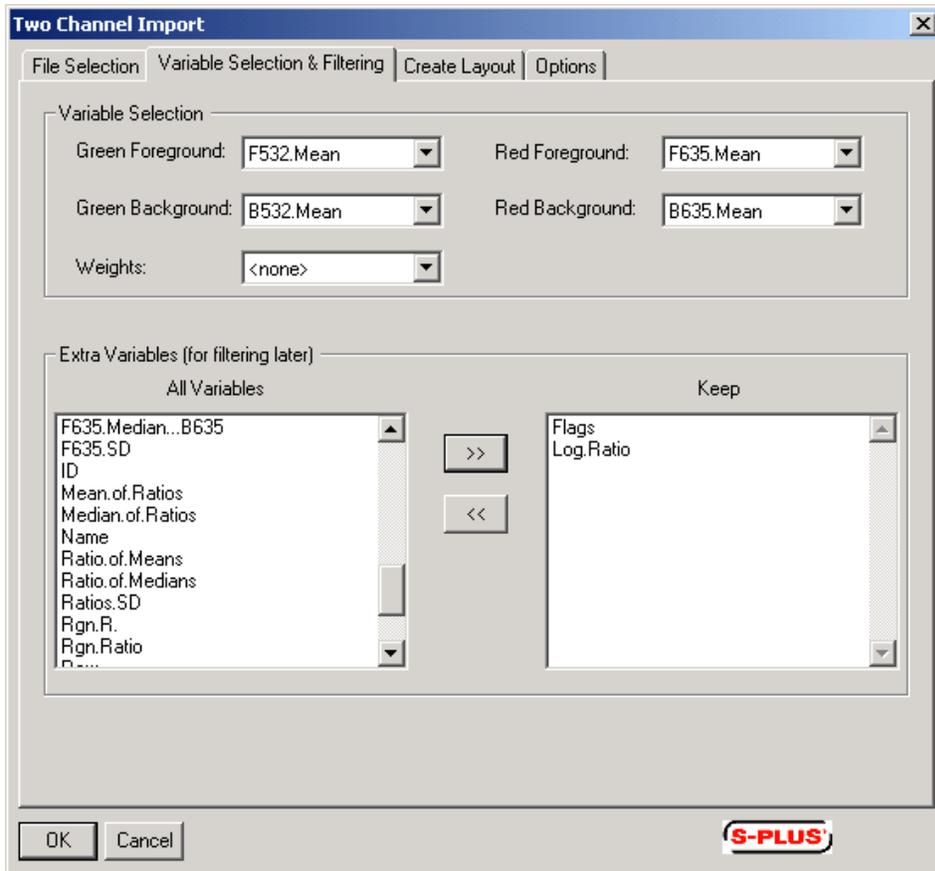
Bland-Altman/ MvA Plots: Intensity log-ratios on y axis and average log sum intensity for the chip pair on the x-axis before and after normalization.

## 3.6.3 User Interface

### 3.6.3.1 Two Channel Import Dialog



Option	Description
<b>File Selection Tab</b>	Tab for selecting and importing 2-Channel data files.
<b>Number of Arrays</b>	Specifies the number of arrays to be imported and scales the import grid accordingly.
<b>Reset Grid</b>	Resizes the import grid based on the number entered.

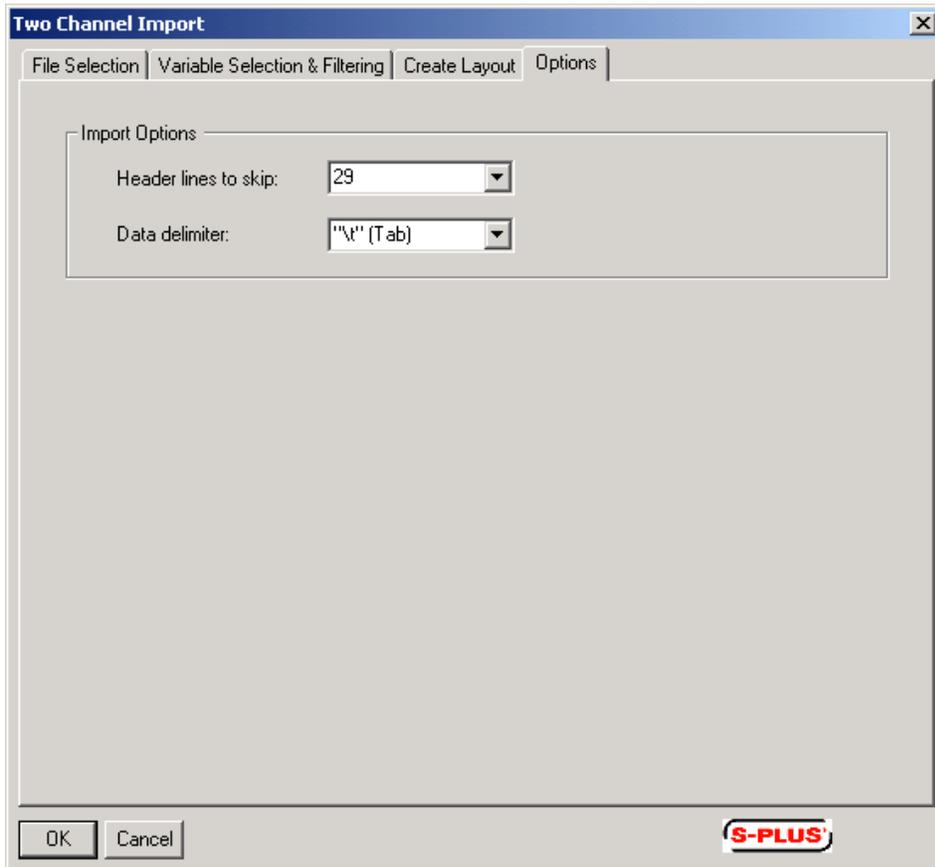


Option	Description
<b>Variable Selection &amp; Filtering Tab</b>	Tab for choosing transformation, filtering, and data import options for Two Channel data files.
<b>Green Foreground</b>	Column in data set to be used as the Green channel foreground intensity values.
<b>Green Background</b>	Column in data set to be used as the Green channel background intensity values.
<b>Red Foreground</b>	Column in data set to be used as the Red channel foreground intensity values.
<b>Red Background</b>	Column in data set to be used as the Red channel foreground intensity values.
<b>Weights</b>	Allows you to specify a column of spot quality weights. These weights are used in subsequent computations to down-weight poor quality spots during normalization.
<b>All Variables</b>	Additional variables that are available from the Two Channel data file that can be selected for import. Click on a variable name in the list to select it. To select more than one column, press <b>Ctrl</b> and click on the variable names in the list. Use the >> button to send the selected variable to Keep field, see below.
>>	Moves selected variables from the <b>All Variables</b> field to the <b>Keep</b> field.

<<	Removes a variable from the <b>Keep</b> field and brings it back to the <b>All Variables</b> field.
<b>Keep</b>	The additional variables selected for import.

Option	Description
<b>Create Layout Tab</b>	Tab for entering the spotted array grid layout.
<b>Grid Rows</b>	Spots are arranged in large blocks or print-tip groups known as the outer grid. The value entered here is the number of rows of these large blocks.
<b>Grid Columns</b>	Spots are arranged in large blocks or print-tip groups known as the outer grid. The value entered here is the number of columns of these large blocks.
<b>Inner Grid Row</b>	Within each print-tip group the number of rows of spots where the cDNA is fixed is entered here. This is the spot matrix or inner grid within each group. It is assumed that the spot matrix size is the same for each print-tip group.
<b>Inner Grid Column</b>	Within each print-tip group the number of columns of spots where the cDNA is fixed is entered here. This is the spot matrix or inner grid within each group. It is assumed that the spot matrix size is the same for each print-tip group.

<b>Control</b>	A column indicating which spots are control spots.
<b>Control Value</b>	Values which label the control spots. In some cases this may be the single value “control”. In others, it may be the numeric values -1 and 1 indicating positive and negative controls.
<b>Gene Name</b>	A column with unique gene or probe names.



Option	Description
<b>Options tab</b>	Tab for detailed specification of parameters for the imported files.
<b>Header lines to skip</b>	The number of header lines to skip in each file before reading the data. Normally this can be detected automatically but it is provided as an option for unusual cases where auto-detection cannot find the row with column names.
<b>Data delimiter</b>	The delimiter separating the fields in each line of the data files. Normally these are tabs but alternative choices include comma, space, colon and semi-colon. Normally the delimiter can be detected automatically but this option is provided for unusual cases where auto-detection can not determine the field delimiter.

► **To reach the Two Channel Import dialog:**  
 Select **Import > Two Channel Array Files...**

### 3.6.3.2 Two-Channel Normalization Dialog

#### Normalization of Two-Channel Data

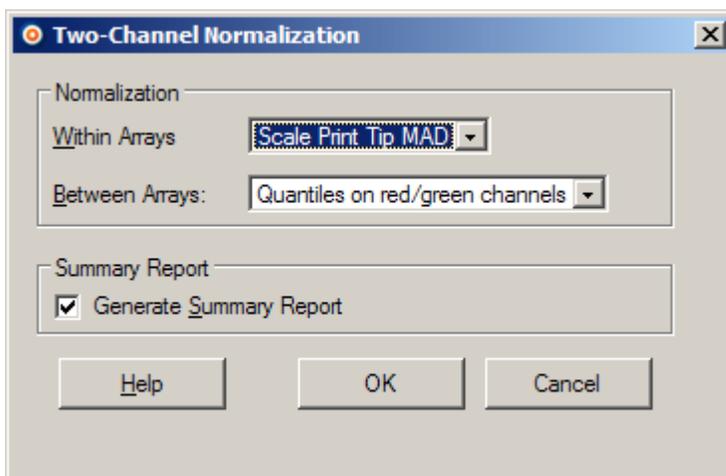
Within Arrays:

There are often systemic variation and imbalances of the red and green fluorescence intensities in two-channel data. This variation is usually not constant across the spots within or between arrays, and can vary according to overall spot intensity, location on the array, plate origin, and possibly other variables. Some causes of the imbalances may be the following:

- Labeling efficiencies and scanning properties of the Cy3 and Cy5 dyes.
- Amounts of Cy3- and Cy5-labeled mRNA.
- Scanning parameters, such as PMT settings.
- Print-tip, spatial, and plate effects.

Between Arrays:

After individual arrays have been normalized for differences in the red and green fluorescence intensities, additional normalization can be done between arrays. DecisionSite for Microarray Analysis offers quantile normalization on the individual red/green channels as well as on the average of the two channels (A). Normalization between arrays is needed if downstream analyses (e.g. ANOVA) compare experimental conditions that vary between arrays.



Option	Description
<b>Within Arrays</b>	Normalize data in each array so that biases in relative probe intensity on a single array, due to effects such as dye differences, are reduced.
> <b>Median</b>	Median normalization by array.
> <b>Print Tip Loess</b>	Normalizes to the loess curve of M vs. A within each print-tip group on each array.
> <b>Scale Print Tip MAD</b>	Normalizes to the loess curve of M vs. A within each print-tip group, followed by within-print-group scale normalization using the median absolute deviation.
> <b>Loess</b>	Normalization to loess curve of M vs. A within each array.
> <b>Two D</b>	2D spatial location normalization. Normalizes to the smoothed intensity surface (loess surface) by print-tip group at each x, y coordinate.
> <b>Global MAD</b>	Scale normalization over each chip using the median absolute deviation

	(MAD), this allows between slide scale normalization.
> <b>Print Tip MAD</b>	Within-print-tip-group scale normalization using the median absolute deviation.
<b>Between Arrays</b>	Normalize data between arrays so that variation, such as scanner setting differences, among the arrays is reduced.
> <b>Quantiles on red/green channels</b>	Quantile normalization on the individual red/green channels
> <b>Quantiles on A</b>	Quantile normalization on the average of the two channels (A).
> <b>None</b>	No normalization is performed between arrays.
<b>Generate Summary Report</b>	Allows you to choose to generate summary reports and be prompted for report type in a subsequent dialog.

► **To reach the Two Channel Normalization dialog:**

1. Select **Import > Two Channel Array Files...**
2. Follow steps 1-12 described under Importing Two Channel Data.

### 3.6.3.3 Two Channel Reports Dialog

The Two Channel Data import of DecisionSite for Microarray Analysis supports two types of reporting plots, box plots and MvA plots.

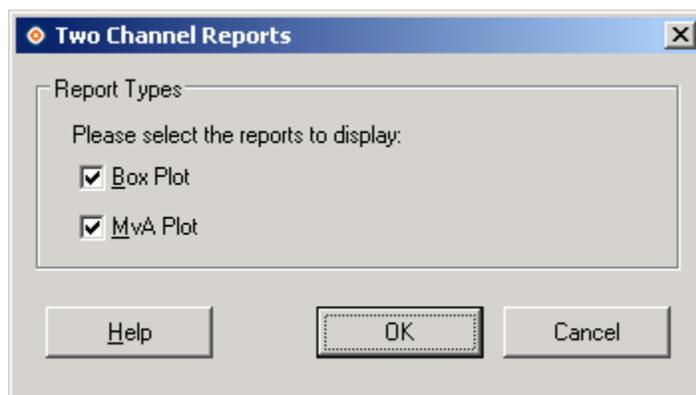
#### MvA Plots

Normalization usually begins with exploratory data analysis and diagnostic plots. Two-channel data typically includes two treatment conditions on one chip. Dudoit et al (2002) and Yang et al. (2001) suggest that the most useful way to view such data in order to identify spot artifacts, and for normalization purposes, is via an M vs. A plot of the intensity log-ratio

$M = \log_2 \left( \frac{R}{G} \right)$  vs. the mean log-intensity  $A = \log_2 \sqrt{RG}$ . This amounts to a 45 degree counter-clockwise rotation of the  $(\log_2 G, \log_2 R)$ -coordinate system, followed by a scaling of the coordinates. This plot highlights the difference between the red and green channels as a function of average intensity across the two channels.

#### Box plots

The y-axis typically shows the intensity log-ratio (M). The x-axis shows the grouping (chip or print-tip).



Option	Description
<b>Box Plot</b>	Box plots with the intensity log-ratio (M) on the Y-axis and the grouping (array or print-tip) on the X-axis.
<b>MvA Plot</b>	This plot highlights the difference between the red and green channels as a function of average intensity across the two channels.

► **To reach the Two Channel Reports dialog:**

1. Click **Import > Two Channel Array Files...**
2. Follow steps 1-16 described under Importing Two Channel Data.

### 3.6.3.4 MIAME Annotation Dialog

Option	Description
<b>Experimenter's Name</b>	Name of scientist running experiment.
<b>Laboratory</b>	Name of the laboratory.
<b>Contact Information</b>	Contact information for scientist running experiment.
<b>Experiment Title</b>	Descriptive title that reflects goal of the experiment (e.g., the title from the related publication).
<b>Experiment Description</b>	A brief description of the experiment (e.g., the abstract from the related publication).
<b>Existing Notes</b>	Link or path to document containing additional information. For example, keywords, experimental factors, design, quality control steps, links to publications or supplemental websites, samples used, extract preparation and labeling, hybridization procedures and parameters, image scanning and data extraction details, and array design.

► **To reach the MIAME Annotation dialog:**

Select **Tools > MIAME...**

## 3.7 Import Affymetrix Data from Database

### 3.7.1 Importing Analysis Data from an Affymetrix Database

Spotfire DecisionSite for Functional Genomics allows you to retrieve information from both remote and local Affymetrix databases. If the information requested is located in an Oracle Affymetrix database, the following procedure is used.

**Note:** The setting up of the Retrieve from Database (Remote) tool is an administrative function that is done on the server. Please contact your Spotfire Administrator if you do not have access to this tool.

For information about how to set up a connection to a local Affymetrix database, please contact your database administrator.

► **Importing analysis data:**

1. Select **Import > Affymetrix Data from Database (Remote)...** or **Affymetrix Data from Database (Local)...**

Response: The Retrieve Affymetrix Data from Database dialog is opened.

2. Click **Retrieve analysis information for specified columns.**

Comment: It is often useful to retrieve summary information before you import your analysis information, so that you can determine whether or not various analyses are relevant and accurate.

3. Click **Columns...**

Response: The Data Import Options dialog is displayed.

4. Select the columns that you want to import.

Comment: The columns are sorted into Absolute Results (which displays columns that can be found on all chips) and Comparison Results (which are found on baseline chips). To import all available columns, click **Select All**.

5. Click **OK**.

Response: The Data Import Options dialog is closed.

6. If your data set contains a list of analysis names (such as in the summary information) you can click **Get selected analysis names from current data set** and select the column with analysis names.

Comment: This will use the Analysis Name column from the previously imported summary data, so you do not have to go through the wizard again. If you do not have any analysis names in the current data set, click **Get analysis names from database**. Make your choices and click **Next >** to continue in the sequential wizard in order to select which analyses to retrieve information about. On the final page of the wizard click **Finish**.

7. Click **Finish**.

Response: Analysis data are loaded into Spotfire DecisionSite. data are automatically pivoted into a Short/Wide format and can immediately be analyzed by the various tools of Spotfire DecisionSite for Functional Genomics.

## 3.7.2 Importing Summary Data from an Affymetrix Database

Spotfire DecisionSite for Functional Genomics allows you to retrieve information from both remote and local Affymetrix databases. If the information requested is located in an Oracle Affymetrix database, the following procedure is used.

**Note:** The setting up of the Retrieve from Database (Remote) tool is an administrative function that is done on the server. Please contact your Spotfire Administrator if you do not have access to this tool.

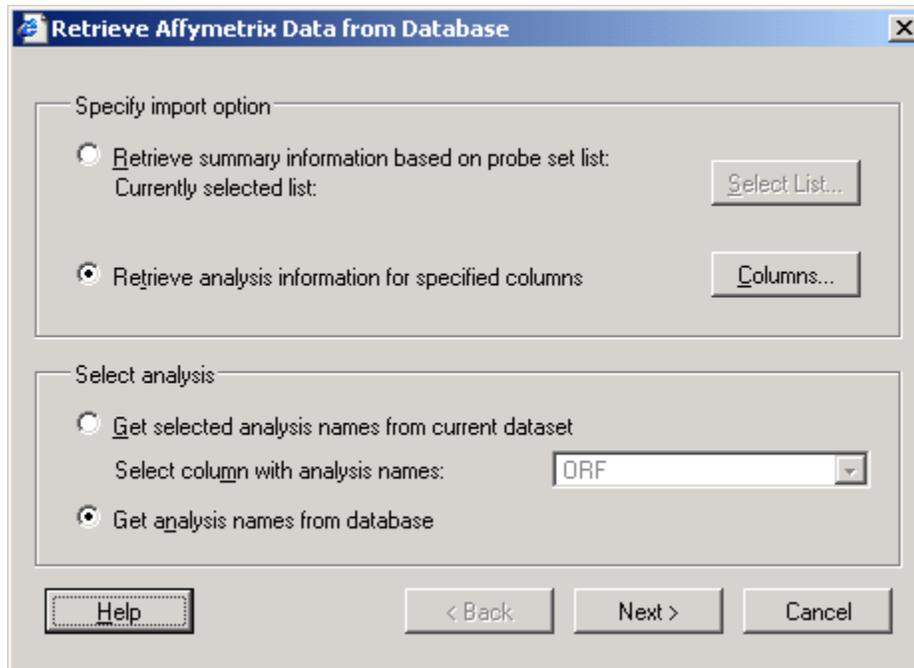
For information about how to set up a connection to a local Affymetrix database, please contact your database administrator.

### ► Importing summary data:

1. Select **Import > Affymetrix Data from Database (Remote)...** or **Affymetrix Data from Database (Local)...**  
Response: The Retrieve Affymetrix Data from Database dialog is opened.
2. Click **Retrieve summary information based on probe set list.**  
Comment: The summary information contains quality control information about the selected chip(s). This is useful for investigating whether or not various analyses are relevant and accurate. Once this has been determined, the analysis information can be retrieved.
3. Click **Select List.../Change List...**  
Response: The Probe set lists portfolio is displayed.
4. Select a relevant probe set list from the portfolio. If you do not have any relevant lists in your portfolio, click **Load Defaults** to add a default list with sublists from the server. Expand the default list and select the species of interest (e.g., Human chips).
5. Click **OK.**  
Response: The Probe set lists portfolio is closed and the selected list is shown in bold face as the Currently selected list.  
Comment: The chosen list will be selected by default the next time you open the tool.
6. Click **Get analysis names from database.**
7. Click **Next >**.
8. Make your choices and click **Next >** to continue in the sequential wizard in order to select which analyses to retrieve information about. On the final page of the wizard click **Finish.**  
Response: Summary data are loaded into Spotfire DecisionSite. Four different line chart visualizations are created: Array Summary, Present Gene Summary, 3' Expression and 3' / 5' Ratio.

After retrieving summary information and studying the results it is often interesting to retrieve analysis data based on what was found previously.

### 3.7.3 Retrieve Affymetrix Data from Database Dialog



Option	Description
<b>Retrieve summary information based on probe set list</b>	Retrieves quality control summary information for the selected chips.
<b>Select List.../Change List...</b>	Opens the <b>Probe set lists</b> portfolio dialog. This is basically your own Portfolio, where you can select any list that includes relevant probe sets. The <b>Load Defaults</b> button will add a default list of control probe sets to the portfolio.
<b>Retrieve analysis information for specified columns</b>	Retrieves actual analysis data for the selected probe sets.
<b>Columns...</b>	Opens the Data Import Options dialog, where you can select which columns to import from your data source.
<b>Get selected analysis names from current data set</b>	Uses the analysis names of the selected column in the current data set for the retrieval of new data.
<b>Get analysis names from database</b>	If this option is selected, the tool will step you through a sequential query against the Affymetrix database. Follow the onscreen instructions and click <b>Next &gt;</b> to continue in the process. When the final page has been reached, click <b>Finish</b> to load the data into Spotfire DecisionSite.
<b>&lt; Back</b>	The < Back button takes you back one step when you are running a sequential query. This is only applicable when you are using the <i>Get analysis names from database</i> option above.
<b>Next &gt;/Finish</b>	Depending on your selections above you will see either the <b>Next &gt;</b> or the <b>Finish</b> button. Next > takes you to the next page in a sequential query, whereas Finish will actually load the data into Spotfire DecisionSite. Data are always

pivoted (transformed into a Short/Wide format) to be ready to analyze using other Functional Genomics tools.

► **To reach the Retrieve Affymetrix Data from Database dialog:**

Select **Import > Affymetrix Data from Database (Remote)...** or **Affymetrix Data from Database (Local)...**

## 3.8 Import Affymetrix Data from Files

### 3.8.1 Importing Affymetrix Data Files

The Import Affymetrix Files tool allows you to open text (TXT) files that have been exported from the Metrics tab of Affymetrix Microarray Suite or from GeneChip. It also allows the import of chip (CHP) files. Multiple files can be added at once as Affymetrix Result Files, however, chip files cannot be added together with any other types of files. When chip files are added as Affymetrix Result Files a Chip Description File (CDF) file or Probe Set Information file (PSI) must also be provided.

► **To import Affymetrix data files:**

1. Select **Import > Affymetrix Data from Files...**  
Response: The Import Affymetrix Files dialog is opened.
2. If this is your first time using the tool, or if you want to add additional files to the available files list, click on the **Add** button. If you already have retrieved the interesting files to the tool, go to step 5.  
Response: Opens a dialog where you can select the Affymetrix files that you want to have access to from within Spotfire DecisionSite.  
Comment: Added files will remain in the list from session to session, unless you remove them using the Remove button.
3. Browse and select the interesting Affymetrix files. It is possible to select several files in the same folder at once by pressing **Ctrl** and clicking on the desired files.
4. Click **Open**.  
Response: The files are added to the list in the Import Affymetrix Files dialog.  
Comment: All the files in the list will be imported into Spotfire DecisionSite. If there is a file in the list that you do not wish to use, you must select it and click **Remove**.
5. Click **Columns...** to specify the columns you want to import.  
Response: The Data Import Options dialog is displayed.
6. Click **OK** to close the Data Import Options dialog.
7. Click **OK** to close the Import Affymetrix Files dialog.  
Response: The data from the selected files are merged and imported into Spotfire DecisionSite as a new data set.

### 3.8.2 Affymetrix Data Files

The Import Affymetrix Files tool allows you to open text (TXT) files that have been exported from the Metrics tab of Affymetrix Microarray Suite or from GeneChip. It also allows the import of chip (CHP) files. These files do not always contain the same columns. If more than one file is selected, the files are merged into a single data set. The retrieved data will also be pivoted into the Short/Wide data format that is required by the analysis tools of Spotfire DecisionSite for Functional Genomics.

A CHP file can be of different result types, Expression Probe Set Results and Genotype Probe Set Results. A CHP file of Expression type contains the following columns (although there may be no values for some of the columns):

- Detection
- Detection p-value
- Signal
- Stat Pairs
- Stat Used Pairs
- Change p-value
- Signal Log Ratio
- Signal Log Ratio Low
- Signal Log Ratio High
- Stat Common Pairs
- Change

A CHP file of Genotype type contains the following columns (although there may be no values for some of the columns):

- Allele Call String
- Confidence
- RAS1
- RAS2
- P-value AA
- P-value AB
- P-value BB
- P-value NoCall

A CHP of Expression type may or may not contain comparison results. Comparison results, if they exist, are found in the columns:

- Change p-value
- Signal Log Ratio
- Signal Log Ratio Low
- Signal Log Ratio High
- Stat Common Pairs
- Change

An Exon CHP file may contain the following columns:

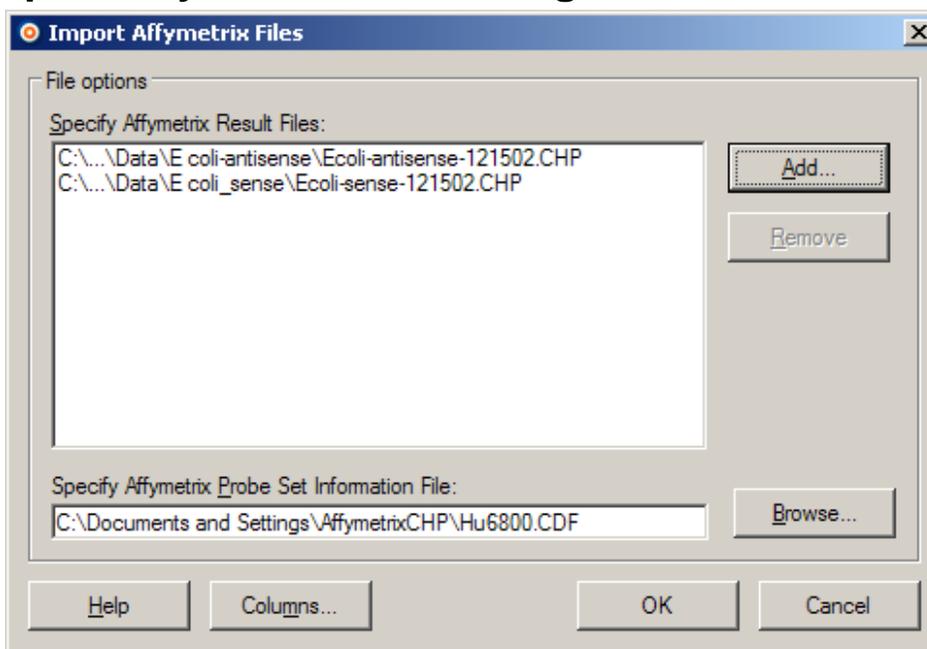
- Exon ID
- Exon Quantification
- Exon P-value

There are two columns that are always included when importing Affymetrix files: Analysis Name and Probe Set Name. The Analysis Name is the name of the Affymetrix file. The file name that the data comes from is instead displayed in a column "FileName for [file name]" that is always displayed (both for CHP and TXT files). The column Probe Set Name is read from the TXT file when importing text files. When importing CHP files, the Probe Set Name column is read from the CDF or PSI file (This is not the case with Exon CHP files, where no such file is used).

When importing CHP files an annotation will be added to each of the columns except for columns Probe Set Name and FileName. The annotation contains the following information: Chip type, Algorithm name and Algorithm version.

For more information on Affymetrix file formats, please visit the Affymetrix website: <http://www.affymetrix.com/support/developer/>.

### 3.8.3 Import Affymetrix Files Dialog



Option	Description
<b>Specify Affymetrix Result Files</b>	Lists the Affymetrix files that will be imported into Spotfire DecisionSite. Add more files by clicking <b>Add</b> . If there is a file in the list that you do not wish to use, you must select it and click <b>Remove</b> .
<b>Add</b>	Opens a dialog where you can select additional Affymetrix files to add to the list.
<b>Remove</b>	Removes a selected file from the list.
<b>Specify Affymetrix Probe Set Information File:</b>	Lists the Chip Description File (CDF) or Probe Set Information file (PSI) to include if CHP files were added.
<b>Columns...</b>	Opens the Data Import Options dialog, where you can select the columns that you want to import from the files.

► **To reach the Import Affymetrix Files dialog:**

Select **Import > Affymetrix Data from Files...**

## 3.9 Import GenePix Data

### 3.9.1 Importing GenePix Files

The Import GenePix Files tool allows you to open GenePix Array List files. If more than one file is selected, the files are merged into a single data set. The retrieved data will also be pivoted into the Short/Wide data format that is required by the analysis tools of Spotfire DecisionSite for Functional Genomics.

► **To import GenePix data files:**

1. Select **Import > GenePix Data...**

Response: The Import GenePix Files dialog is opened.

2. If this is your first time using the tool, or if you want to add additional files to the available files list, click on the **Add** button. If you already have retrieved the interesting files to the tool, go to step 5.

Response: Opens a dialog where you can select the GenePix files that you want to have access to from within Spotfire DecisionSite.

Comment: Added files will remain in the list from session to session, unless you remove them using the Remove or Clear buttons.

3. Browse and select the interesting GenePix file(s). It is possible to select several files in the same folder at once by pressing **Ctrl** and clicking on the desired files.
4. Click **Open**.

Response: The file(s) are added to the list in the Import GenePix Files dialog.

5. Select the file or files that you want to import into Spotfire DecisionSite by clicking on them in the list.

6. Click **Columns...** to specify the columns you want to import.

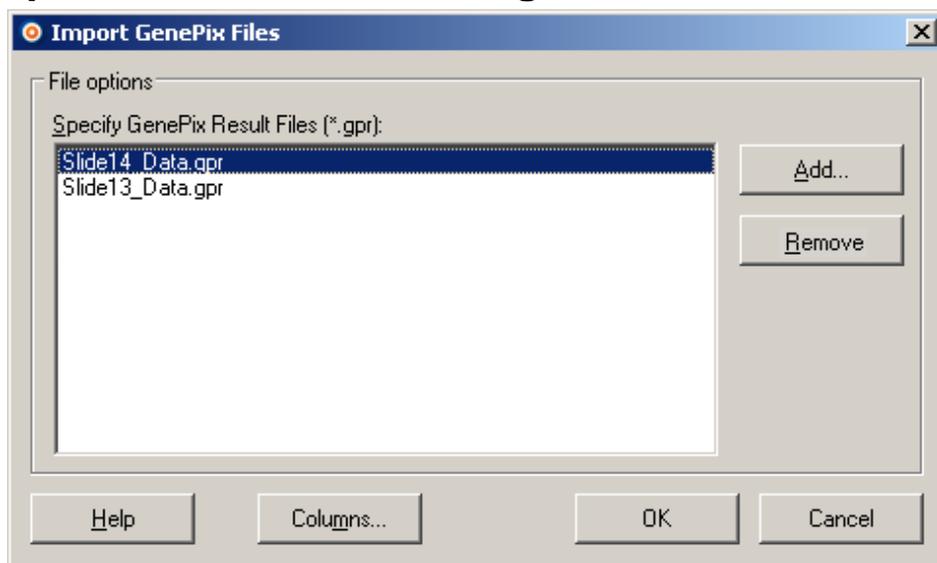
Response: The Data Import Options dialog is displayed.

Comment: The columns are sorted into Absolute Results (which displays columns that can be found on all chips) and Comparison Results (which are found on baseline chips). To import all available columns, click **Select All**.

7. Click **OK** to close the Data Import Options dialog.
8. Click **OK** to close the Import GenePix Files dialog.

Response: The data from the selected file(s) are merged and imported into Spotfire DecisionSite as a new data set.

## 3.9.2 Import GenePix Files Dialog



Option	Description
<b>Specify GenePix Result Files (*.gpr)</b>	Lists the available GenePix files. Add more files by clicking <b>Add</b> .
<b>Add</b>	Opens a dialog where you can select additional GenePix files to add to the list.
<b>Remove</b>	Removes a selected file from the list.

<b>Clear</b>	Clears the entire list.
<b>Columns...</b>	Opens the Data Import Options dialog, where you can select the columns that you want to import from the files.

► **To reach the Import GenePix Files dialog:**

Select **Import > GenePix Data...**

## 3.10 Import SAS Data

### 3.10.1 Importing SAS Data Files

In order to open SAS data files in Spotfire DecisionSite, you will need the SAS OLEDB driver. More information on how to get this can be found at <http://www.spotfire.com/sr>.

► **To import SAS data files:**

1. **File > Import > Import Data...**
2. In the **Select Data Source** dialog, select **File**.
3. In the **Open** dialog, select the file containing the SAS data. Click **Open**.  
Response: The SAS Data Import - Column Selection dialog is opened.
4. In the **Available SAS columns** list, click to select the columns that you want to import.

Comment: For multiple selection, press **Ctrl** and click on the desired columns in the Available SAS columns list. You can sort the columns in the list alphabetically by clicking on the Column name bar.

Click on the **Add >>** button to send the selected columns to the **Imported columns** field.

Select whether you want to map your data to Spotfire compatible types.

Comment: See SAS Column Formatting for more information on this.

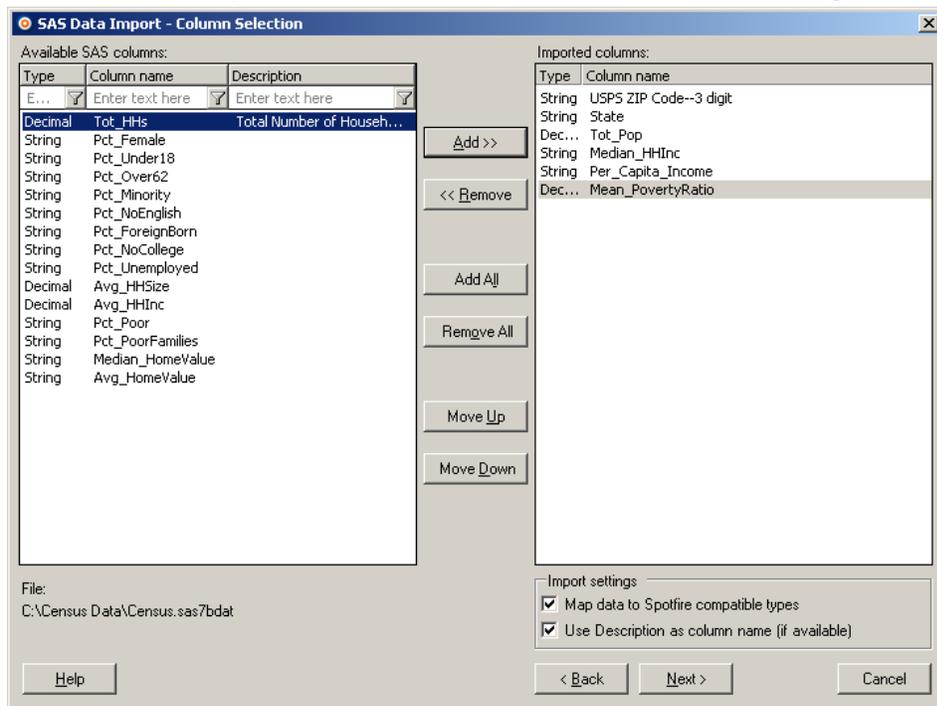
Select whether you want the description to be the column name once imported into Spotfire DecisionSite.

Click **Next >**.

Response: The Import Data - Data Conditioning dialog is opened.

5. Select a conditioning method if desired and click **Finish**.  
Response: The data from the selected SAS file is imported into Spotfire DecisionSite as a new data set.

## 3.10.2 SAS Data Import - Column Selection Dialog



Option	Description
<b>Available SAS columns:</b>	The columns in the SAS file available to be imported into Spotfire DecisionSite. Click a column name in the list to select it. To select more than one column, press <b>Ctrl</b> and click the column names in the list. Then click <b>Add &gt;&gt;</b> to send the selected column to the Imported Columns field.
Enter text here 	If you have a data set with many columns, you can right-click on the header of the columns in the Available columns list box and select <b>Show Search Field</b> from the pop-up menu. This will display a search field where you can type a search string and limit the number of items in the list. It is possible to use the wildcard characters * and ? in the search.
<b>Add &gt;&gt;</b>	Moves selected columns from the Available SAS columns field to the Imported columns field.
<b>&lt;&lt; Remove</b>	Removes a column and brings it back to the Available SAS columns field.
<b>Add All</b>	Adds all columns from the Available SAS columns field to the Imported columns field.
<b>Remove All</b>	Removes all columns from the Imported columns field and brings them back to the Available SAS columns field.
<b>Move Up</b>	Moves the selected column up in the list.
<b>Move Down</b>	Moves the selected column down in the list.
<b>File:</b>	The pathname of the SAS data file.

<b>Map data to Spotfire compatible types</b>	Allows you to map the data types to Spotfire compatible ones. If this check box is cleared, the SAS formatting will be unchanged.
<b>Use Description as column name (if available)</b>	Allows you to specify whether to use the SAS description as the column name once imported into DecisionSite. If this check box is cleared, the current column name will be unchanged after import.

► **To reach the SAS Data Import - Columns Selection dialog:**

1. Select **File > Import > Import Data...**
2. In the **Select Data Source** dialog, select **File**.
3. In the **Open** dialog, select the SAS data file. Click **Open**.

### 3.10.3 SAS Column Formatting

Spotfire DecisionSite allows you to import SAS Data files of the format **.sas7bdat** and **.sd2** into DecisionSite. It is also possible to open **.sd7** files if they are first renamed to have a **.sas7bdat** extension. Other file formats are not supported at this time.

If the "Map data to Spotfire compatible types" check box is selected in the SAS Data Import - Column Selection dialog, or if a SAS file is opened without the data import dialog; Spotfire DecisionSite attempts to reproduce the data type that SAS would for the same data. If it is not selected, raw data will be read from the SAS data file and columns will be of the type string or decimal.

The table below shows how the SAS formats are used to map the data to Spotfire DecisionSite specific data types:

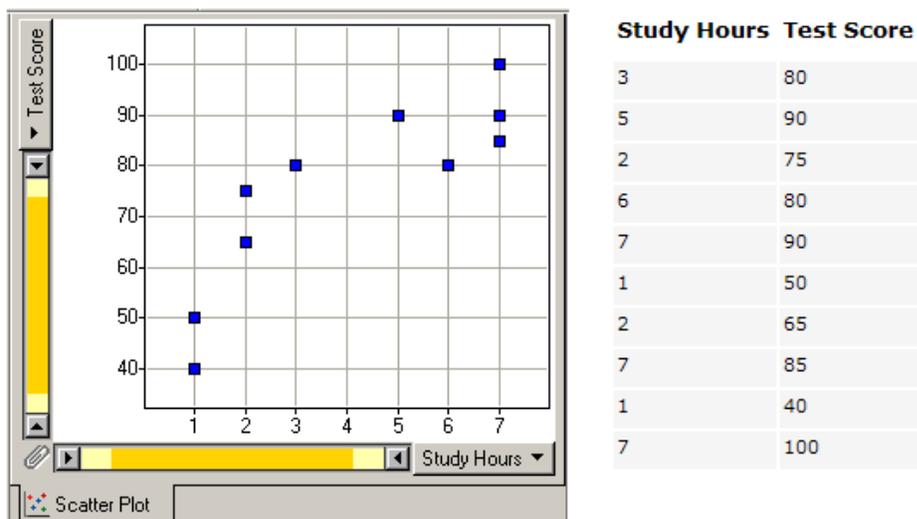
<b>SAS Format</b>	<b>Spotfire Type</b>
date	Date
dateampm	DateTime
datetime	DateTime
day	Integer
ddmmyy	Date
downame	String
dtdate	DateTime
dtmonyy	DateTime
dyyear	Integer
dyyyqc	DateTime
hour	Integer
julian	String
mmddy	Date
mmyy	Date
monname	String

month	Integer
monyy	Date
octal	String
qtr	Integer
qtrr	String
timeampm	String
tod	Time
weekdate	Date
weekdatx	Date
weekday	Integer
worddate	Date
worddatx	Date
xyymmdd	Date
year	Integer
yymm	Date
yymmdd	Date
yymmn	Date
yymon	Date
yyq	String
yyqr	String

## 4 Visualizations

### 4.1 Scatter Plots

Scatter plots are similar to line graphs in that they use horizontal and vertical axes to plot data points. However, they have a very specific purpose. Scatter plots show how much one variable is affected by another. Each record (or row) in the data set is represented by a marker whose position depends on its values corresponding to the X and Y axes.



The above picture demonstrates how scatter plots can be used. Say, for example, that you want to show whether studying longer hours helps you improve your test grades.

The scatter plot shows that according to this set of data, the longer you study, the better grade you will get on your test.

A third variable can be set to correspond to the color or size of the markers, thus adding yet another dimension to the plot.

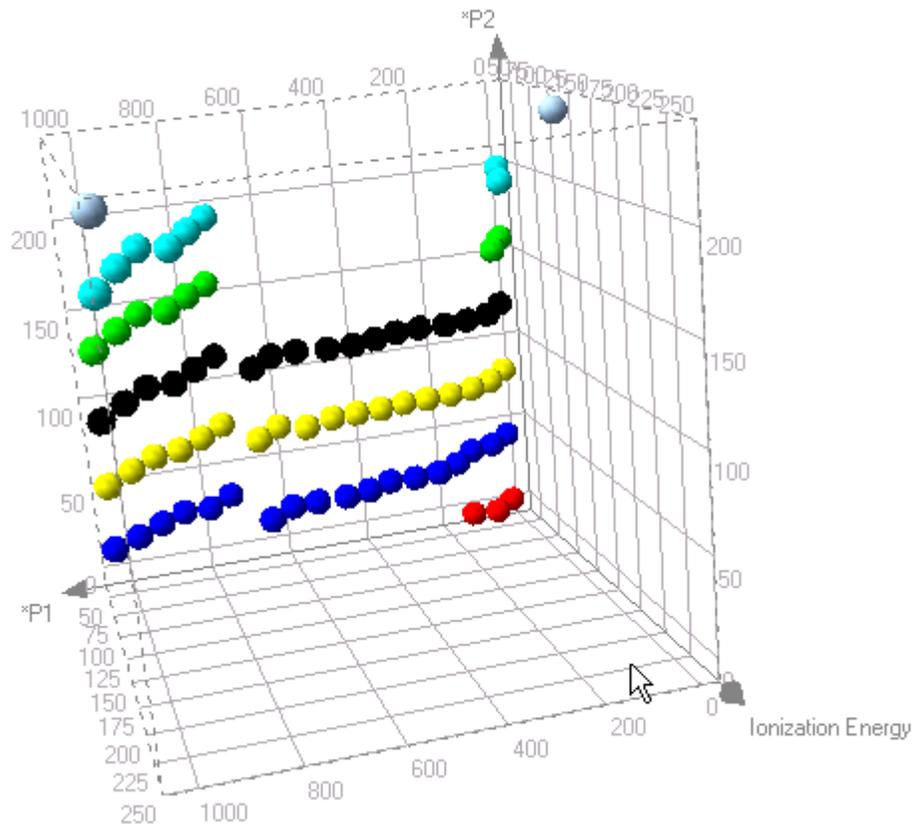
Two-dimensional scatter plots are the default visualization of many data sets.

#### ► Make a new 2D scatter plot in one of the following ways:

- Press **Ctrl+1** on the keyboard.
- Click the **New Scatter Plot** button on the toolbar, .
- Select **New Scatter Plot** from the **Visualization** menu.

By right-clicking in a visualization a pop-up menu appears. This context menu lets you access many features in a fast and easy way.

A 3D scatter plot is used to show the relationship between three variables. It shows the data set in three dimensions, using three columns as axes. Each record (or row) in the data set is represented by a marker whose position depends on its values corresponding to the X, Y and Z-axis. A fourth variable can be set to correspond to the color or size of the markers, thus adding yet another dimension to the plot.



3D scatter plots allow a lot of information to be encoded into visualizations. They are especially useful when analyzing data that is not clustered along any of the axes (columns) of the data set.

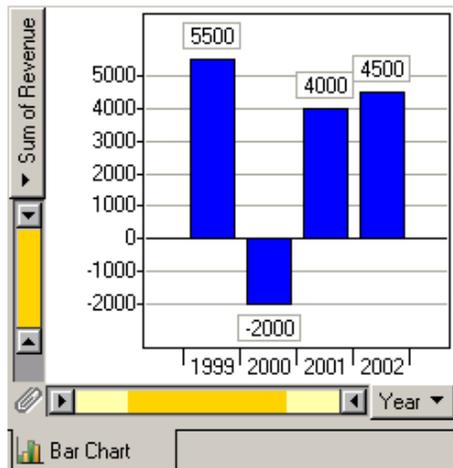
► **Make a new 3D scatter plot in one of the following ways:**

- Press **Ctrl+2** on the keyboard.
- Click the **New 3D Scatter Plot** button on the toolbar, .
- Select **New 3D Scatter Plot** from the **Visualization** menu.

3D visualizations have the Z-axis selector and zoom bar along the top edge of the visualization. The Z-axis initially points towards the viewer, out from the screen.

## 4.2 Bar Charts

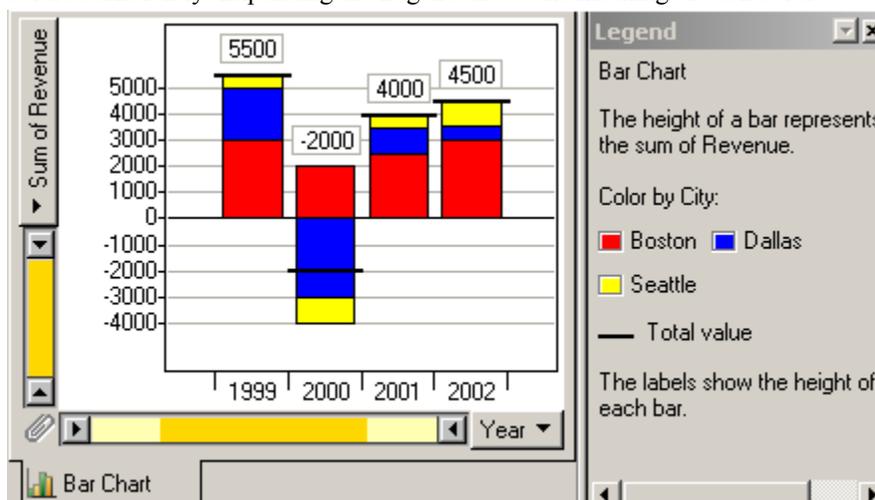
A Bar Chart is a way of summarizing a set of categorical data. It displays the data using a number of bars of the same width, each of which represents a particular category. The length of each bar is proportional to the count, sum or the average of the values in the category it represents, such as age group or geographical location. In DecisionSite it is also possible to color or split each bar into another categorical column in the data, which enables you to see the contribution from different categories to each bar in the bar chart.



Year	City	Revenue
1999	Boston	3000
1999	Dallas	2000
1999	Seattle	500
2000	Boston	2000
2000	Dallas	-3000
2000	Seattle	-1000
2001	Boston	2500
2001	Dallas	1000
2001	Seattle	500
2002	Boston	3000
2002	Dallas	500
2002	Seattle	1000

The above picture demonstrates how bar charts can be used. Say, for example, that you want to show the total yearly revenue of a company with offices in three different cities. The bar chart sums the revenue for the three cities and displays them per year.

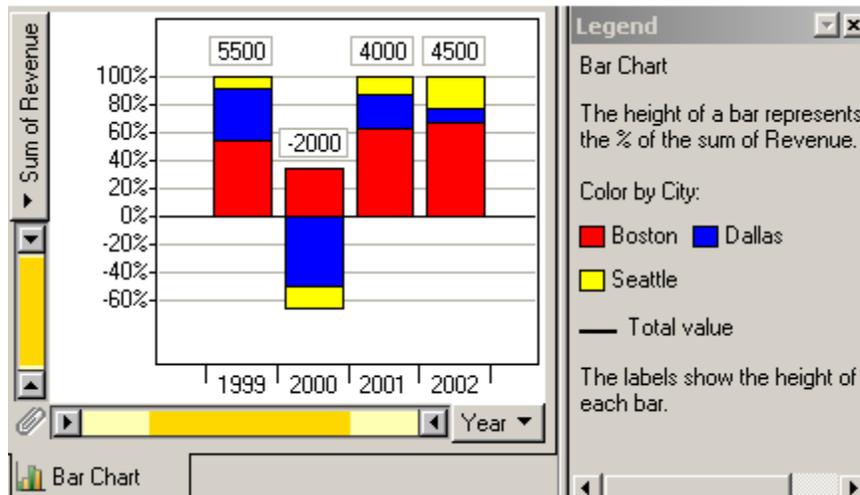
Bar charts can also be categorically colored, which means that the partial sums of the bars are colored differently. Expanding the Legend shows the meaning of each color.



When categorical coloring is applied, you have the option to display the categories in four different ways:

- Stacked bars
- Side-by-side bars
- 100% stacked bars
- 100% side-by-side bars

If you want to compare the proportions of different categories for, e.g., different time periods, you can use either of the 100% layout options in the Properties dialog. With 100% stacked bars, all bars will be of equal height (100%), unless some negative values exist in the data.



In the example above, one can see that the Seattle revenue (yellow) has affected the total revenue more during 2002 than in previous years, whereas the Dallas revenue (blue) has decreased in importance. See Bar chart layout details for more information.

If the categories are split to several columns, categorical coloring can also be shown via differently colored bars in multiple columns (see below).

#### ► Make a new bar chart in one of the following ways:

- Press **Ctrl+4** on the keyboard.
- Click the **New Bar Chart** button on the toolbar, .
- Select **New Bar Chart** from the **Visualization** menu.

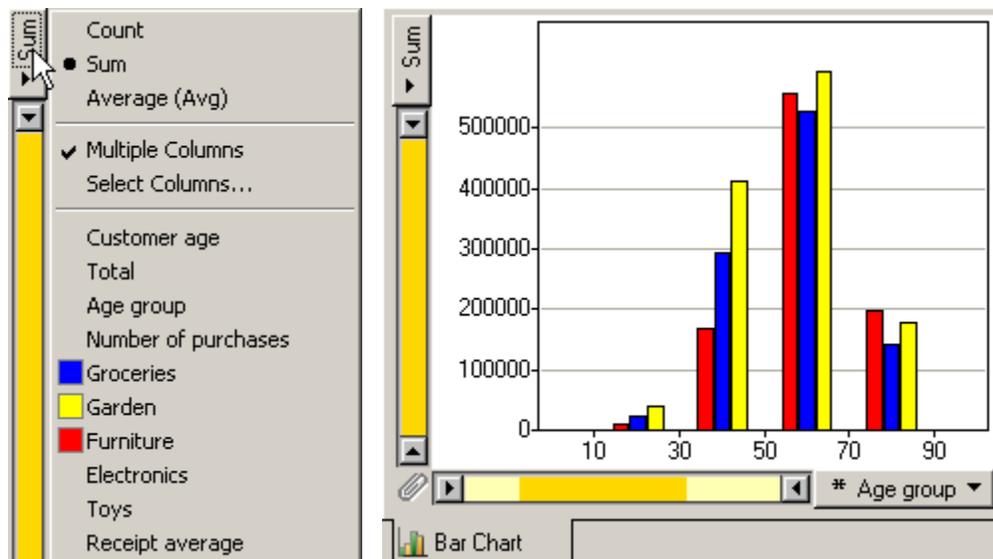
#### Count / Sum / Average

The height of the bars can be set to represent three different aggregation methods: Count, Sum or Average. You select this by clicking on the Axis Selector for the Y-axis.

- **Count** – the height of a bar represents the number of records with a particular value.
- **Sum** – the height of the bar indicates the total sum of the values of all records in that bar.
- **Average** – the height of the bar indicates the average value of all records in that bar.

#### Multiple Columns

You can display multiple columns as side-by-side bars. This is useful if you want to compare many parameters at the same time, and the categorical data exist in different columns. (When the categorical data is included in a single column, you should instead use one of the side-by-side options in the Layout section of the Bars tab, see Categorical Coloring Layout below.)



### ► To Display Multiple Columns:

1. Click on the Axis Selector for the Y-axis.
2. Select **Multiple Columns**.  
Response: The Multiple Columns option will be selected with a check mark the next time you open the list.
3. Click on the Axis Selector for the Y-axis.
4. Select an additional column to display. Selected columns will be indicated by a colored square.

**Note:** You can also click on the **Select Columns...** option, which will display the **Bar Chart Columns tab** of the **Properties** dialog. From this dialog you can easily add or remove several columns to the bar chart.

### Sorting using Right-Click

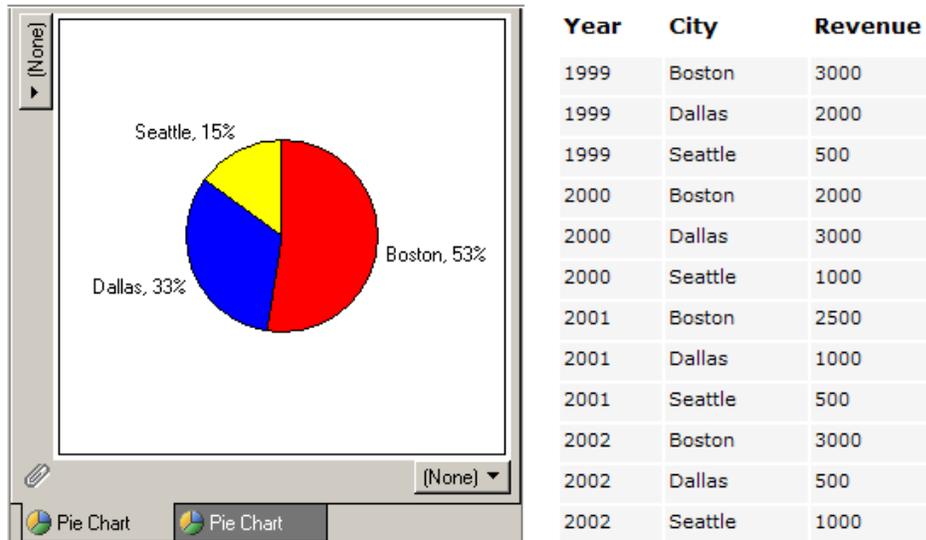
By right-clicking in a visualization a pop-up menu appears. This context menu lets you access many features in a fast and easy way. If you are not using Multiple Columns you can sort the bars in ascending or descending order; selecting the Reverse sort order will arrange your bars in the reverse order of the current sort order. This is an instantaneous sorting of the bars; if you filter the data with the query devices so the height of the bars change, their horizontal order will not change until you choose to sort them again.

**Note:** Ascending and descending sorting is available when you are viewing single columns with fixed coloring or categorical coloring in stacked bar layout. You cannot use sorting when you are using multiple columns or either of the categorical coloring 100% bars layout options.

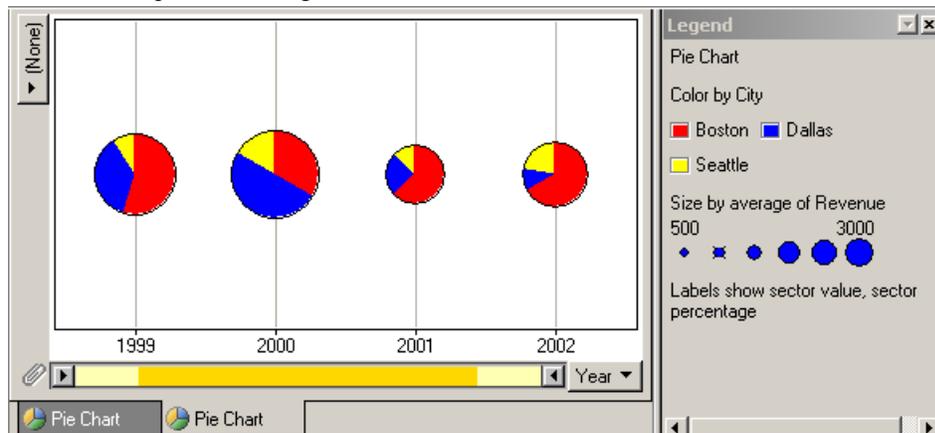
**Tip:** If you want to sort multiple column bar charts, first apply the sorting you want to a bar chart with only the sorting column on the Y-axis. Then, select Multiple Columns and add more columns to your visualization.

## 4.3 Pie Charts

Pie charts are circle graphs divided into pieces, each piece displaying the size of some related piece of information. Pie charts are used to show percentages of a whole.



A pie chart visualization can consist of one or more pies. Multiple pies are used to split the data by different categories in a column. This is accomplished by setting the X-axis and/or Y-axis selectors to represent a categorical column in the data set.



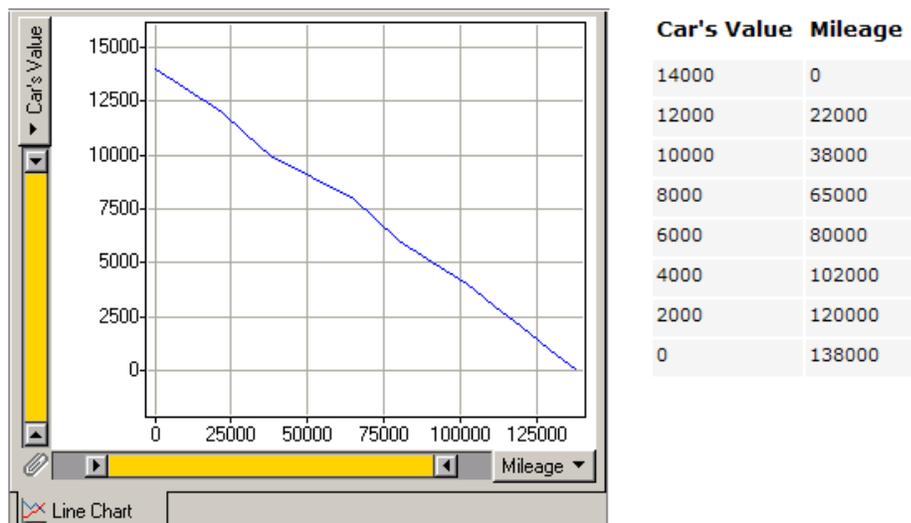
► **Make a new pie chart in one of the following ways:**

- Press **Ctrl+5** on the keyboard.
- Click the **New Pie Chart** button on the toolbar, .
- Select **New Pie Chart** from the **Visualization** menu.

By right-clicking in a visualization a pop-up menu appears. This context menu lets you access many features in a fast and easy way.

## 4.4 Line Charts

A line chart is a way to summarize how two pieces of information are related and how they vary depending on one another. Line charts are useful for visualizing data that behaves like a function with respect to the variable on the X-axis, such as time series data. This visualization type is ideal for showing trends or changes in data over a period of time, at even intervals. Line charts emphasize time flow and rate of change rather than the amount of change.



The above picture demonstrates how line charts can be used. Say, for example, that you want to show how fast a car devaluates the more mileage it gets. The line chart shows that according to this set of data, the longer a car is driven, the more its value decreases.

► **Make a new line chart in one of the following ways:**

- Press **Ctrl+6** on the keyboard.
- Click the **New Line Chart** button on the toolbar, .
- Select **New Line Chart** from the **Visualization** menu.

By right-clicking in a visualization a pop-up menu appears. This context menu lets you access many features in a fast and easy way.

## 4.5 Profile Charts

A profile chart maps each record as a line, or profile. Each attribute of a record is represented by a point on the line. This makes profile charts similar in appearance to line charts, but the way data is translated into a plot is substantially different.

Consider, for example, a data set with three different applicants for a job position. Through tests or interviews, the recruiter may have provided percentage estimates of each candidate in terms of experience, social competence, and creativity. The data may look as follows:

Applicant	Experience	Grades	Creativity
Lisa	85	95	60
Joe	70	75	95
Anne	100	80	80

For each applicant, it is now possible to plot a personality profile. This will give a good (if somewhat simplified) overview of characteristics, and a possibility to visually match an applicant against a "model profile" for the job. The profile chart would look as follows:



► **To create a profile chart:**

1. Press [Ctrl+7], or click the **New Profile Chart** button on the toolbar, or select **Visualization > New Profile Chart**.
2. Go to the axis selector of the X-axis and uncheck columns that you do not want to include in the chart, such as identifier columns.
3. Use the **Properties** dialog to adjust the various properties of the chart.

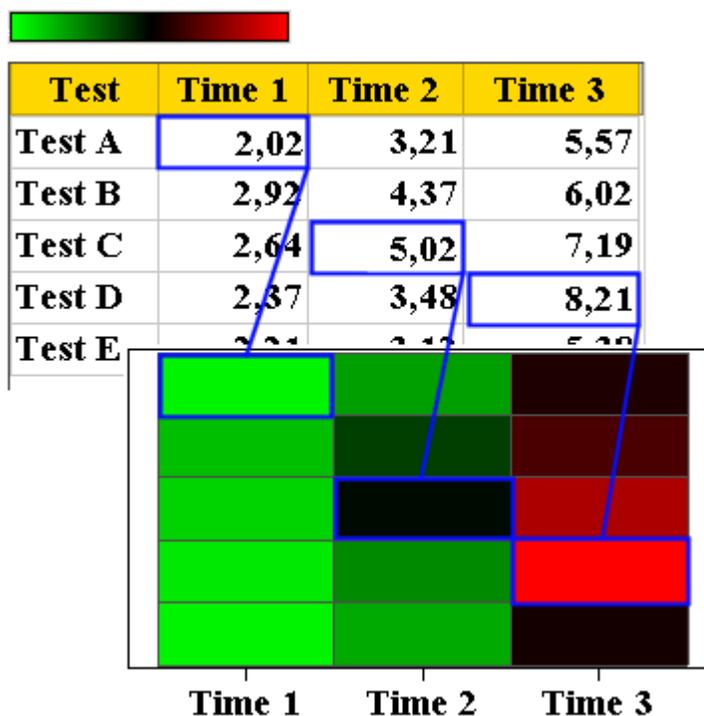
By right-clicking in a visualization a pop-up menu appears. This context menu lets you access many features in a fast and easy way.

## 4.6 Heat Maps

Heat Map plots are also known as Intensity plots or Matrix plots. A Heat Map can be likened to a spreadsheet, where the values in the cells are instead represented by colors.

Heat Maps can be used to identify clusters of records with similar values, as these are displayed as "areas" of similar color.

The easiest way to understand a heat map is to think of a table or spreadsheet which contains colors instead of numbers. The default color gradient sets the lowest value in the heat map to bright green, the highest value to a bright red, and mid-range values to black, with a corresponding transition (or gradient) between these extremes.



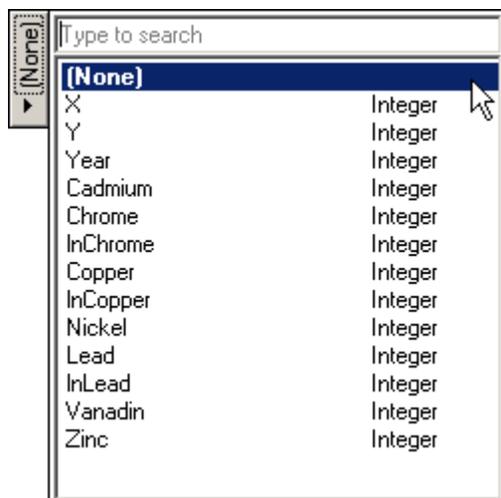
### ► To create a Heat Map:

1. Press [Ctrl+8], or click the **New Heat Map** button on the toolbar, or select **Visualization > New Heat Map**.
2. Go to the axis selector of the Y-axis and select the columns you wish to order the rows by.
3. Use the **Properties** dialog to adjust the various properties of the chart.

### Order of rows

By default, the order of the rows in the heat map is set to **None**, meaning that they are in the same order as they were before the data set was imported. However, you may want to sort the rows differently, such as if a certain column was pre-generated to contain a relevant sorting order. The order of the rows is shown numerically in the X-axis selector of the Heat Map.

Click on the vertical axis selector to select which column (or None) to order the rows by.

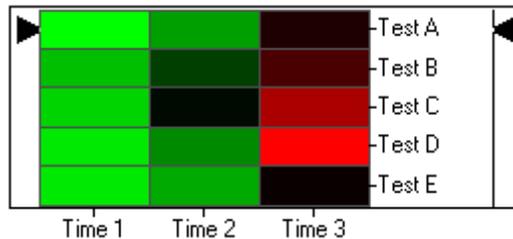


## Activating and Marking Records

Making a record active or marking several records in a heat map plot differs somewhat from other plots. In a heat map, one row always equals one record. Consequently you always select or mark one or more entire rows, which equals one or many records.

### Making a record Active

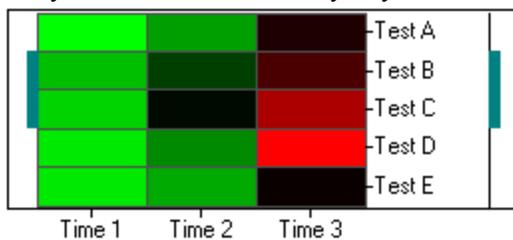
When you click on a row, a black triangle appears at both ends of the selected row to indicate that it is active. Information about the row is displayed in the Details-on-Demand window.



### Marking Records

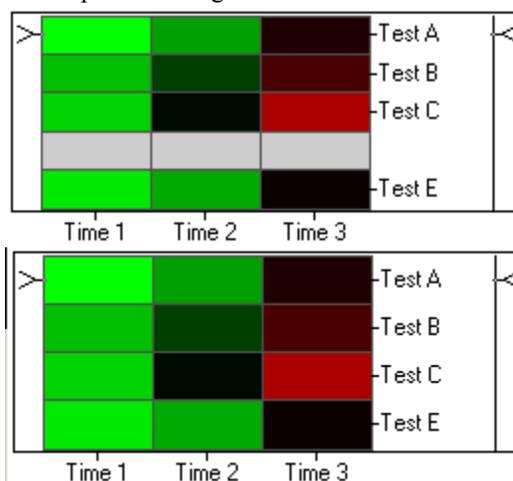
By clicking and holding the mouse button while the mouse pointer is on a row and dragging it to cover several rows, these rows all become marked. This is indicated by a small bar shown at the left and right of the rows in question. Details on these records are shown in the Details-on-Demand window.

By right-clicking in a visualization a pop-up menu appears. This context menu lets you access many features in a fast and easy way.



### Show/hide deselected records

Records that have been deselected by using the query devices become gray (default color) in the heat map. To hide these records, clear the **Show deselected** check box in the Heat Map tab of the Properties dialog.



**Note:** If you have had a dendrogram associated to the heat map, this will no longer be valid after hiding the deselected values. In this case, the dendrogram tree will be removed. You can show the dendrogram again by selecting the Show deselected check box.

## Row Labels

It is possible to show row labels either to the left or to the right of the heat map. This setting, plus the selection of the column to display as row labels, are set on the Heat Map tab of the Properties dialog.

When row labels have been displayed, it is possible to adjust the space available for the labels by dragging the line between the heat map and the row labels with the mouse pointer. If the height of the rows is so small that it is impossible to see row labels, row labels will not be shown on every row. Instead, the number of row labels that fit into the heat map will be displayed at an equal distance from each, for example only on every fifth row. If rows have been deselected, no row labels will be shown for these rows.

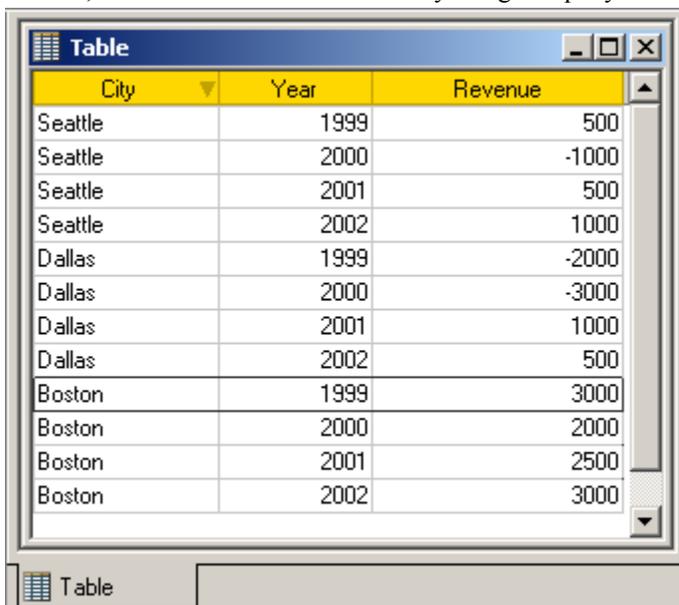
Row labels that are too long to be displayed correctly will be truncated and end with an ellipsis (...). In this case, hovering over the row label with the mouse pointer will display a ToolTip of the entire row label text.

## 4.7 Tables

The Table visualization presents the data as a table of rows and columns. The Table can handle the same number of rows and columns as any other visualization in DecisionSite.

In the Table, a row represents a record. By clicking on a row, you make that record active, and by holding down the mouse button and dragging the pointer over several rows, you can mark them.

You can sort the rows in the table according to different columns by clicking on the column headers, or filter out unwanted records by using the query devices.



City	Year	Revenue
Seattle	1999	500
Seattle	2000	-1000
Seattle	2001	500
Seattle	2002	1000
Dallas	1999	-2000
Dallas	2000	-3000
Dallas	2001	1000
Dallas	2002	500
Boston	1999	3000
Boston	2000	2000
Boston	2001	2500
Boston	2002	3000

### ► To create a Table:

1. Press **[Ctrl+9]**, or click the **New Table** button on the toolbar, or select **Visualization > New Table**.
2. Click on the header of the column you wish to sort the rows by, or rearrange the order of the columns by dragging and dropping the column headers horizontally.
3. Use the **Properties** dialog to further adjust the various properties of the chart.

By right-clicking in a visualization a pop-up menu appears. This context menu lets you access many features in a fast and easy way.

You can sort the vertical order of the rows in the table. This can be done in several steps, for example: first sort according to the values in column 1, then by the values in column 5, then by the values in column 3, etc.

► **To sort the data:**

1. Click on the header of the first column you wish to sort the data by.
2. Press Shift and click on another column header to make a subsequent sort according to the values in that column.
3. Repeat step 2 on other columns as many times as you like.

A small digit will appear in the column headers indicating the sorting order.

**Note:** Click an additional time on a column header to toggle between Ascending and Descending row order.

**Note:** For more information on how strings are sorted in a Table see the topic String.

► **To change the column order:**

1. Click on a column header and hold the mouse button down.
2. You can now drag and drop that column horizontally. Move the header to the position you want it to be placed.
3. Release the mouse button when you wish to insert the column.

**Note:** You can move a column to the first or last position by right-clicking in the column header and selecting **Move First** or **Move Last** from the menu that appears.

► **To resize the column width:**

Place the mouse pointer to the right of the column header you want to resize (just between it and the next column header). The cursor changes into a cross with arrows.

By double-clicking, the column width will automatically expand so that all the items in the column can be displayed without being truncated.

If you want to rescale the column width by hand, you can instead hold down the mouse button and move the mouse horizontally, which will adjust the width. Release the mouse button when you are satisfied.

**Note:** You can also set the width of a column by right-clicking in the column heading, and selecting **Column Width** from the menu that appears. Enter the width in number of characters and press **OK**.

In a table with many columns you often need to scroll horizontally. However, sometimes you may want certain columns to always be displayed regardless of scrolling. This is achieved by freezing one or more columns.

► **To freeze columns when scrolling horizontally:**

1. Place the columns you want to freeze to the far left, using drag and drop.
2. Select **Edit > Properties** and choose the **Table** tab.
3. Select the number of **Frozen columns** from the drop-down list box.
4. Close the Properties dialog.
5. The leftmost column(s) you specified will be displayed at all times, when you are scrolling horizontally.

## **Activating and Marking Records**

Moving the mouse over a record will highlight it with a thin black rectangle.

To make a record Active simply click on it. The Active record is indicated by a thick black rectangle around it. You can use the arrow keys to move the active record indicator up or down, thus making another record active instead.

There are several ways to help you mark a set of records in the Table, as explained in the table below. Marked records are by default indicated by a dark green background.

The following instructions explain how to mark one or more records in the Table:

► **To mark one single record:**

**Mouse:**

Drag the mouse over the record while holding down the left mouse button. A dotted rectangle will indicate the drag operation.

**Keyboard + mouse:**

Click on the record you want to mark. Then click on it again, while holding down the Shift key.

**Keyboard:**

Press the Spacebar to mark the currently active record (only in table visualizations).

► **To mark a range of records:**

**Mouse:**

Drag the mouse over the records you want to mark. A dotted rectangle will indicate the drag operation.

**Keyboard + mouse:**

Click on the first record in the range. Hold down the Shift key and click on the last record in the range. The records in the range will be marked.

**Keyboard only:**

Move the active record to the first record in the range using the up and down arrow keys. Press the Spacebar to mark this record and to start a new "marking session". Hold down the Shift key while pressing the up/down arrow keys. The records will be marked one after another.

► **To mark multiple records:**

**Keyboard + mouse:**

Drag the mouse over the records in the first range. Hold down the Ctrl key and drag over another range. The records will be added to the set of marked records.

Alternative: Hold down the Ctrl key while clicking on individual records. This will include the clicked records in the set of marked records.

**Keyboard only:**

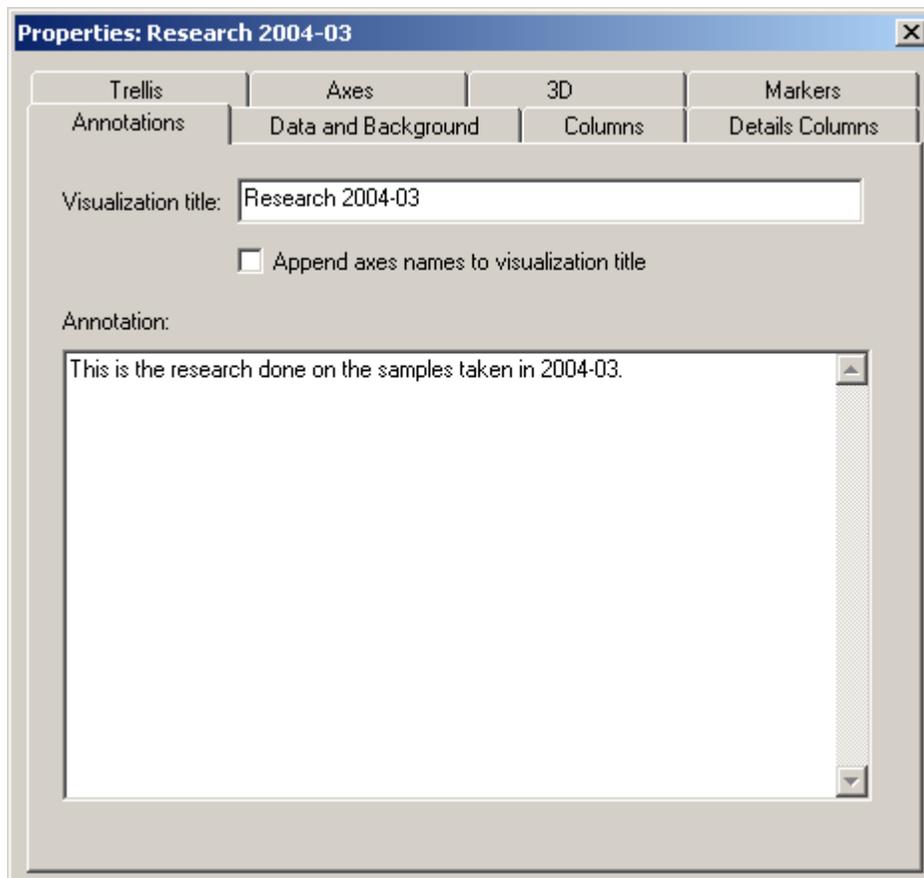
Mark a range of records as described above. Continue to move the active record with the arrow keys. Hold down the Ctrl key and press the Space key to add the currently active record to the set of marked records.

## 4.8 Properties Dialog

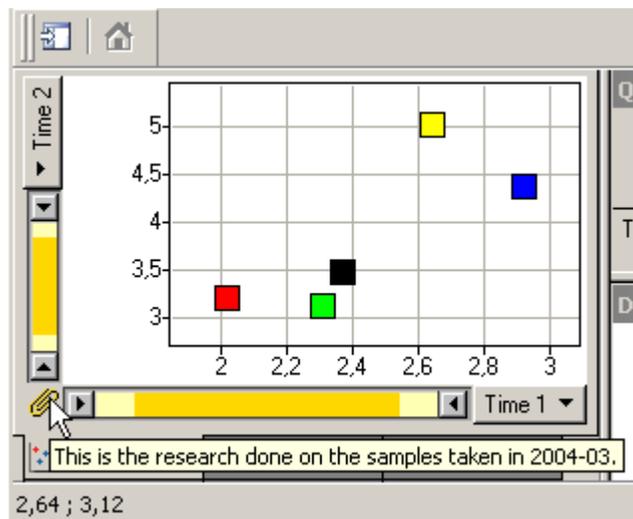
### 4.8.1 Annotations Tab

#### 4.8.1.1 Annotations Tab

Edit > Properties > Annotations tab



You can give any visualization a title and an annotation. The title will appear as the caption of the window. It can also appear in the heading of printouts. The annotation will appear as a ToolTip when you place the mouse pointer over the paper clip at the bottom-left corner of the visualization.



► **To set title and annotation:**

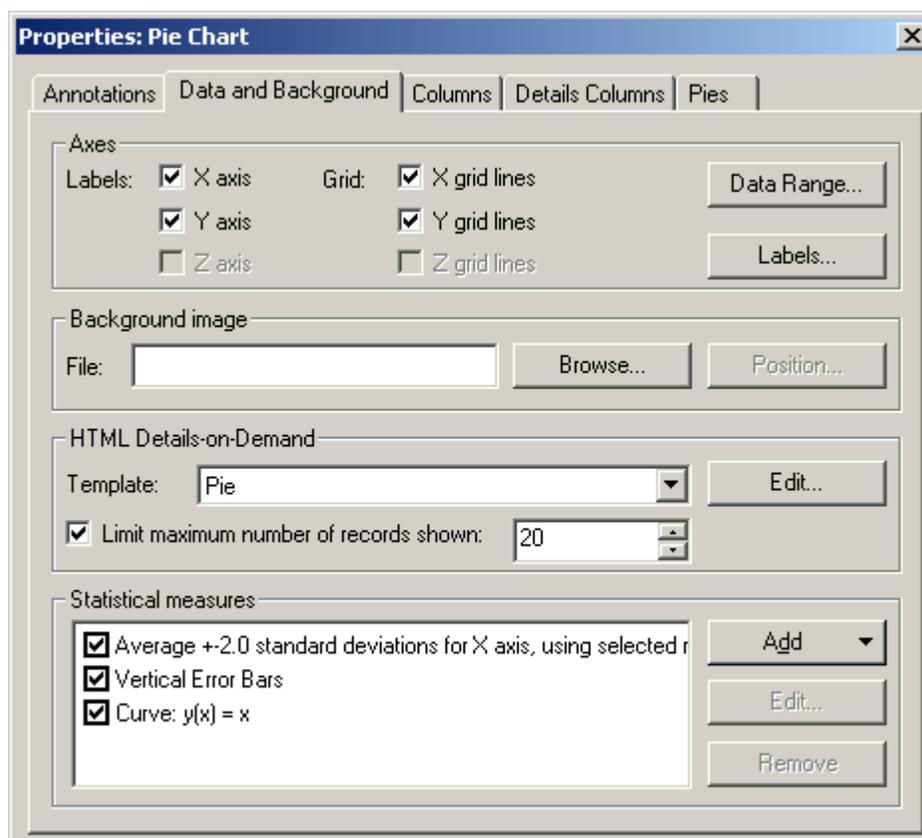
1. Go to the **Annotations** tab of the **Properties** dialog.
2. Type a title and/or an annotation.
3. Select the check box **Append axes names to visualization title** if you want the current axes to be appended to the title.

You can type in a lot of text in the **Annotation** field, as well as cut and paste to and from other Windows applications; this can only be done with text, however. This is a good place for adding information about the purpose and methods used in the visualization, features to look for and other helpful information concerning the data. The annotation can be printed together with the visualization, by selecting the Include annotation option available in the Print Layout Wizard on the **File** menu.

## 4.8.2 Data and Background Tab

### 4.8.2.1 Data and Background Tab

Edit > Properties > Data and Background tab



Option	Description
<b>Axes</b>	The Axes section allows you to control axis labels, data range and grid lines for bar charts, pie charts, line charts and heat maps. This section does not appear for scatter plots since these have a separate Tab for more advanced settings, see Axes for Scatter Plots.
<b>Background image</b>	Background image lets you select a file to use as background. You can also specify how the background image is positioned.
<b>HTML Details-on-Demand</b>	Details-on-Demand lets you choose templates for formatting the HTML display of record details.
<b>Statistical measures</b>	Statistical measures offers control over the standard deviation marking lines, error bars, and different types of curves and curve fits. Available for 2D scatter plots and pie charts only. In bar charts, you can select to add a vertical reference line from the

Add menu under Statistical measures.

## 4.8.2.2 Axes

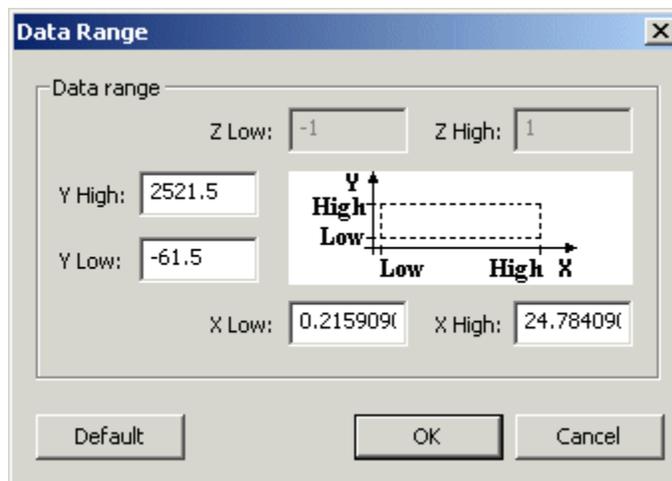
Edit > Properties > Data and Background tab

The Axes section of the Data and Background dialog appears in all plots except for Scatter Plots. Scatter Plots can handle more advanced axis labels and have a separate properties tab for this, see Axes tab for Scatter Plots. For all other plots please continue below.

The **Axes** section of the **Data and Background** tab lets you define attributes for labels, axes and grids. The check boxes allow you to control which labels and grid lines to display.

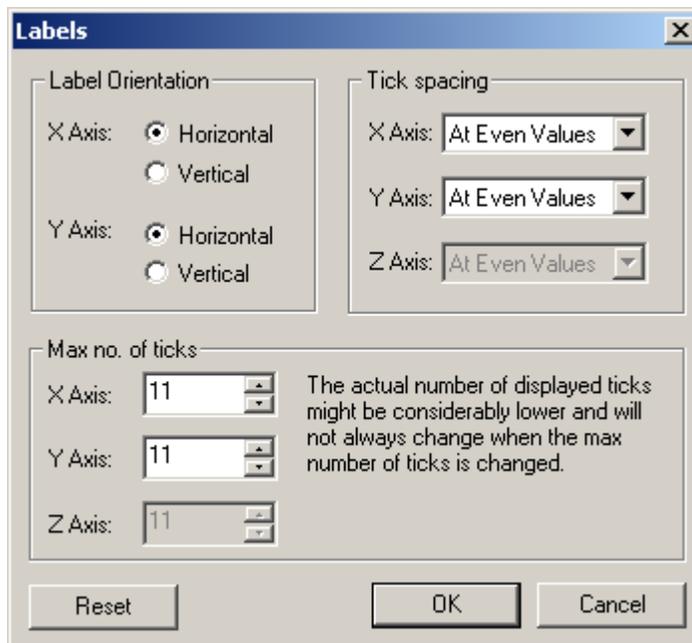
### Data Range

In the **Data Range** dialog, the minimum and maximum values of the axes can be set. This allows you to get more space around the data whose range is otherwise set to the range of the records of the data set.



### Labels

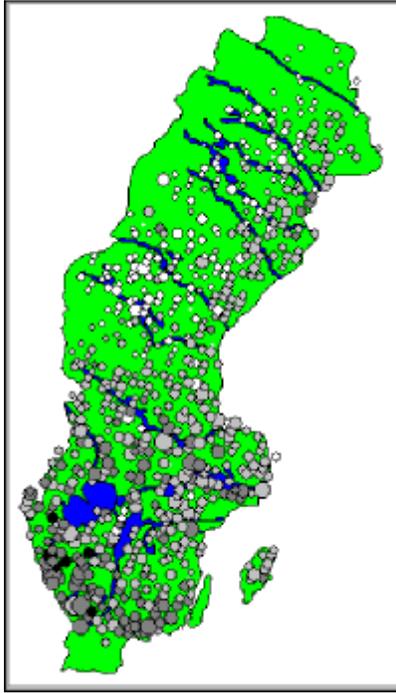
If you click the **Labels...** button you can set the label orientation, the label spacing and the maximum number of labels for each of the axes.



Option	Description
<b>Label Orientation</b>	Specifies whether the labels should be oriented horizontally or vertically on the X-axis and on the Y-axis.
<b>Tick spacing</b>	For spacing you can select to show axis ticks in four ways: <b>Even Distribution</b> will attempt to distribute ticks evenly between the highest and lowest value . <b>At Values</b> will not place a tick where there is no value. <b>At All Values</b> will place ticks at all values (within density constraint). <b>At Even Values</b> will attempt to place ticks at evenly spaced whole numbers.
<b>Max no. of ticks</b>	Specifies the maximum number of allowed ticks. However, the actual number of displayed ticks might be less than this number depending on which option you have selected under Tick spacing above.
<b>Reset</b>	Resets all settings in this dialog to its default value.

## 4.8.2.3 Background Images

### 4.8.2.3.1 Image Files and Background Maps



Background maps, images, and figures may be displayed along with visualization markers in a Spotfire DecisionSite visualization. Such images can ease the interpretation of the data by providing a context in which it can be interpreted. For example, some aspects of the environmental database described earlier can be examined more easily if data is seen together with a map of Sweden. Another example where an image provides context to the data is the metabolic pathway for yeast genes used in the microarray sample file included in the Spotfire DecisionSite distribution.

Background images can be added to 2D scatter plots, line charts, profile charts, bar charts and pie charts.

### Formats of background images and maps

Supported background image formats:

- Windows bitmap images (\*.bmp)
- JPEG images (\*.jpg, \*.jpeg)
- PNG bitmap images (\*.png)
- TGA files (\*.tga)
- PCX files (\*.pcx)

Supported background map formats:

- MapInfo Interchange Format files (\*.mif). These are typically tagged with for example with zip codes, which Spotfire DecisionSite can use to position visualization markers.
- Spotfire mapping files (\*.sfm)

### 4.8.2.3.2 Adding a Background Image

Edit > Properties > Data and Background tab

#### ► To add a background image to the current visualization:

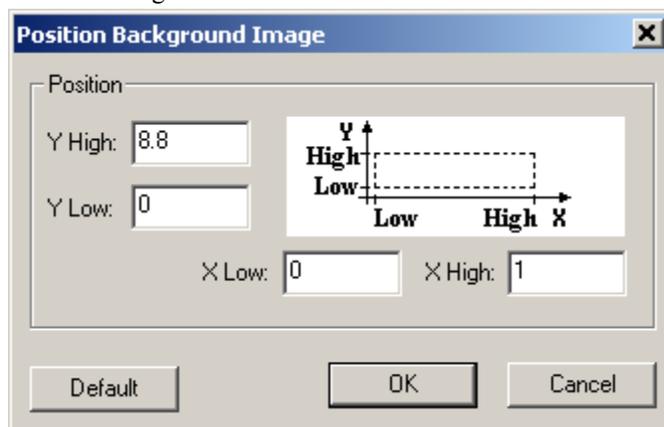
1. In the Properties dialog, open the **Data and Background** tab.
2. Enter the path and name of the image file to use in the file box.  
**Tip:** The **Browse...** button can be used to search the file system for appropriate files. You can also enter an URL to an image available on a server.
3. Click **Position...** in the **Background Image** section to adjust the positioning of the image relative to the markers.

**Tip:** If desired, adjust the **Data Range...** in the Axes section to increase the visible area of your visualization. This might be necessary if you want the picture area to be larger than the area covered by markers.

### 4.8.2.3.3 Position a Background Image

Edit > Properties > Data and Background tab > Position...

On the Data and Background tab of the Properties dialog, click the **Position...** button. The dialog that appears allows you to specify how the background image is positioned, by giving the coordinates for two opposing corners. These coordinates refer to the current X and Y-axes. This means that the corners are "pinned" to values in the data range. Zooming and panning will cause the image to stretch and scroll with the data.



Option	Description
<b>Y High</b>	Specifies the top position of the background image.
<b>Y Low</b>	Specifies the bottom position of the background image.
<b>X Low</b>	Specifies the left edge of the background image.
<b>X High</b>	Specifies the right edge of the background image.
<b>Default</b>	Reverts to the default coordinates.

### 4.8.2.3.4 Adding MapInfo Background Files

MapInfo is a leading geographic information system software package. MapInfo Interchange Format (MIF) is an ASCII format developed by Mapping Information Systems Corporation (<http://www.mapinfo.com/>) to facilitate the transfer of data from other geographical information system packages to MapInfo.

Spotfire DecisionSite can import MIF files to use as background maps. This allows you to position visualization markers in two dimensions based on a single column such as zip code, area code, or area name.

Suppose, for example, that you have a data file with information about various countries, such as name, population, language, etc. However, the data set includes no information about geographical coordinates. By using a MIF file as background, you get not only a background map, but also two new columns of data. Each record is given map coordinates depending on which country it represents.

► **To use a MIF file as background:**

1. Create a scatter plot visualization.
2. Activate the **Properties** dialog and select the **Data and Background** tab.
3. Click the **Browse...** button by the **Background Image** field and select **MapInfo Interchange Files**, then browse to the file you want as a background.
4. Click **Open**.  
The **Match Data and Background** dialog is displayed, where it is possible to match a database column with a tag in the MIF file.
5. In the left field, select the column in your data set that identifies geographical position, in this case **Country**.
6. In the right field, select the MapInfo tag in the MIF file that relates to the same information, in this case **Country**. (The names are not necessarily the same.)
7. In the two text fields, enter names for the new columns that will be added to your data set, specifying X and Y position.
8. Make sure **Use current axes** is cleared. If you select this option, then no new coordinates will be extracted from the MIF file. You will then only get a background image.
9. If you want to add *all* the information in the MIF file (i.e., not just the coordinates) to your data set, then select **Make new columns for background columns**.
10. Click **OK**.

Comment: Spotfire DecisionSite will try to match data and background. The background image is shown, and the axes changed to the new coordinate columns.

#### 4.8.2.3.5 Spotfire DecisionSite Mapping Files (SFM Files)

The Spotfire DecisionSite mapping file (\*.sfm) format first establishes a coordinate system, which relates the data set's coordinate system to that of the polygon set being defined. After that, a number of polygons are defined. A polygon is defined by a fill color, an origin point, a border color, the number of points and the X, Y, and Z coordinates of the points.

The Z coordinates are ignored, but they must be included. The format of the file as follows (with variables in italics):

```
COORDSYS xmin xmax ymin ymax zmin zmax
ADD
POLY fillcolor xorigin yorigin zorigin
!yes
numberofpoints
x1 y1 z1
x2 y2 z2
...
```

A sample file could look as follows:

```
COORDSYS 0.0 1.0 0.0 1.0 0.0 1.0
ADD
POLY LimeGreen 0.0 0.0 -0.02 0.0
!yes
5
0.677419 0.976261 0.0
0.680645 0.977745 0.0
0.680645 0.983680 0.0
0.677419 0.985163 0.0
0.677419 0.988131 0.0
```

The *env.sfm* file in the Spotfire DecisionSite distribution serves as an example of this background map format.

To map a data file to a Spotfire mapping file:

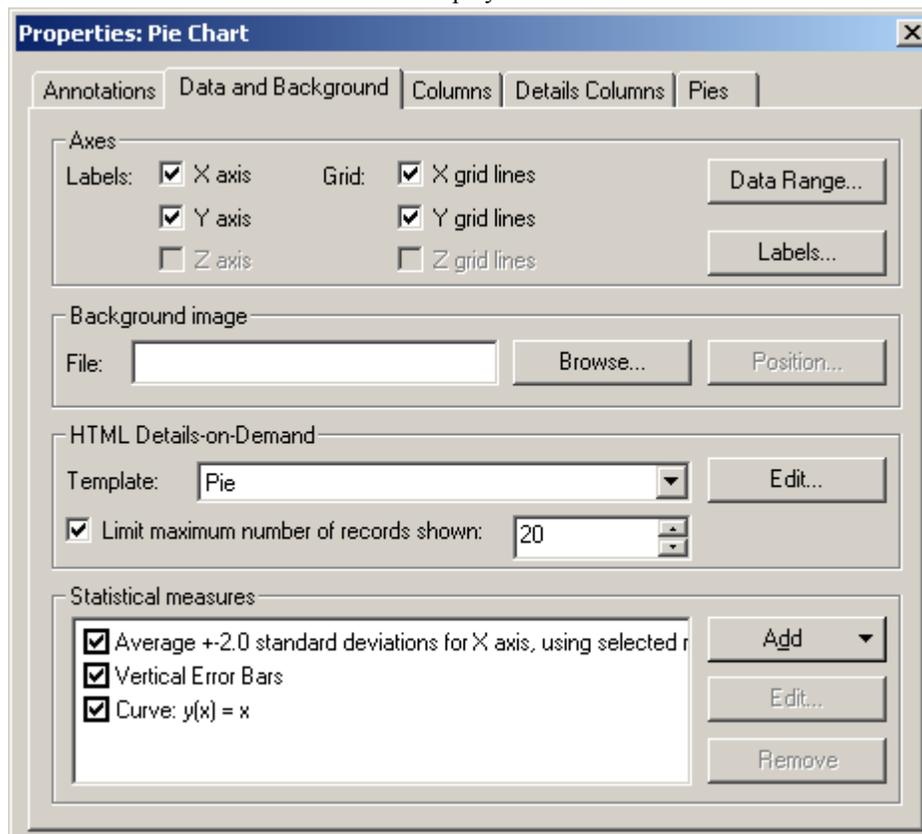
In your visualization, select the two axes from the data that serve as coordinates.

In the **Data and Background** tab in the **Properties** dialog, select an SFM file which has a coordinate system matching the coordinates in the axes file.

## 4.8.2.4 HTML Details-on-Demand

Edit > Properties > Data and Background tab

The information of each record can be displayed in an external or internal HTML browser.



HTML Details-on-Demand templates are accessed through the **Data and Background** tab.

## 4.8.2.5 Statistical Measures

### 4.8.2.5.1 Statistical Measures

Edit > Properties > Data and Background tab

Some statistics and curves can be visualized directly in 2D scatter plots. This section of the **Edit > Properties > Data and Background** dialog offers control of several kinds of statistical measures:

**Average and Standard Deviation** – X-axis and Y-axis average and standard deviation marking lines. The standard deviation is an indication of how dispersed the probability distribution is about its center.

**Error Bars** – Error bars are used to indicate the estimated error in a measurement. Errors bars indicate the uncertainty in the x and/or y values.

**Orthogonal Straight Line Fit** – This is suitable when it is reasonable to assume randomness for both the X-axis values and the Y-axis values.

**Curve** – This option lets you enter a custom expression using the full power of the SXL language, which is drawn as a curve overlaying the visualization.

**Curve Fit** – This adds a best fit curve to the graph using one of several different models. Curve fit should be used when there is no randomness for the markers along the X-axis.

**Note:** If you designate X and Y axes for a Pie Chart, you can add some statistical measures to that visualization as well.

► **To add a measure or a curve to a visualization:**

1. Open the **Properties** dialog and select the **Data and Background** tab.
2. Click on the **Add** button.
3. Choose a measure from the drop-down list.
4. Make the appropriate settings in the dialog that appears.
5. Click **OK**.

► **To edit a statistical measure:**

1. Select a measure from the list by clicking on it.
2. Click on the **Edit** button.

or

- Double-click on the statistical measure in the list.

► **To remove a statistical measure:**

1. Select a statistical measure from the list by clicking on it.
2. Click on the **Remove** button, or press **Delete** on your keyboard.

You can show or hide a statistical measure without removing it permanently from the list.

► **To show/hide a statistical measure:**

- Select the check box beside a statistical measure to show it in the scatter plot.
- Clear the check box beside a statistical measure to hide it in the scatter plot.

#### 4.8.2.5.2 Average and Standard Deviation

The statistical measure "Average" displays the X-axis and Y-axis standard deviation marking lines.

The standard deviation,  $s$ , is an indication of how dispersed the probability distribution is about its center. It is computed as follows:

$$s = \sqrt{\frac{\sum_{i=1}^n (x_i - \bar{x})^2}{n - 1}}$$

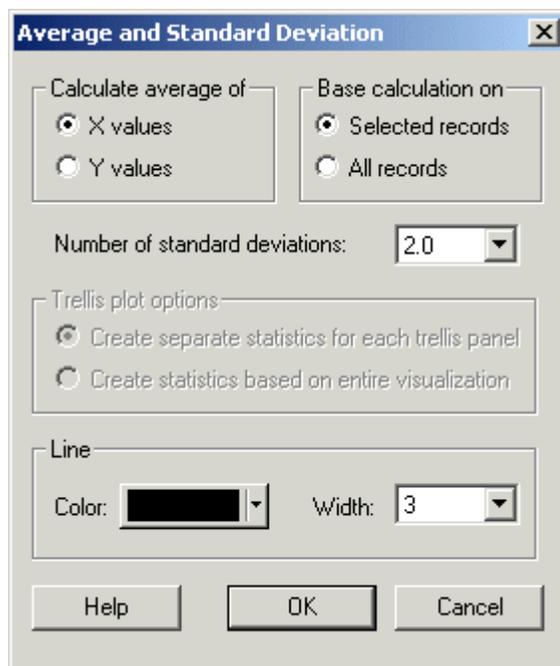
where

$n$  is the number of values in the group and

$\bar{x}$  is the mean value of the group.

**Note:** In this application, the standard deviation is calculated for the data in the data set, as opposed to calculation of standard deviation for the mean value only.

## User Interface

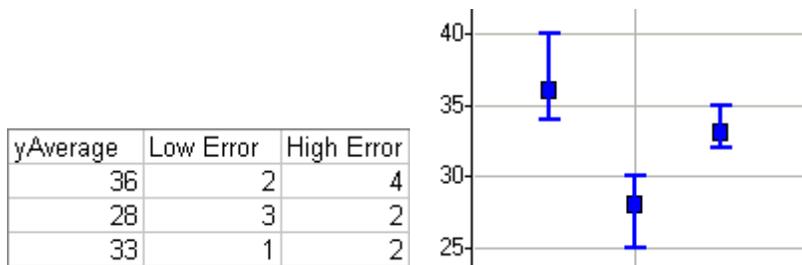


Option	Description
<b>Calculate average of</b>	Specifies whether the average of the X values or the Y values should be calculated.
<b>Base calculation on</b>	Specifies whether the statistical measure should be calculated based on <b>All records</b> in the data set regardless of any filtering done with the query devices, or whether the calculation should be based on the <b>Selected records</b> so that filtering with the query devices will affect the result.
<b>Number of standard deviations</b>	Specifies how many standard deviations away from the (bolder) average line the deviation lines will be drawn.
<b>Trellis plot options</b>	Specifies whether the average displayed in each trellis panel will be calculated based on the records specific to that trellis panel only, or if the average will be based on all records regardless of trellis condition and therefore be the same for every trellis panel.
<b>Color</b>	The color of the displayed line.
<b>Width</b>	The width (in pixels) of the displayed line.

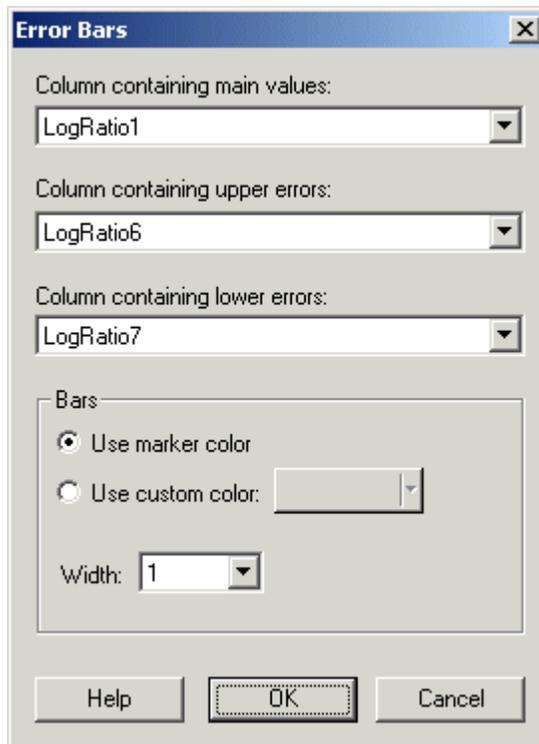
### 4.8.2.5.3 Error Bars

Error bars are used to indicate the estimated error in a measurement. In other words, they indicate the uncertainty in the x and/or y values.

Unlike other statistical measures in Spotfire DecisionSite, no calculations are performed to produce the error bars. Instead the data needed is assumed to be in the data set, in the form of three columns representing an average value, a high error and a low error. The marker itself shows the average value, and the high and low error values make up the error bar.



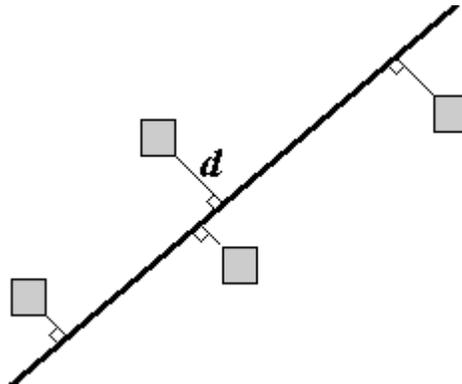
### User Interface



Option	Description
<b>Column containing main values</b>	Specifies which column contains the main (or average) values.
<b>Column containing upper errors</b>	Specifies which column contains the upper error values.
<b>Column containing lower errors</b>	Specifies which column contains the lower error values.
<b>Use marker color</b>	Select this option to use the marker color for the error bars.
<b>Use custom color</b>	Select this option to use a custom color for the error bars.
<b>Width</b>	The width (in pixels) of the error bars.

#### 4.8.2.5.4 Orthogonal Straight Line Fit

Orthogonal straight line fit is calculated by choosing the line that minimizes the least square sum of the distance  $d$  perpendicular to the line, of all the selected markers (see picture below). It should be used when the distance between the markers along both the X-axis and the Y-axis varies.



### User Interface

Option	Description
<b>Base calculation on</b>	Specifies whether the line should be calculated based on all records in the data set regardless of any filtering done with the query devices, or whether the calculation should be based on the selected records so that filtering with the query devices will affect the result.
<b>Trellis plot options</b>	Specifies whether the orthogonal straight line fit displayed in each trellis panel will be calculated based on only the records specific to that trellis panel, or if the fit will be based on all records regardless of trellis condition and therefore be the same for every trellis panel.
<b>Color</b>	The color of the displayed line.
<b>Width</b>	The width (in pixels) of the displayed line.

## Results

If Orthogonal Straight line fit is active and the Legend is visible, information about Statistical measures will be displayed there. The correlation value, **R**, which is displayed, is the standard Pearson's correlation and is calculated like this:

$$R = \frac{\sum_i (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_i (x_i - \bar{x})^2 \sum_j (y_j - \bar{y})^2}}$$

**Note:** The Legend will not display the R value if you have several Trellis panels.

### 4.8.2.5.5

## Curve

The Curve feature allows you to specify a curve to be displayed on top of a scatter plot or pie chart, given that you have specified X- and Y-axes in the pie charts. You simply enter an expression where the curve is defined as "y as a function of x" and it will be drawn on top of the plot. To aid you in creating powerful expressions, you can use the Spotfire Expression Language (SXL). All the functions of SXL can be selected and inserted from the **Function** list in the dialog.

### Examples:

$y(x) = 10+x$

$y(x) = \text{Average}(x)+100$

$y(x) = 10*\sin(x*\text{PI}())+5$

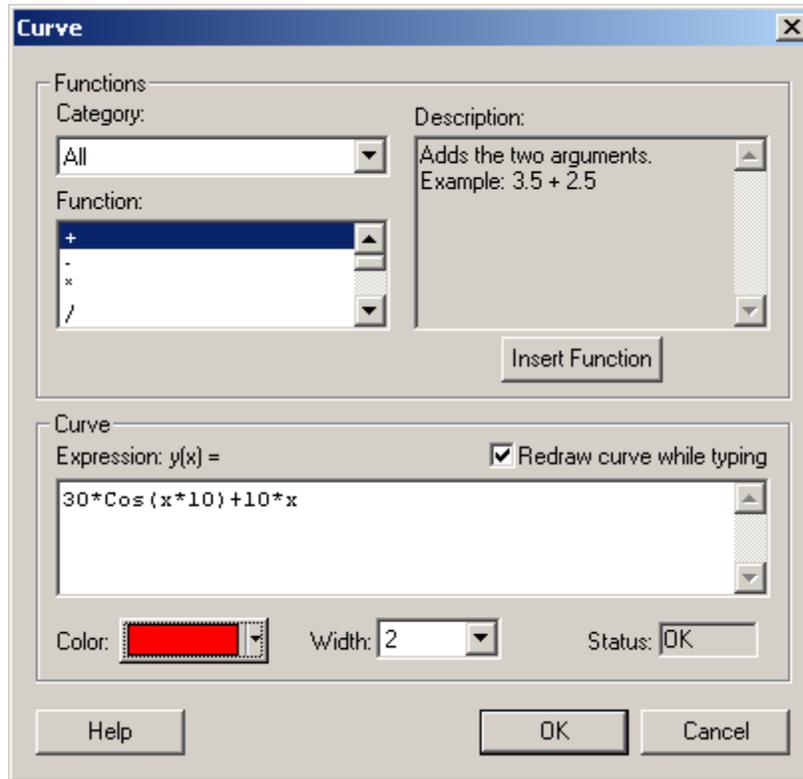
You can also select the color and width of the curve. In the **Status** field there is also a syntax verification of the entered expression, where you can easily see if the expression is correct.

If the expression is valid, and the **Redraw curve while typing** check box is selected, the curve will be drawn and immediately updated on screen when you edit your expression, so you can always check to see if it looks like you intended.

## Transformations

The x and y values are unaffected by transformations, but the mapping onto the plot will be affected. This means that a straight line equation such as  $y(x) = x$ , will turn into a curve if the X-axis column uses a Log transform.

## User Interface



### Category

Select a category of functions to limit the choices in the **Function** list.

- All
- Operators
- Math Functions
- Statistical Functions
- Text Functions
- Logical Functions
- Date & Time Functions
- Conversion Functions

### Function

Select a function by clicking on it, and click the **Insert Function** button to insert it to the **Expression** field. You can also double-click on a function to insert it.

If you place the cursor at a specific location in the **Expression** field, the function will be inserted there.

### Description

This field provides a brief description of the selected function. For more detailed descriptions, please see Spotfire Expression Language (SXL).

### Expression

This is the text field in which you build your expression. You can insert functions to it from the list, or enter text as in any standard text editor.

Cut/Copy/Paste works in the field using standard **Ctrl+X** / **Ctrl+C** / **Ctrl+V**.

Highlighting a section of the expression, and clicking Insert Function will add the selected function to the expression with the highlighted section as an argument.

Also, Undo/Redo functionality is available by pressing **Ctrl+Z**.

**Note:** Very long expressions will be displayed truncated in the Visualization Legend. To avoid this, insert a blank space with suitable distance. This will not affect the expression, but will allow the Legend to display it over several rows.

### Color

Select the color of the curve by clicking on this button.

### Width

Select the width (in pixels) of the curve by clicking on this drop-down list.

### Status

This field shows if the current expression is valid or not. If the expression is correct, then **OK** will be shown.

If this field shows an **#EXPR!** error, there is a problem with the syntax of the expression. Moving the mouse pointer over the field or clicking on it, will display an explanation of what is wrong. Pressing **F5** will also display the error description. Pressing **F4** will move the cursor to the position in the expression where the error lies.

### Redraw curve while typing

If this check box is selected, the curve will be drawn and updated in the plot while you edit the expression. This is useful to verify that the curve actually looks like you intended, but if you are using very large data sets and complex expressions for the curve, it may be a good idea to turn it off in order to improve performance.

## 4.8.2.5.6 Curve Fit

### 4.8.2.5.6.1 Curve Fit

Curve fit (regression analysis) allows you to summarize a collection of sample data points by fitting them to a model that will describe the data and display a curve or a straight line on top of a scatter plot or a pie chart. Unlike the Curve feature, Curve Fit is not a fixed curve, but rather a line that can be changed upon changing the input data during filtering or zooming.

Curve fitting can be used either to determine the parameter values of a known regression model or to find a model that fits the data better than other models.

**Tip:** If a curve fit is active and the Legend is visible, information about the curve fit will be displayed there. Select **View > Legend** to display it. More information is also available via View Result, see below.

### Transformations

The x and y values are unaffected by transformations, but the mapping onto the plot will be affected. This means that a straight line equation such as  $y(x) = x$ , will turn into a curve if the X-axis column uses a Log transform.

### Limitations on data

All types of input data cannot be used to calculate curves using all different types of models.

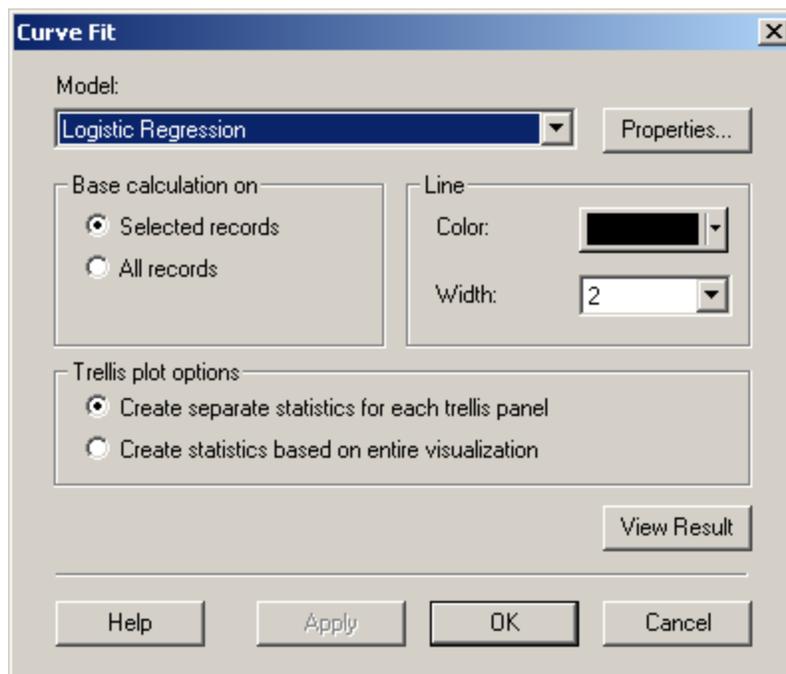
All models require:

- more than one data point to use in the calculation
- that not all data points have the same x- and y-values (lie on top of each other)
- that not all data points have the same x-value

In addition, the logarithmic model, the power model and the logistic regression model require that all data points have positive x-values. The power model also requires that all y-values have the same sign (positive or negative).

The logistic regression requires that no values are lower than the specified min value or higher than the specified max value and that not all data points have the same y-value. If any of the above limitations occur, no curve will be drawn, and an error message will be displayed in the Legend.

## User Interface



## Model

Specifies the type of curve to display in your visualization. Choose from:

<b>Straight Line</b>	$y=a+bx$
<b>Logarithmic</b>	$y=a+b\ln x$
<b>Exponential</b>	$y=ae^{bx}$
<b>Power</b>	$y=ax^b$
<b>Logistic Regression</b>	$y=\min+(max-\min)/(1+(X50/x)^{Hill})$
<b>2nd order Polynomial</b>	$y=a+bx+cx^2$
<b>3rd order Polynomial</b>	$y=a+bx+cx^2+dx^3$
<b>4th order Polynomial</b>	$y=a+bx+cx^2+dx^3+ex^4$
<b>5th order Polynomial</b>	$y=a+bx+cx^2+dx^3+ex^4+fx^5$

See Curve Fit Models for more information.

### **Properties...**

Available for Logistic regression only. Lets you specify values for max and min. If no values are specified, they will be automatically calculated.

**Note:** If you specify max and min values within the range of your data, you must filter out all data points outside of your specified range using the query devices or zooming in order to obtain a curve. (For example, no curve will be calculated if the min value equals the lowest value of y in your data set, unless you filter out this value and base the calculation on selected values only.)

### **Base calculation on**

Specifies whether the statistical measure should be calculated based on all records in the data set regardless of any filtering done with the query devices, or whether the calculation should be based on the selected records so that filtering with the query devices will affect the result.

### **Color**

The color of the displayed line.

### **Width**

The width (in pixels) of the displayed line.

### **Trellis plot options**

Specifies whether the curve fit displayed in each trellis panel will be calculated based on only the records specific to that trellis panel, or if the fit will be based on all records regardless of trellis condition and therefore be the same for every trellis panel.

### **View Result**

Opens the Curve Fit: Result dialog, where detailed results from the fit is shown and can be copied into other applications.

### **Apply**

Applies the curve fit to the visualization. Allows you to test one or many curve fits in your visualization without having to close the Curve Fit dialog.

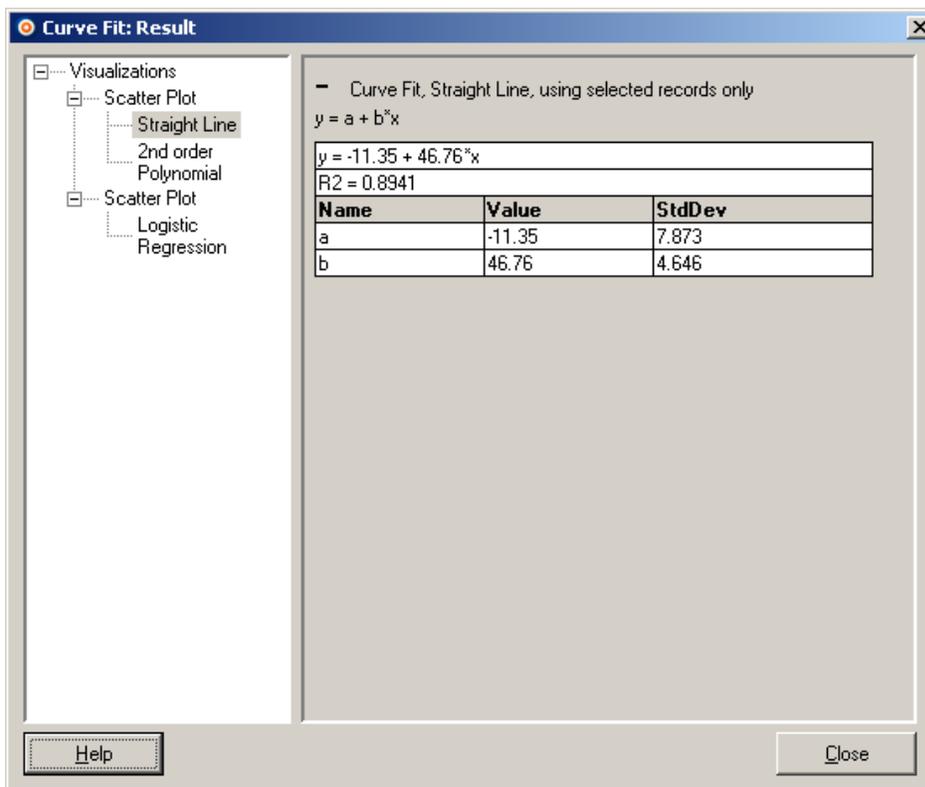
#### **4.8.2.5.6.2**

### **Curve Fit: Result Dialog**

The Curve Fit Result dialog displays detailed information about all curve fits that were enabled when you clicked on the button. Click on a specific curve fit in the Visualizations tree to view its details.

**Tip:** Select all text in the gray part of the dialog and copy the information, if you want to include the results in a report.

## User Interface



The left pane shows a tree view of the different visualizations that have one or more curve fits applied. Click on the desired curve fit to view the details in the right pane of the dialog.

The right pane displays detailed information about the used equations and parameters of the selected curve. See Curve Fit Theory and Curve Fit Models for more information about the various parameters.

### ► To reach the Curve Fit: Result dialog:

Right-click in the scatter plot or pie chart where you have applied a curve fit and select **View Curve Fit Result** from the pop-up menu.

**Tip:** You can also reach this dialog from the Curve Fit dialog, e.g., if you are testing several different curves using the Apply-button. In the Curve Fit dialog, click on the **View Result** button to display the results.

### 4.8.2.5.6.3

#### Curve Fit Models

There are several different models available for curve fitting. See Curve Fit for information about how to apply the various curves. The Curve Fit models below can be used when there is no randomness for the markers along the X-axis.

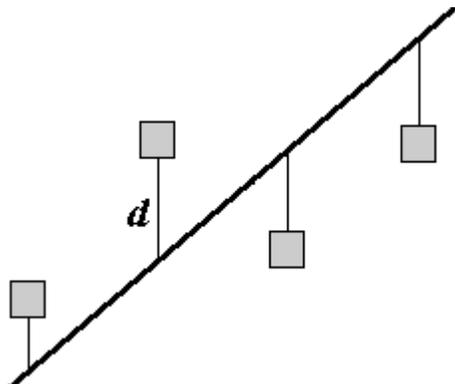
#### Straight Line

The straight line fit is calculated by choosing the line that minimizes the least square sum of the vertical distance  $d$ , of all the selected markers (see picture below) by using the following equation:

$$y = ax + b$$

where  $a$  is the slope and  $b$  is the intercept.

For example, you could plot days along the X-axis and have one marker for each day. The distance between the markers along the X-axis is the same, thus making straight line fit appropriate.



### Logarithmic

The logarithmic fit calculates the least squares fit through points by using the following equation:

$$y = a + b \ln x$$

where  $a$  and  $b$  are constants, and  $\ln$  is the natural logarithm function. This model requires that  $x > 0$  for all data points. DecisionSite uses a nonlinear regression method for this calculation. This will result in better accuracy of the calculation compared to using linear regression on transformed values only.

### Exponential

The exponential fit calculates the least squares fit through points by using the following equation:

$$y = ae^{bx}$$

where  $a$  and  $b$  are constants, and  $e$  is the base of the natural logarithm.

Exponential models are commonly used in biological applications, e.g., for exponential growth of bacteria. DecisionSite uses a nonlinear regression method for this calculation. This will result in better accuracy of the calculation compared to using linear regression on transformed values only.

### Power

The Power fit calculates the least squares fit through points by using the following equation:

$$y = ax^b$$

where  $a$  and  $b$  are constants. This model requires that  $x > 0$  for all data points, and either that all  $y > 0$  or all  $y < 0$ . DecisionSite uses a nonlinear regression method for this calculation. This will result in better accuracy of the calculation compared to using linear regression on transformed values only.

### Logistic Regression

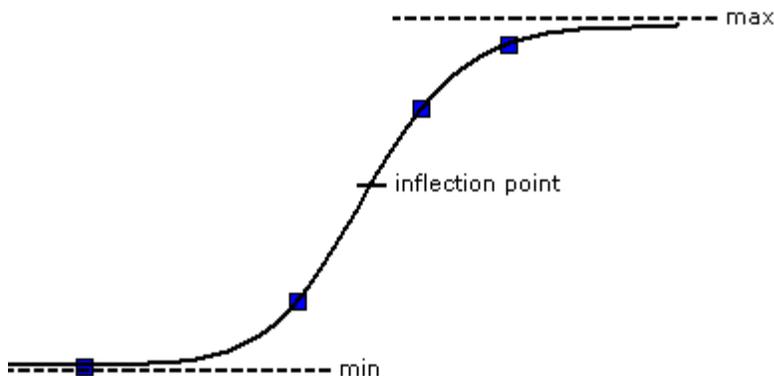
The logistic regression fit is a dose response ("IC50") model, also known as sigmoidal dose response. The four parameter logistic model is the most important one.

Dose-response curves describe the relationship between response to drug treatment and drug dose or concentration. These type of curves are often semi-logarithmic, with  $\log$  (drug concentration) on the X-axis. On the Y-axis one can show measurements of enzyme activity, accumulation of an intracellular second messenger or measurements of heart rate or muscle contraction.

The current implementation of the logistic regression fit uses the following equation:

$$y = \min + \frac{\max - \min}{1 + \left(\frac{X50}{x}\right)^{Hill}}$$

where min and max are the lower and upper asymptotes of the curve, Hill is the slope of the curve at its midpoint and X50 is the x-coordinate of the inflection point (x, y). This model requires that  $x > 0$  for all data points and that you use at least four records to calculate the curve.



**Note:** The logistic regression model of DecisionSite does not assume logarithmic values of  $x$  and  $X50$ , unlike some other curve fitting software. Hence, if your input data is logarithmic you might want to create a column that is not logarithmic before you apply the logistic regression curve fit, in order to obtain similar results to the ones you are used to. (For example, by using Data > New Column > By Expression.) If you want the curve to be displayed on a logarithmic form, right-click in the Query Devices window and select Set Property > Log Scale.

## 2nd order Polynomial

The second order polynomial fit, or quadratic curve, calculates the least squares fit through points by using the following equation:

$$y = a + bx + cx^2$$

where  $a$ ,  $b$  and  $c$  are constants. This model requires that you use at least three records to calculate the curve.

## 3rd order Polynomial

The third order polynomial fit calculates the least squares fit through points by using the following equation:

$$y = a + bx + cx^2 + dx^3$$

where  $a$ ,  $b$ ,  $c$  and  $d$  are constants. This model requires that you use at least four records to calculate the curve.

## 4th order Polynomial

The fourth order polynomial fit calculates the least squares fit through points by using the following equation:

$$y = a + bx + cx^2 + dx^3 + ex^4$$

where  $a$ ,  $b$ ,  $c$ ,  $d$  and  $e$  are constants. This model requires that you use at least five records to calculate the curve.

## 5th order Polynomial

The fifth order polynomial fit calculates the least squares fit through points by using the following equation:

$$y = a+bx+cx^2+dx^3+ex^4+fx^5$$

where a, b, c, d, e and f are constants. This model requires that you use at least six records to calculate the curve.

If you have a low number of unique x-values, a polynomial curve can be calculated in an unlimited number of ways. This means that you may end up with a curve that does not look like expected. If this should happen, you probably should not apply this model to your data. The polynomial models have all been partially solved by using the LAPACK software package, see References.

#### 4.8.2.5.6.4 Curve Fit Theory

Generally, curve fit algorithms determine the best-fit parameters by minimizing a chosen merit function. In order to optimize the merit function, it is necessary to select a set of initial parameter estimates, and then iteratively refine the merit parameters until the merit function does not change significantly between iterations. The Levenberg-Marquardt algorithm has been used for nonlinear least squares calculations in the current implementation.

The goodness of fit is shown as an R2-value. A value of R2=1.0 indicates a perfect fit, whereas R2=0.0 indicates that the regression model might be unsuitable for this type of data.

The standard deviation (StdDev) shown in the Curve Fit: Result dialog is the standard deviation of the differences between the actual data points and the calculated curve. It approaches 0 if the selected model accurately describes the data.

#### R2

The R2-value measures how much of the variation in the data points that can be explained by the selected regression model:

$$R^2 = \frac{SSR}{SST} = 1.0 - \frac{SSE}{SST} \quad 0 \leq R^2 \leq 1$$

where

$$SSR = \sum_{i=1}^n (\hat{Y}_i - \bar{Y})^2 \quad \text{(the regression sum of squares)}$$

$$SSE = \sum_{i=1}^n (Y_i - \hat{Y}_i)^2 \quad \text{(the residual or error sum of squares)}$$

$$SST = \sum_{i=1}^n (Y_i - \bar{Y})^2 \quad \text{(the total sum of squares, SST= SSE+SSR)}$$

and  $\hat{Y}_i$  represents the  $i^{\text{th}}$  fitted value (calculated using the selected model) of the dependent variable Y.

#### Limitations to curve fitting

Since the calculation of the curve is an iterative process, the calculation must stop somewhere. In some cases the maximum number of iterations might be reached before the best possible curve has been calculated. In that case, a message will inform you of this in the Legend (select View > Legend to display it). In some cases, for example if the data is widely scattered or too few data points are available, the iterative process might also result in a curve that converges on a false minimum.

When a model is applied during data analysis, it is important not only to look at the R2-value and how well the curve fits the current markers in the scatter plot. It is also good to consider

what the curve would look like for more extreme values and determine if the model is reasonable in a scientific or statistical context. The number of unique x-values must be larger than, or equal to, the number of degrees of freedom in order to obtain a unique curve. If the curve can be solved in an infinite number of ways, it is not sure that the presented curve will be relevant to your data.

## References

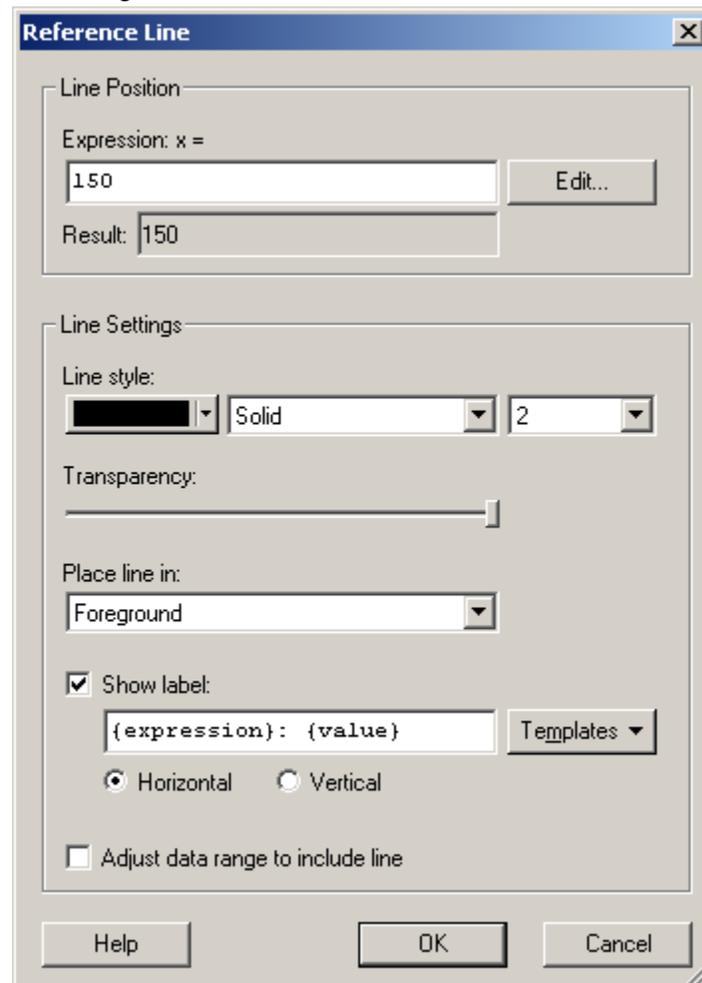
Heath, M.T., (2002), Scientific Computing: An Introductory Survey, 2nd ed., McGraw-Hill, New York.

Anderson, E., Bai, Z., Bischof, C., Blackford, S., Demmel, J., Dongarra, J., Du Croz, J., Greenbaum, A., Hammarling, S., McKenney, A., Sorensen, D., (1999), LAPACK Users' Guide, 3rd ed., Society for Industrial and Applied Mathematics, Philadelphia, PA, ISBN = 0-89871-447-8

## 4.8.2.6 Reference Lines in Bar Chart

### 4.8.2.6.1 Reference Line Dialog

This dialog is used to create vertical reference lines in a bar chart.



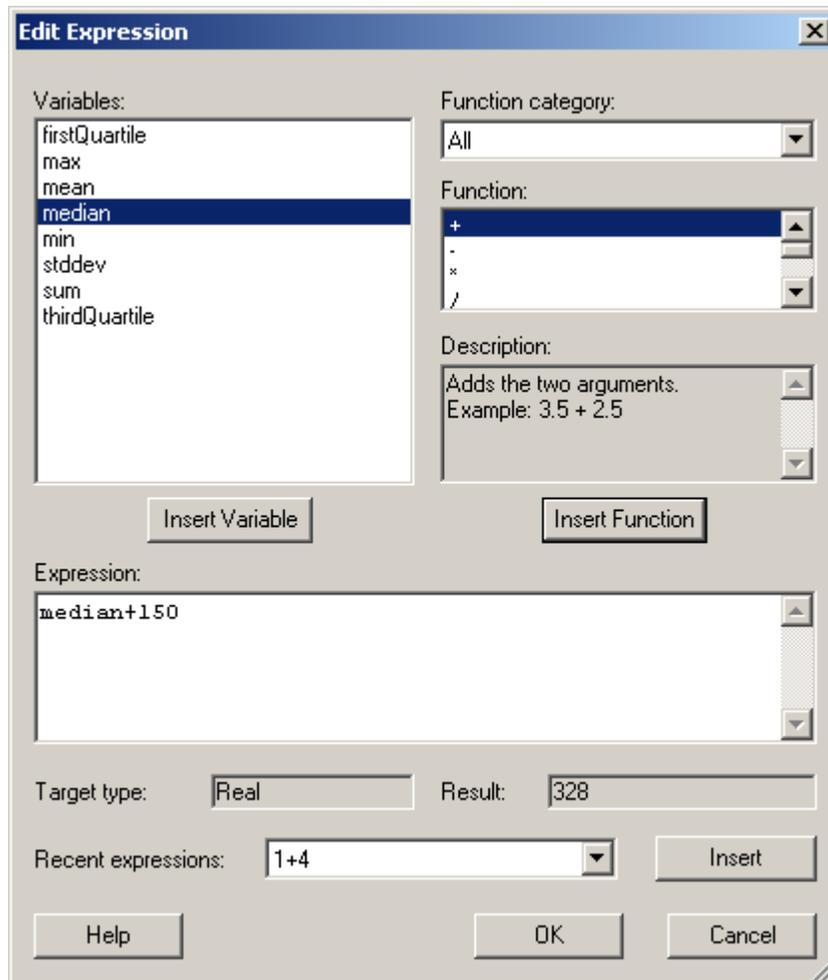
Option	Description
Expression	Type the expression you want to be presented as a reference line in

	<p>the text field. If you want a line drawn at a specific number, you simply type that number in the text field. You can also type more complicated expressions, including a number of functions and variables such as mean and median directly in the field. For more information about the available functions and variables, click on Edit... (see below).</p> <p>Note that variables such as median and mean are always calculated on all data and not on the data filtered by the query devices or zooming.</p>
<b>Edit...</b>	Opens the Edit Expression dialog, where you can combine different variables and functions into an expression, as well as read a short description of all available functions.
<b>Result</b>	Displays the result of the expression.
<b>Line style</b>	Allows you to change the color, style and line width of the reference line.
<b>Transparency</b>	Allows you to change the transparency of the reference line. A completely solid line is obtained by moving the thumb to the far right.
<b>Place line in</b>	Determines whether the line should be placed in the Foreground or in the Background of the bars.
<b>Show label</b>	<p>Select this check box to show a label for the reference line. Clear the check box to remove the label.</p> <p>You can type a label text directly in the text field or, you can use one of the available templates, see below.</p>
<b>Templates</b>	<p>Displays a drop-down menu from where you can select a template for how the label should be presented.</p> <p>Choose from <b>Value</b> (which simply shows the x-axis value of the reference line), <b>Expression</b> (which shows the expression, e.g., "median+150"), <b>Expression: Value</b> (e.g., "median+150:328") or <b>Display Name</b> (which shows the name of the reference line as it is presented in the legend (e.g., "Vertical reference line: x = median+150")).</p>
<b>Horizontal</b>	Click this radio button for a horizontal label.
<b>Vertical</b>	Click this radio button for a vertical label.
<b>Adjust data range to include line</b>	Select this check box to adjust the data range so that the reference line becomes visible even if it is outside the data range for the current data set.

► **To reach the Reference Line dialog:**

1. Create a bar chart with a continuous column on the X-axis.
2. Select **Edit > Properties**.
3. Go to the **Data and Background** tab.
4. Click on **Add** and select **Vertical Reference Line...** from the drop-down menu.

### 4.8.2.6.2 Edit Expression Dialog



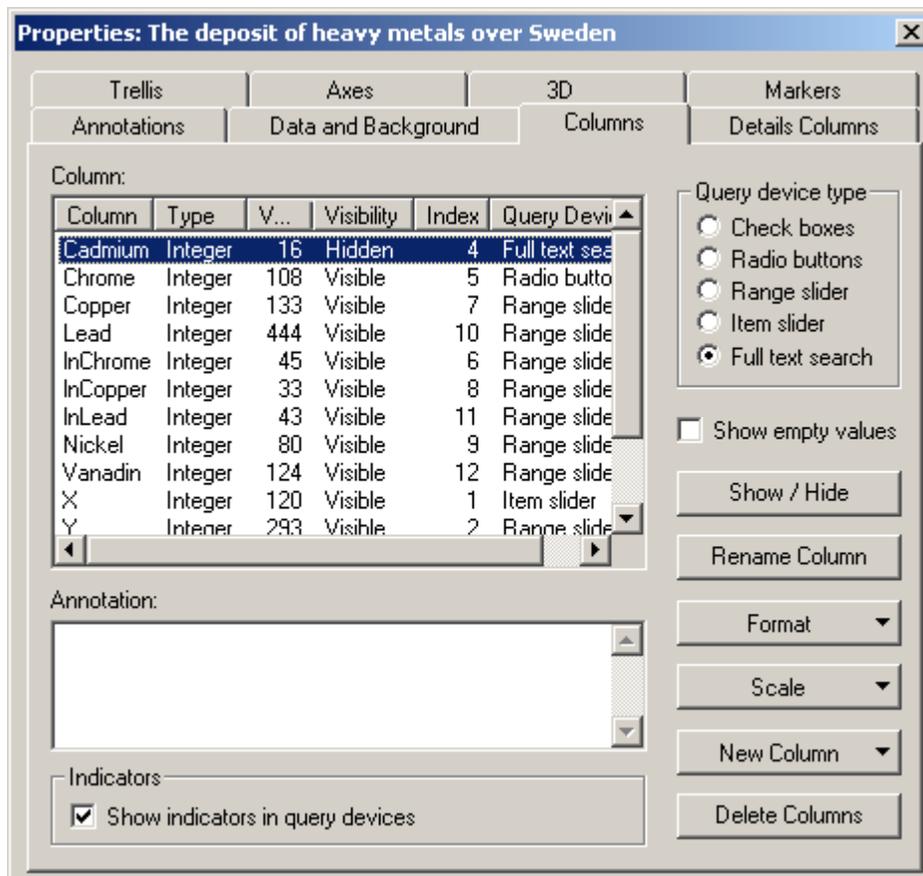
Option	Description
<b>Variables</b>	Lists the available variables which can be used to create your expression. Insert a variable into your expression with the <b>Insert Variable</b> button.
<b>Function category</b>	Select a category of functions to limit the choices in the <b>Functions</b> list: All Operators Math Functions Statistical Functions Text Functions Logical Functions Date & Time Functions Conversion Functions
<b>Function</b>	Select a function by clicking on it, and click the <b>Insert Function</b> button to insert it to the <b>Expression</b> field. You can also double-click on a function to insert it.  If you place the cursor at a specific location in the <b>Expression</b> field, the function will be inserted there.

<b>Description</b>	Provides a brief description of the selected function. For more detailed descriptions, please see Spotfire Expression Language (SXL).
<b>Expression</b>	<p>This is the text field in which you build your expression. You can insert variables and functions to it from the lists, or enter text as in any standard text editor.</p> <p>Cut/Copy/Paste works in the field using standard <b>Ctrl+X / Ctrl+C / Ctrl+V</b>.</p> <p>Highlighting a section of the expression, and clicking Insert Function will add the selected function to the expression with the highlighted section as an argument.</p> <p>Also, Undo/Redo functionality is available by pressing <b>Ctrl+Z</b>.</p> <p><b>Note:</b> Very long expressions will be displayed truncated in the Visualization Legend. To avoid this, insert a blank space with suitable distance. This will not affect the expression, but will allow the Legend to display it over several rows.</p>
<b>Target type</b>	Displays the data type of the result.
<b>Result</b>	<p>This field displays the result of applying the current expression to the data set.</p> <p>If this field shows an error message, then there is a problem with the expression. Clicking on the field will display an explanation of what is wrong. Pressing <b>F5</b> will also display the error description. Pressing <b>F4</b> will move the cursor to the position in the expression where the error lies.</p> <p>There are three kinds of error messages:</p> <p>#EXPR! – there is a problem with the syntax of the expression.</p> <p>#NUM! – the expression evaluates to infinity or other illegal number.</p> <p>#ARG! – there is a problem with one or many arguments.</p>
<b>Recent expressions</b>	This list contains the fifteen most recent expressions you have created.
<b>Insert</b>	Inserts the selected recent expression to the cursor position of the expression field.

## 4.8.3 Columns Tab

### 4.8.3.1 Columns tab

Edit > Properties > Columns tab



This dialog is used to set column properties columns—how they are viewed, what query device to associate with the column, annotations, name, scale, etc.

Option	Description
<b>Column</b>	Lists all the existing columns in the data set. Select a column name and use the controls described below to control that column. Click on the headers (e.g., Column, Type, etc.) to sort the columns accordingly.
<b>Annotation</b>	Enter any text that you want to associate with this column. This text will appear when you place the mouse pointer over the paper clip icon next to a query device.
<b>Show indicators in query devices</b>	Displays a paper-clip icon in the upper right corner of the query device when the column has an annotation, and displays the letter 'e' when the column contains empty values.
<b>Query device type</b>	Shows what query device type is assigned to the selected column in the list.
<b>Show empty values</b>	Shows (or hides) all records where a value is missing in the selected column.
<b>Show/Hide</b>	Toggles the query device associated with this column.
<b>Rename Column</b>	Allows you to enter a new name for the column.
<b>Format</b>	Configures how to display the format for various columns (Number Formatting, Date and Time Formatting, Date Formatting or Time Formatting). For example, how to represent negative values, number of decimal digits, etc.

	Select one or more columns from the list, click the <b>Format</b> button, and select a formatting option to access the formatting dialog. <b>Note:</b> Formatting may change the perceived type of a column. For example, a date column will be presented as a string column when week day formatting is applied. See <i>Rearranging the Data by Formatting</i> for more information. Selecting <b>Format &gt; None</b> from the drop-down menu, resets the options to the default settings.
<b>Scale</b>	Sets the scale of the selected column or columns when mapped to an axis in the visualization. Scale options: <b>Original</b> , <b>Ln(1+x)</b> , <b>Log</b> , <b>Exp</b> , <b>Exp10</b> , <b>Inverse Scale</b> , and <b>Reverse sorting</b> .
<b>New Column</b>	Adds a new column either <b>by Binning</b> or <b>from an Expression</b> .
<b>Delete Columns</b>	Deletes the selected column from memory. The underlying file is not affected unless you save the data set.

This dialog can also be accessed by double-clicking in the upper right corner of any query device.

### 4.8.3.2 Annotating Columns

Edit > Properties > Columns tab

It is possible to annotate individual columns. This text will appear when you place the mouse pointer over the paper clip next to a query device.

#### ► To enter an annotation for a column:

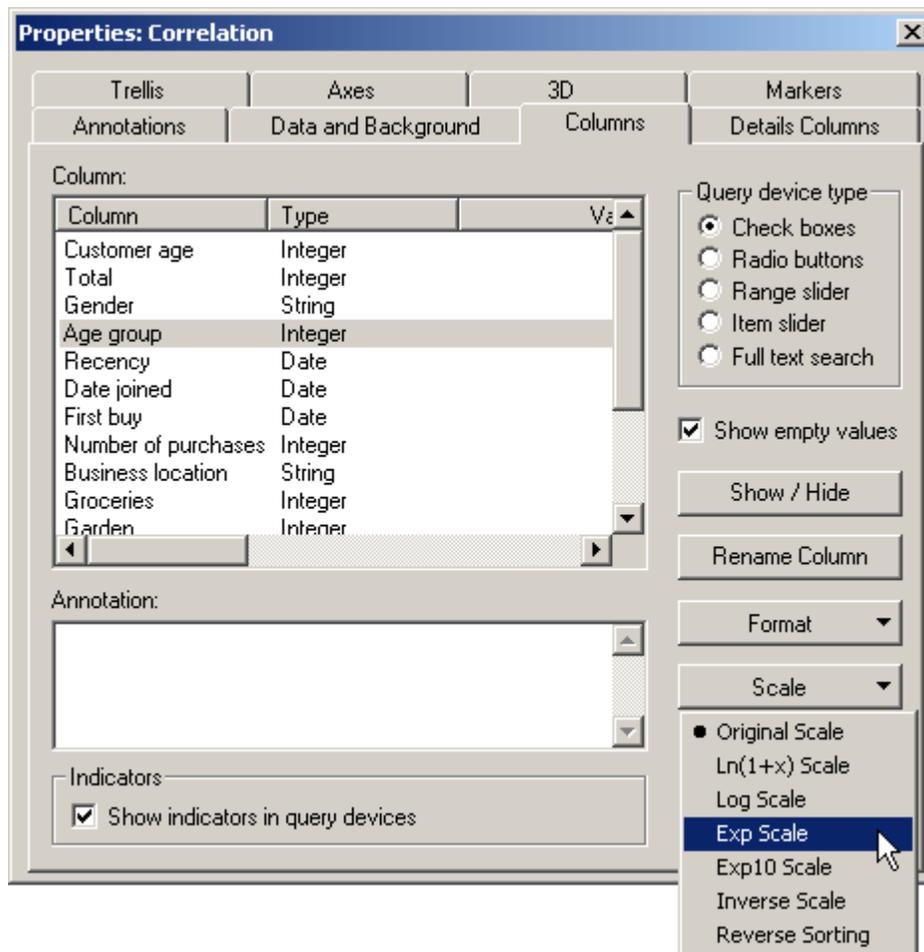
1. Go to the **Columns** tab of the **Properties** dialog.
2. Select a column.
3. Enter your text in the **Annotation** field.

You can also edit annotations for a column by double-clicking the paper-clip next to the corresponding query device, or by selecting **Edit Annotations...** from the query device pop-up menu.

### 4.8.3.3 Transforming Axis Scale

A numerical column can be set to display its values using a variety of scales instead of the linear scale, which is default: Natural Log Scale ( $\ln(x+1)$ ), Logarithmic Scale (**Log**), Exponential to the bases of  $e$  (**Exp**) and  $10$  (**Exp10**), Inverse Scale ( $1/x$ ), and Reverse Scale. The last option changes the sort order for the selected column. This is accomplished by right-clicking on the query device representing the column, and from the **Set Property** sub-menu selecting the transformation desired.

Another way to change the scale is from the **Columns** tab of the **Properties** dialog, by marking the column to rescale and selecting the transformation from the Set Scale pull down box.



The transformation can be removed and the scale reset to linear by choosing **Original Scale**.

#### 4.8.3.4 Number Format

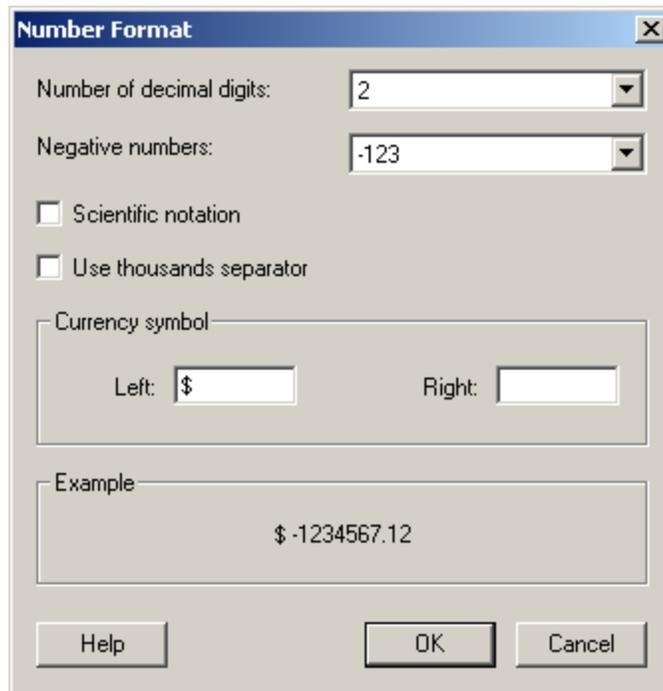
You can specify how you want DecisionSite to display number formatting for integer and decimal columns. You can set the number of decimal digits, how to display negative numbers, to display numbers using scientific notation, select whether or not to use thousands separators, and also add a currency symbol to be displayed together with the actual value.

**Note:** If you prefer, you can set default number formatting for all Integer type columns and all Decimal type columns, instead of specifying this for each column individually. Such default settings will be applied every time you open a new data set in DecisionSite Client. Default settings are made in the Fonts & Numbers tab of the Options dialog.

##### ► To set Number Formatting for a column:

1. Open the **Properties** dialog by selecting **Edit > Properties** and click on the **Columns** tab.
2. Select one or more columns you wish to set number formatting for.
3. Click on the **Format** button.

- Select **Number...** which opens the Number Format dialog.



- Specify the **Number of decimal digits** and how to display **Negative numbers**.
- Specify whether or not you wish to display the numbers in **Scientific notation**. (For example: 1,23E+006.)  
**Note:** When using Scientific notation, the **Use thousands separator** check box is cleared and grayed out, as it is no longer applicable.
- Decide whether or not to **Use thousands separator**.  
**Note:** The symbol used for thousands separator and decimal separator is determined by the Windows Locale setting.
- If desired, enter **Unit labels** in the **Left** or the **Right** text field.  
Comment: This could be a currency symbol or any other unit. The maximum length is 12 characters.
- Click **OK**.

Selecting **Format > None** from the Format drop-down menu, resets the options to the default settings.

### 4.8.3.5 Date and Time Format

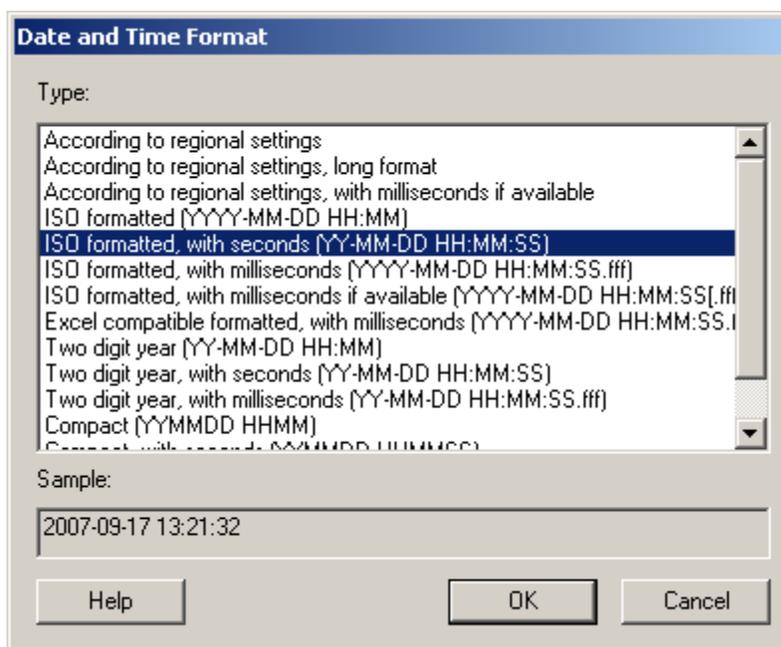
You can specify how you want DecisionSite to display date and time formatting for time stamp columns. You can set the date and time to be shown either according to regional settings, with or without milliseconds, or according to a number of other date and time formats.

By changing the date format for a date or time stamp column, you can obtain a whole new set of factors to filter your data by. See *Rearranging the Data by Formatting* for more information.

#### ► To set Date and Time Formatting for a column:

- Open the **Properties** dialog by selecting **Edit > Properties** and click on the **Columns** tab.
- Select one or more columns you wish to set time formatting for.
- Click on the **Format** button.

- Select **Date and Time...** which opens the Date and Time Format dialog.



- Click on a format type.  
Response: An example of what the selected date and time format would look like is shown in the Sample field.
- When you are satisfied with the selected format, click **OK**.

Selecting **Format > None** from the Format drop-down menu, resets the format to the default setting.

**Tip:** If you want to change the date and time formatting for a single column you can also reach the Date and Time Format dialog from the pop-up menu of the Query Devices panel. Right-click on the column of interest and select **Set Property > Format > Date and Time...** from the pop-up menu.

### 4.8.3.6 Date Format

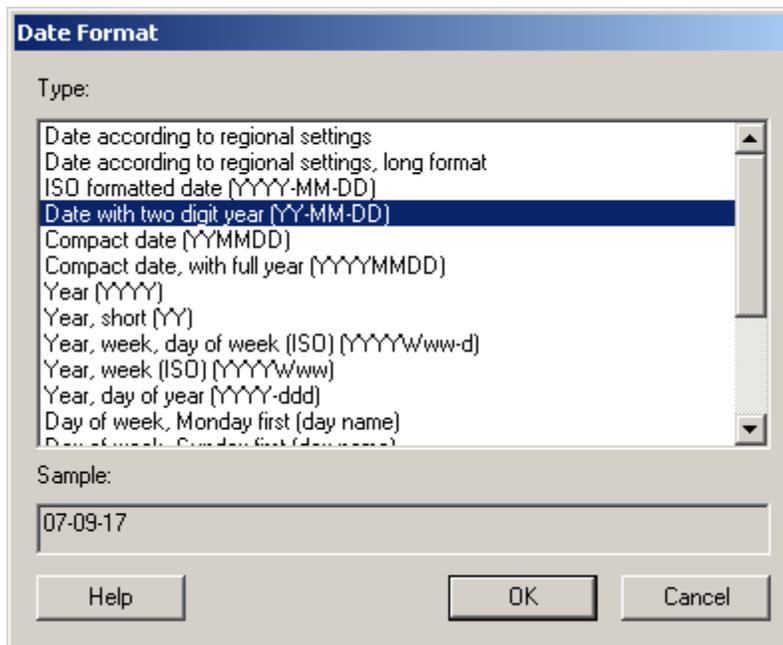
You can specify how you want DecisionSite to display date formatting for time stamp columns. You can set the date to be shown either according to regional settings or according to a number of other date formats.

By changing the date format for a date or time stamp column, you can obtain a whole new set of factors to filter your data by. See *Rearranging the Data by Formatting* for more information.

#### ► To set Date Formatting for a column:

- Open the **Properties** dialog by selecting **Edit > Properties** and click on the **Columns** tab.
- Select one or more columns you wish to set date formatting for.
- Click on the **Format** button.

- Select **Date...** which opens the Date Format dialog.



- Click on a format type.  
Response: An example of what the selected date format would look like is shown in the Sample field.
- When you are satisfied with the selected format, click **OK**.

Selecting **Format > None** from the Format drop-down menu, resets the format to the default setting.

**Tip:** If you want to change the date formatting for a single column you can also reach the Date Format dialog from the pop-up menu of the Query Devices panel. Right-click on the column of interest and select **Set Property > Format > Date...** from the pop-up menu.

### 4.8.3.7 Time Format

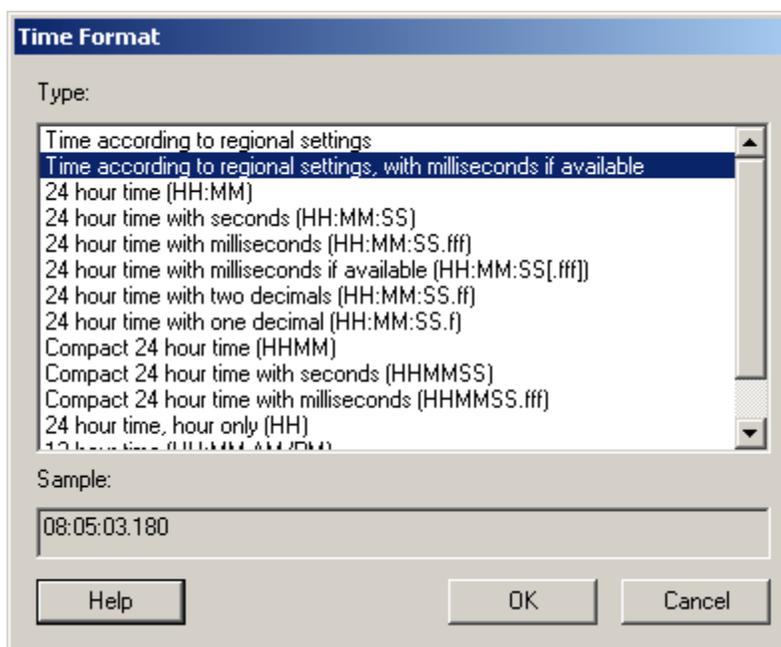
You can specify how you want DecisionSite to display time formatting for time and time stamp columns. You can set the time to be shown either according to regional settings, with or without milliseconds, or according to a number of other time formats.

By changing the time format for a time column, you can change the number of unique values in your data set. See *Rearranging the Data by Formatting* for more information.

#### ► To set Time Formatting for a column:

- Open the **Properties** dialog by selecting **Edit > Properties** and click on the **Columns** tab.
- Select one or more columns you wish to set time formatting for.
- Click on the **Format** button.

- Select **Time...** which opens the Time Format dialog.



- Click on a format type.  
Response: An example of what the selected time format would look like is shown in the Sample field.
- When you are satisfied with the selected format, click **OK**.

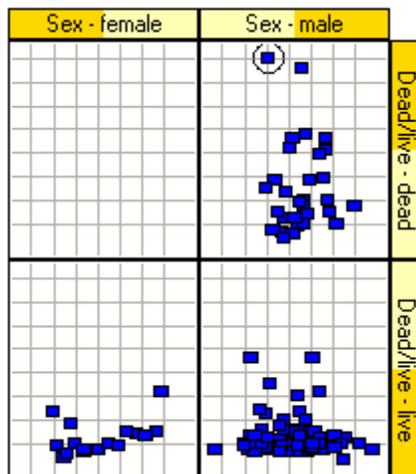
Selecting **Format > None** from the Format drop-down menu, resets the format to the default setting.

**Tip:** If you want to change the time formatting for a single column you can also reach the Time Format dialog from the pop-up menu of the Query Devices panel. Right-click on the column of interest and select **Set Property > Format > Time...** from the pop-up menu.

## 4.8.4 Trellis Tab

### 4.8.4.1 What is a Trellis plot?

Trellis plots enable you to quickly recognize similarities or differences between different subsets. Trellis plots provide the means to create a systematic layout for scatter plots, bar charts, profile charts and heat maps. Each individual pane in a Trellis plot displays a subset of the original data set, where the subset is defined by certain *conditions*. By this we mean that all the records in a particular subset have the same value for one or more attributes. A condition specifies one attribute.



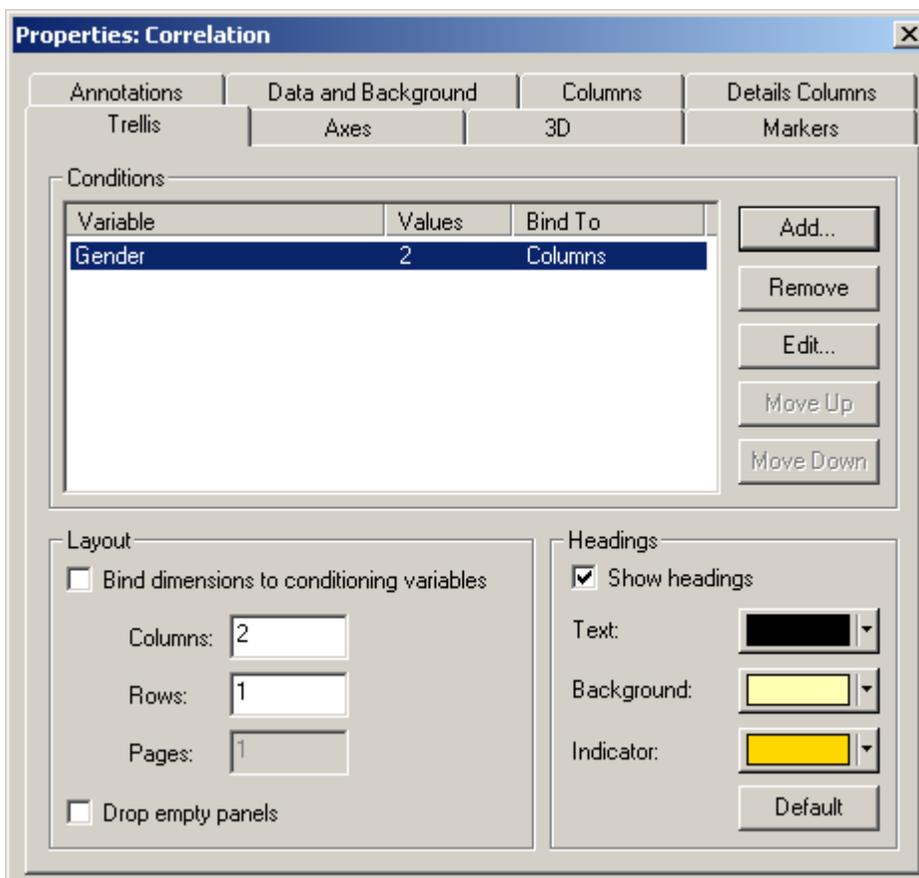
A Trellis plot is a way of breaking up a visualization (scatter plot, profile chart or heat map) into several panels, each one displaying a particular sub set of the data. The example above displays a Trellis plot with two conditions: Sex and Dead/Alive.

► **To create a Trellis plot:**

1. Create a new scatter plot, profile chart or heat map.
2. Open the **Properties** dialog.
3. Go to the **Trellis** tab.
4. In the **Conditions** box, click **Add...**
5. In the **Trellis condition** dialog, select the variable (column name) by which you want to separate the plots.
6. Click **OK**.

#### 4.8.4.2 Trellis Tab

Edit > Properties > Trellis tab



Option	Description
<b>Conditions</b>	A condition specifies a variable by which the data is divided into subsets. Each value of the conditioning variable will yield a separate subset. Adding a second condition will split each subset, etc.
<b>Layout</b>	You can control the layout of the plots in terms of rows, columns and pages. There are two ways of doing this: <b>Automatically</b> , by binding a dimension to each conditioning variable. <b>Manually</b> , by specifying the exact dimensions of the Trellis plot. You can also select whether or not to show empty trellis panels by clearing or selecting the <b>Drop empty panels</b> check box.
<b>Headings</b>	Specifies whether or not to show headings. You can also change the colors used in the headings.

### 4.8.4.3 Trellis Conditions

Edit > Properties > Trellis tab

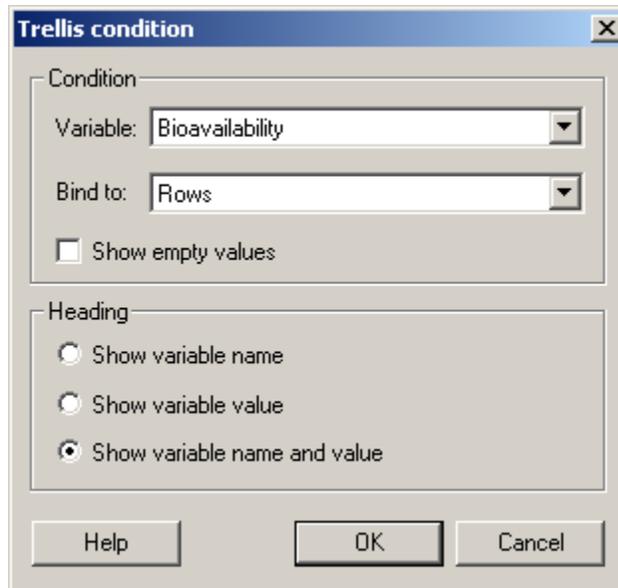
A condition specifies a variable by which the data is divided into subsets. Each value of the conditioning variable will yield a separate subset. Adding a second condition will split each subset, etc.

If, for example, two Boolean variables are used as conditioning variables, this will result in four separate plots representing the combinations True-True, True-False, False-True and False-

False. If a Boolean variable is used in conjunction with a variable that has five different values, this will yield ten plots. From this follows that variables with a continuous distribution and a wide range of values (e.g. Real values) should be binned before forming a Trellis plot. Otherwise the number of plots quickly becomes unmanageable.

► **To add a condition:**

1. In the **Properties** dialog, under the **Trellis** tab, click **Add...**
2. In the **Trellis condition** dialog, select a variable and a dimension to bind it to.
3. Optionally, use the radio buttons in the **Heading** box to control what information to show in the heading for this variable.
4. Click **OK**.



**Empty values**

Selecting the **Show empty values** option will generate an extra trellis panel containing records for which the conditioning variable is undefined.

► **To remove a condition:**

1. Select a condition from the list on the **Trellis** tab.
2. Click **Remove**.

► **To modify an existing condition:**

1. Select a condition from the list.
2. Click **Edit...**
3. In the **Trellis condition** dialog, make the desired changes.
4. Click **OK**.

► **To change the order of conditions:**

1. Select a condition from the list.
2. Click **Move up** or **Move down**.

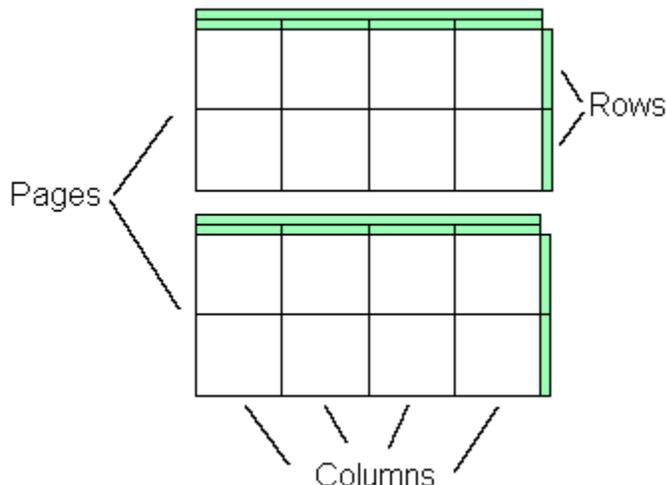
**Tip:** The settings in the Trellis condition dialog can also be reached and changed by right-clicking on any trellis panel heading.

### 4.8.4.4 Trellis Layout

Edit > Properties > Trellis tab

You can control the layout of the plots in terms of rows, columns and pages. There are two ways of doing this:

- Automatically, by binding a dimension to each conditioning variable.
- Manually, by specifying the exact dimensions of the Trellis plot.



Example of three conditioning variables bound to rows, columns and pages.

#### ► To arrange the plots automatically:

1. In the **Properties** dialog, under the **Trellis** tab, make sure the check box labeled **Bind dimensions to conditioning variables** is selected.
2. Click **Add...**
3. In the Trellis Condition dialog, select a variable and a dimension to bind it to.  
Comment: If Bind to: Columns is selected, all trellis panels will be displayed side by side with the title at the top. If Bind to: Rows is selected, the trellis panels will be under each other with the title on the right hand side of all rows. If Bind to: Pages is selected, each trellis panel will be displayed on a separate page and you will have to scroll down to see all panels.
4. Repeat steps 2 and 3 for any additional conditions.

**Tip:** Experiment with different layouts while still in the Trellis Condition dialog. The visualization is updated dynamically, so you can immediately see the results of your current settings.

#### ► To set layout manually:

1. In the **Properties** dialog, under the **Trellis** tab, make sure the check box labeled **Bind dimensions to conditioning variables** is cleared.
2. Enter the number of trellis panels that you want to show next to each other simultaneously, both horizontally (columns) and vertically (rows). The number of pages is automatically updated to make sure there is room for the specified panels – you can never change the number of pages directly.

### 4.8.4.5 Trellis Headings

Edit > Properties > Trellis tab

## Show Headings

You can select whether or not to show trellis panel headings from the **Trellis** tab of the **Properties** dialog. Select the check box to show all headings. Clear the check box to hide all headings. You can also right-click on any trellis panel header and select **Heading > Hide All Headers** from the pop-up menu.

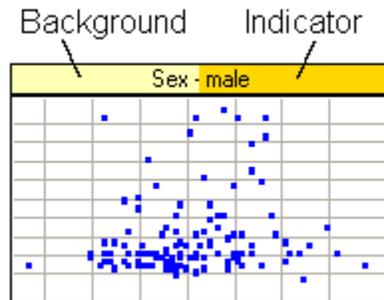
## Heading Color

The colors used in the headings of columns, rows and pages can be set manually from the **Trellis** tab of the **Properties** dialog.

**Text** is the color of the text in all headings.

**Background** is the background color of all headings.

**Indicator** is the color of the bar that indicates the relative size and position of the range of values.



**Note:** The indicator bar represents the size of the range of values represented by a column, row or page, not the number of records with that value.

## Heading Text

What to show in the heading text is specified from the Trellis condition dialog, reached by clicking Add... or Edit... on the **Trellis** tab of the **Properties** dialog. You can specify which of three options should be shown as the heading for the trellis panels.

- Show variable name
- Show variable value
- Show variable name and value

### 4.8.4.6 Empty Panels

It is possible to insert empty panels anywhere in the layout. This can be useful when manually configuring a multi-page layout. Normally in such a layout, a page flows to the next as soon as it is full. This may not always be appropriate.

Consider, for example, a situation with twenty-four panels arranged in a three-by-three layout. This would yield two pages with nine panels on each, and a final page with only six panels. By inserting an empty panel on each page, the result would be three pages with eight (non-empty) panels on each.

#### ► To insert an empty panel:

1. In the **Trellis** tab of the **Properties** dialog, make sure **Bind dimensions to conditioning variables** is cleared.
2. Right-click in the heading field of the panel where you want the empty panel to be inserted.
3. Select **Insert Empty Panel**.

If an empty panel is inserted on the first page, it will appear at the same position on each subsequent page. An empty panel inserted on the second page will appear on even pages, etc.

You may also be in the situation where some of the combinations of variables used for the trellis panels result in panels without any records. These panels can easily be hidden.

► **To hide empty panels:**

1. Right-click in the heading field of any trellis panel.
2. Select **Drop Empty Panels** from the pop-up menu.

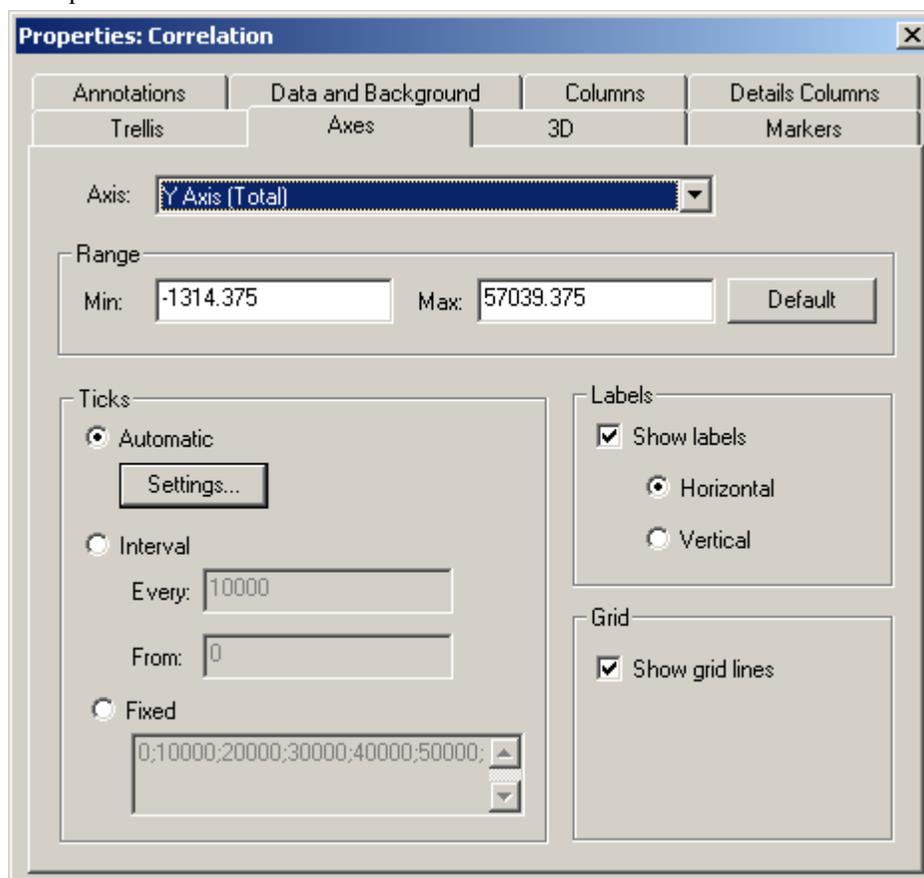
Comment: You can also select the Drop empty panels check box in the Layout field of the Trellis tab in the Properties dialog.

## 4.8.5 Axes Tab

### 4.8.5.1 Axes Tab

Edit > Properties > Axes tab

Axis labels for Scatter Plots are controlled from the **Axes** tab of the **Properties** dialog. For other plots see Axes.



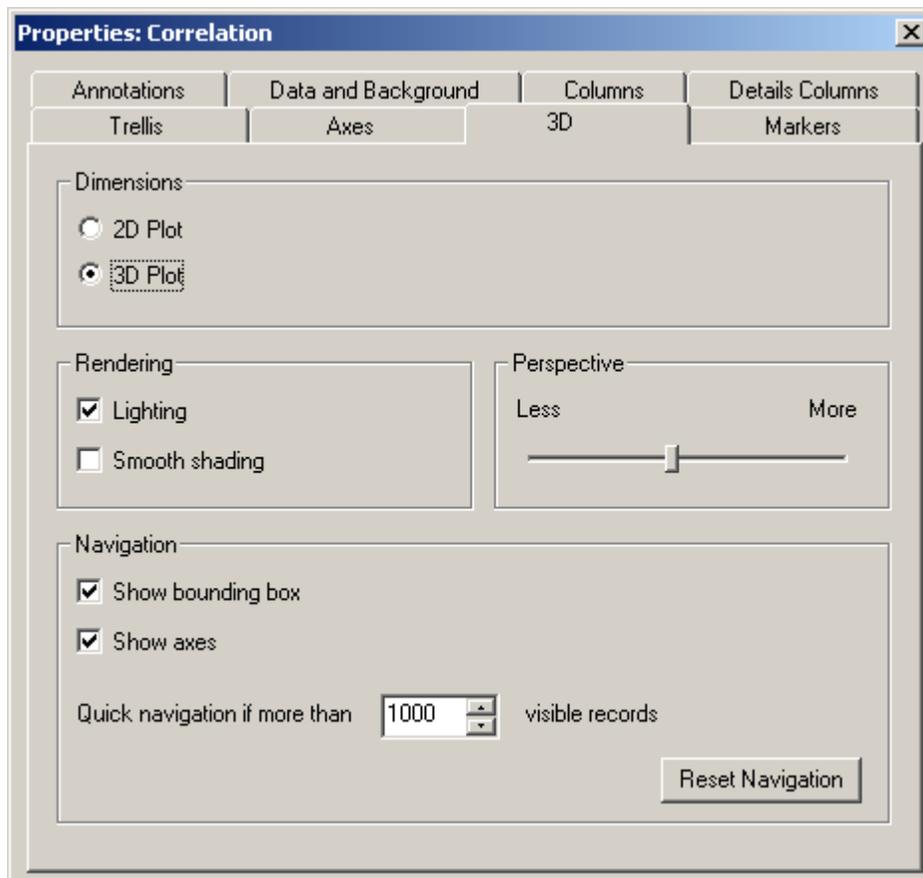
Option	Description
Axis	Select the axis whose labels you want to edit. All other settings made in the <b>Axes</b> dialog are specific to the axis you have currently selected here.

<b>Range</b>	The minimum and maximum values specify the range of the axis labels. Default will set the range to encompass the entire data range.
<b>Ticks</b>	<p>There are three options for tick mark control:</p> <p><b>Automatic</b> – this option will attempt to display a suitable number of labels at even intervals. You can modify this somewhat by clicking the <b>Settings</b> button, which opens the Ticks dialog. Select the <b>Spacing</b> you want, and the <b>number of Ticks</b> to be displayed. For spacing you can select to show axis labels in four ways:</p> <ul style="list-style-type: none"> <li>Even Distribution – will attempt to distribute labels evenly between the highest and lowest value</li> <li>At Values – will not place a label where there is no value</li> <li>At All Values – will place labels at all values</li> <li>At Even Values – will attempt to place labels at evenly spaced whole numbers.</li> </ul> <p><b>Interval</b> – this option lets you specify an exact interval for the labels, which you enter in the <b>Every</b> field. You may also specify from which value the labels should be drawn, in both directions. For example, if you set Every: 10 and From: 1920, labels would appear in steps of -10 and +10 originating from the value 1920.</p> <p><b>Fixed</b> – this option lets you specify the exact values for which you want labels to appear. Simply type the values into the field separated by a semicolon. Example: 1920;1922;1930;1955;1991</p> <p>This can also be used to specify the number of decimals to be shown on the axes.</p> <p>Another feature of the <b>Fixed</b> option is that you may name a tick mark to display a string instead of the value, like this: 0.0;3.14=Pi;5.0;10.0 which would display the text "Pi" as a label instead of 3.14.</p>
<b>Labels</b>	<p>The <b>Show labels</b> check box sets whether or not to display labels for the current axis.</p> <p>The <b>Horizontal</b> or <b>Vertical</b> radio buttons sets whether the labels for the current axis should be displayed horizontally or vertically.</p>
<b>Grid</b>	The <b>Show grid lines</b> check box sets whether or not to display grid lines for the current axis.

## 4.8.6 3D Tab

### 4.8.6.1 3D Tab

Edit > Properties > 3D tab



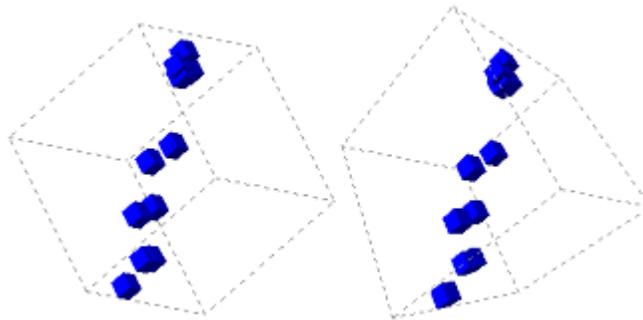
Option	Description
<b>Dimensions</b>	<p>You can choose whether to display a 2D Scatter Plot or a 3D Scatter Plot by selecting the appropriate radio button.</p> <p>A 3D visualization can be 'flattened' into a 2D scatter plot or, conversely, a 2D plot can be made into one with 3D attributes. In the latter case Spotfire DecisionSite will suggest a third axis using the same algorithm as with 2D scatter plots.</p>
<b>Rendering</b>	<p>With the <b>Lighting</b> check box cleared, the glyphs will be flat, as if illuminated evenly from all sides, a sphere will appear as a filled circle and a cube from certain angles will look like a hexagon and from other angles like a square.</p> <p>The <b>Smooth Shading</b> alternative will smooth edges of adjacent polygons on the surface of the glyphs; mostly useful when the filled sphere is used, this makes the sphere appear rounder.</p>
<b>Perspective</b>	<p>The perspective slider modifies the 'field of view' of the 3D visualization. Using the mouse, drag the slider towards the right for a 'wide angle' perspective.</p>
<b>Navigation</b>	<p>This section provides various helpful settings for quicker navigation of the 3D scatter plot.</p>

### 4.8.6.2 3D – Perspective

Edit > Properties > 3D tab



The perspective slider modifies the 'field of view' of the 3D visualization. Using the mouse, drag the slider towards the right for a 'wide angle' perspective. With the slider in the left-most position the view becomes orthogonal, a projection where the size of the markers is retained no matter the distance. The keyboard arrow keys allow fine-tuning of the perspective when the slider has been activated.

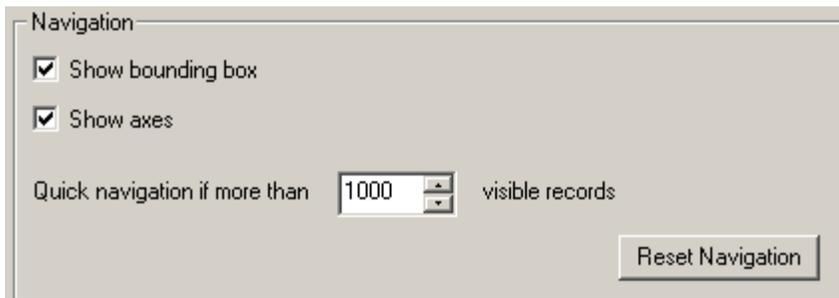


Orthogonal view (left) and exaggerated perspective (right).

**Note:** When viewing 3D plots the perspective view will make markers that are 'closer' to the viewer look bigger and so care must be taken if you also want size to reflect some attribute. Orthogonal projection where markers retain size irrespective of distance may be preferable.

### 4.8.6.3 3D – Navigation

Edit > Properties > 3D tab



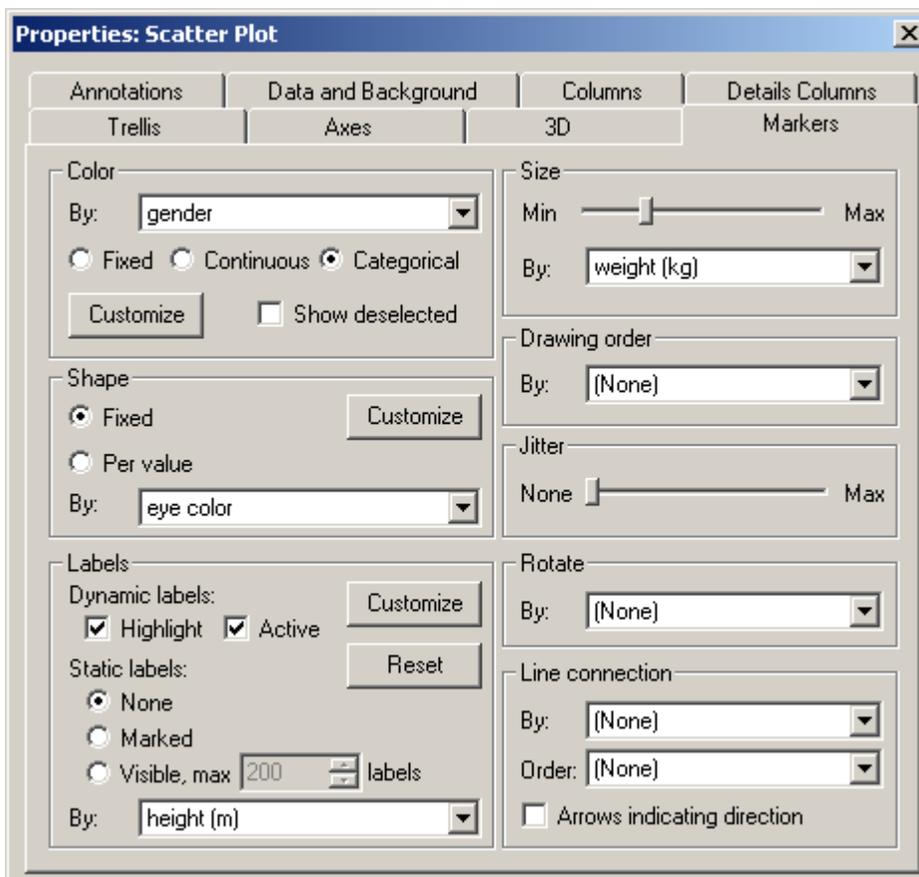
Option	Description
<b>Show bounding box</b>	This draws a dotted cube around the edges of the visualization volume, which often aids in locating a marker in the 3D space.
<b>Show axes</b>	This draws the arrows representing the X, Y and Z axes.
<b>Quick navigation if more than...visible records</b>	This lets you speed up rotation, zooming, etc by drawing markers as dots while navigating. Markers are restored to their normal shapes as soon as you stop navigating. Use this feature if the lag times become too great during 3D navigation.
<b>Reset Navigation</b>	This button resets the orientation of the visualization—X (horizontal), Y (vertical), and Z (depth)—but does not affect zooming or perspective.

**Note:** The Reset button in the toolbar will reset not only navigation, but also all query devices.

## 4.8.7 Markers Tab of the Scatter Plot

### 4.8.7.1 Markers Tab of the Scatter Plot

Edit > Properties > Markers tab



Option	Description
<b>Color</b>	Markers can be colored to reflect the value of a particular attribute. There are three modes for coloring: Fixed, Continuous and Categorical.
<b>Shape</b>	The shape of markers can be fixed, or made to reflect the value of a particular column. Click <b>Fixed</b> or <b>Per value</b> to alternate between these modes.
<b>Labels</b>	It is possible to tag each marker with a label, showing the value of a particular column. You can select to show both Dynamic labels (Highlight and/or Active) and Static labels (None/Marked/Visible) at the same time. Dynamic labels are always placed on top of any static labels. The static labels include the following options: <b>None</b> – No labels are visible. <b>Marked</b> – Only records that are marked will have labels next to them.

	<p><b>Visible, max</b> – All visible records (up to a specified maximum number) will have labels next to them, provided that the number of visible markers does not exceed the specified max number. If so, no labels are shown.</p> <p>Select the column you wish to label by, from the drop-down list <b>By</b>. Click on <b>Customize</b> to open the Customize Labels dialog, where you can change the color and line width of the label frames and lines, as well as the size available to labels.</p> <p>You can drag labels to any position within the visualization area. Click on <b>Reset</b> to return all marker labels to their original position.</p> <p>If you are running DecisionSite for Lead Discovery, you can also select to display the chemical structure for each record in the label. This is done by right-clicking in the scatter plot and selecting <b>Structure Marker Labels</b> from the pop-up menu.</p> <p>Select Structure Marker Labels &gt; Remove to revert to the column selected here.</p>
<b>Size</b>	<p>The size of markers can be made to reflect the value of a particular column. Select a column from the drop-down list under <b>Size</b>. Moving the slider changes the size of all markers, while maintaining the size ratio of different markers.</p>
<b>Drawing order</b>	<p>It is possible to specify the order in which the markers of a scatter plot will be drawn. This is done by specifying a column that will determine the drawing order.</p> <p><b>Note:</b> By setting both <b>Size by</b> and <b>Drawing order by</b> to the same column, the smaller markers will be drawn on top of the larger ones.</p>
<b>Jitter</b>	<p>Jittering displaces markers slightly and randomly, thereby making aggregations stand out visually. Attention is brought to areas where many records overlap.</p>
<b>Rotate</b>	<p>The rotation of markers can be made to reflect the value of a column. Using asymmetrical markers and rotating them according to a chosen variable takes advantage of the human ability to visually detect regions with different surface structure.</p>
<b>Line connection</b>	<p>Line connection means that a line is drawn between records that share some property. To follow a progression, markers can also be connected in ascending order according to some other property. The order of lines can be made clearer by use of arrows indicating direction (pointing from lower to higher value in the <b>Order</b> column).</p>

### 4.8.7.2 Color

Edit > Properties > Markers tab



Markers can be colored to reflect the value of a particular attribute. There are three modes for coloring: Fixed, Continuous and Categorical. The mode is set in the **Properties** dialog.

Option	Description
<b>Fixed</b>	Fixed coloring means that all markers are the same color (except deselected and marked).
<b>Continuous</b>	<p>Continuous coloring means that the maximum and minimum specified values in the selected column are each assigned a color. Intermediate values are then assigned colors on a scale ranging between the two extreme colors. In scatter plots, any column can be used for continuous coloring. Any values not included in the range are given a specific color.</p> <p>Colors, representing minimum and maximum values are set with the <b>Customize</b> dialog. <b>Begin</b> and <b>End</b> categories define the color limits.</p> <p>When one of the categories is selected, you can choose which color will represent that end of the value range. A line with the color scale is displayed below the corresponding query device.</p>
<b>Categorical</b>	Categorical coloring means that each value in the chosen column is given its own color. However, categorical coloring makes most sense if there are less than ten unique values. To control which color is assigned to each value, click <b>Customize</b> .
<b>Customize Colors</b>	<p>Regardless of coloring mode, the choice of colors can be controlled by clicking <b>Customize</b> on the <b>Markers</b> tab of the <b>Properties</b> dialog.</p> <p>Depending on the current coloring mode, the top-most list will display the fixed color, Begin and End colors (continuous mode), or the color associated to each category (categorical mode). The other list displays colors associated with deselected, empty and marked records. ("Empty" refers to records for which no value is specified in the column used for coloring.)</p>

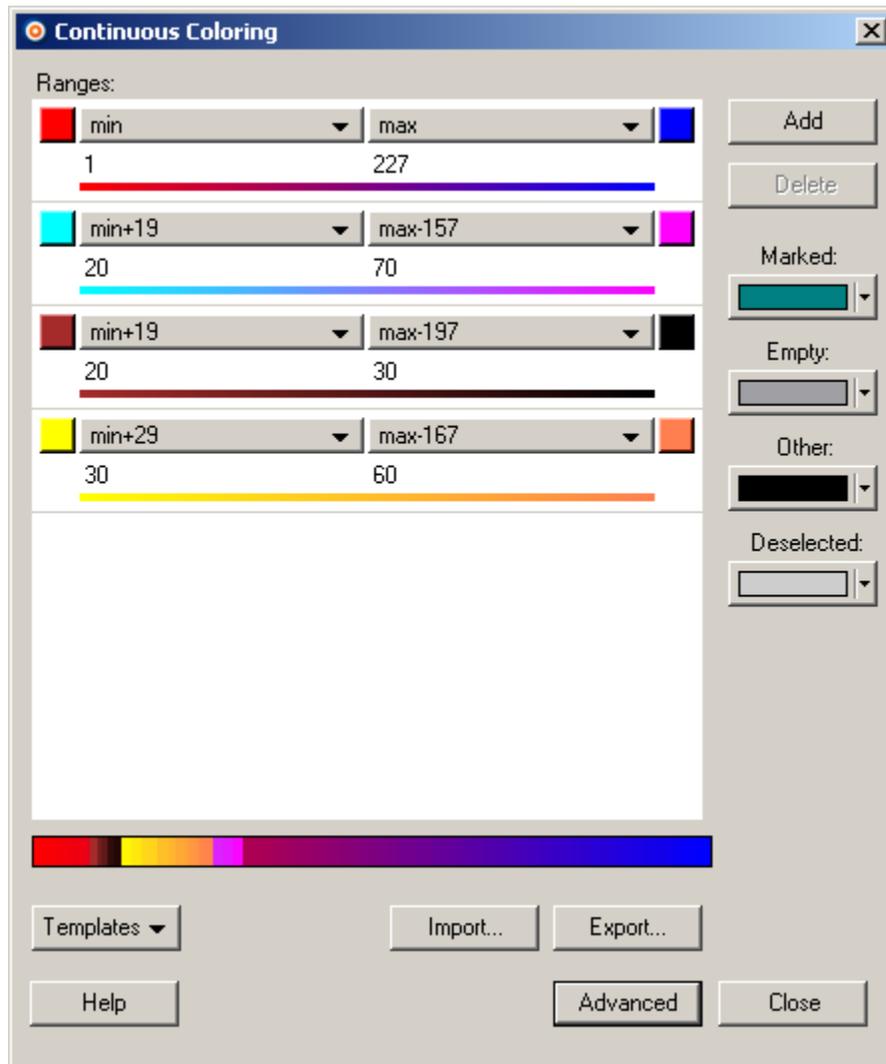
### 4.8.7.3 Overlapping Color Ranges

It is possible to specify overlapping color ranges. This means that the value of a marker can be inside several ranges, but the marker will always only have one color. DecisionSite uses the following method to determine which color range will be used to set the color of the marker:

If the value of a marker is included in several ranges, the gradient with the highest start value is selected. However, if multiple gradients exist with the same low start value, the gradient with the lowest end value is selected.

Also note that categorical values are more important than continuous ones. In other words, if you have a value that you have set to a specific categorical color, this color will be used even if the value is also defined within a color range.

**Example:**



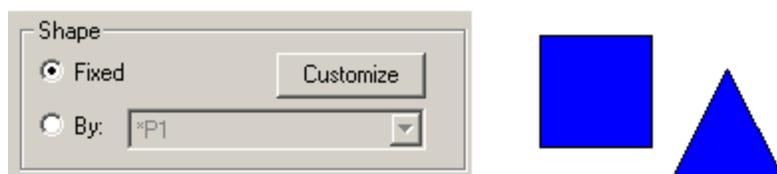
If you have set the Ranges as above:

- Value 1 is colored according to the first range.
- Value 20 is colored according to the third range.
- Value 30 is colored according to the last range.

When the dialog is opened the color gradients are sorted such that the highest priority is at the bottom, next highest just above that, and so on. If new gradients are added, the order is changed, but you can restore the order by right-clicking and selecting **Sort gradients**, which will cause the list to reflect the drawing order.

### 4.8.7.4 Shape and Rotation

Edit > Properties > Markers tab



The shape of markers can be fixed, or made to reflect the value of a particular column. Click **Fixed** or **By** to alternate between these modes. Only columns with less than 23 distinct values can be used for controlling shapes. Click **Customize** to choose appropriate shapes for each value.

There are twelve shapes available for 3D markers:

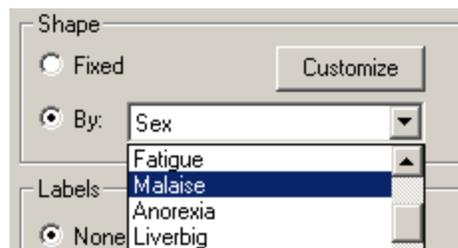
Solid Cube	Wire Cube	Arrow (Pyramid)	Minus
Solid Sphere	Wire Sphere	Diamond	Bar
Solid Tetrahedron	Wire Tetrahedron	Cross	Point

These shapes consist of polygonal surfaces or lines. They all show shading and other '3D' characteristics. Some shapes are particularly useful in conjunction with rotation.

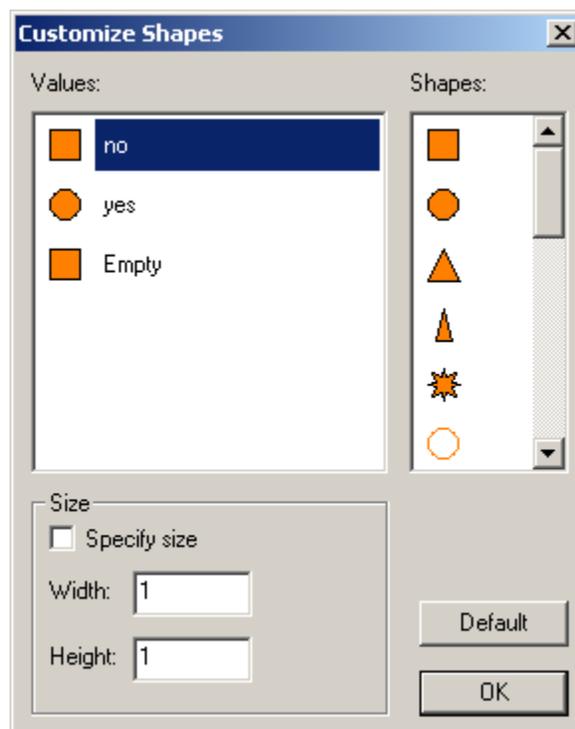
It is possible to customize the shape and size of the markers in a scatter plot.

#### ► To customize markers:

1. Open a scatter plot.
2. Select **Edit > Properties**.
3. Select the **Markers** tab.
4. Select a column to determine the shape of the markers.



5. Click on **Customize**.



6. Select a value ("no", "yes" or "Empty" in the example above).
7. Select a shape for that value.
8. Select the **Specify size** check box.  
When this option is selected, the custom size overrides the usual size slider in the properties Marker tab.
9. Enter **Width** and **Height**.  
These values are relative to the scale used in the current visualization. Look at the scale used in the current visualization and determine how large you wish your markers to be.

**Note:** The horizontal and vertical scale may be different, which means that a perfect square might not have the same **Width** and **Height** values.

**Note:** Use **Reverse sorting** if you want the markers to be drawn in the opposite order. Right-click in the Query Device you wish to sort by, select **Set Property** and **Reverse sorting**.

### Rotation

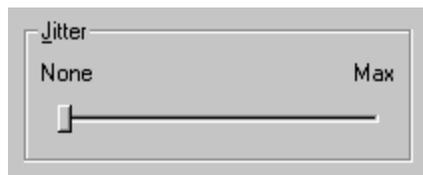


The rotation of markers can be made to reflect the value of a column. Using asymmetrical markers and rotating them according to a chosen variable takes advantage of the human ability to visually detect regions with different surface structure. The maximum rotation is 90 and so the most useful shapes for this effect are the arrow, the minus, and the bar.

In 3D plots, the marker rotation is implemented around the Z-axis.

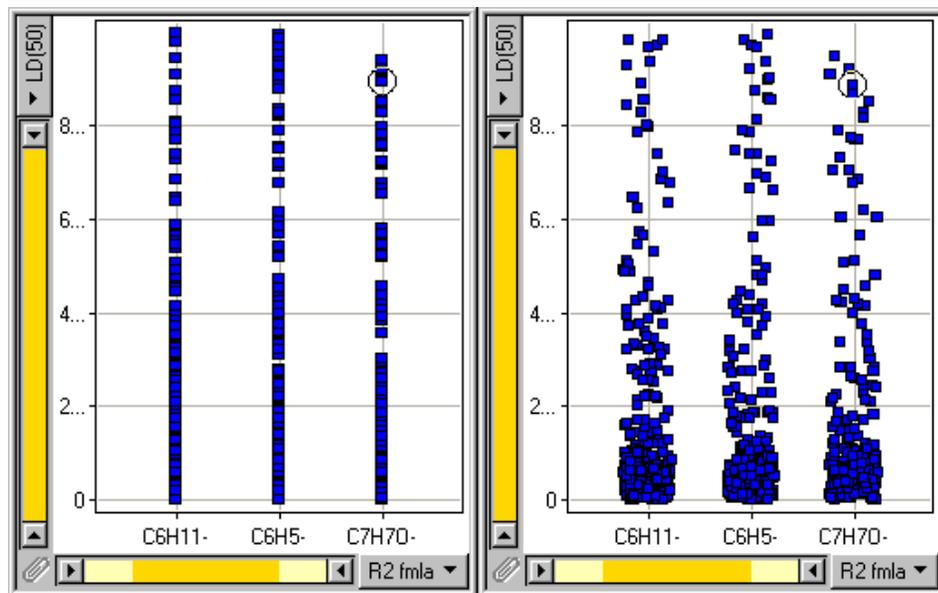
## 4.8.7.5 Jitter

Edit > Properties > Markers tab



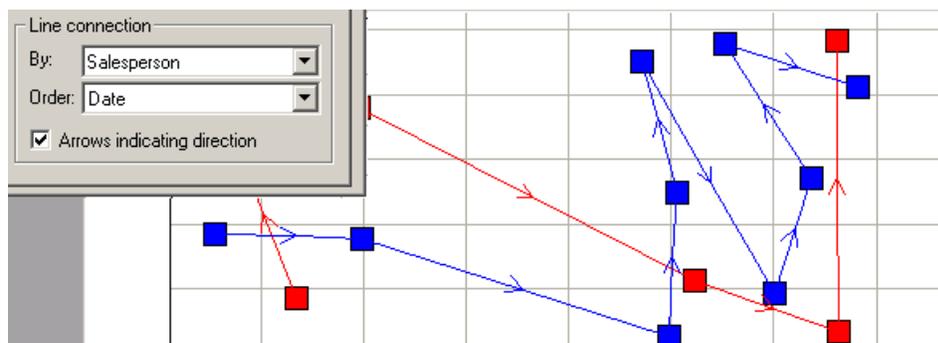
Jittering displaces markers slightly and randomly, thereby making aggregations stand out visually (below, right). Attention is brought to areas where many records overlap. Such regions can then be investigated further, by zooming, changing axes, etc. Use the slider to increase or decrease jittering.

Scatter plots, line charts, profile charts and pie charts support jittering.



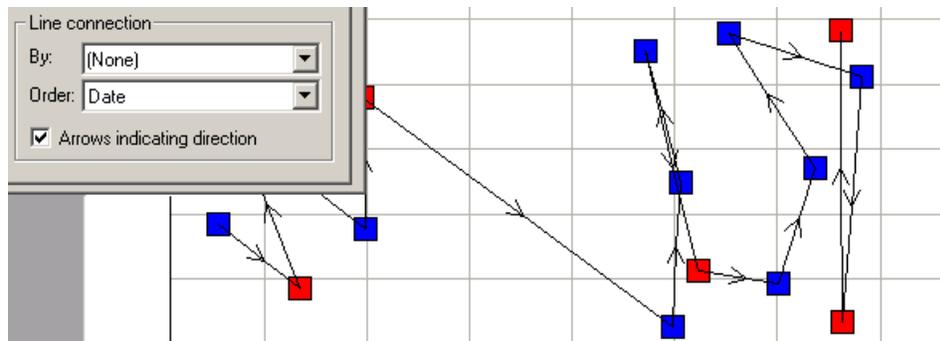
#### 4.8.7.6 Line Connection

Edit > Properties > Markers tab



Line connection means that a line is drawn between records that share some property. To follow a progression, markers can also be connected in ascending order according to some other property. The order of lines can be made clearer by use of arrows indicating direction (pointing from lower to higher value in the **Order** column). To demonstrate the usefulness of line connection, in the example data above, the locations of two salespersons, indicated by red and blue, are plotted. The two salespersons visit various locations at different points in time. Without the lines and arrows indicating direction, we would be unable to see in which order the blue salesperson visited the different locations.

Setting the **By:** selection to (None) causes the Line connections to disregard which individual salesperson went to what location, and will instead plot a timeline showing which locations were visited by any salesperson in order of the date the locations were visited:



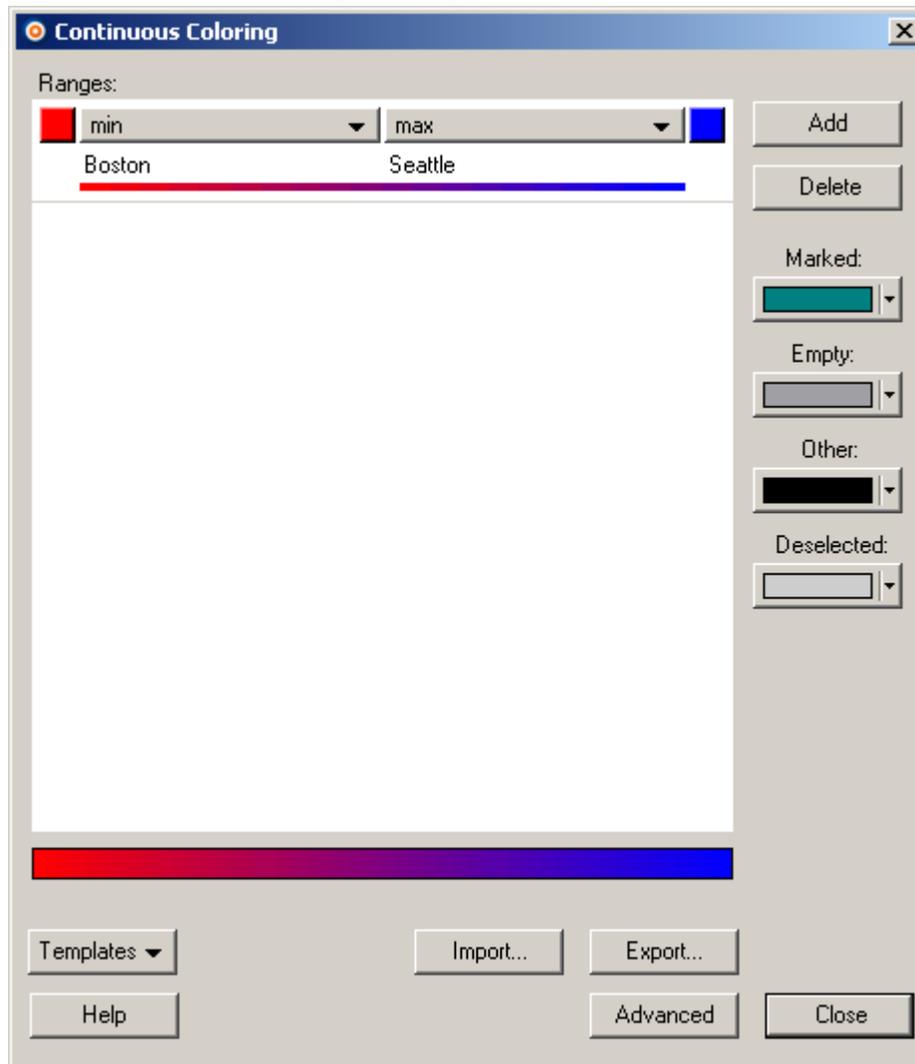
## 4.8.7.7 User Interface

### 4.8.7.7.1 Fixed Coloring Dialog



Option	Description
<b>Fixed</b>	Shows the color of the markers in the data set.
<b>Marked</b>	Shows the color of the records that have been marked.
<b>Empty</b>	Shows the color of the empty records. Empty refers to records that have at least one empty field. These records are not shown at all in visualizations where an axis corresponds to the missing field.
<b>Undefined</b>	Shows the color of values that are not included in a range (continuous).
<b>Deselected</b>	Shows the color of the deselected values. Deselected refers to records that do not fulfill the constraints of the query devices.

### 4.8.7.7.2 Continuous Coloring Dialog



Option	Description
<b>Ranges</b>	Displays the values in the chosen column, and the color for each value. <b>Note:</b> When the dialog is opened the color gradients are sorted such that the highest priority is at the bottom, next highest just above that, and so on. If new gradients are added, the order is changed, but you can restore the order by right-clicking and selecting <b>Sort gradients</b> .
<b>Add</b>	Adds a new item to the list of Color ranges. Using this, you can assign specific colors to values, and create your own coloring arrangement.
<b>Delete</b>	Removes a selected value. Ctrl+click to select multiple items for deletion.
<b>Marked</b>	Shows the color of the records that have been marked.
<b>Empty</b>	Shows the color of the empty records. Empty refers to records that have at least one empty field. These records are not shown at all in visualizations where an axis corresponds to the missing field.

<b>Other</b>	Shows the color of values that are not included in a range (continuous).
<b>Deselected</b>	Shows the color of the deselected values. Deselected refers to records that do not fulfill the constraints of the query devices.
<b>Templates &gt;</b>	
<b>&gt; Two color gradient for all records</b>	Applies a two-color color arrangement to your data, one color as your minimum value, and one as your maximum value.
<b>&gt; Three color gradient for all records</b>	Applies a three-color color arrangement to your data, one color as your minimum value, one as your maximum value, and the third color as a central value.
<b>&gt; Two color gradient for visible records</b>	Applies a two-color color arrangement to your visible data.
<b>&gt; Three color gradient for visible records</b>	Applies a three-color color arrangement to your visible data.
<b>&gt; Two color gradient highlighting outliers</b>	Applies a two-color color arrangement to your data, but outliers are highlighted in another color, rather than being included in the continuous coloration.
<b>&gt; Two color gradient resisting outliers</b>	Applies a two-color arrangement to your data in which all values before $\text{median}-2*\text{stddev}$ are colored the first color (red), and all values after $\text{median}+2*\text{stddev}$ are colored the final color (blue). Outliers are colored either red or blue. Values close to the median are easily distinguished.
<b>Import...</b>	Imports a color arrangement from a file.
<b>Export...</b>	Exports a color arrangement to a file. This enables you to save a color arrangement and reuse it.
<b>Advanced</b>	Switches you to the Advanced Coloring dialog where you can have more control over the way you color your values and ranges.

► **To change a color in Continuous mode:**

1. Click on the square of the color that you want to modify.
2. Select a color from the palette or click **More colors...** to see the complete color palette.

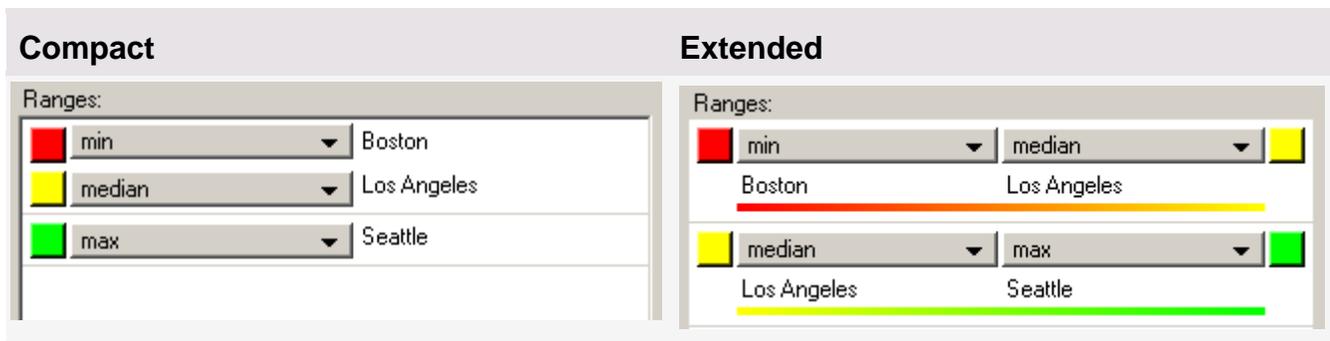
► **To change the Marked, Empty or Deselected color:**

1. Click the button of the color that you want to modify.
2. Select a color from the palette or click **More colors...** to see the complete color palette.

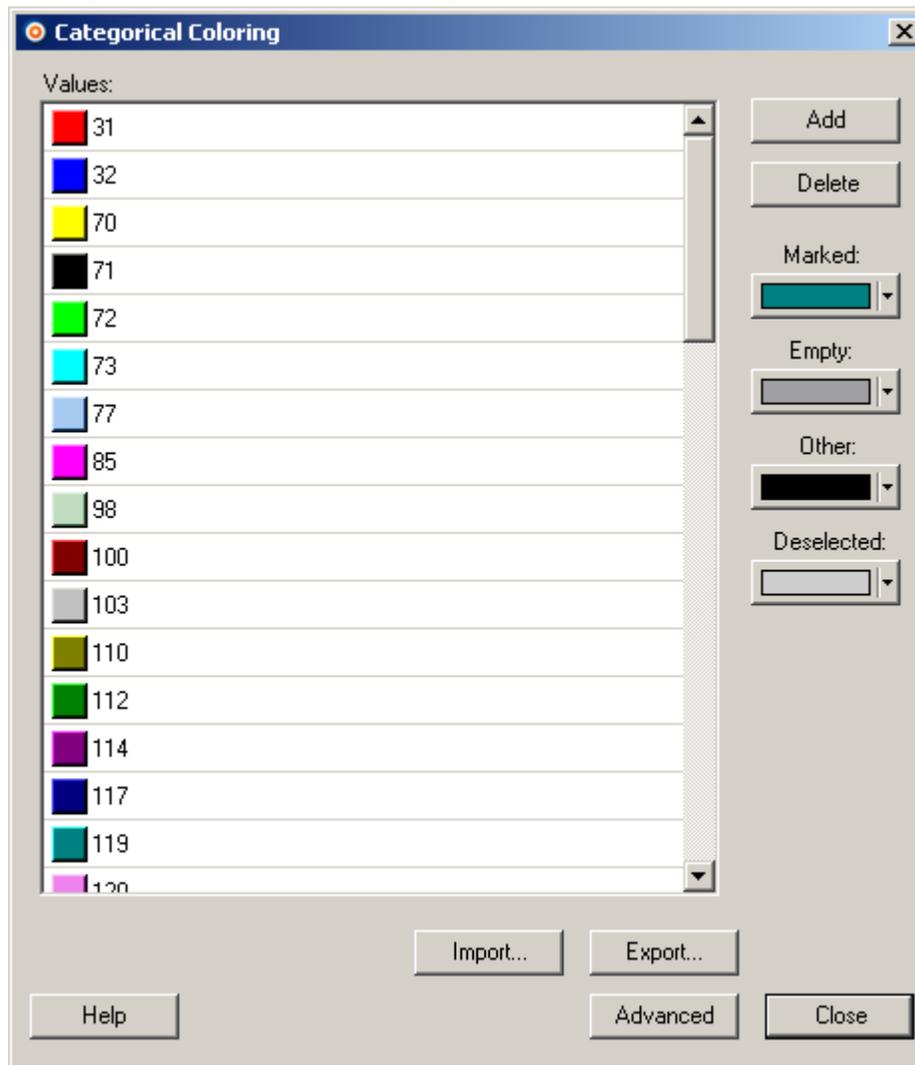
► **To switch between the Compact and Extended color views:**

Right-click in the Continuous Coloring dialog and select either **Compact color view** or **Extended color view**.

Compact color view is useful when you are creating a connected gradient, i.e., when there are overlaps or holes. If, for example, you have a connected gradient through the points  $\text{min} \rightarrow \text{median} \rightarrow \text{max}$ , and you wish to change median to average, you only need to change one item in the Compact color view, whereas you would have to change two items ( $\text{min} \rightarrow \text{median}$  and  $\text{median} \rightarrow \text{max}$ ) in the Extended color view.



### 4.8.7.7.3 Categorical Coloring Dialog



Option	Description
Values	Displays the values in the chosen column, and the color for each value. <b>Note:</b> When the dialog is opened the values are sorted. If new values are added, the order is changed, but you can restore the order by right-clicking and selecting <b>Sort gradients</b> .

<b>Add</b>	Adds a new item to the list of Color values. Using this, you can assign specific colors to values, and create your own coloring arrangement.
<b>Delete</b>	Removes a selected value. Ctrl+click to select multiple items for deletion.
<b>Marked</b>	Shows the color of the records that have been marked.
<b>Empty</b>	Shows the color of the empty records. Empty refers to records that have at least one empty field. These records are not shown at all in visualizations where an axis corresponds to the missing field.
<b>Other</b>	Shows the color of values that are not specified in the Values list.
<b>Deselected</b>	Shows the color of the deselected values. Deselected refers to records that do not fulfill the constraints of the query devices.
<b>Import...</b>	Imports a color arrangement from a file.
<b>Export...</b>	Exports a color arrangement to a file. This enables you to save a color arrangement and reuse it.
<b>Advanced</b>	Switches you to the Advanced Coloring dialog where you can have more control over the way you color your values and ranges.

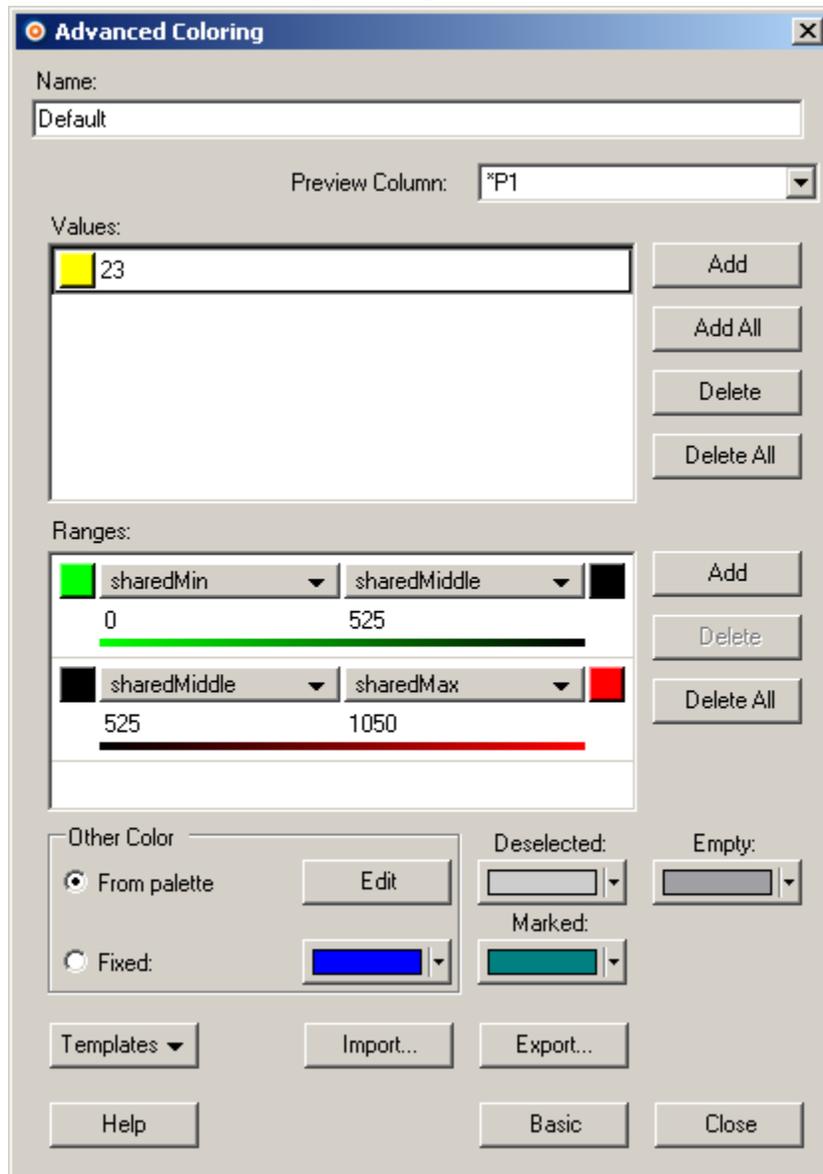
► **To change a color in Categorical mode:**

1. Click on the square of color that you want to modify.
2. Select a color from the palette or click **More colors...** to see the complete color palette.

► **To change the Marked, Empty, Other or Deselected color:**

1. Click the button of the color that you want to modify.
2. Select a color from the palette or click **More colors...** to see the complete color palette.

### 4.8.7.7.4 Advanced Coloring Dialog



Option	Description
<b>Name</b>	Displays the name of the coloring arrangement. Type to enter a new name.
<b>Preview Column</b>	Lists the columns from which you can add values to the <b>Values</b> list.
<b>Values</b>	Displays the values in the chosen column ( <b>Preview Column</b> ), and the color for each value. If a value has a defined categorical color, this color will be used even if the value is also defined within a color range.
<b>Add</b>	Adds a new item to the list of Values. Using this, you can assign specific colors to values, and create your own coloring arrangement.
<b>Add All</b>	Adds all available values from the selected <b>Color by</b> column to the Values list.

<b>Delete</b>	Removes a selected value. Ctrl+click to select multiple items for deletion.
<b>Delete All</b>	Deletes all items in the Values list.
<b>Ranges</b>	Shows the color of the empty records. Empty refers to records that have at least one empty field. These records are not shown at all in visualizations where an axis corresponds to the missing field.
<b>Add</b>	Adds a new item to the list of Ranges. Using this, you can assign specific colors to values, and create your own coloring arrangement.
<b>Delete</b>	Removes a selected value. Ctrl+click to select multiple items for deletion.
<b>Delete All</b>	Deletes all items in the Ranges list.
<b>Other Color &gt;</b>	<p>Determines which color is used for markers that do not get a color from any other setting. The color a marker gets is decided in the following order:</p> <ul style="list-style-type: none"> <li>Markers associated with a data row with empty/null value in the color column are set to the empty color</li> <li>Markers filtered out by query devices or zoom sliders are set to the deselected color.</li> <li>Marked items are drawn using the marked color.</li> <li>Markers that are included in the value list are set to the color specified there. The value list may include values that are not part of the current data set, but you know those values could be included in a future data set, thus it is possible to set up color arrangements that have predefined colors for all anticipated values.</li> <li>Markers that are included in a color range (from the Ranges list) are set to a color from that range. <b>Note:</b> Because it is possible to specify overlapping ranges, a marker can be inside several ranges. See <a href="#">Overlapping Color Ranges</a> for more information.</li> <li>Any other markers are set to either a fixed color, or a color from a palette, depending on your selections. A palette is a list of colors. If there are more unique values in the color column than there are colors in the palette, colors will be reused.</li> </ul>
<b>&gt; From palette</b>	Causes each marker to get an individual color from the color palette list. <b>Note:</b> If there are more than 97 values, colors will be reused.
<b>&gt; Edit</b>	Launches the Edit Palette dialog where you can adjust the RGB values of individual colors.
<b>&gt; Fixed</b>	Lets you choose the color that the markers will get.
<b>Deselected</b>	Shows the color of the deselected values. Deselected refers to records that do not fulfill the constraints of the query devices.
<b>Marked</b>	Shows the color of the records that have been marked.
<b>Empty</b>	Shows the color of the empty records. Empty refers to records that have at least one empty field. These records are not shown at all in visualizations where an axis corresponds to the missing field.
<b>Templates &gt;</b>	
<b>&gt; Two color gradient for all</b>	Applies a two-color color arrangement to your data, one color as your

<b>records</b>	minimum value, and one as your maximum value.
> <b>Three color gradient for all records</b>	Applies a three-color color arrangement to your data, one color as your minimum value, one as your maximum value, and the third color as a central value.
> <b>Two color gradient for visible records</b>	Applies a two-color color arrangement to your visible data.
> <b>Three color gradient for visible records</b>	Applies a three-color color arrangement to your visible data.
> <b>Two color gradient highlighting outliers</b>	Applies a two-color color arrangement to your data, but outliers are highlighted in another color, rather than being included in the continuous coloration.
> <b>Two color gradient resisting outliers</b>	Applies a two-color arrangement to your data in which all values before $\text{median}-2*\text{stddev}$ are colored the first color (red), and all values after $\text{median}+2*\text{stddev}$ are colored the final color (blue). Outliers are colored either red or blue. Values close to the median are easily distinguished.
<b>Import...</b>	Imports a color arrangement from a file.
<b>Export...</b>	Exports a color arrangement to a file. This enables you to save a color arrangement and reuse it.
<b>Basic</b>	Returns you to the basic Categorical or Continuous or Heat Map Coloring dialog.

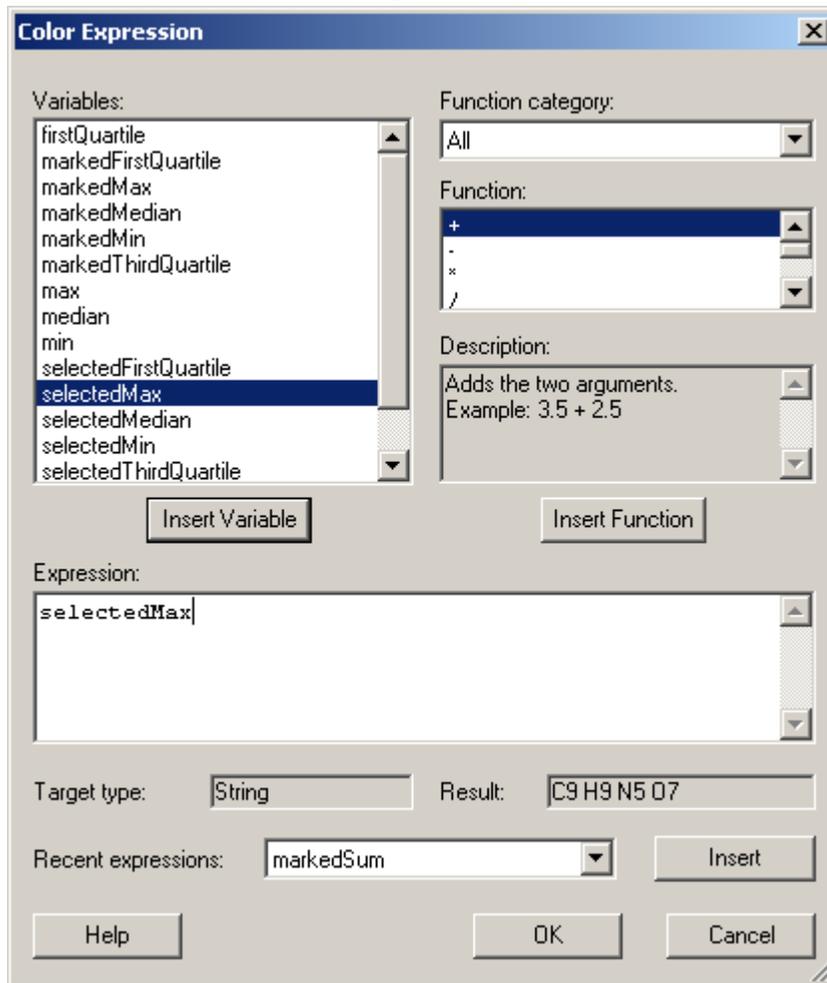
► **To change a color of the Values or Ranges:**

1. Click on the square of color that you want to modify.
2. Select a color from the palette or click **More colors...** to see the complete color palette.

► **To change the Marked, Empty or Deselected color:**

1. Click the button of the color that you want to modify.
2. Select a color from the palette or click **More colors...** to see the complete color palette.

### 4.8.7.7.5 Color Expression Dialog

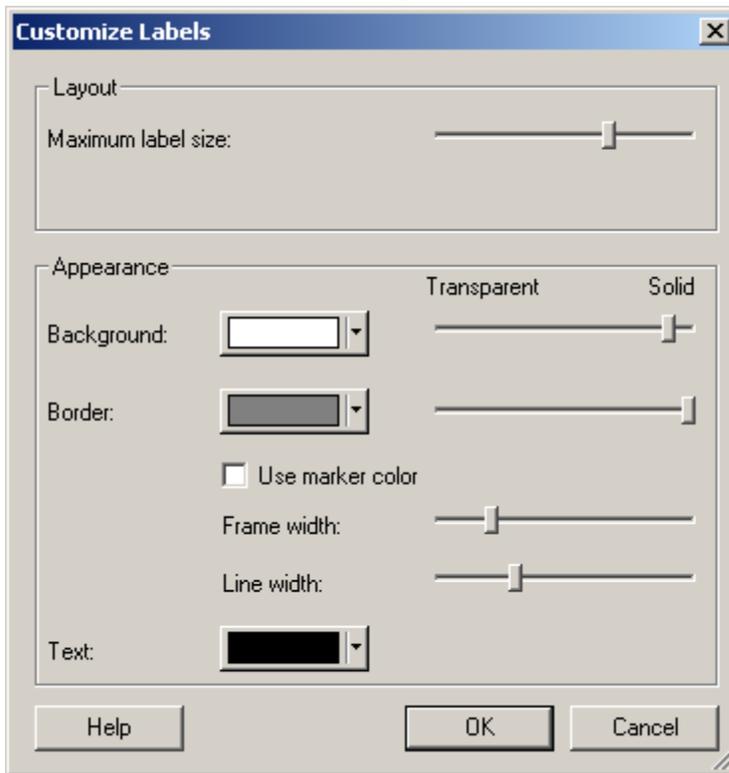


Option	Description
<b>Variables</b>	Lists the available variables which can be used to create your expression. Insert a variable into your expression with the <b>Insert Variable</b> button.
<b>Function category</b>	Select a category of functions to limit the choices in the <b>Functions</b> list: All Operators Math Functions Statistical Functions Text Functions Logical Functions Date & Time Functions Conversion Functions
<b>Function</b>	Select a function by clicking on it, and click the <b>Insert Function</b> button to insert it to the <b>Expression</b> field. You can also double-click on a function to insert it.  If you place the cursor at a specific location in the <b>Expression</b> field, the function will be inserted there.

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<b>Description</b>	Provides a brief description of the selected function. For more detailed descriptions, please see Spotfire Expression Language (SXL).
<b>Expression</b>	<p>This is the text field in which you build your expression. You can insert variables and functions to it from the lists, or enter text as in any standard text editor.</p> <p>Cut/Copy/Paste works in the field using standard <b>Ctrl+X</b> / <b>Ctrl+C</b> / <b>Ctrl+V</b>.</p> <p>Highlighting a section of the expression, and clicking Insert Function will add the selected function to the expression with the highlighted section as an argument.</p> <p>Also, Undo/Redo functionality is available by pressing <b>Ctrl+Z</b>.</p> <p><b>Note:</b> Very long expressions will be displayed truncated in the Visualization Legend. To avoid this, insert a blank space with suitable distance. This will not affect the expression, but will allow the Legend to display it over several rows.</p>
<b>Target type</b>	Displays the data type of the result.
<b>Result</b>	<p>This field displays the result of applying the current expression to the first row of the data set.</p> <p>If this field shows an error message, there is a problem with the expression. Clicking on the field will display an explanation of what is wrong. Pressing <b>F5</b> will also display the error description. Pressing <b>F4</b> will move the cursor to the position in the expression where the error lies.</p> <p>There are three kinds of error messages:</p> <p>#EXPR! – there is a problem with the syntax of the expression.</p> <p>#NUM! – the row evaluates to infinity or other illegal number.</p> <p>#ARG! – there is a problem with one or many arguments.</p>
<b>Recent expressions</b>	This list contains the twenty most recent expressions you have created.
<b>Insert</b>	Inserts the selected recent expression to the cursor position of the expression field.

## 4.8.7.7.6 Customize Labels Dialog

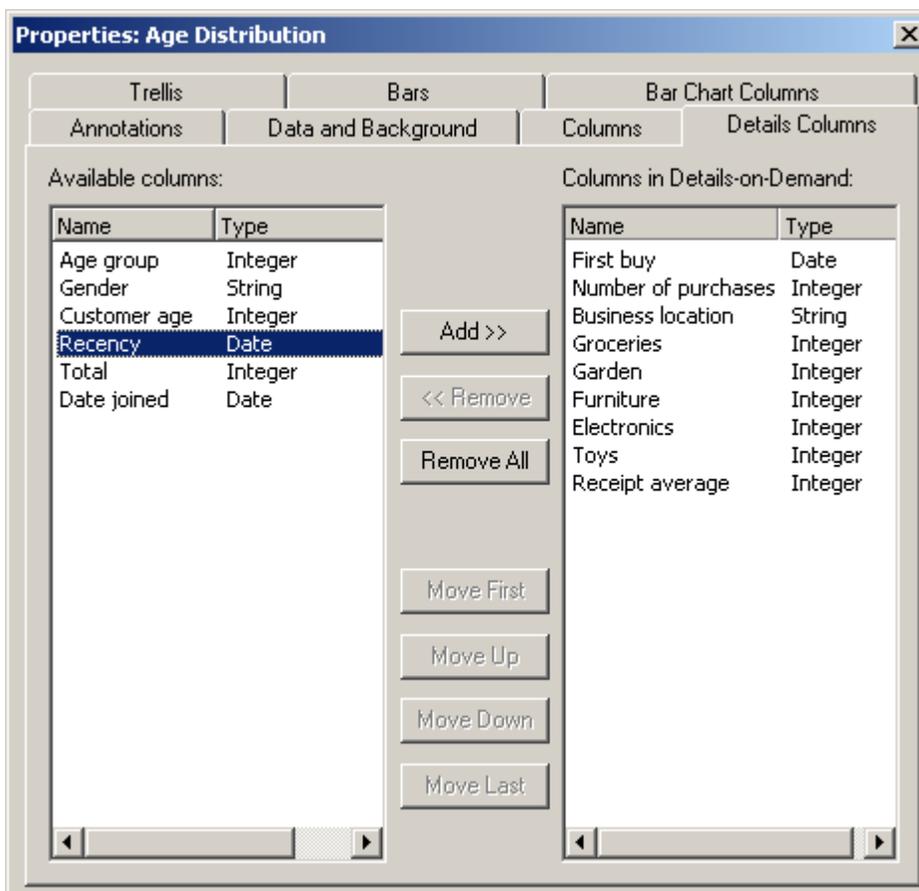


Option	Description
<b>Maximum label size</b>	Allows you to change the maximum label size that you wish to allow.
<b>Background</b>	Allows you to change the color of the background on the label. You can also adjust the transparency of the background using the slider.
<b>Border</b>	Allows you to change the color of the frame surrounding the label as well as the line leading to the border. The transparency of the border can also be adjusted.
<b>Use marker color</b>	Select this check box to use the same color on the label frame and line as is used on each item. <b>Note:</b> In bar charts, only the segment labels will be affected by this setting, not the bar labels.
<b>Frame width</b>	Adjusts the thickness of the surrounding frame.
<b>Line width</b>	Adjusts the thickness of the line leading from the marker to the label.
<b>Text</b>	Allows you to change the color of the label text.

## 4.8.8 Details Columns Tab

### 4.8.8.1 Details Columns Tab

Edit > Properties > Details Columns tab



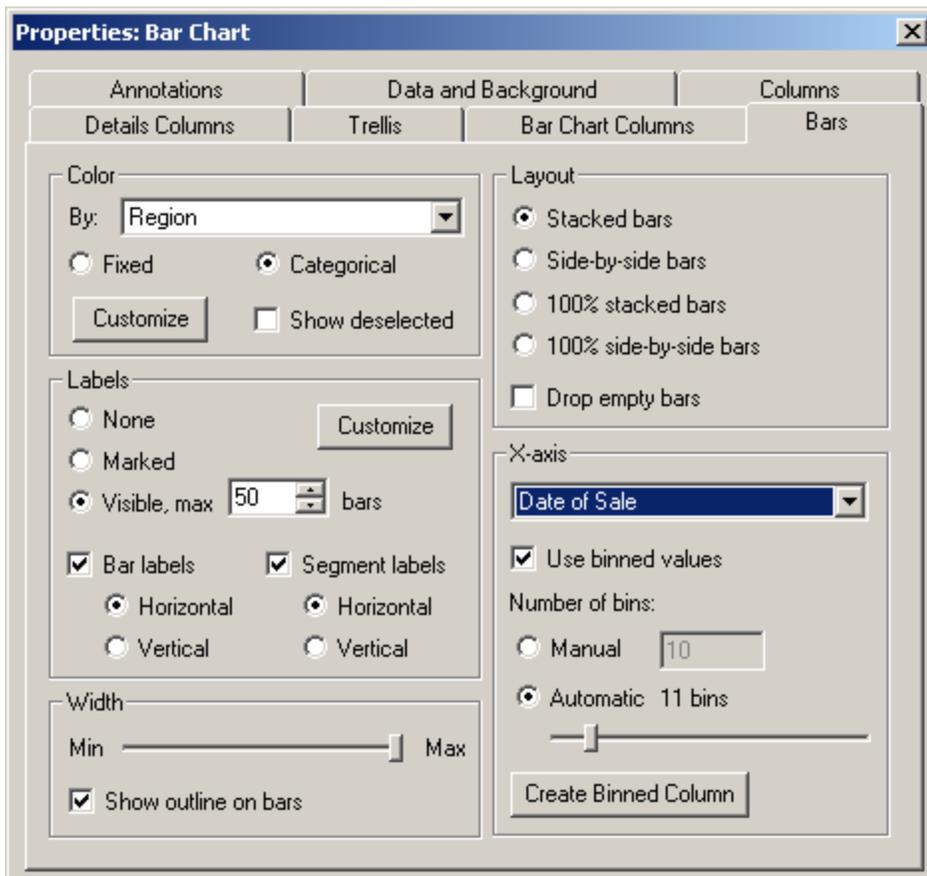
Option	Description
<b>Available columns</b>	These columns are not included in the bar chart. <b>Note:</b> You can right-click on the Name header to get a pop-up menu where you can select other attributes you would like to be visible.
<b>Columns in Details-on-Demand</b>	These columns are displayed as information in the Details-on-Demand window. <b>Note:</b> The Details-on-Demand table cannot display more than a few hundred columns (depending on the width the columns). This means that in a very wide data set you might not be able to view all columns in the Details-on-Demand simultaneously.
<b>Add &gt;&gt;</b>	Select a column from the left list and press the <b>Add &gt;&gt;</b> button to move it to the right list, and include it in the details-on-demand.
<b>&lt;&lt; Remove</b>	Select a column from the right list and press the <b>&lt;&lt;Remove</b> button to move it back to the available columns list, and remove it from the details-on-demand.
<b>Remove All</b>	Removes all columns from the right list, and moves them to the available columns list.
<b>Move First</b>	Select a column from the right list and press the <b>Move First</b> button to move it to the top. This changes the order the columns are displayed in the details-on-demand.
<b>Move Up</b>	Select a column from the right list and press the <b>Move Up</b> button to move it a step up. This changes the order the columns are displayed in the details-on-demand.

<b>Move Down</b>	Select a column from the right list and press the <b>Move Down</b> button to move it a step down. This changes the order the columns are displayed in the details-on-demand.
<b>Move Last</b>	Select a column from the right list and press the <b>Move Last</b> button to move it to the bottom. This changes the order the columns are displayed in the details-on-demand.

## 4.8.9 Bars Tab

### 4.8.9.1 Bars Tab

Edit > Properties > Bars tab



Option	Description
<b>Color</b>	If fixed coloring is used, one color is assigned to the entire bar or, if you are using multiple columns, to the part of a bar that originates in a single column. When using categorical coloring for bar charts, the bars are divided into sections according to the column selected in the drop down menu. Categorical coloring is not available for multiple columns display.
<b>Labels</b>	You can select to display labels for the bars in the bar chart, to see the exact values they represent. <b>None</b> – No labels are displayed. <b>Marked</b> – Only the bars that are marked will display labels. <b>Visible, max</b> – All visible bars will have labels next to them, provided

	<p>that the number of visible bars does not exceed the specified max number. If so, no labels are shown.</p> <p>Click on <b>Customize</b> to open the <b>Customize Labels</b> dialog, where you can change the color and line width of the label frames and lines, as well as the size available to labels.</p> <p>Select the <b>Bar labels</b> check box to display labels above the bars. Select the <b>Segment labels</b> check box to display labels on bar segments.</p> <p>You can also specify whether you want <b>Horizontal</b> or <b>Vertical</b> labels.</p>
<b>Width</b>	<p>Drag the slider to modify the width of the bars.</p> <p>If you select the <b>Show outline on bars</b> check box, black outlines will be drawn around the bars.</p>
<b>Layout</b>	<p>When categorical coloring is applied, you can choose between four different ways of displaying the bars. <b>Stacked bars</b> will place all columns in a category on top of each other, in effect summarizing them. <b>Side-by-side bars</b> will place the bars beside each other for comparison. The 100%-options are used if you want to compare the proportions of different categories for, e.g., different time periods. With <b>100% stacked bars</b>, all bars will be of equal height (100%), unless some negative values exist in the data. 100% side-by-side bars displays bars side by side, but proportionally so that each group sums up to 100% (if the Sum measure is selected). See <b>Bar Chart Layout Details</b> for more information.</p> <p>Selecting the <b>Drop empty bars</b> check box, will hide all bars containing no records from the visualization, letting the visible bars use the space along the horizontal axis. Filtering with the query devices will cause bars to appear/disappear dynamically if this option is selected.</p>
<b>X-axis</b>	<p>Use the drop-down list to change the column to use on the X-axis.</p> <p>If the X-axis in your bar chart represents a numeric value, you can select to bin (group) the records from several bars into larger "binned" bars. Rather than showing a separate bar for say, 1987, 1988, 1989, etc., you can show a single bar for 1980-1989, another bar for 1990-1999, etc.</p> <p>Do this by first selecting the <b>Use binned values</b> check box. This setting can also be reached from the right-click menu of the axis selector. Then you can either can choose your own number of bins by typing the number into the <b>Manual</b> field, or, select <b>Automatic</b> and adjust the slider to display a suitable number of bars.</p> <p>Moving the slider sets a maximum number of bins (1-1000), and the bar chart displays a number of bars as close to this as possible depending on the range of the data.</p> <p><b>Note:</b> Automatic binning of the bar charts uses a form of even interval binning, which is optimized for interactivity and has heuristics to automatically adjust to fit logical tick marks on the X-axis.</p> <p>Click on <b>Create Binned Column</b> to add a new column to the data set containing the binned values. <b>Create Binned Column</b> can also be reached from the right-click menu of the axis selector.</p>

### 4.8.9.2 Bar Charts – Color

Edit > Properties > Bars tab

## Fixed Coloring

If fixed coloring is selected, one color is assigned to all bars. If you are displaying Multiple Columns, the bars of each column will by default be a different color.

### ► To Specify the Fixed Color for a Column:

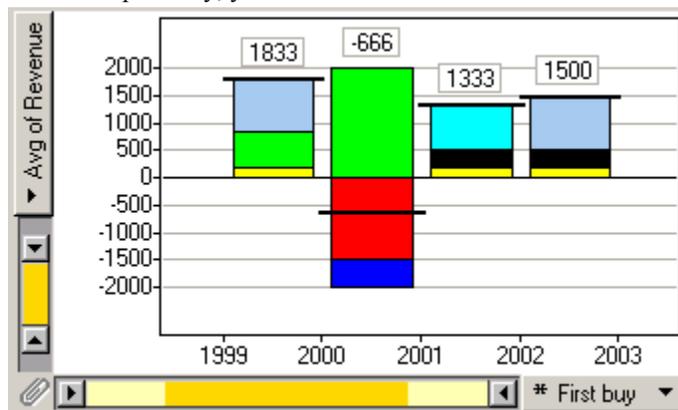
1. Select **Edit > Properties**.
2. Select the **Bars** tab.
3. Select the radio button called **Fixed**.
4. Click on the **Customize** button.
5. Select a column from the list, and pick a color for it in the palette to the right.
6. Click **OK**.

## Categorical Coloring

In single column mode you can use categorical coloring for the bars, which means that each bar is divided into differently colored sections, representing another column of your data set. See Bar Chart Layout Details for more information about different layout options.

### ► To Specify Categorical Coloring:

1. Select **Edit > Properties**.
2. Select the **Bars** tab.
3. Select the radio button called **Categorical**.  
**Note:** You cannot set Categorical coloring when using Multiple Columns.
4. Select the column you want to color the sections by.
5. Optionally, you can also click the **Customize** button to set the specific colors used.



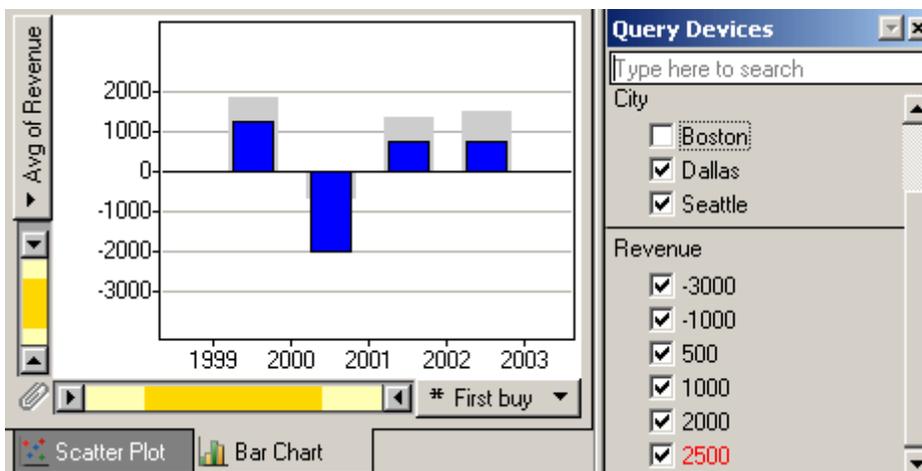
Bar chart with categorical coloring, displaying the Average Value line.

## Total Sum Line / Average Value Line

When using categorical coloring and there are negative segments in the bar, it can still be very useful to see how high the bar would be if all the positive and negative segments were summed up. This is indicated by a black line crossing each bar. If the bars are set to show the Sum of the values the line indicates the Total Sum, and if the bars are set to show the average of the values the line indicates the Average Value. Such a value can be both positive and negative.

## Show deselected

If you select the **Show deselected** check box, a gray shadow will appear behind the regular bars. This indicates how the bars would look if all the records in the data set are included. Filtering with a query device or zooming in another plot deselects records in bars, causing the bars to change, but you can always compare them to the background shadows which remain the same.



You can change the color of the shadow by clicking on the **Customize** color button in the **Bars** tab of the **Properties** dialog.

### 4.8.9.3 Bar Chart Layout Details

When categorical coloring is applied, you have the option to display the categories in four different ways:

- Stacked bars
- Side-by-side bars
- 100% stacked bars
- 100% side-by-side bars

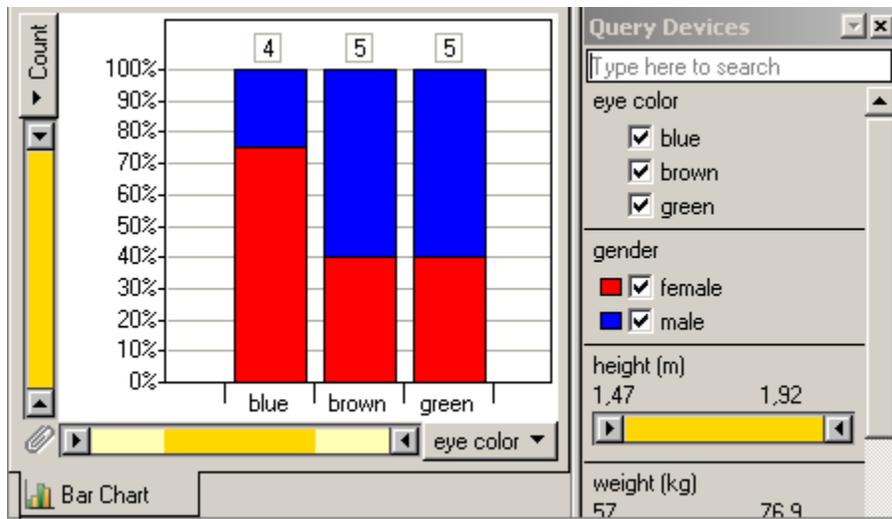
The categorical coloring layout is changed in the Properties dialog (**Edit > Properties > Bars** tab). Different layout modes are more or less useful for different types of aggregations: Sum, Average and Count. Below is a description of what you will see when you use the different layout options and aggregations.

#### Count

With Count, the height of a bar represents the number of records with a particular value. All layout options will display positive bars and show the contribution of each category to the total of the group.

Example:

In a data set containing personal data, the different eye color categories contain a different number of people (4,5,5). Also, by using the 100% stacked bar option, it is easy to see that women are slightly over-represented in the blue eye color category.



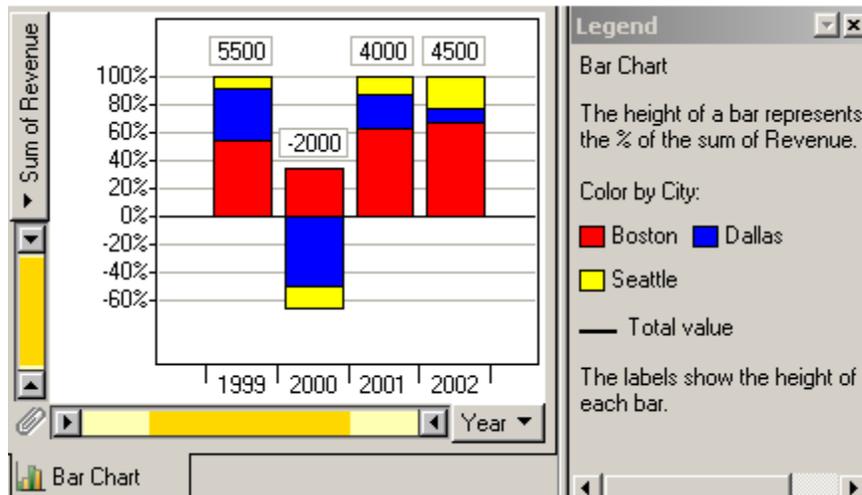
### Sum

With Sum, the height of the bar indicates the total sum of the values of all records in that bar. The various categorical coloring layout options show the contribution of all categories to the total sum.

Option	Height of each category
<b>Stacked bars</b>	Represents the sum of the values in that category.
<b>Side-by-side bars</b>	Represents the sum of the values in that category.
<b>100% stacked bars</b>	Represents how many percent of the total sum for the group that is constituted of the sum of the values in the category. The exact percentage of each category can be seen in the details-on-demand window, when clicking on a bar category.
<b>100% side-by-side bars</b>	Represents how many percent of the total sum for the group that is constituted of the sum of the values in the category. The exact percentage of each category can be seen in the details-on-demand window, when clicking on a bar category.

Example:

If you want to compare the proportions of different categories for, e.g., different time periods, you can use either of the 100% layout options in the Properties dialog. With 100% stacked bars, all bars will be of equal height (100%), unless some negative values exist in the data.



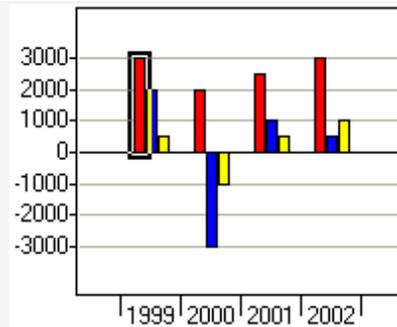
In the example above, one can see that the Seattle revenue (yellow) has affected the total revenue more during 2002 than in previous years, whereas the Dallas revenue (blue) has decreased in importance.

### Average

**Note:** The representation of the bars may be difficult to understand if your data contains both positive and negative values. Use this type of representation with moderation for data with mixed signs.

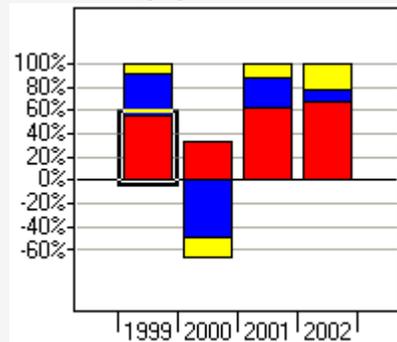
Click on a bar or a bar category and view the details-on-demand window for more information about the various bars and categories.

Option	Height of each category	Details-on-Demand information
<b>Stacked bars</b>	Represents the average of the values in that category divided by the number of categories ( $Avg_{cat}/n$ ).	The exact percentage of each category's average compared to the total average of the entire group ( $(Avg_{cat}/Avg_{group}) * 100$ ).
<b>Side-by-side bars</b>	Represents the average of the values in that category ( $Avg_{cat}$ ).	The average of category as well as the average of the entire group.



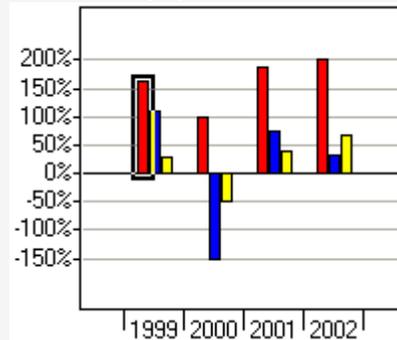
**100% stacked bars**

Represents the average of the category divided by the average of the group and the number of categories as a percentage  $((Avg_{cat}/Avg_{group})*(100/n))$ .



**100% side-by-side bars**

Represents the average of the values in that category divided by the average of the group  $((Avg_{cat}/Avg_{group})*100)$ .



The exact percentage of each category's average compared to the total average of the entire group  $((Avg_{cat}/Avg_{group})*100)$ .

**Details-on-Demand**

Active bar at Year = 1999:  
 Contains 3 records  
 The average of Revenue is 1833.33333333  
 Height: 100.0%

For City = Boston:  
 Contains 1 record  
 The average is 3000

Divided by City:		
Value	Average	Percentage
Boston	3000	163.6
Dallas	2000	109.1
Seattle	500	27.3

The exact percentage of the selected category's average compared to the total average of the entire group  $((Avg_{cat}/Avg_{group})*100)$ .

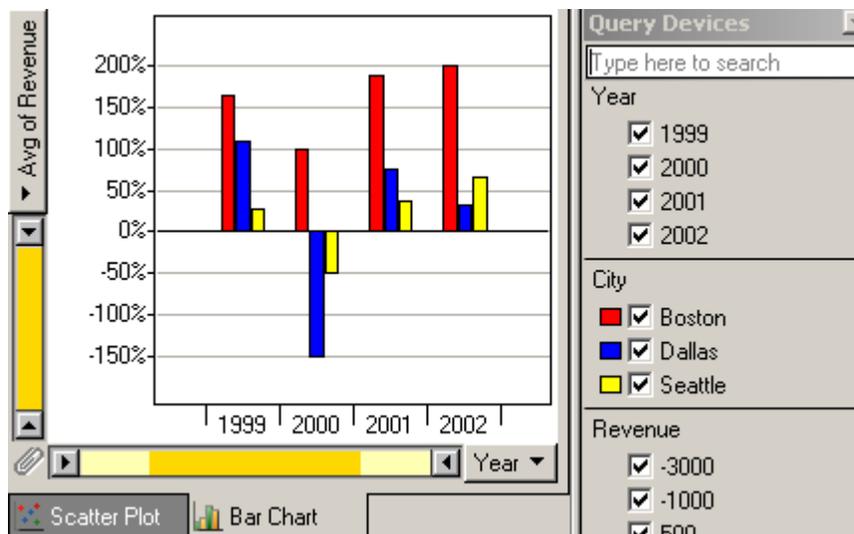
**Details-on-Demand**

Active bar at Year = 1999:  
 Contains 1 record  
 The average for City = Boston is 3000, Height: 163.6%

All bars in group:  
 Contains 3 records  
 The average of Revenue is 1833.33333333

**Example:**

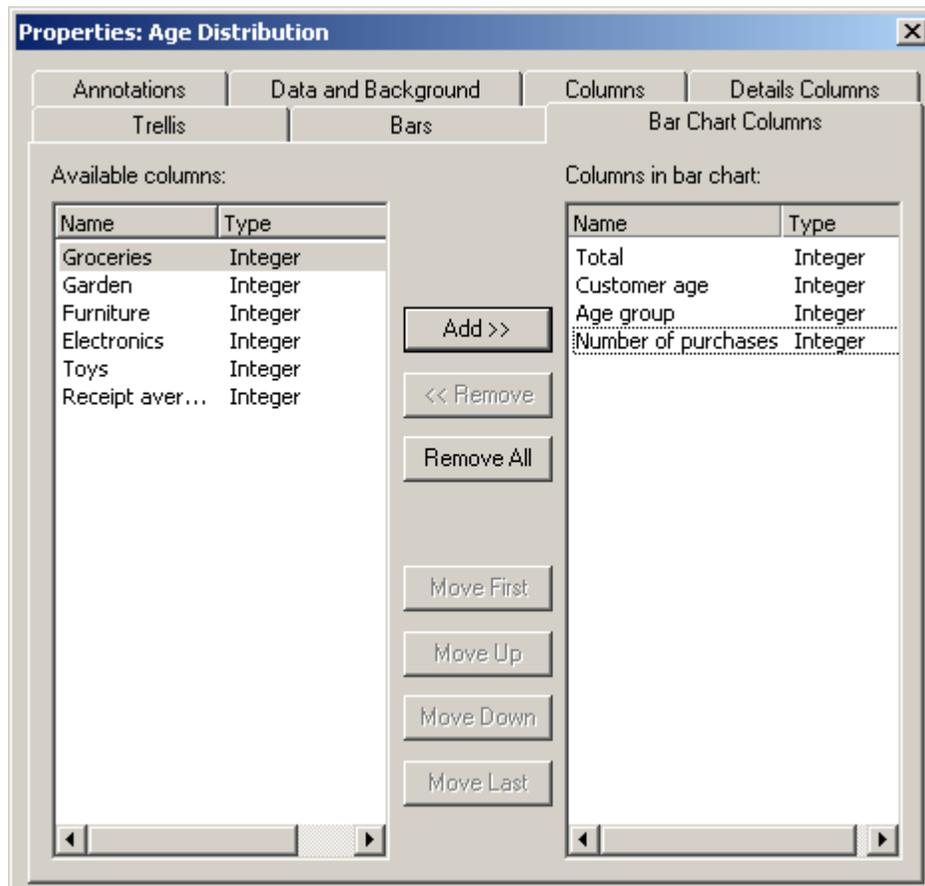
When you are using Average to represent the height of the bars, the 100% side-by-side bars option will display the percentage of the category average compared to the group average. That means that if the average for the specific category is higher than the average for the whole group, the bars will reach a height of more than 100%, see below.



## 4.8.10 Bar Chart Columns Tab

### 4.8.10.1 Bar Chart Columns Tab

Edit > Properties > Bar Chart Columns tab

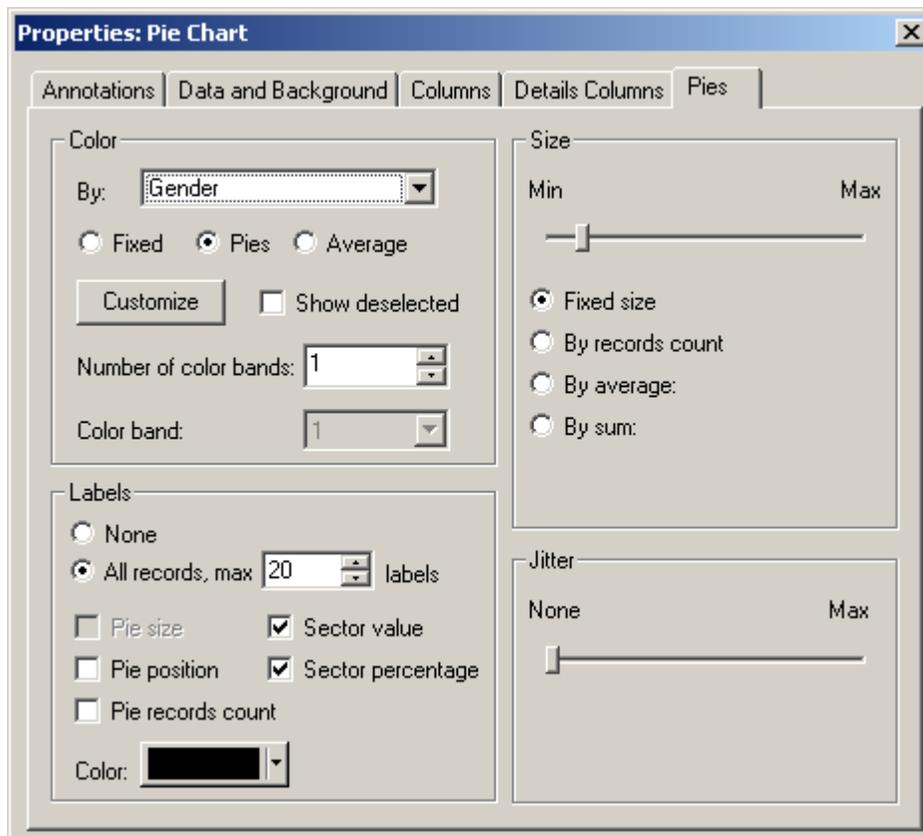


Option	Description
<b>Available columns</b>	These columns are not included in the bar chart. <b>Note:</b> You can right-click on the Name header to get a pop-up menu where you can select other attributes you would like to be visible.
<b>Columns in bar chart</b>	These columns are included in the bar chart. The order of this list corresponds to the order the columns are shown in the Bar Chart visualization.
<b>Add &gt;&gt;</b>	Select a column from the left list and press the <b>Add &gt;&gt;</b> button to move it to the right list, and include it in the bar chart.
<b>&lt;&lt; Remove</b>	Select a column from the right list and press the <b>&lt;&lt;Remove</b> button to move it back to the available columns list, and remove it from the bar chart.
<b>Remove All</b>	Removes all columns from the right list, and moves them to the available columns list.
<b>Move First</b>	Select a column from the right list and press the <b>Move First</b> button to move it to the top. This changes the order the bars are displayed.
<b>Move Up</b>	Select a column from the right list and press the <b>Move Up</b> button to move it a step up. This changes the order the bars are displayed.
<b>Move Down</b>	Select a column from the right list and press the <b>Move Down</b> button to move it a step down. This changes the order the bars are displayed.
<b>Move Last</b>	Select a column from the right list and press the <b>Move Last</b> button to move it to the bottom. This changes the order the bars are displayed.

## 4.8.11 Pies Tab

### 4.8.11.1 Pies Tab

Edit > Properties > Pies tab



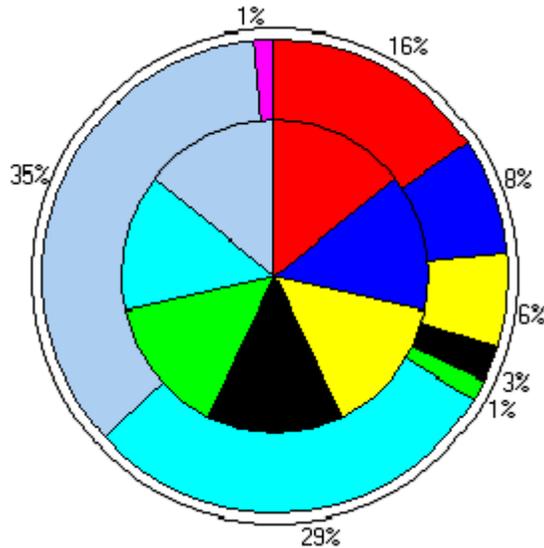
Option	Description
<b>Color</b>	A pie chart can consist of one or more bands, each reflecting the distribution of values in a certain column. Set <b>Number of color bands</b> to the desired number, then select one band at a time using <b>Color band</b> . Color settings are set for each band individually.
<b>Labels</b>	Five different labels can be added to the pie charts: <b>Pie size</b> shows the number of records associated with the pie, or average or sum, depending on the settings under <b>Size</b> . <b>Pie sector value</b> shows the value associated with each sector in the outermost band. <b>Pie sector percentage</b> shows the percentage of the pie that each sector covers in the outermost band. <b>Pie records count</b> shows the number of records in the pie. <b>Pie position</b> shows the position of the pie. Requires the use of axes.
<b>Size</b>	The maximum size of the pies in the pie chart can be varied with the <b>Size</b> slider. Under the <b>Size</b> slider there are four options of radio buttons with the following functions: <b>Fixed size</b> – pies are sized all the same. <b>By records count</b> – pies are sized according to the number of records in each pie. <b>By average</b> – pies are sized according to the average value of the records in the pie. <b>By sum</b> – pies are sized according to the sum of the records in the pie.
<b>Jitter</b>	The <b>Jitter</b> function, at the bottom right of the <b>Properties</b> dialog, can be used in the same way with pie charts as when working with scatter plots.

The overlapping pies will be randomly displaced so that hidden information will be made visible. At least one axis has to be in use.

### 4.8.11.2 Pie Charts - Color

Edit > Properties > Pies tab

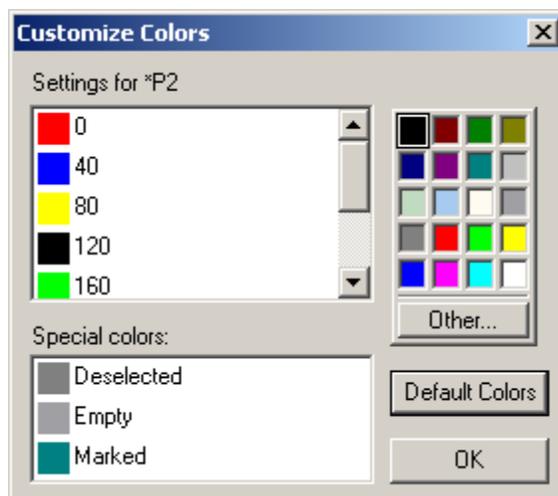
A pie chart can consist of one or more bands, each reflecting the distribution of values in a certain column. Set **Number of color bands** to the desired number, then select one band at a time using **Color band**. Color settings are set for each band individually. The image shows a pie chart with multiple color bands.



For whole pies or bands, three coloring modes are available:

- **Fixed** – One color is assigned to the entire pie or band.
- **Pies** – The normal way of coloring: the band to be colored is divided into sections whose size is determined according to the distribution of the selected column.
- **Average** – Assigns one color to each band or pie. The color is given according to the average value of the records in the chosen column for that pie/band.

Use the **Customize** button to choose color.



► **To change a color:**

1. Select the category that you want to modify.
2. Select a color from the palette.

► **To revert to default coloring, click Default Colors.**

► **To select a color from the complete palette, click Other....**

**Note:** Empty refers to records that have at least one empty field. These records are not shown at all in visualizations where an axis corresponds to the missing field.

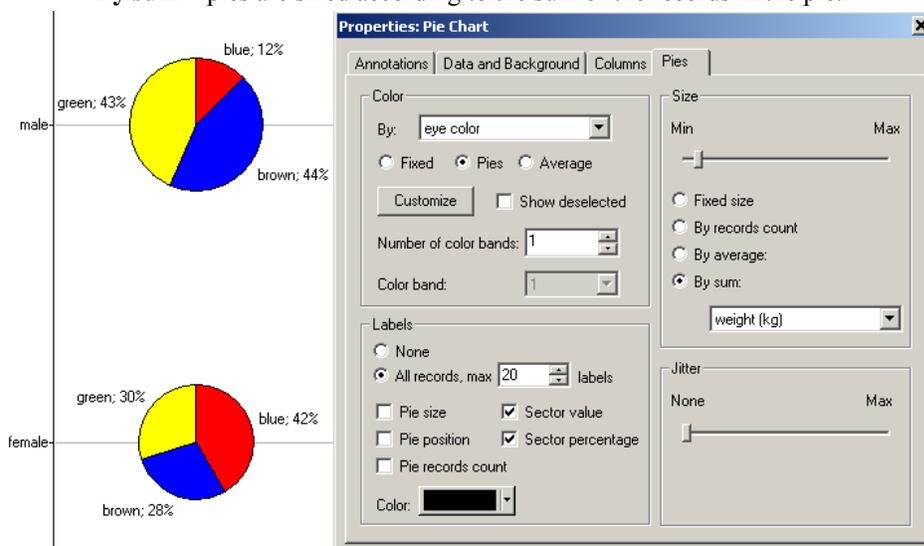
Use **Show deselected** if all records in the data set should be included in the pies. The deselected records are displayed as a separate sector. The color of this sector can be altered with the color selector under **Customize** the color of the sector representing empty markers and the marking color can be changed in the same way.

### 4.8.11.3 Pie Charts - Size

Edit > Properties > Pies tab

The maximum size of the pies in the pie chart can be varied with the **Size** slider. Under the **Size** slider there are four options of radio buttons with the following functions:

- **Fixed size** – pies are sized all the same.
- **By records count** – pies are sized according to the number of records in each pie.
- **By average** – pies are sized according to the average value of the records in the pie.
- **By sum** – pies are sized according to the sum of the records in the pie.

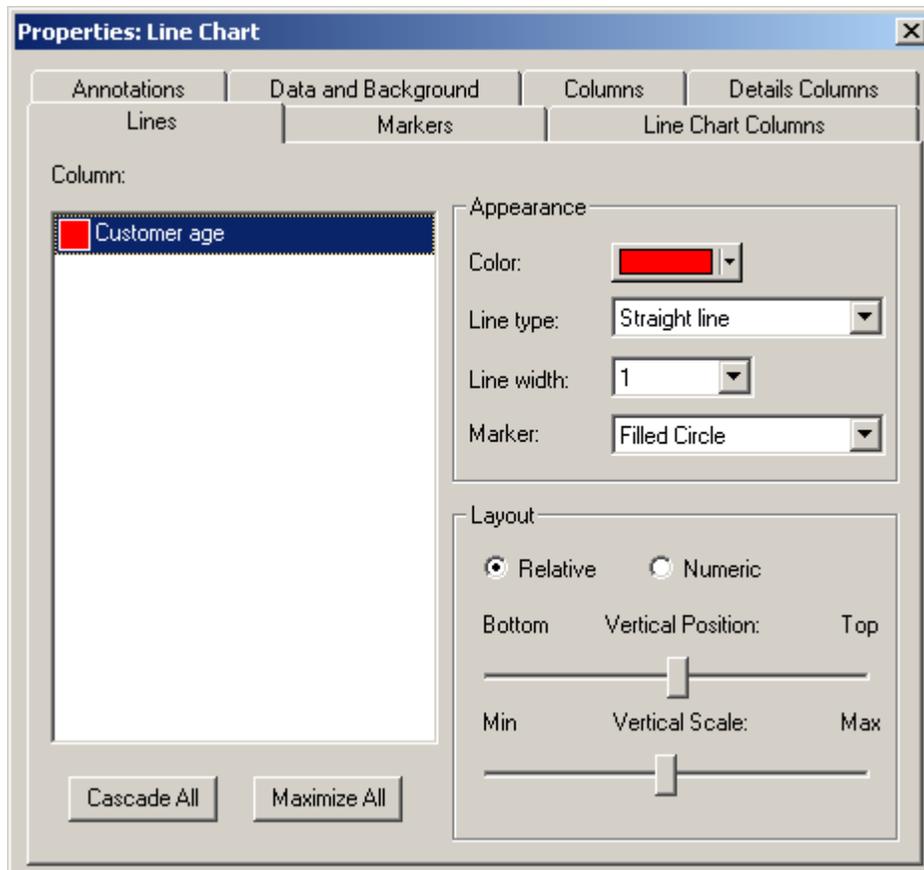


When high *negative* values are used for sizing (By average or By sum), pies will appear large. A red filled circle within the pie will indicate that the value used for sizing is negative. If the sum or average is zero, this will yield invisible pies.

## 4.8.12 Lines Tab

### 4.8.12.1 Lines Tab

Edit > Properties > Lines tab



Option	Description
<b>Appearance</b>	Here you set the properties for each column, that is, each line. Select the column you want to edit, and view the properties in the list boxes on the right. Adjusting the controls will change the appearance of the selected column.
<b>Layout</b>	When <b>Scale Mode</b> is set to <i>Individual</i> (see Markers property page) it is possible to control the vertical position and amplitude of the plotted curves. This makes it easy to compare the shapes of the curves. Position and scale can be set either using sliders, or by entering numerical values. You can at any time switch between the two modes by pressing either of the two radio buttons labeled <b>Relative</b> or <b>Numeric</b> .

### 4.8.12.2 Line Charts – Appearance

Edit > Properties > Lines tab

On the **Lines** of the **Properties** dialog tab you set the properties for each column, i.e., each line. Select the column you want to edit, and view the properties in the list boxes on the right. Adjusting the controls will change the appearance of the selected column.

### Color

The color used for this column. The column is used for lines and markers as well as for axis labels in the Individual Scale mode.

### Line type

Determines the type of the line used to connect points. Alternatives:

**None** – no line will be drawn

**Straight line** – points will be connected with a straight line

**Step** – points will be connected with a right angle. The first line is horizontal

### Line width

Indicates the width of the line in pixels. The default setting is 1.

Thick lines take considerably longer time to draw. It is therefore a good idea to use a low value for Line width when viewing large data sets.

### Marker

Allows you to select a shape to use for markers. If **Marker** is set to None, no markers are shown in the plot.

Please note that no markers will be drawn unless **Show Markers** is turned on in the **Markers** tab.

## 4.8.12.3 Line Charts – Layout

Edit > Properties > Lines tab

When **Scale Mode** is set to *Individual* (see Markers property page) it is possible to control the vertical position and amplitude of the plotted curves. This makes it easy to compare the shapes of the curves. Position and scale can be set either using sliders, or by entering numerical values. You can at any time switch between the two modes by pressing either of the two radio buttons labeled **Relative** or **Numeric**.

### Vertical Position (Relative)

Moves the selected curve up and down in the visualization window. This may be desirable when you want to compare two curves by superimposing them on one another.

### Vertical Scale (Relative)

Scales the selected curve. If you move the slider to *Min* the curve will appear almost flat. When set to *Max* the curve amplitude will equal the window height of the visualization.

### High (Numeric)

Sets the highest value of the visible range.

### Low (Numeric)

Sets the lowest value of the visible range.

### Cascade all

Sets the Scale and Position of all columns so that each of them will occupy a separate slot of the window height.

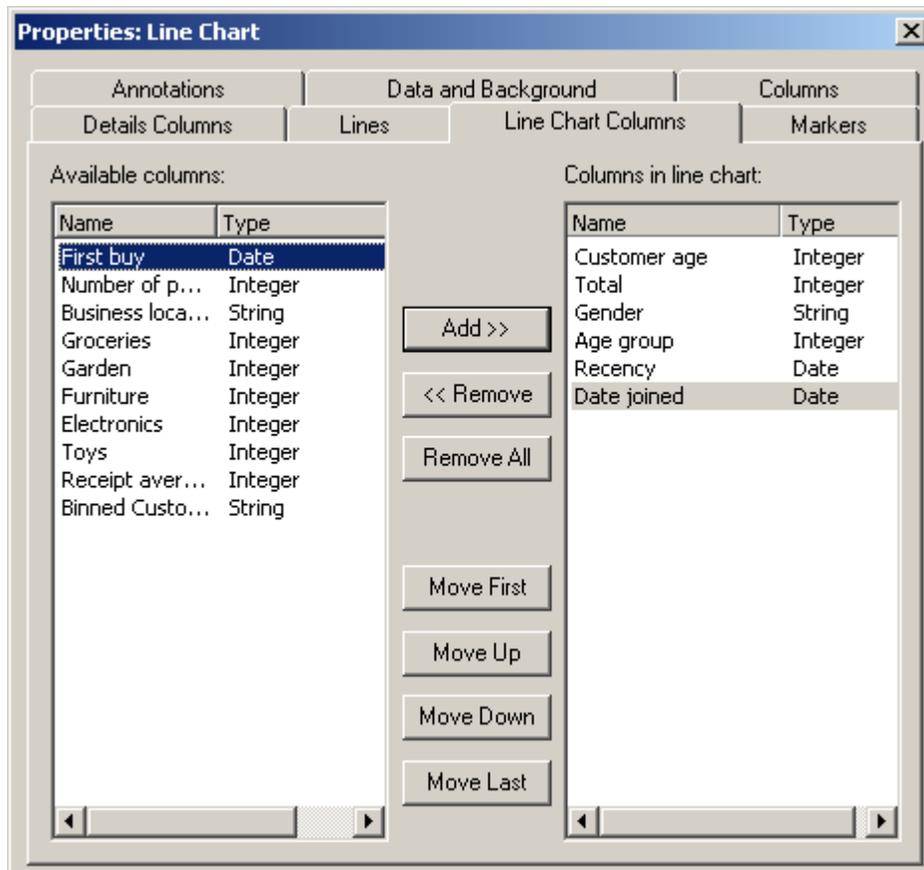
### Maximize all

Set the Scale and Position on every column so they utilize the whole height of the window.

## 4.8.13 Line Chart Columns Tab

### 4.8.13.1 Line Chart Columns Tab

Edit > Properties > Line Chart Columns tab



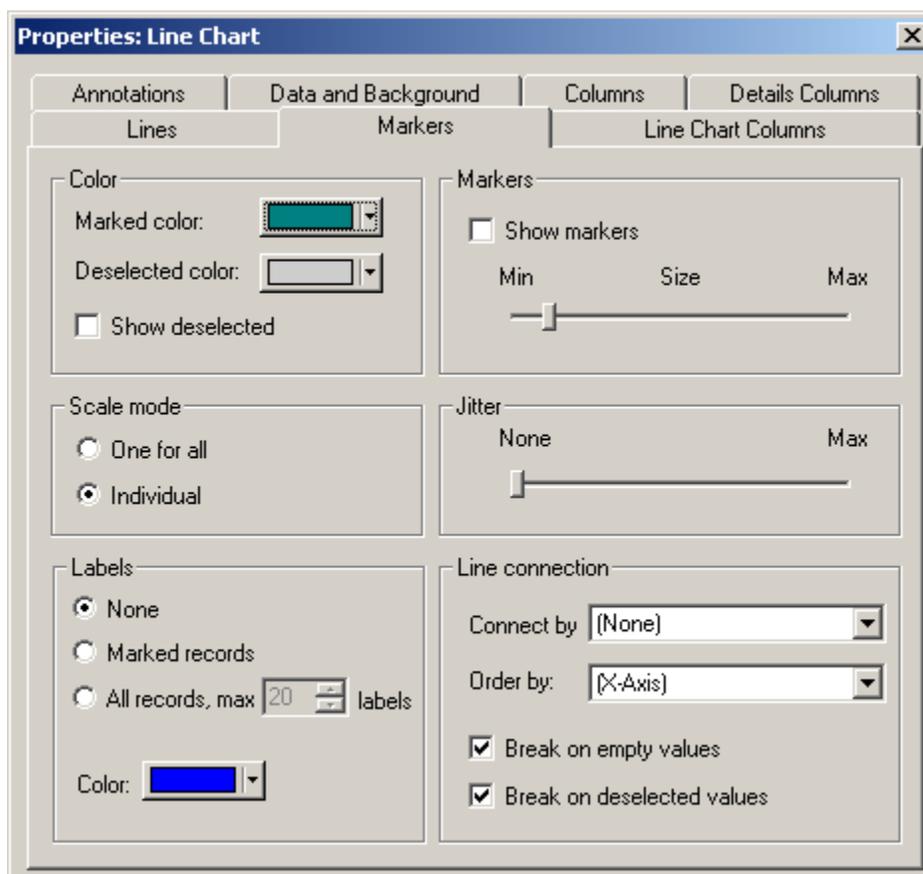
Option	Description
<b>Available columns</b>	These columns are not included in the line chart. <b>Note:</b> You can right-click on the Name header to get a pop-up menu where you can select other attributes you would like to be visible.
<b>Columns in line chart</b>	These columns are included in the line chart. The order of this list corresponds to the order the columns are shown in the Line Chart visualization.
<b>Add &gt;&gt;</b>	Select a column from the left list and press the <b>Add &gt;&gt;</b> button to move it to the right list, and include it in the line chart.
<b>&lt;&lt; Remove</b>	Select a column from the right list and press the <b>&lt;&lt;Remove</b> button to move it back to the available columns list, and remove it from the line chart.
<b>Remove All</b>	Removes all columns from the right list, and moves them to the available columns list.
<b>Move First</b>	Select a column from the right list and press the <b>Move First</b> button to move it to the top. This changes the order the lines are displayed.
<b>Move Up</b>	Select a column from the right list and press the <b>Move Up</b> button to

	move it a step up. This changes the order the lines are displayed.
<b>Move Down</b>	Select a column from the right list and press the <b>Move Down</b> button to move it a step down. This changes the order the lines are displayed.
<b>Move Last</b>	Select a column from the right list and press the <b>Move Last</b> button to move it to the bottom. This changes the order the lines are displayed.

## 4.8.14 Markers Tab of the Line chart

### 4.8.14.1 Markers Tab of the Line chart

Edit > Properties > Markers tab



Option	Description
<b>Color</b>	The colors used for drawing marked and deselected records are edited here. Whether deselected records should be drawn or not is determined with the <b>Show Deselected</b> check box. <b>Note:</b> the color used to plot the records is the same as the connecting line, and thus configured on a per column basis on the <b>Lines</b> tab.
<b>Scale mode</b>	The line chart works in two modes: one in which all columns are plotted against a common Y-axis, and one where each column has a Y-axis of its own. <b>One for all</b> In this mode there is a single Y-axis scale for all columns. The range of

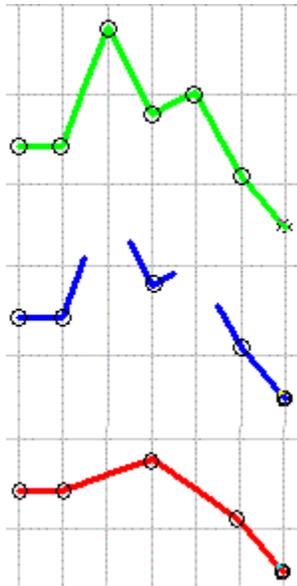
	<p>this axis is automatically adjusted to fit all the columns currently being visualized.</p> <p><b>Note:</b> Since the values of the plotted columns may be of different magnitude, some lines might not be visible due to their low amplitude in relation to the scale of the Y-axis. Select Individual scale mode, or use the zoom bar on the Y-axis to zoom in on curves with low amplitude.</p> <p><b>Individual</b></p> <p>In this mode each column has a Y-axis scale of its own. This is useful when you want to visualize data of different types and magnitude in one plot, or when the shapes of the curves are more interesting than the absolute values. In Individual mode you can control the vertical position and scale of each plotted column using the sliders on the <b>Lines</b> tab.</p>
<b>Labels</b>	For line charts, labels show the values of the column being plotted. Functionality is otherwise the same as for scatter plots.
<b>Markers</b>	The markers check box determines if markers should be drawn or not. The size of markers is controlled with the <b>Size</b> slider. The shape and color of the markers are controlled on column basis on the <b>Lines</b> tab.
<b>Jitter</b>	Jittering has the same functionality as for scatter plots. That is, the X and Y coordinates are slightly moved to make it possible to tell data points with the same coordinate apart. The slider sets the amount of random displacement.
<b>Line connection</b>	You can choose which column to use for discriminating between lines ( <b>Connect by</b> ), and the order in which data points are connected within each line ( <b>Order by</b> ). The order can be set to any column, to <i>Row Number</i> , or to <i>None</i> . The column on the X-axis is used by default. Selecting <i>None</i> turns line connection off.

#### 4.8.14.2 Line Charts – Line Connection

Edit > Properties > Markers tab

You can choose which column to use for discriminating between lines (**Connect by**), and the order in which data points are connected within each line (**Order by**). The order can be set to any column, to *Row Number*, or to *None*. The column on the X-axis is used by default. Selecting *None* turns line connection off.

Line connection works in a slightly different way for line charts compared to scatter plots. In scatter plots, points will be connected no matter how many intermediate points are deselected (filtered out). In a line chart, you can control how you want to handle values that are missing or deselected.



In the first chart, no values are deselected.

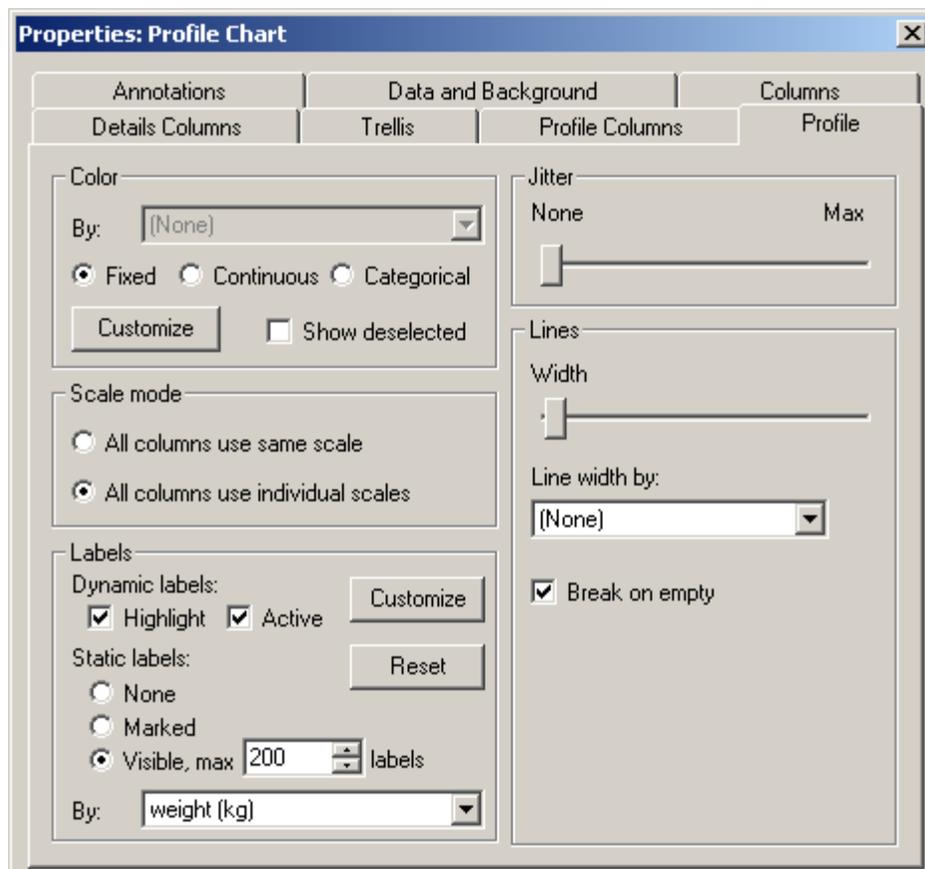
In the second, high values have been deselected and **Break on deselected values** has been turned on. Broken lines then extend half way to the deselected value.

In the third chart, high values have been deselected and **Break on deselected values** turned off.

## 4.8.15 Profile Tab

### 4.8.15.1 Profile Tab

Edit > Properties > Profile tab

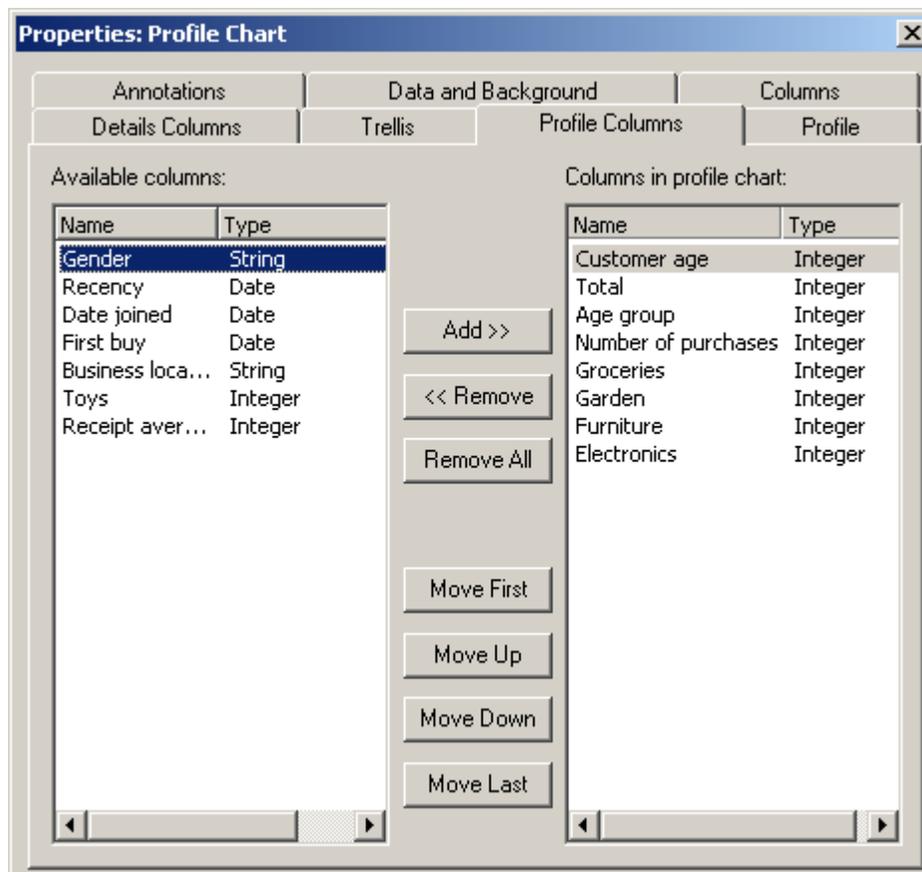


Option	Description
<b>Color</b>	Markers can be colored to reflect the value of a particular attribute. There are three modes for coloring: Fixed, Continuous and Categorical. Coloring in profile charts is identical to scatter plots.
<b>Scale mode</b>	<p>The vertical dimension in a profile chart represents the value of each attribute. The scale can either be the same for all columns, or individual for each column.</p> <p>In the first case, the scale used for all columns ranges from the lowest to the highest value in <i>all columns</i> being plotted. This should be used when the values in the plotted columns are of the same unit and similar magnitude. To use this mode, select <b>All columns use same scale</b>. In the second case, the scale for each column ranges from the lowest value in the column to the highest value in the column. To use this mode, select <b>All columns use individual scales</b>.</p>
<b>Labels</b>	<p>It is possible to tag each profile with a label, showing the value of a particular column. You can select to show both Dynamic labels (Highlight and/or Active) and Static labels (None/Marked/Visible) at the same time. Dynamic labels are always placed on top of any static labels. The static labels include the following options:</p> <p><b>None</b> – No labels are visible.</p> <p><b>Marked</b> – Only records that are marked will have labels next to them.</p> <p><b>Visible, max</b> – All visible records (up to a configurable maximum number) will have labels next to them, provided that the number of visible records does not exceed the specified max number. If so, no labels are shown.</p> <p>Click on <b>Customize</b> to open the Customize Labels dialog, where you can change the color and line width of the label frames and lines, as well as the size available to labels.</p> <p>You can drag labels to any position within the visualization area. Click on <b>Reset</b> to return all profile labels to their original position.</p> <p>Select the column you wish to label by, from the drop-down list <b>By</b>.</p> <p>If you are running DecisionSite for Lead Discovery, you can also select to display the chemical structure for each profile in the label. This is done by right-clicking in the profile chart and selecting <b>Structure Marker Labels</b> from the pop-up menu. Select Structure Marker Labels &gt; Remove to revert to the column selected here.</p>
<b>Jitter</b>	Jittering displaces markers slightly and randomly, thereby making aggregations stand out visually. Attention is brought to areas where many records overlap. Such regions can then be investigated further, by zooming, changing axes, etc. Use the slider to increase or decrease jittering.
<b>Lines</b>	<p>The width of all lines is adjusted by moving the <b>Width</b> slider. Select a column under <b>Line width by</b> to associate the width of individual lines with the value of a particular attribute.</p> <p>Empty values can be dealt with in two ways: either by leaving a gap in the profile, or by connecting the values on each side with a straight line. To leave a gap, select <b>Break on empty</b>.</p>

## 4.8.16 Profile Columns Tab

### 4.8.16.1 Profile Columns Tab

Edit > Properties > Profile Columns tab



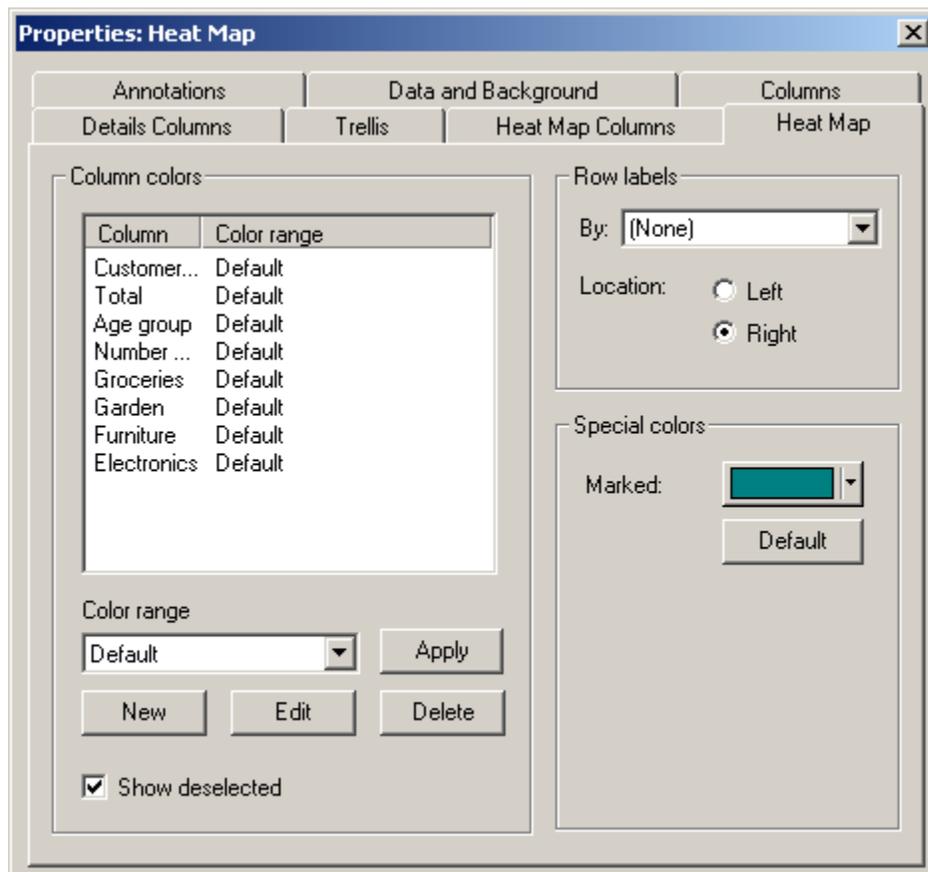
Option	Description
<b>Available columns</b>	These columns are not included in the profile chart. <b>Note:</b> You can right-click on the Name header to get a pop-up menu where you can select other attributes you would like to be visible.
<b>Columns in profile chart</b>	These columns are included in the profile chart. The order of this list corresponds to the order the columns are shown in the Profile Chart visualization.
<b>Add &gt;&gt;</b>	Select a column from the left list and press the <b>Add &gt;&gt;</b> button to move it to the right list, and include it in the profile chart.
<b>&lt;&lt; Remove</b>	Select a column from the right list and press the <b>&lt;&lt;Remove</b> button to move it back to the available columns list, and remove it from the profile chart.
<b>Remove All</b>	Removes all columns from the right list, and moves them to the available columns list.
<b>Move First</b>	Select a column from the right list and press the <b>Move First</b> button to move it to the top. This changes the order the lines of the profile chart are displayed.

<b>Move Up</b>	Select a column from the right list and press the <b>Move Up</b> button to move it a step up. This changes the order the lines of the profile chart are displayed.
<b>Move Down</b>	Select a column from the right list and press the <b>Move Down</b> button to move it a step down. This changes the order the lines of the profile chart are displayed.
<b>Move Last</b>	Select a column from the right list and press the <b>Move Last</b> button to move it to the bottom. This changes the order the lines of the profile chart are displayed.

## 4.8.17 Heat Map Tab

### 4.8.17.1 Heat Map Tab

Edit > Properties > Heat Map tab



The **Heat Map** tab of the **Properties** dialog is used to modify the color range of the heat map and to display or hide row labels and deselected records. The default color range is set to green for minimum values, black for intermediate values and red for maximum values.

### Apply color range to column

To apply a specific color range to one or more columns, select the appropriate columns from the list, then choose a range from the **Color range** drop-down list, and finally click the **Apply** button.

### Create new color scheme

To change the color range of one or more columns, you need to create a new range. Click on the **New** button to open the Create Color Scheme dialog.

### Edit existing color scheme

You can also edit the coloring of an already existing color range. Select a certain color range from the **Color range** drop-down list and click on the **Edit** button to open the Edit Color Scheme dialog. Changes made to this color range will have effect on the columns already linked to the range.

### Delete color range

To delete a color range, select the color range from the **Color range** drop-down list and click on the **Delete** button. Any columns linked to the deleted range will automatically be reset to the Default color range.

### Show/hide deselected records

To hide records that have been deselected by using the query devices from the heat map, clear the **Show deselected** check box.

**Note:** If you have had a dendrogram associated to the heat map, this will no longer be valid after hiding the deselected values. In this case, the dendrogram tree will be removed. You can show the dendrogram again by selecting the Show deselected check box.

### Show/hide row labels

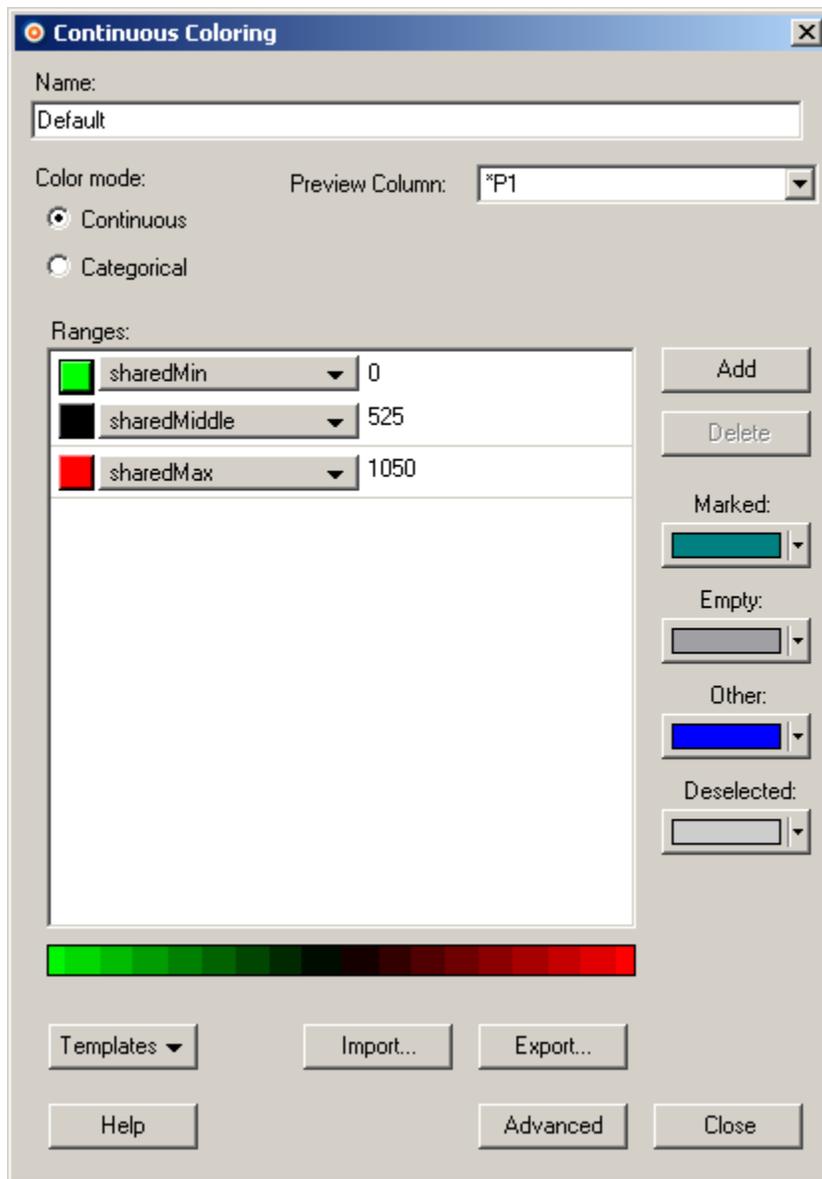
To show row labels next to the heat map, select a column where appropriate labels are located from the **Row labels By:** drop-down list. Choose the location of the labels by clicking the **Left** or **Right** radio button.

**Tip:** If you want to include information from more than one column in the row labels, use the New Column from Expression tool to concatenate the columns prior to applying row labels on your heat map.

To remove the row labels, select [None] in the drop-down list.

## 4.8.17.2 Create/Edit Heat Map Coloring

Edit > Properties > Heat Map Tab > New/Edit Color Range



Type a Name of the new color scheme in the text field at the top. Then select **Categorical Coloring** or **Continuous Coloring**.

### Categorical Coloring

Categorical Coloring means that each unique value in the heat map is represented by its own color. This is most useful when dealing with a smaller number of varying values, or when looking for identical values in a heat map.

You can change which color to represent a certain value by selecting a value from the list, and then choosing a new color for it from the palette.

### Continuous Coloring

Continuous Coloring means that the color range is linear from one specific color to another color, via a third middle color. By default this is set to show low values in shades of green, intermediate values going towards black, and high values in shades of red.

Select new colors to represent the Min, Mid or Max values, by clicking on their corresponding color button and picking a new color from the palette that appears.

Continuous Coloring is divided into three sub-options:

- **Shared custom range:**  
With this option, you can specify an exact Min, Mid and Max value for the color range instead of having these values being automatically determined. All selected columns will be colored according to these values regardless of their own individual Min and Max values.
- **Shared auto range:**  
With this option, there is a separate shared auto range per data-type category:
  - Date/DateTime
  - Time
  - Integer/Decimal

String columns are not grouped at all, and each column will get an individual range spanning from the first string to the last.

- **Individual auto range:**  
With this option, the Min, Mid and Max values for the range are automatically set to the lowest, median and highest values respectively, that exist in each individual column. All selected columns will be colored according to their own individual Min and Max values.

### 4.8.17.3 Advanced Coloring Dialog

Option	Description
<b>Name</b>	Displays the name of the coloring arrangement. Type to enter a new name.
<b>Preview Column</b>	Lists the columns from which you can add values to the <b>Values</b> list.
<b>Values</b>	Displays the values in the chosen column ( <b>Preview Column</b> ), and the color for each value. If a value has a defined categorical color, this color will be used even if the value is also defined within a color range.
<b>Add</b>	Adds a new item to the list of Values. Using this, you can assign specific colors to values, and create your own coloring arrangement.
<b>Add All</b>	Adds all available values from the selected <b>Color by</b> column to the Values list.

<b>Delete</b>	Removes a selected value. Ctrl+click to select multiple items for deletion.
<b>Delete All</b>	Deletes all items in the Values list.
<b>Ranges</b>	Shows the color of the empty records. Empty refers to records that have at least one empty field. These records are not shown at all in visualizations where an axis corresponds to the missing field.
<b>Add</b>	Adds a new item to the list of Ranges. Using this, you can assign specific colors to values, and create your own coloring arrangement.
<b>Delete</b>	Removes a selected value. Ctrl+click to select multiple items for deletion.
<b>Delete All</b>	Deletes all items in the Ranges list.
<b>Other Color &gt;</b>	<p>Determines which color is used for markers that do not get a color from any other setting. The color a marker gets is decided in the following order:</p> <ul style="list-style-type: none"> <li>Markers associated with a data row with empty/null value in the color column are set to the empty color</li> <li>Markers filtered out by query devices or zoom sliders are set to the deselected color.</li> <li>Marked items are drawn using the marked color.</li> <li>Markers that are included in the value list are set to the color specified there. The value list may include values that are not part of the current data set, but you know those values could be included in a future data set, thus it is possible to set up color arrangements that have predefined colors for all anticipated values.</li> <li>Markers that are included in a color range (from the Ranges list) are set to a color from that range. <b>Note:</b> Because it is possible to specify overlapping ranges, a marker can be inside several ranges. See <a href="#">Overlapping Color Ranges</a> for more information.</li> <li>Any other markers are set to either a fixed color, or a color from a palette, depending on your selections. A palette is a list of colors. If there are more unique values in the color column than there are colors in the palette, colors will be reused.</li> </ul>
<b>&gt; From palette</b>	Causes each marker to get an individual color from the color palette list. <b>Note:</b> If there are more than 97 values, colors will be reused.
<b>&gt; Edit</b>	Launches the Edit Palette dialog where you can adjust the RGB values of individual colors.
<b>&gt; Fixed</b>	Lets you choose the color that the markers will get.
<b>Deselected</b>	Shows the color of the deselected values. Deselected refers to records that do not fulfill the constraints of the query devices.
<b>Marked</b>	Shows the color of the records that have been marked.
<b>Empty</b>	Shows the color of the empty records. Empty refers to records that have at least one empty field. These records are not shown at all in visualizations where an axis corresponds to the missing field.
<b>Templates &gt;</b>	
<b>&gt; Shared auto range</b>	<p>With this option, there is a separate shared auto range per data-type category:</p> <ol style="list-style-type: none"> <li>3. Date/DateTime</li> <li>4. Time</li> <li>5. Integer/Decimal</li> </ol>

	String columns are not grouped at all, and each column will get an individual range spanning from the first string to the last.
> <b>Individual auto range</b>	Sets the Min, Mid and Max values for the range automatically to the lowest, median and highest values respectively, that exist in each individual column. All selected columns will be colored according to their own individual Min and Max values.
> <b>Shared custom range</b>	Lets you specify an exact Min, Mid and Max value for the color range instead of having these values being automatically determined. All selected columns will be colored according to these values regardless of their own individual Min and Max values.
<b>Import...</b>	Imports a color arrangement from a file.
<b>Export...</b>	Exports a color arrangement to a file. This enables you to save a color arrangement and reuse it.
<b>Basic</b>	Returns you to the basic Categorical or Continuous or Heat Map Coloring dialog.

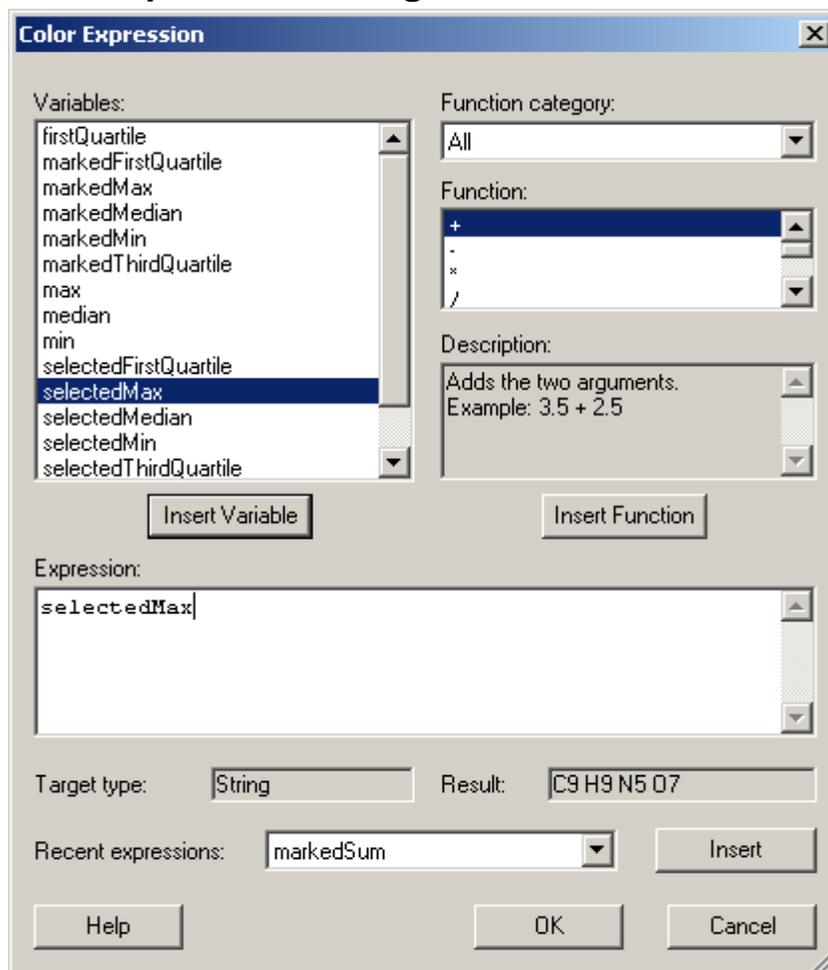
► **To change a color of the Values or Ranges:**

1. Click on the square of color that you want to modify.
2. Select a color from the palette or click **More colors...** to see the complete color palette.

► **To change the Marked, Empty or Deselected color:**

1. Click the button of the color that you want to modify.
2. Select a color from the palette or click **More colors...** to see the complete color palette.

## 4.8.17.4 Color Expression Dialog



### Variables

Lists the available variables which can be used to create your expression. Insert a variable into your expression with the **Insert Variable** button.

### Category

Select a category of functions to limit the choices in the **Functions** list.

- All
- Operators
- Math Functions
- Statistical Functions
- Text Functions
- Logical Functions
- Date & Time Functions
- Conversion Functions

### Function

Select a function by clicking on it, and click the **Insert Function** button to insert it to the **Expression** field. You can also double-click on a function to insert it.

If you place the cursor at a specific location in the **Expression** field, the function will be inserted there.

### Description

This field provides a brief description of the selected function. For more detailed descriptions, please see Spotfire Expression Language (SXL).

### Expression

This is the text field in which you build your expression. You can insert variables and functions to it from the lists, or enter text as in any standard text editor.

Cut/Copy/Paste works in the field using standard **Ctrl+X** / **Ctrl+C** / **Ctrl+V**.

Highlighting a section of the expression, and clicking Insert Function will add the selected function to the expression with the highlighted section as an argument.

Also, Undo/Redo functionality is available by pressing **Ctrl+Z**.

**Note:** Very long expressions will be displayed truncated in the Visualization Legend. To avoid this, insert a blank space with suitable distance. This will not affect the expression, but will allow the Legend to display it over several rows.

### Recent expressions

This list contains the twenty most recent expressions you have created. You can select one of these and click the Insert button to insert the expression into the **Expression** field. This will not replace the entire content of the field, only insert the selected expression at the cursor position.

### Result

This field displays the result of applying the current expression to the first row of the data set.

If this field shows an error message, there is a problem with the expression. Clicking on the field will display an explanation of what is wrong. Pressing **F5** will also display the error description. Pressing **F4** will move the cursor to the position in the expression where the error lies.

There are three kinds of error messages:

#EXPR! – there is a problem with the syntax of the expression.

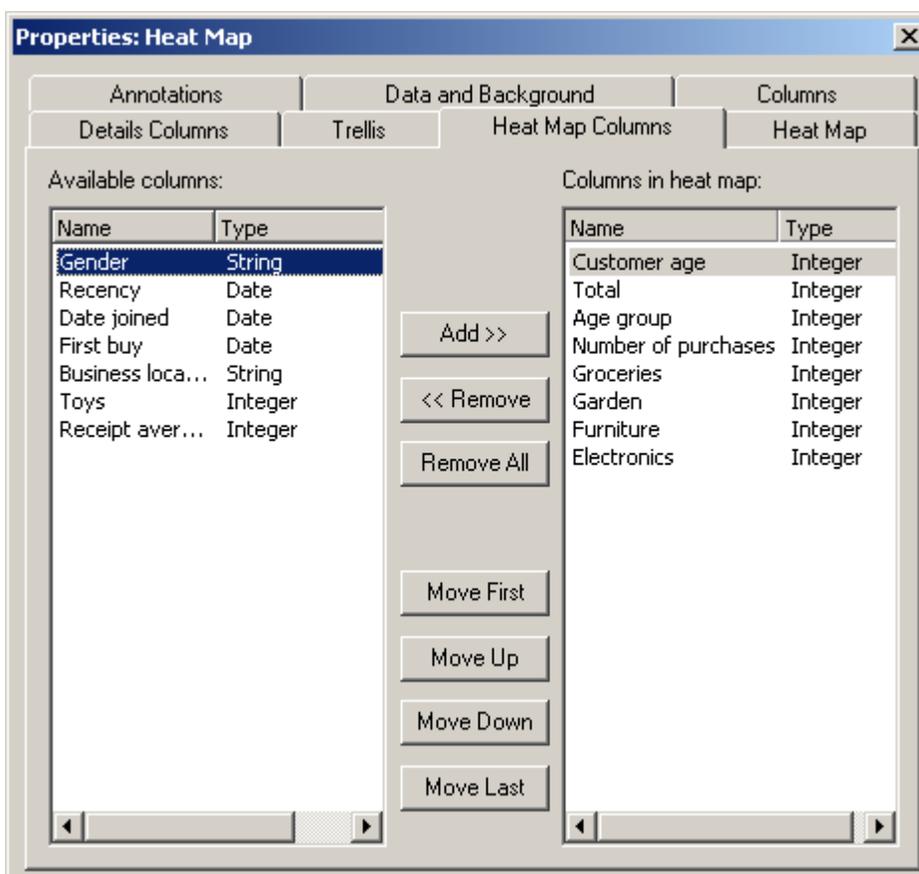
#NUM! – the row evaluates to infinity or other illegal number.

#ARG! – there is a problem with one or many arguments.

## 4.8.18 Heat Map Columns Tab

### 4.8.18.1 Heat Map Columns Tab

Edit > Properties > Heat Map Columns tab



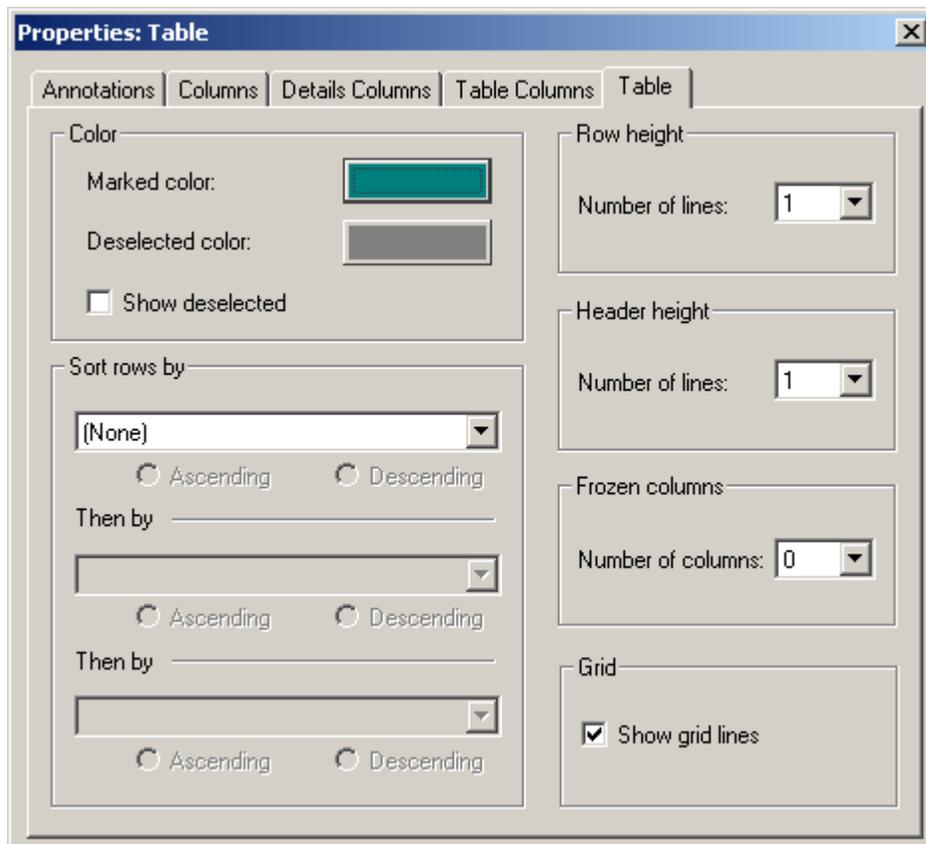
Option	Description
<b>Available columns</b>	These columns are not included in the heat map. <b>Note:</b> You can right-click on the Name header to get a pop-up menu where you can select other attributes you would like to be visible.
<b>Columns in heat map</b>	These columns are included in the heat map. The order of this list corresponds to the order the columns are shown in the Heat Map visualization. You can also see this numerically in the X-axis selector of the Heat Map.
<b>Add &gt;&gt;</b>	Select a column from the left list and press the <b>Add &gt;&gt;</b> button to move it to the right list, and include it in the heat map.
<b>&lt;&lt; Remove</b>	Select a column from the right list and press the <b>&lt;&lt;Remove</b> button to move it back to the available columns list, and remove it from the heat map.
<b>Remove All</b>	Removes all columns from the right list, and moves them to the available columns list.
<b>Move First</b>	Select a column from the right list and press the <b>Move First</b> button to move it to the top. This changes the order the lines are displayed.
<b>Move Up</b>	Select a column from the right list and press the <b>Move Up</b> button to move it a step up. This changes the order the columns are displayed in the heat map.
<b>Move Down</b>	Select a column from the right list and press the <b>Move Down</b> button to move it a step down. This changes the order the columns are displayed in the heat map.

**Move Last** Select a column from the right list and press the **Move Last** button to move it to the bottom. This changes the order the columns are displayed in the heat map.

## 4.8.19 Table Tab

### 4.8.19.1 Table Tab

Edit > Properties > Table tab



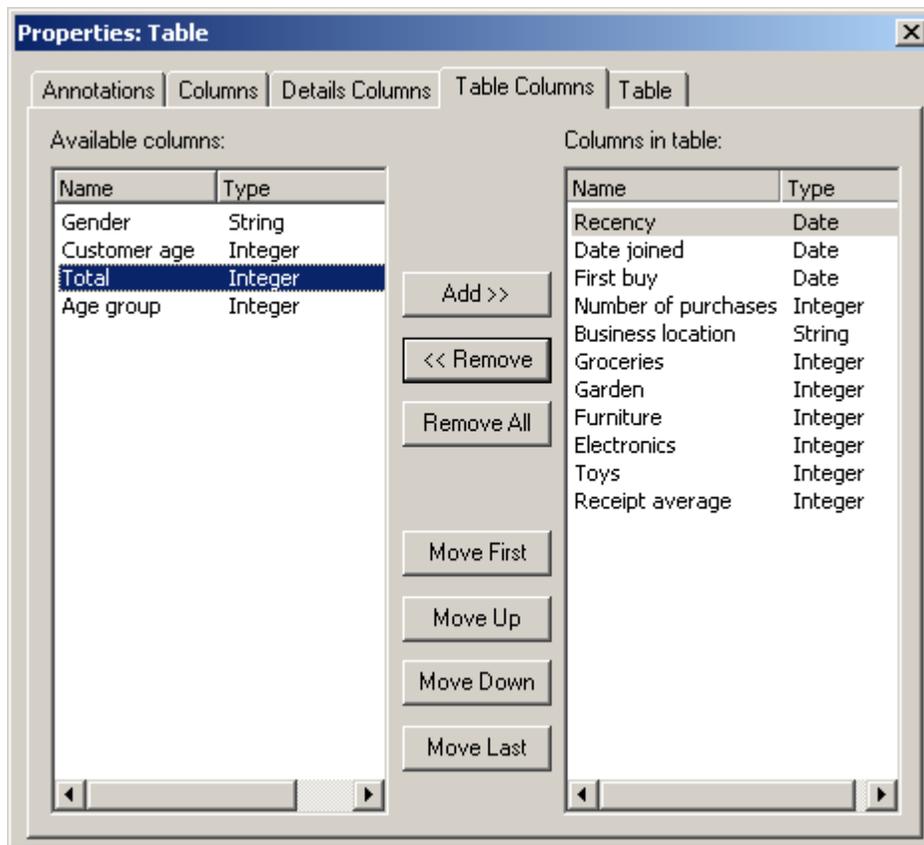
Option	Description
<b>Color</b>	<p>You can change the color that indicates marked and deselected markers by clicking on the corresponding button. You can also choose whether or not to display deselected records in the table by selecting or clearing the check box.</p> <p><b>Note:</b> Deselected records cannot be marked or made active in any way. Even though it is possible to make them visible by selecting the <b>Show deselected</b> check box, they are not included when marking a group of records.</p>
<b>Sort rows by</b>	<p>You can sort the order of the rows in the table. From the Properties dialog this can be done by up to three columns, but if you wish to sort by more than three columns simply use the Shift+click functionality.</p> <p>In the <b>Properties</b> dialog, first select a primary column to sort the rows</p>

	<p>by, and select whether the order should be Ascending or Descending. You may then select a secondary column to sort by, and even a third if you so desire.</p> <p><b>Note:</b> You can also sort the rows quickly by just clicking on the header of a column. Clicking several times will toggle between ascending or descending order. By holding down Shift and clicking on another column header you can sort by several columns.</p>
<b>Row height</b>	This drop-down list box lets you choose how high each row in the table should be. Height is measured in number of lines. It can be useful to increase the number of lines if there is a great deal of information in each cell, as several lines makes the text wrap inside each cell.
<b>Header height</b>	This drop-down list box lets you choose how high the headers in the table should be. Height is measured in number of lines. It can be useful to increase the number of lines if there is a great deal of information in each column header, as several lines makes the text wrap inside each cell.
<b>Frozen columns</b>	<p>In a table with many columns you often need to scroll horizontally. However, sometimes you may want certain columns to always be displayed regardless of scrolling. This is achieved by freezing one or more columns.</p> <p>Place the columns you want to freeze to the far left of the table, then use this drop-down list box to specify the number of columns you want to freeze.</p>
<b>Grid</b>	Select this check box to show grid lines in the table.

## 4.8.20 Table Columns Tab

### 4.8.20.1 Table Columns Tab

Edit > Properties > Table Columns tab



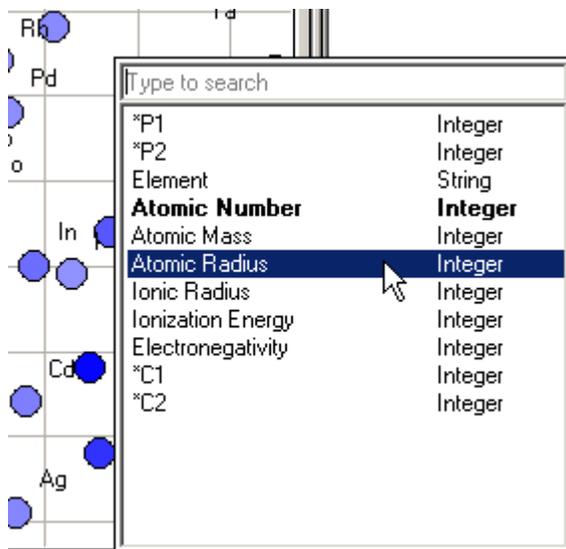
Option	Description
<b>Available columns</b>	These columns are not included in the table. <b>Note:</b> You can right-click on the Name header to get a pop-up menu where you can select other attributes you would like to be visible.
<b>Columns in table</b>	These columns are included in the table. The order of this list corresponds to the order the columns are shown in the Table visualization.
<b>Add &gt;&gt;</b>	Select a column from the left list and press the <b>Add &gt;&gt;</b> button to move it to the right list, and include it in the table.
<b>&lt;&lt; Remove</b>	Select a column from the right list and press the <b>&lt;&lt;Remove</b> button to move it back to the available columns list, and remove it from the table.
<b>Remove All</b>	Removes all columns from the right list, and moves them to the available columns list.
<b>Move First</b>	Select a column from the right list and press the <b>Move First</b> button to move it to the top. This changes the order the columns are displayed in the table.
<b>Move Up</b>	Select a column from the right list and press the <b>Move Up</b> button to move it a step up. This changes the order the columns are displayed in the table.
<b>Move Down</b>	Select a column from the right list and press the <b>Move Down</b> button to move it a step down. This changes the order the columns are displayed in the table.
<b>Move Last</b>	Select a column from the right list and press the <b>Move Last</b> button to

move it to the bottom. This changes the order the columns are displayed in the table.

## 4.9 Working with Visualizations

### 4.9.1 Changing Visualization Axes

To change the column to be mapped to each axis, click on an axis selector, and select a column name. For example, to see the Mendeleevian layout of the periodic.csv example data set, select *P1* for the X-axis and *P2* for the Y-axis.



**Note:** You can also select which column to use as an X, Y or Z-axis by right-clicking on the Query Device representing that column, and selecting **Set Property > Axis** from the pop-up menu.

### 4.9.2 Zooming and Panning

Zooming can be done in two ways: by using the zoom bars or by using the mouse.

#### Mouse Shortcuts

2D Scatter Plots, Bar Charts, Pie Charts, Line Charts, Profile Charts, and Heat Maps.

Action	Mouse maneuver	Comment
Zoom in	Ctrl + Right-click	The scroll wheel has the same function
Zoom out	Ctrl + Shift + Right-click	

In 3D Scatter Plots, the zoom bars are used as in 2D. Additionally, the following means of navigation are available.

Action	Mouse action 1	Mouse action 2	Pointer icon	Comment
Rotate	Ctrl + drag using the right mouse button	Drag using the middle mouse button		Rotation is around the visualization center

Zoom	Shift + drag using the right mouse button	Shift + drag using the middle mouse button		Moves in the direction of view
Roll	Shift + Ctrl + drag using the right mouse button	Shift + Ctrl + drag using the middle mouse button		Rotation is in the plane of the screen; down-wards and right cursor motion rotate clockwise
Zoom in on a specific marker	Click on a marker and use the mouse wheel	Ctrl + drag using the middle mouse button		Keeps the selected marker in the same place on screen

**Note:** Clicking the **Reset Navigation** button on the **3D** tab of the **Properties** dialog will undo all navigation adjustments.

### Zoom bars

Dragging the end arrows of the zoom bars (along the edges of the visualization window) zooms in on a portion of the visualization. Dragging the bar itself (by placing the mouse pointer on the yellow bar and dragging) pans across different areas of the entire visualization.



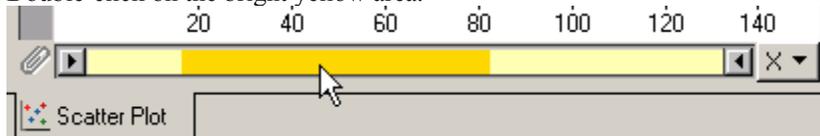
#### Altering the length of the X-axis zoom bar

The pale yellow area represents the selected range of values, whereas the bright yellow area represents the range of existing values within the selected range.

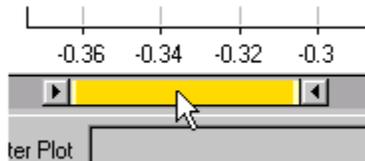
The zoom bar can be adjusted to encompass only the currently selected data.

#### ► Setting the zoom bar span to the current selection:

1. Double-click on the bright yellow area.



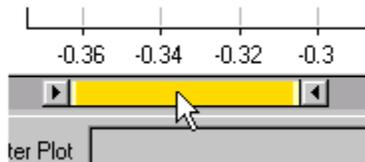
Response: The scatter plot and the zoom bar are now adjusted to focus on the selected markers.



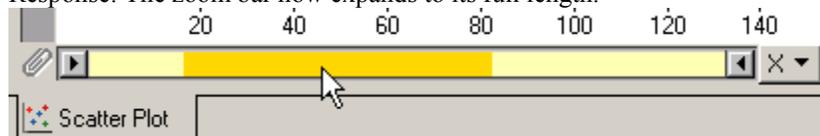
**Tip:** You can also right-click on the Zoom bar and select **Zoom to Selection** from the pop-up menu. To zoom in on one side but not on the other, double-click on the left or right drag box.

#### ► Resetting the zoom bar span:

1. Double-click on the center of the zoom bar.



Response: The zoom bar now expands to its full length.



**Tip:** You can also right-click on the Zoom bar and select **Reset Zooming** from the pop-up menu.

**Note:** By double-clicking on the left or right drag box of the zoom bar, you can narrow down the left or right span.

#### ► Setting the zoom bar to a specific value:

1. Click on an end arrow of the zoom bar.
2. Type the desired value.

The scatter plot and the zoom bar are now adjusted to show the value you entered.

**Note:** Note that no "edit field" will appear in which to type the value. Simply type the value after clicking, a temporary ToolTip will be displayed, and the slider will adjust itself to the specified number.

#### ► Setting the Data Range to Selected records:

1. Move the drag box of the zoom bar to narrow the selection.
2. Right-click on the zoom bar.
3. Select **Data Range from Zooming** from the pop-up menu.

The zoom bar expands to its full width, but with the Data Range set to encompass only the selected records. Three dots are displayed to indicate that the range is not the original full range.

#### ► To reset the Data Range:

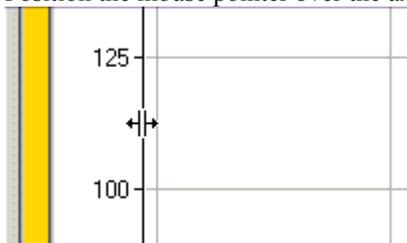
1. Right-click the zoom bar and select **Reset Data Range**.

## 4.9.3 Axis Labels

Axis labels are by default displayed along both the horizontal and vertical axes. These can be adjusted in several ways.

#### ► To adjust the axis label width/height:

1. Position the mouse pointer over the axis. The mouse pointer changes, as seen below.



2. Press down the mouse button and drag the axis to the width or height desired.

**Note:** If the axis labels are hidden, simply grab the axis and drag it to make the labels visible again.

### Label options

By right-clicking in the axis label area, a pop-up menu appears. It contains several options:

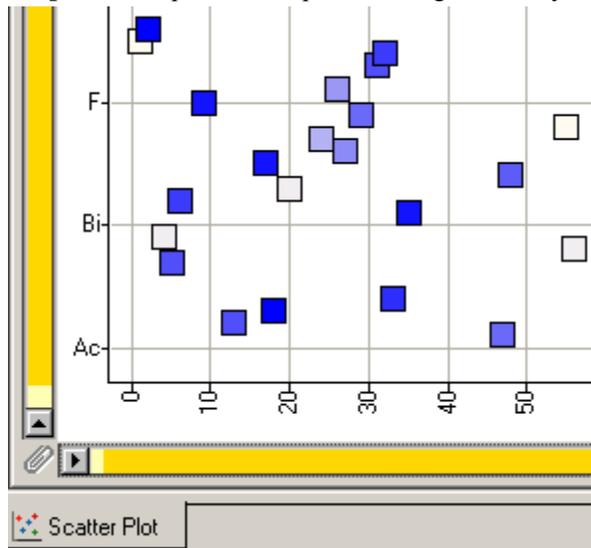
**Hide** – Hides the vertical or horizontal axis labels. Drag the axis (see above) to make the labels visible again.

**Fewer Labels** – Fewer labels are displayed on the axis.

**More Labels** – More labels are displayed on the axis.

**Label Orientation** – Sets the label text orientation to either Horizontal or Vertical (see below).

**Properties** – Opens the Properties dialog in which you can set Label spacing and density.



## 4.9.4 Applying Templates

If you open many data sets of a similar nature in DecisionSite Client, you may wish to create a template of the usual visualizations you always create, certain query device settings you always initially make, etc. For information on how to save a template see Saving Spotfire Files.

A template file is basically a standard Spotfire file which can be used to apply predefined visualization settings to a new data set. When you want to apply a template to a data set, you can therefore choose to apply the settings from either a Template file (SFT), a Spotfire Analysis File (SFS) or a Spotfire XML File (XSF, which is the same thing as an SFS file only in XML format).

### ► To Apply a Template:

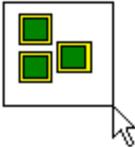
1. Open your data set in DecisionSite Client.
2. Select **File > Apply Template...**
3. Select the template file you want to apply.
4. Click **Open**.

Response: The template is applied on your data.

## 4.9.5 Marking, Activating, and Highlighting Records

### 4.9.5.1 How to Mark, Activate and Highlight

In DecisionSite, there are three ways to interact with the data set: marking, activating and highlighting.

Action	Marking	Activating	Highlighting
Indicator in visualizations			
How to do it	Hold down the left mouse button and draw a rectangle around one or more objects (or press <b>Shift</b> before you press the button, and drag for a lasso effect).	Click on a single object.	Hover with the mouse pointer over an object.

**Note:** An "object" can be a single record (as in scatter plots) or an aggregation of records (such as pie charts).

The effect of performing these actions varies with the tool and type of visualization. Go to the sections describing each tool to find out more, or click the Help window's **Back** button to return to where you were!

### 4.9.5.2 Marking

The purpose of marking records may be to view details, or to distinguish records in order to copy, erase, or in other ways manipulate them.

#### ► To mark one or more records:

1. Click and hold the left mouse button, and drag the mouse: the pointer will delineate a rectangle.
2. Enclose the markers of interest in this rectangle. When the mouse button is released, the marked objects will be given a different color and outline.

**Note:** Marking a pie or bar is equivalent to marking all the records that are included in that pie or bar.

#### ► To add more records to the marked set:

1. Press and hold **Ctrl**.
2. Click on markers you want to add, one by one. Alternatively, use the mouse to draw a rectangle around several markers (while still pressing **Ctrl**).

#### Marking with the lasso

A set of graphical objects, be they pies, bars or scatter plot markers, can be "lasso selected", i.e., be surrounded by a line drawn in an arbitrary shape. Press the **Shift** key and the left mouse button, then draw a line capturing the markers. Note that a straight line connects the beginning and the endpoints of the lasso marquee. The line delineates the area that will be included in the selection.

**Note:** For a record to be marked, its exact coordinates must be within the bounds of the selecting line. Just slicing through part of an enlarged marker will not suffice.

#### Setting colors for marked objects

Marked records will be given an identifying color in all visualizations. You can define this color through the **Customize** color button of the **Properties** dialog.

## Unmarking

Re-marking any marked object(s) while Ctrl is pressed will unmark them. If Ctrl is not pressed, only the new selection will be marked. Unmark all data by selecting **Edit > Marked Record(s) > Unmark**; or by pressing [Ctrl+E]. Alternatively you can unmark everything by marking an empty area of any visualization.

## Message box when marking

If a set of markers is already marked, and you mark a new set, a message box will appear, warning you that you will lose the previous marking. You can turn this feature off by checking the box labeled **Never show alert again**. If, at a later time, you would like this feature back, select **Edit > Marked Record(s) > Unmark**, and check the box in the dialog. You can also use the **Customize** dialog.

### 4.9.5.3 Activating

Clicking on a single record will make a persistent circle surround the corresponding marker in all scatter plot visualizations. A record thus chosen is referred to as **active**.

The arrow keys will cause the nearest record in the direction of the arrow to become active. The Tab key will move the active record indicator to the next record in the data set. If you have a group of records marked, using the keys will only cycle through these.

The details of an active record are presented in the Details-on-Demand window. The record will continue showing details until another record is made active or a group of records marked with the lasso or rectangle method.

### 4.9.5.4 Highlighting

Moving the mouse pointer close to or on top of a graphical object will highlight it. A thin circle will cling to the marker until the pointer is moved a certain distance away.



Highlighted marker

Highlighting shows where in each visualization a data point lies, because the same record is highlighted in each visualization.

### 4.9.5.5 Actions Involving the Marked Set

The following commands concern the set of marked records. They can all be found via the **Edit** menu or in the right-click context menus of the visualizations.

Option	Description
<b>Marked Record(s) &gt; Unmark</b>	<b>Ctrl+E</b> . Unmarks all records in the data set.
<b>Marked Record(s) &gt; Invert</b>	<b>Ctrl+I</b> . Inverts the marking so that all unmarked records become marked and vice versa.
<b>Marked Record(s) &gt; Select</b>	<b>Ctrl+M</b> . Sets query devices to include only the marked records. This hides the unmarked records.
<b>Marked Record(s) &gt; Undo Select</b>	<b>Shift+Ctrl+M</b> . Undoes the previous selection.
<b>Marked Record(s) &gt; Delete</b>	<b>Delete</b> . Removes corresponding records from the data set. The action is irreversible and immediately affects the loaded data set. However,

the data source (e.g., the file) will remain unchanged until you explicitly overwrite it by saving.

**Data > New Column > From Marked Records...** Creates a new column. By default, marked records will get the value Yes, and unmarked records the value No.  
**Note:** Found under the **Data** menu.

### 4.9.5.6 Resetting Visualizations

After having zoomed in, selected, deselected and performed a number of manipulations on the markers, pies and/or bars, the set of records shown in the visualizations may become disarrayed. The command **Reset to All** in the **Edit** menu (**Ctrl + R**) will get the visualization back in order again, resetting the query devices and restoring zoomed visualizations.

Deleted records will be gone, however, and can only be restored by closing the visualization without saving it and then opening the original data set once again.

### 4.9.5.7 Copying Records

These commands under the **Edit** menu copy the data stored in the loaded data set, or a sub-set of it, to the clipboard. The copied information can then be exported, pasted into a spreadsheet program, such as Microsoft Excel or another program, e.g. Notepad.

**Copy** [Ctrl+C] copies the records corresponding to the markers, bars and pies marked with the lasso or rectangle marking tool to the Windows clipboard in text format. It also copies an image of the visualization to the clipboard, which can be pasted into other applications by using a Paste Special option.

**Copy Special > Marked Records** copies the records corresponding to the markers, bars and pies marked with the lasso or rectangle marking tool to the Windows clipboard in text format.

**Copy Special > Selected Records** copies only the records within the limits set by the query devices to the Windows clipboard in text format.

**Copy Special > All Records** copies all records to the Clipboard. Data in all the records in the data set is copied to the Clipboard in text format.

**Copy Special > Visualization** copies the active visualization display as a Windows Metafile image. This image can be pasted into other Windows compatible applications such as MS Word, Paint, PowerPoint etc. As Metafile images are vector-based graphics they can be enlarged or shrunk at will without losing detail. Axes, labels and grid lines are included in the image. These images can be manipulated from within the new host applications.

### 4.9.5.8 Information About the Data Set

The record meter in the status bar at the bottom of the Spotfire DecisionSite gives continuous information about visualization statistics. You can see at a glance what portion of all the data is currently visible, marked, etc. The same information is displayed as text.



Colors should be read as follows:

Green – Records that are selected and marked.

Yellow – Records that are selected and unmarked.

Gray – Records that are selected, but lack a value required for representation on the current axes, and hence are invisible.

The sum of the above makes up the set of selected records. The length of the record meter in relation to the box in which it sits is an indication of the relative size of the current selection. To display or hide the status bar, use the **Status Bar** command in the **View** menu.

## 4.9.6 Organizing the Desktop

### 4.9.6.1 Arranging Visualizations

There are several ways to reposition windows; the commands governing these functions all reside in the **Window** menu:

**Auto Hide Axis Selectors** – when the visualization is small enough, this option automatically hides the zoom bars and the axis selectors.

**Hide Window Frame** – hides the title bar, giving more space to the visualizations—only available when several visualizations have been tiled.

**Auto Tile** – arranges all the windows on screen according to an internal algorithm. The active visualization will be made the largest, and placed in the upper left-hand corner.

**Cascade** – arranges the visualization windows so that they partially overlap each other, leaving each window accessible by clicking on the title bar.

**Tile Horizontal** – splits the window area horizontally, giving each visualization equal area.

**Tile Vertical** – splits the window area vertically, giving each visualization equal area.

**Tip:** An alternative way of organizing visualizations is to use a Trellis plot. This allows you to split an existing plot into panes, and organize these in a grid. Note that this feature is currently available only for scatter plots (2D and 3D), bar charts, profile charts and heat maps. See *What is a Trellis Plot?* for more information.

### 4.9.6.2 Showing and Hiding Windows

Spotfire DecisionSite consists of several windows. It can be desirable to rearrange the application's layout to organize visualizations and information for more effective analysis.

The **View** menu displays a list of the Spotfire DecisionSite windows. Each window can be shown or hidden by selecting or clearing the check mark next to the name of the window, respectively. The windows are listed and described below:

**Toolbars** – the row of clickable buttons right below the menus. See *Toolbar Buttons* for more information.

**Status Bar** – the information field at the bottom of the application window. The status bar displays information about pointer position, number and portion of records that are visible and marked, etc.

**Full Screen** – by selecting this option, all Toolbars are hidden and the Visualization, Query Device and Details-on-Demand window are maximized to fill the whole screen. By clicking on the small icon (below) the Toolbars are returned. You can also go to Full Screen mode by pressing **F11**.



**Workbook** – when this option is selected, each visualization is given a separate tab.

**Details-on-Demand (Text)** – the window where information about the marked records, the highlighted scatter plot marker, bar or pie object, etc., appears.

**Details-on-Demand (HTML)** – information about the highlighted or marked scatter plot marker(s), bar or pie object(s), etc., formatted according to the HTML templates stored in the current SFS file.

**Details-on-Demand (External Browser)** – as above, but launches a separate browser.

**Query Devices** – the window that contains all the query devices.

**Legend** – the window that explains the significance of the current visualization settings, e.g., which columns are used for size, rotation, color, etc.

**Guides Toolbar** – the row of clickable buttons pertaining to the Guides pane.

**Guides Pane** – the browser window used to view Guides, and to run Spotfire DecisionSite applications (plug-ins).

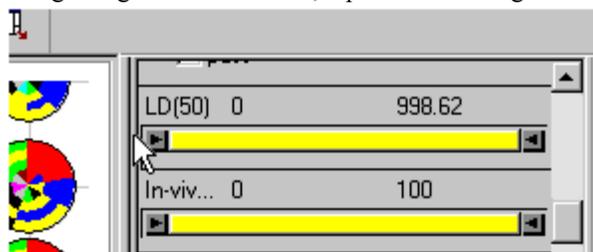
### 4.9.6.3 Moving and Resizing Windows

Spotfire DecisionSite has a certain default setup; the Guides pane appears on the left, while the larger area in the centre is for the visualization(s). The right side is occupied by the Query Device window and the Details-on-Demand window.

Since this may not be the most effective layout for all purposes, it is possible to move and resize the windows.

To resize a window, click on a window border and drag it to the desired position.

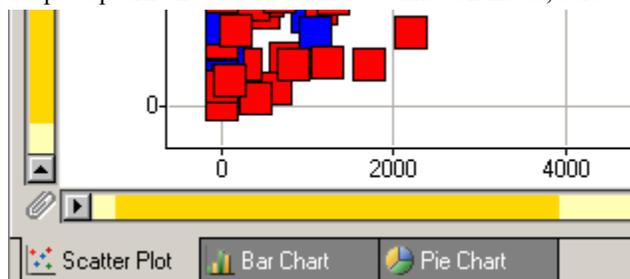
To move a window, click on the title bar or gripper bar at the top of the window, and drag the window to the desired position. Alternatively, press the left mouse key while pointing at the left or right edge—there is a thin, 3 pixel band—to grab the window for repositioning.



### 4.9.6.4 Workbook Mode

Workbook mode can be used to put each visualization on its own tab. A click on a tab activates the corresponding visualization and allows manipulation and modification of its attributes.

To put Spotfire DecisionSite into Workbook mode, select **Workbook** from the **View** menu.



You can change the order of the tabs by right-clicking on a tab and selecting **Move > First/Left/Right/Last** from the pop-up menu.

#### Combining Workbook with Auto tile

With **Windows > Auto Tile** off, pages in the Workbook retain the size that they had been given; decreasing the size of the application window will crop portions of some visualizations.

With the **Auto Tile** function on, clicking on a Workbook tab gives the chosen visualization priority position and size.

### 4.9.6.5 Duplicate Visualization

By selecting **Visualization > Duplicate Visualization** you can create a copy of the currently selected visualization. This is useful if you have created a visualization with different settings, and you wish to create an identical copy in which you then want to change some aspect and compare the two.

## 4.9.6.6 Customizing Visualizations

The **Tools > Options > Visualization Settings** tab allows you to control certain aspects of the visualizations.

### Hiding axis selectors

Axis selectors can be made to automatically disappear when the visualization size is less than a certain threshold value. Click **Auto Hide Axis Selectors** and set threshold values to enable this function. The **Default** button restores default threshold values and disables Auto-hide.

### Controlling default settings for new visualizations

The **Save** button on the **Visualization Settings** tab of the **Options** dialog allows you to set the preferred initial settings for new visualizations.

The settings of the current visualization are used as a template for initial visualizations of similar type. In this context, 2D and 3D scatter plots are linked, i.e., default settings for 3D visualizations will also apply to 2D scatter plots.

The following settings are saved for all visualizations:

- **Color** – e.g., categorical or continuous coloring, beginning and ending colors for continuous coloring, marked and deselected marker color, etc., but not which column governs coloring.
- **Size** – the size of markers (but not which column governs size).
- **Labels** – the label mode (None, Marked, All), the number of labels displayed and their color, displacement, orientation, positioning and density.
- **Gridtype** – show grid or not.
- **Append axis names to visualization title**
- **Show deselected** – whether or not deselected records should be displayed.

In addition, marker shape is also saved for scatter plots, outline or no outline is saved for bar charts, scale mode is saved for profile charts and line charts as well as the show marker option for line charts.

No column-specific settings are saved, e.g., **Rotate by** is not saved since it refers to a specific column. Settings from the **3D** tab such as navigation, rendering and perspective are not saved; neither are **Data and Background** tab settings as they are column specific.

The **Reset** button will remove the configuration that you have previously saved and restore the default values.

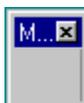
## 4.9.6.7 Customizing Toolbars

Tools > Customize > Toolbars tab

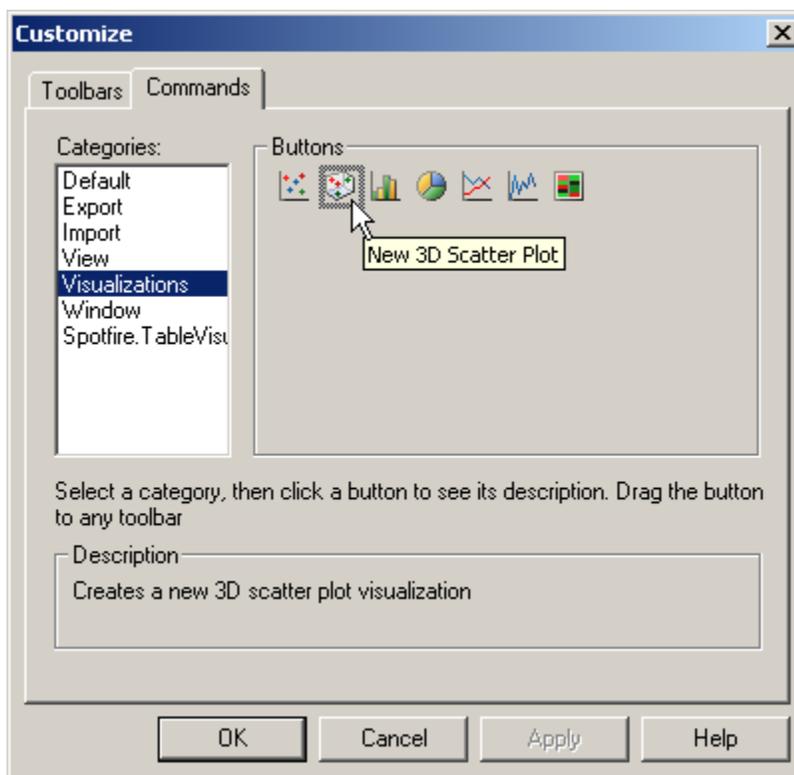
You can tailor Spotfire DecisionSite's toolbars to allow you to rapidly access features that you use regularly.

### ► To customize toolbars:

1. Select **Tools > Customize...**
2. Go to the **Toolbars** tab.
3. Click **New...**
4. Enter a name for the new toolbar and click **OK**.
5. Make sure the new toolbar is selected in the list. Your toolbar should be visible as a small box on your screen:



6. Go to the **Commands** tab.
7. Select a category of commands.



8. Drag any button to your new toolbar (or to any of the standard toolbars).
9. Click **OK**.

### 4.9.6.8 Fonts & Numbers Tab

#### ► To change the fonts:

Select **Tools > Options > Fonts & Numbers**. This opens the **Fonts & Numbers** tab of the **Options** dialog in which you can specify which font should be used for different categories of the application:

- Annotations - the font used for the annotation when printing.
- Axis labels - the font used for the axis labels, on screen, when printing or exporting.
- Details on Demand - on screen.
- Headers and Footers - shown when printing.
- Legend - on screen, when printing or exporting.
- Marker labels - the font used for the marker labels, on screen, when printing or exporting.
- Query Devices - on screen.
- Title - when printing.
- Visualization - texts in visualizations (not labels), on screen, when printing or exporting.

Select one or more categories and click on the Change Font button. This displays the Font selection dialog in which you can select which font, font style and font size should be used for the selected categories.

► **To reset the fonts:**

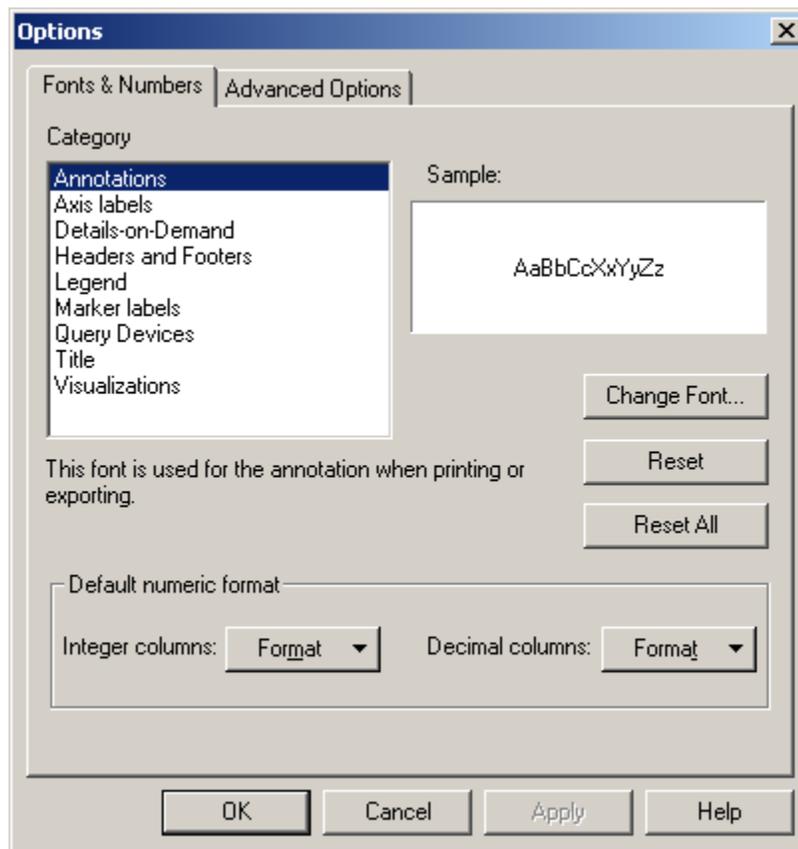
- Select one or more categories and click on the **Reset** button, to reset the font for these categories to the default font.
- Click on the **Reset All** button to reset all categories to the default font.

You can specify how you want DecisionSite Client to display number formatting for all Integer type values and Decimal type values. You can set the Number of decimal digits, how to display Negative numbers, and whether or not to use Thousands separators. The settings you make in this dialog will be set as default, and take effect when you load a new data set in to DecisionSite Client.

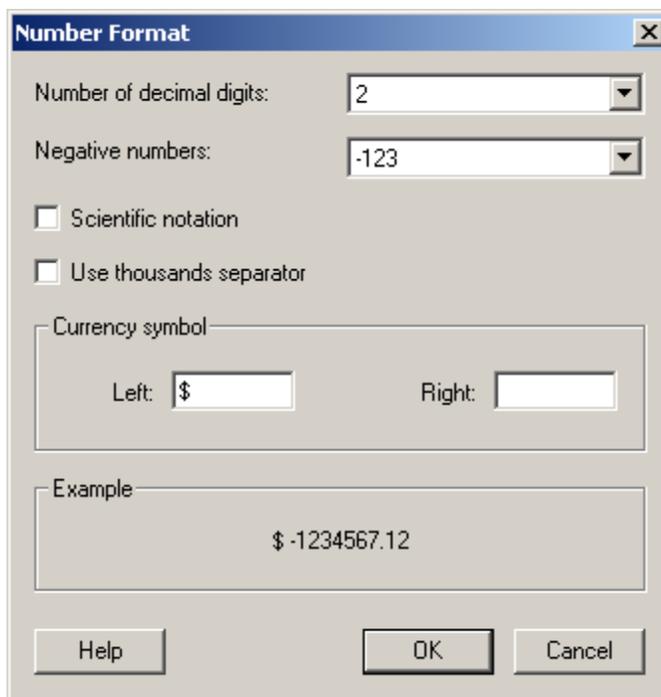
You can set other number formatting for specific columns later if you want to. See Number Format for Columns.

► **To set Number Formatting:**

1. Select **Tools > Options > Fonts & Numbers**.



2. Click on either the **Integers...** or **Decimals...** button and select either **None** formatting or a custom one under **Number...**



3. Specify the **Number of decimal digits**, how to display **Negative numbers**, and whether or not to **Use thousands separators**.  
**Note:** The symbol used for thousands separators and decimal separator is determined by the Windows Locale setting.
4. Click **OK**.

### 4.9.6.9 Advanced Options Tab

The **Advanced Options** tab of the **Tools > Options** dialog provides some options for fine-tuning your Spotfire DecisionSite environment. Use the check boxes to enable or disable any of the following features (the first four only take effect after Spotfire DecisionSite is restarted):

Option	Description
<b>Show grippers on docked windows</b>	Displays a small banner in docked windows, which can be used when dragging the window to a new position. Drag the banner to move the docked window. Examples of docked windows are the Details-on-Demand window and the Legend window.
<b>Show full column names in query devices</b>	When this option is selected, column names are displayed on a separate row inside each query device. Clearing the check box will display the column names and the values on the same row, in some cases truncating the column name, but instead the query devices will be more compact, thus displaying more query devices in the window.
<b>Show warning when changing marked records</b>	Displays a dialog each time you mark a new set of records.
<b>Use OpenGL hardware acceleration</b>	If you experience problems displaying 3D Scatter Plots, try turning off the OpenGL acceleration.

<b>Use DirectX9 for smooth line rendering, if available</b>	Enables the use of hardware-accelerated DirectX 9 for smooth line rendering. (This setting only has effect if there is a DirectX 9 capable graphics card available in your computer.)
<b>Ignore case in full text search</b>	This sets the default behavior for full-text search query devices. This means that when you import a new data set or change a query device into a full-text search, it will be either case sensitive or not, depending on this setting. However, you can also specify whether or not each individual full-text search query device should be case sensitive by right-clicking on it. In the pop-up menu that appears, select <b>Set Property &gt; Search options &gt; Ignore Case</b> . By using this alternative, different query devices can have different settings.
<b>Use Regular Expression in full text search</b>	This sets the default behavior for full-text search query devices. This means that when you import a new data set or change a query device into a full-text search, it will either use regular expressions or not, depending on this setting. However, you can also specify whether or not each individual full-text search query device should use regular expressions by right-clicking on it. In the pop-up menu that appears, select <b>Set Property &gt; Search options &gt; Use Regular Expression</b> . By using this alternative, different query devices can have different settings. <b>Note:</b> When you save the visualization, the settings for each query device are saved in the SFS file and will remain when you open the file again. However, since the case sensitivity and regular expression settings are not available in versions older than DecisionSite 7.1, the full-text search query devices in older SFS files that are opened in DecisionSite 7.1 or later, will be based on the default settings in the <b>Advanced options</b> tab.
<b>Show Bar Chart version 7.x toolbar button</b>	In DecisionSite 8.0 a new improved bar chart was introduced. For legacy reasons it is still possible to create a version 7.x bar chart. Select this check box and restart DecisionSite Client to display a toolbar button which lets you create a version 7.x bar chart.
<b>Export data using column formatters</b>	Select this option to use the current formatting of all columns upon export. See Export Data for more information.

**You can also set:**

- The default width of the query device window
- Vertical or horizontal auto-tiling
- Default file location; this is the directory you want Spotfire DecisionSite to open when you select **File > Open**. Entering a single period character in this field means that Spotfire DecisionSite's *Spotfire/DecisionSite/Data/* directory will be the default.

## 4.9.7 View Tip

### 4.9.7.1 What is View Tip?

View Tip is a tool for rapid assessment of potentially interesting visualizations. It suggests visualizations based on the correlation between data in the columns, the number of unique values, and the distribution of data. In some cases the View Tip also suggests colors where this is appropriate.

View Tip is a convenient way of quickly getting to know a data set. As you browse through the different miniatures plots, you realize that View Tip is a natural first step when you start exploring unknown data.

### To use the View Tip function:

Open the data set in Spotfire DecisionSite, and select **View Tip...** from the **Visualization** menu. Click on an item in the Scatter plots or Histograms list, or use the arrow keys to quickly browse either list.

When you have found an interesting visualization that you want to investigate further, click **Create View** to generate the corresponding visualization in Spotfire DecisionSite.

Click **Close**.

**Note:** Selecting a Histogram will create a "Version 7.x Histogram".

## 4.9.7.2 View Tip Algorithms

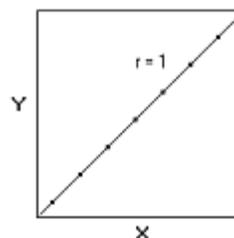
### Ordering of scatter plots

View Tip calculates the correlation between different combinations of columns, and orders the suggested visualizations according to the degree of linear correlation.

The most common measure of correlation is the Pearson Product Moment Correlation (called Pearson's correlation for short). When computed in a sample, it is designated by the letter  $r$  and is sometimes called Pearson's  $r$ . Pearson's correlation reflects the degree of linear relationship between two variables. Pearson's ranges from +1 to -1.

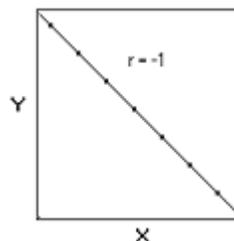
#### Positive correlation

A correlation of +1 means that there is a perfect positive linear relationship between variables. This scatter plot depicts such a relationship. It is a positive relationship because high scores on the X-axis are associated with high scores on the Y-axis.



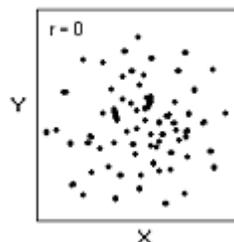
#### Negative correlation

A correlation of -1 means that there is a perfect negative linear relationship between variables. This scatter plot depicts such a relationship. It is a negative relationship because high scores on the X-axis are associated with low scores on the Y-axis.



#### Zero-correlation

A correlation of 0 means there is no linear relationship between the two variables, as shown in this graph. Correlation is rarely, if ever 0, 1, or -1.



With behavioral data, there is almost never a perfect linear relationship between two variables. The more the points tend to fall along a straight line, the stronger the linear relationship. View Tip calculates the absolute value for  $r$ , and then determines the rank of the scatter plots accordingly.

## 5 Query Devices

### 5.1 What is a Query Device?

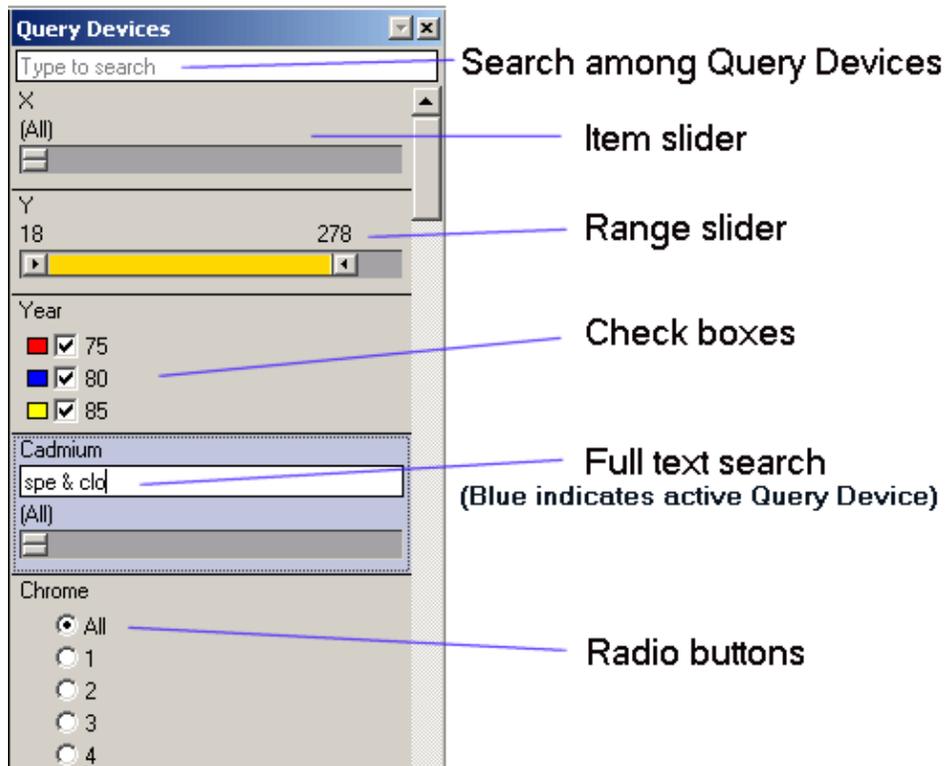
A query device works like a filter, imposing constraints on the loaded data set. For example, a query device may exclude all records with values above a certain threshold. Only records that comply with the query device settings are visible in visualizations. When manipulating a query device, you can instantly see how the current setting affects the visible data. The visible data (and any empty values for the active axis) is also referred to as **selected**.

When a data set is loaded, each column in the underlying data set becomes associated with one query device. The type of device depends on the type of data in the column. Spotfire DecisionSite has five types of query devices: range sliders, item sliders, full-text search, check box query devices, and radio button query devices. (Also, the zoom bars work like range sliders.)

#### Searching for a Query Device

When using a data set with many columns, you often have just as many query devices. Sometimes it can be hard to find the query device you wish to manipulate by scrolling through the query device panel. A quick way to find a certain query device is to use the search function at the top of the query device panel. If you know the name of the column (Query Device) you want, simply begin typing it into the search box and the desired query device should come into focus. Any columns with names that do not match this are hidden from the query device panel. As you enter text, the query device panel is continuously updated with the query devices that begin with the current substring. To show all query devices again, just clear the search box. The query device search expression is based on case-insensitive substring matching of the column name. For example: Typing in "a" will match a column named "Apple" as well as a column named "Pear" but it will not match a column named "Lemon".

You can also navigate between the query devices using your keyboard. F3+up arrow or F3+down arrow will move you up or down one query device. F3+home or F3+end will move you to the first or last query device, and F3+page up or F3+page down will move you up or down one screen length among the query devices.

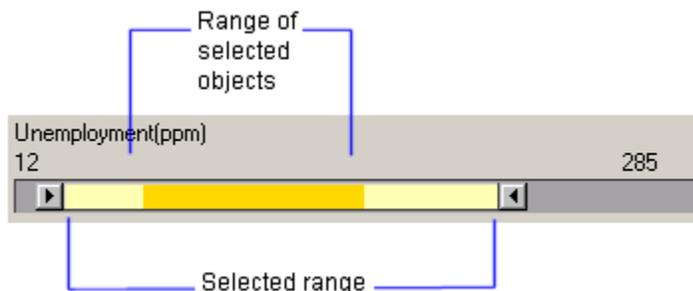


You can also navigate between the query devices using your keyboard. F3+up arrow or F3+down arrow will move you up or down one query device. F3+home or F3+end will move you to the first or last query device.

## 5.2 Range Sliders

Range sliders allow the selection of a range of values. The left and right drag box can be used to change the lower and upper limit of the range, meaning that only records with values within the chosen range are selected and therefore visible in the visualization. Labels above the slider indicate the selected span. The range can also be adjusted with the arrow keys when the query device is active: left and right arrows move the lower limit (left drag box), and up and down arrow keys move the upper limit. The slider automatically jumps to values in the data set (not necessarily the visible or selected records).

The currently selected interval of the range slider can be grabbed and moved to pan the selected range—this provides a powerful way of sweeping over different "slices" of a data set. Click and drag the yellow portion of the range slider to do this. Observing the reactions the other sliders to such a sweep can give some interesting clues to correlation between parameters in the data set.



An important feature of the range slider is that the values are distributed on a linear scale according to the values of the data. Thus if values are unevenly distributed, this will be reflected in the range slider.

**Note:** This is not the case with item sliders, where values are evenly distributed along the range of the slider, regardless of what values appear in the column.

**Note:** For more information on how strings are sorted in a query device please see Strings.

## Adjusting the Range Slider span

The range slider can easily be adjusted to encompass only the currently selected data.

### ► Setting the range slider span to the current selection:

1. Double-click on the center of the range slider.



2. The range slider is now adjusted so as to show only the effective area:



3. To reset the range slider, double-click on the center of it again. The range slider is then reset to its maximum width.

### ► Setting the left range slider span:

1. Double-click on the left drag box.



2. The range slider is now adjusted:



3. To reset the left range slider span, double-click on the left drag box of it again. The range slider is then reset to its maximum width.

**Note:** This function also applies to the zoom bars functionality.

Sometimes you might wish to filter the data in a column using a smaller range than the full range of the column. If so, you can set a range slider to encompass only a smaller range.

### ► Setting the Data Range to Selected records:

1. The original Range Slider span is 0 to 40.



2. Move the drag box to narrow down the selection.



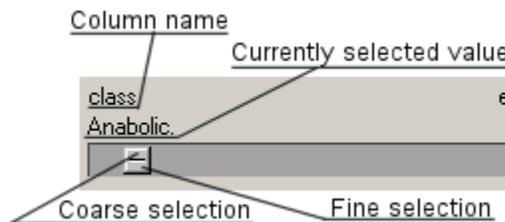
3. Right-click on the Range Slider to bring up the Query Device pop-up menu.
4. Select **Data Range > From Selected**. The Range Slider expands to its full width, but with the range 27 to 40. Three dots are displayed to indicate that the range is not the original full range.



5. To reset the span, right-click the Range Slider and select **Data Range > Reset**.

## 5.3 Item Sliders

In an item slider query device, data items are represented by their numerical values on a continuous linear scale. However, the item slider selects only a single item at a time. The selected value is displayed as a label above the slider. As a special case, all items are selected when the slider handle is at the extreme left of the scale.



The item slider features two levels of granularity—a coarse grain slider for moving rapidly between items, and a fine grain slider for moving more slowly between adjacent items.

**Note:** The scope of an item slider is dependent on the settings of other query devices. This means that the item slider range constantly changes as you manipulate the query devices. Items that fall outside of the current selection or zooming become unavailable and will be grayed out.

**Note:** For more information on how strings are sorted in a query device please see String.

If you are working with large data sets—consisting of perhaps several hundreds of thousands of records—it can be quite tricky to get the slider to stop at the desired value. The solution to this problem is to use the fine-resolution handle together with the keyboard.

To pin-point a certain entry with the item slider:

Click the upper handle of the slider, and drag the box to the approximate position of the entry by keeping an eye on the currently selected value above the slider.

Fine tune with the fine resolution handle.

When the input focus is set on the slider (marked by a dotted line), you can use the arrow keys on your keyboard to adjust the slider to the exact position of the entry. Up and right arrows move to the next value, down and left to the previous one.

When the item slider drag box is moved to its leftmost position, all values for the slider are selected. This is indicated by the label (**All**) above the slider.

## 5.4 Full-text Search

### 5.4.1 Full-text Search

The full-text search query device allows you to search for (sub)strings within columns. It also allows you to search for a pattern by using Regular Expressions. For example, you can enter a pattern that means "a letter followed by two digits".

By *normal-text search*, we refer to search strings that don't contain regular expressions. The search can be made arbitrarily complex by use of logical operators AND (&) and OR (blank space). Search expressions are evaluated from left to right.

Once the search string has been entered, press Enter on your keyboard to execute the search. All records matching the search criteria will be shown in the visualization window.

The operators allowed in normal searches are:

white-space	logical OR
&	logical AND
" "	search for the exact sub-string within double quotes

The full-text search query device also supports Cut/Copy/Paste of text strings using the CTRL+X, CTRL+C and CTRL+V.

You can specify whether a full-text search query device should use regular expressions or not, by right-clicking on it. In the pop-up menu that appears, select or deselect **Set Property > Search Options > Use regular expression**.

#### Case sensitivity

When importing a new data set or changing a query device into a full-text search, the resulting full-text search query device(s) will be either case sensitive or not. This is determined by a setting in the **Tools > Options > Advanced options** tab called **Case sensitive full-text search**. If this check box is selected then searches done with the query devices will be case sensitive.

However, you can also specify whether or not each individual full-text search query device should be case sensitive by right-clicking on it. In the pop-up menu that appears, select **Set Property > Search Options > Ignore case**. By using this alternative, different query devices can have different settings.

When you save the visualization, the settings for each query device are saved in the SFS file and will remain when you open the file again. However, since the case sensitivity and regular expression settings are not available in versions older than DecisionSite 7.1, the full-text search query devices in older SFS files opened in DecisionSite 7.1 or later, will be based on the default settings in the **Advanced options** tab..

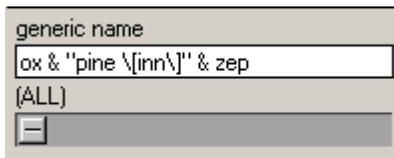
**Note:** When a query device is changed into a full-text search query device, the "Show Empty Values" option from the Properties dialog is automatically set to False. This means that empty values are not included in the search result.

### 5.4.2 Using the Full-text Slider

The slider integrated in the full-text search query device is really just an item slider with one important difference: the *scope* of the slider corresponds to the result of the full-text search. This means that if you set the slider in its leftmost position (All), all items *that match the search criteria* will be shown (which doesn't necessarily mean all the records in the data set).

Use the slider to select individual items among those that match the search criteria. Drag the upper portion and the scrolling will be rapid. If the search has resulted in many hits, some will not appear with the coarse selector. When in the appropriate region of hits, drag the fine-tuning lower portion to locate the specific value you want.

As with other sliders, once activated they can be adjusted with the keyboard arrows. Keyboard selection is always fine-grained, value by value.



Let's look at the example in the figure above. Note that the brackets must be preceded by a backslash since brackets have a special meaning in regular expressions (see Regular Expressions below).

**carb ox & "pine \[inn\]" & zep**

Spotfire DecisionSite will evaluate the search expression in the following way

**(carb OR ox) AND ("pine [inn]") AND zep**

In plain English this means: "Show me all items where the column Generic Name contains names that include the sub-strings **carb** or **ox**, and also contains the full string **pine [inn]** as well as the sub string **zep**."

This means that OXCARBAZEPINE [INN] would be matched, but not AMOXAPINE [U;INN] or CARBAMAZEPINE [U;INN].

**Note:** The scope of a full-text slider is dependent on the settings of other query devices. This means that the slider range constantly changes as you manipulate the query devices. Items that fall outside of the current selection or zooming become unavailable and will be grayed out.

## 5.4.3 Introduction to Regular Expressions

Regular expressions constitute the standard pattern matching language, used heavily for searching and parsing text in most UNIX and Perl software.

Regular expressions allow you to construct a template or pattern for what you're searching for. You can then use your pattern template to determine whether a given text fragment matches your pattern.

For example, suppose you wanted to find all records beginning with the letter *n*. You would then want to construct a regular expression that would have the meaning "has a letter *n* as the first character on the line". The regular expression for this is:

**^n**

The ^ in regular expression syntax means "beginning of line". Therefore ^n means "line beginning with the letter n".

Next, we want to find records whose first word begins with *n*, and whose second word begins with the letter *g*. Let's say we also don't care whether the letters are upper or lower case. Here is the regular expression meaning "all lines whose first word begins with *n* and whose second word begins with *g*":

**^n.\s+g.+**

The three main components of the pattern are 'n', '\s', and 'g'. The *n* means the letter *n*, the *g* the letter *g*, and the *\s* is a special character meaning "white space", or "any spaces", which could be a space, a tab, or a line break. Notice that both the *n* and the *g* are followed by a period. The period in regular expression syntax means "any character". Therefore, *n.* or *g.* means *n* followed any character and *g* followed by any character, respectively.

Finally, notice the 3 plus signs. A plus sign (+) in regular expressions means "one or more" and it always applies to the character immediately preceding it. Therefore, *a+* means "one or more a's", "*\s+*" means "one or more white spaces", etc. Since *.* means "any character", then, *.+* means "one or more of any character", and "*n.+*" means "the letter *n* followed by one or more letters."

Therefore, `^n.+s+g.+` means "an n at the beginning of the line followed by one or more characters followed by one or more spaces, tabs, etc., followed by a g, followed by one or more characters".

For a more thorough tutorial on regular expressions, a good source is the *O'Reilly & Associates nutshell guide* to either *Sed & Awk* or *Perl*. These are UNIX programming languages which are based heavily on regular expression pattern matching, and the O'Reilly guide for each of these languages contains a chapter devoted to regular expressions.

Microsoft's MSDN web site offers a complete reference to the symbols that can be used with Spotfire DecisionSite full text query devices.

## 5.4.4 List of Regular Expression Symbols

Symbol	Description
	Positions
<code>^</code>	Only match the beginning of a string. " <code>^T</code> " matches the first "T" in "To Be Or Not To Be"
<code>\$</code>	Only match the ending of a string. " <code>t\$</code> " matches the last "t" in "A cat in the hat"
<code>\b</code>	Matches any word boundary " <code>ly\b</code> " matches "ly" in "probably not"
	Literals
<b>Alphanumeric</b>	Matches alphabetical and numerical characters literally.
<code>\n</code>	Matches a new line
<code>\f</code>	Matches a form feed
<code>\r</code>	Matches carriage return
<code>\t</code>	Matches horizontal tab
<code>\v</code>	Matches vertical tab
<code>\?</code>	Matches ?
<code>\*</code>	Matches *
<code>\+</code>	Matches +
<code>\.</code>	Matches .
<code>\ </code>	Matches
<code>\{</code>	Matches {
<code>\}</code>	Matches }
<code>\\</code>	Matches \
<code>\[</code>	Matches [
<code>\]</code>	Matches ]
<code>\(</code>	Matches (
<code>\)</code>	Matches )
	Character Classes
<code>[xyz]</code>	Match any one character enclosed in the character set. " <code>[a-e]</code> " matches "b" in "basketball".

[^xyz]	Match any one character not enclosed in the character set. "[^a-e]" matches "s" in "basketball".
.	Match any character except \n.
\w	Match any word character. Equivalent to [a-zA-Z_0-9].
\W	Match any non-word character. Equivalent to [^a-zA-Z_0-9].
\d	Match any digit. Equivalent to [0-9].
\D	Match any non-digit. Equivalent to [^0-9].
\s	Match any whitespace character. Equivalent to [\t\r\n\v\f].
\S	Match any non-whitespace character. Equivalent to [^\t\r\n\v\f].
	Repetition
{x}	Match exactly x occurrences of a regular expression. "\d{5}" matches 5 digits.
(x,)	Match x or more occurrences of a regular expression. "\s{2,}" matches at least 2 space characters.
{x,y}	Matches x to y number of occurrences of a regular expression. "\d{2,3}" matches at least 2 but no more than 3 digits.
?	Match zero or one occurrences. Equivalent to {0,1}. "a?s?b" matches "ab" or "a b".
*	Match zero or more occurrences. Equivalent to {0,}.
+	Match one or more occurrences. Equivalent to {1,}.

## 5.5 Check Boxes

The Check box query device presents a set of check boxes—one for each unique value present in the column. One or several boxes may be selected or cleared to determine which values are to appear in the visualizations. If all records with a certain value are deselected by some other query device the label of that value becomes red.



Values not present among currently selected records are highlighted in red (lighter gray in black and white printing)

A check box query device applied to the column Subject of the Film database. Coloring is set to categorical; ticking a check box causes all records of that particular color to show (unless they are deselected by another query device).

By default Spotfire DecisionSite assigns check boxes to any column containing ten values or less. Initially boxes all are selected, which makes all records in the data set visible. For quick selecting or clearing of all the values, right click on the check boxes query device, and select **All** or **None** from the pop-up menu.

Like radio buttons, check boxes provide options that are either On or Off. Check boxes differ from radio buttons in that you typically use check boxes for independent or nonexclusive choices.

## 5.6 Radio Button

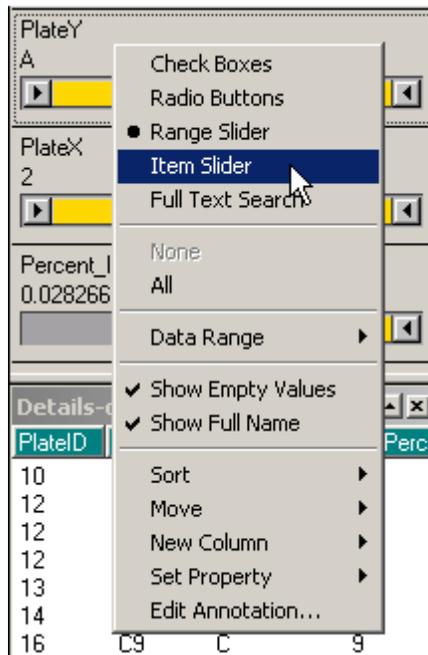
In a radio button query device, a radio button represents each data item. Radio buttons, also referred to as option buttons, represent a single choice within a limited set of mutually exclusive choices. That is, in any group of option buttons, only one option in the group can be set at a time. However an "All" option is always present among the radio buttons, which lets you select all records. Items that are selected in the global context are marked with black labels, while globally deselected items have red labels.

The radio buttons query device, like the check boxes, presents a list of all values stored in a column, but allows only one value to be selected at any given time. When a new value is selected, the old one is deselected.



## 5.7 Changing the Type of Query Devices

Spotfire DecisionSite makes an initial suggestion of what query device to use for each column in the data set. The type of query device to use for the column can then be changed, with one restriction: check boxes and radio buttons can only be used for columns having less than 500 unique values.



The query device pop-up menu. The currently selected query device is marked with a bullet.

► **To change the type of query device:**

- Right-click the query device to make the pop-up menu appear. Select the appropriate query device option from the pop-up menu, or
- select the Columns tab of the Properties dialog. This tab contains a list of all the columns in the data set. Mark a column and select the type of query device to use for that column.

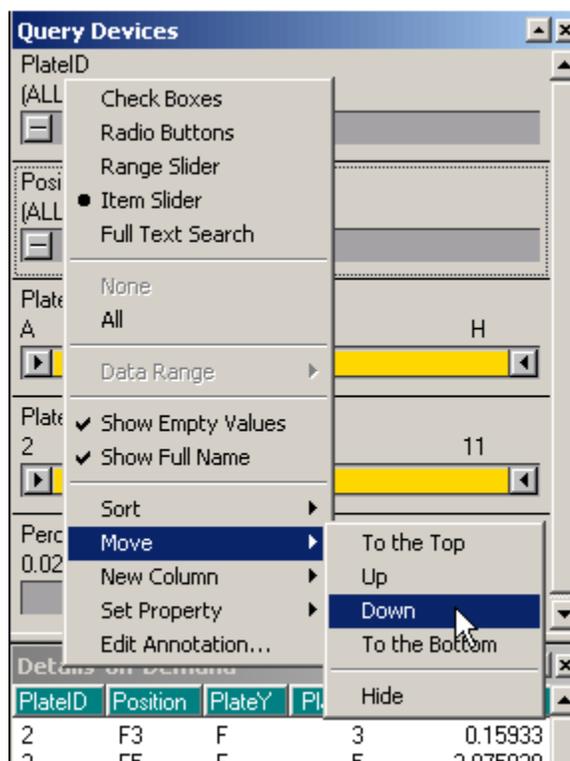
## 5.8 Moving Individual Query Devices

Working with data sets containing a large number of columns does not necessarily mean that you need to manipulate them all at once. A more useful strategy is to select a few parameters, to see how they interact with each other. For this reason you may want to regroup them and rearrange their order, so that you do not have to scroll up and down to keep track of the changes.

The initial order of the Query Devices depends on the structure of the data set loaded into Spotfire DecisionSite or the SQL query that was used to acquire data. You can change this as needed by rearranging columns in the originating spreadsheet program or writing the SQL query in a certain order.

► **To change the order of the query devices:**

1. Right-click on the query device to be moved. A pop-up menu will open.



2. Place the cursor over the **Move** option. A submenu will appear.
3. Choose the command that reflects the direction in which to move the device. The options **Up** and **Down** move it one step upwards or downwards respectively. The options **To the top** and **To the bottom** make the query device the topmost or bottommost device respectively.

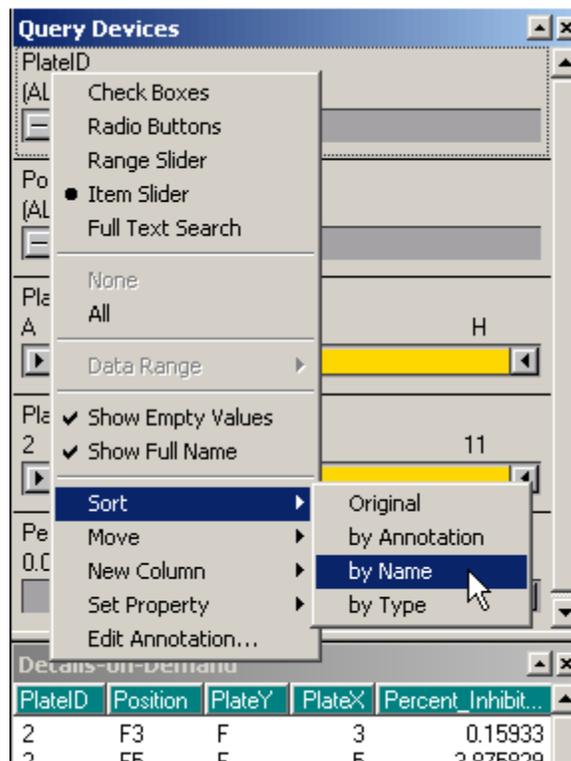
## 5.9 Sorting the Query Devices

The order of the query devices can be sorted in four ways: by original order, by annotation, by name, or by type. For example, you can group all range sliders together, or sort the query devices in alphabetical order.

### ► To sort the query devices:

1. Right-click on a query device.

2. Select **Sort** from the pop-up menu.

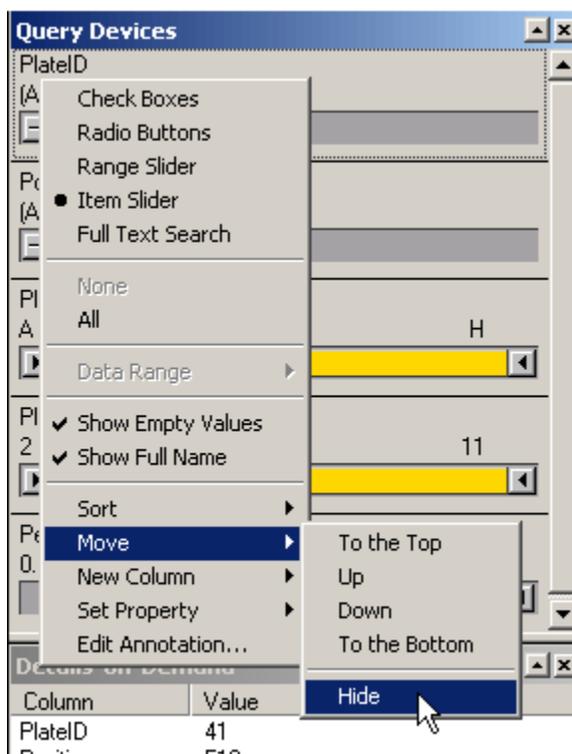


3. Select **Original**, **by Annotation**, **by Name**, or **by Type**.

**Note:** Sorting **by Type** means the type of Query Device, not the type of the column itself (Integer, String, etc.).

## 5.10 Hiding a Query Device

Right-click on the query device to be hidden. From the **Move** sub-menu of the pop-up menu that appears, choose **Hide**. Or deselect **Show Query Device** in the **Columns** tab of the Properties dialog, while having the correct column marked. A hidden query device can only be brought back by reselecting the **Show Query Device** option in the **Columns** tab.



To hide the Query devices window altogether, either clear the check mark next to Query devices in the View menu or click on the small X beside the parallel bars at the edge of the window.



## 5.11 Entering a Value for a Slider

A minimum or maximum value can be typed into a **range slider**, **item slider** or the **full-text search slider**. There are two ways of doing this:

### ► To enter a minimum value:

1. Double-click on the number above the left drag box.
2. Type the desired minimum value, and press ENTER.



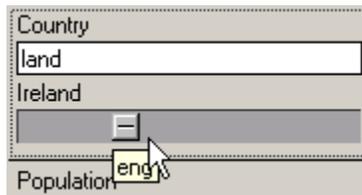
### ► To enter a minimum value:

1. Click on the left drag box.
2. Type the desired minimum value.



► **To move the full-text search slider:**

1. Click on the drag box.
2. Type the desired value.



Note the difference between entering a value in the full-text search field (which filters out a subset of the data set, in this example all countries containing the letters "land"), and entering a value on the drag box (which moves the slider, in this example the first country containing the letters "Eng").

**Note:** Note that no "edit field" will appear in which to type the value. Simply type the value after clicking, and the slider will adjust itself.

**Note:** An item slider or full-text search slider will adjust itself to the existing value nearest possible to the value you typed, where as a range slider will adjust to the exact value you typed.

## 5.12 Indicators

The Query Devices can display two types of indicators: a paper clip icon which indicates that the column has an annotation, and a letter 'e' which indicates that the column contains empty values.

In order to see these indicators you must switch on this option. Do this by opening the **Columns** tab of the **Properties** dialog. Then select the check box marked **Show indicators in query devices**.

### Annotating columns

See Annotating Columns for more information.

### Empty values

By default, the query device shows records with null or empty values. When a column contains empty values a black colored letter 'e' is displayed in the upper right corner of the query device.

You can choose to hide records with empty values by clearing the check box **Show Empty values** from the **Columns** tab of the **Properties** dialog, or by deselecting the menu item **Show Empty Values** from the query device pop-up menu. The 'e' will then turn red.

## 5.13 Changing Column Name

You can easily change the name of a column and its corresponding query device by double-clicking on the query device.

► **To change the column name:**

1. Double-click on the name of the query device you wish to rename.
2. Type a new column name in the text field that appears, and press Enter.

## 5.14 Quick Access to Color and Size Properties

A quick way of setting the color or size property in the current visualization is to right-click on the query device representing the column, and selecting the appropriate property from the **Set property** sub menu that appears.

## 5.15 Initial Query Device Selection

Spotfire DecisionSite's default choice of query devices is based on the column content and the number of unique values present in the data set for that attribute.

If a column contains 10 unique values or less, check boxes will be assigned as query device.

For columns containing more than 10 values, an item slider is chosen for alphanumeric (string) attributes, such as names and descriptions. Range sliders are assigned to numeric columns like date, time, and decimal or integer values.

## 6 Details-on-Demand and Legend

### 6.1 Details-on-Demand

The Details-on-Demand window displays the actual values of marked or active records. For objects that consist of multiple records (such as pies, bars, etc.) the Details-on-Demand window displays information appropriate to that object, such as average value, number of values, etc.

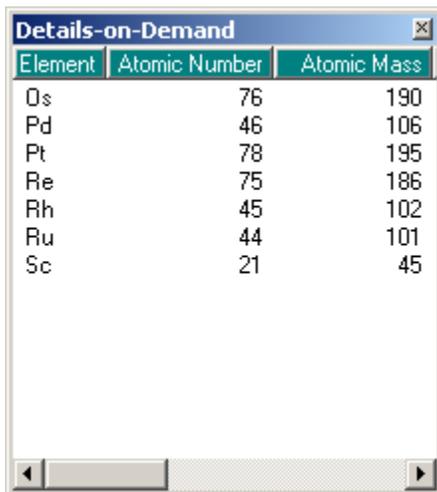
#### Presenting the Details-on-Demand

There are three different ways in which the information can be presented:

- As plain text in the details frame (default).
- As an HTML document based on Microsoft Internet Explorer displayed in the Details-on-Demand window.
- As an HTML based document in an external browser.

The HTML based details information can be formatted using the templates in the **Data and Background** tab of the **Properties** dialog. The bar chart and the pie chart have their own HTML templates. Details for the other visualizations are controlled by a set of templates working on active or marked records. The HTML based presentation can use all functions provided by modern browsers, e.g., images, tables, links to the Internet and Java applets. Further manipulation of the HTML template is described below.

### 6.2 Plain Text



The screenshot shows a window titled "Details-on-Demand" containing a table with three columns: "Element", "Atomic Number", and "Atomic Mass". The table lists data for seven elements: Os, Pd, Pt, Re, Rh, Ru, and Sc.

Element	Atomic Number	Atomic Mass
Os	76	190
Pd	46	106
Pt	78	195
Re	75	186
Rh	45	102
Ru	44	101
Sc	21	45

By default, Details-on-Demand displays data in plain text. The details window is placed in the lower right corner of the main window. It can of course be moved to another location if desirable. The details for a single active record are presented in a vertical table, those for several marked records in a horizontal table.

#### Adjusting column width

The width of the columns in the Details-on-Demand text display can be adjusted. By default the width is as wide as the header of the column. To change the width, place the mouse pointer on the separating line in the column header. The mouse pointer will change shape as shown in the illustration below. Click-and-drag the separator to the desired position. If you double click on the separator, the column width will collapse or expand to fit the longest value in the table.

Element	Atomic Number	Atomic Mass
Os	76	190
Pd	46	106
Pt	78	195
Re	75	186
Rh	45	102
Ru	44	101

**Note:** Columns can be completely hidden from view. To find a column that accidentally has been minimized, move the separator along the column headers until it is changed into a double separator as seen below, then click and drag to resize the hidden column.

Element	Atomic Number
Os	76
Pd	46
Pt	78
Re	75
Rh	45

### Sorting values in columns

The values in all columns in the Details-on-Demand window can be sorted alphabetically and/or numerically. You can use either increasing or decreasing sort order.

#### ► To sort a Details-on-Demand column:

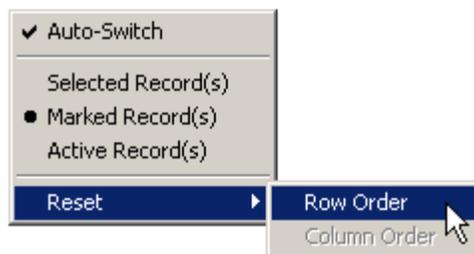
1. Click on a column heading.

Element	Atomic Number	Atomic Mass
Os	76	190
Pd	46	106
Pt	78	195
Re	75	186
Rh	45	102

2. The column is now sorted in increasing order. Click on the column heading again to toggle between increasing and decreasing order. Note the small arrow beside the column title, showing the sorted order.

Element	Atomic Num...	Atomic Mass
Os	76	190
Pd	46	106
Pt	78	195
Re	75	186
Rh	45	102

3. To revert to the original order, right-click in the Details-on-Demand window and select **Reset > Row Order** from the pop-up menu.

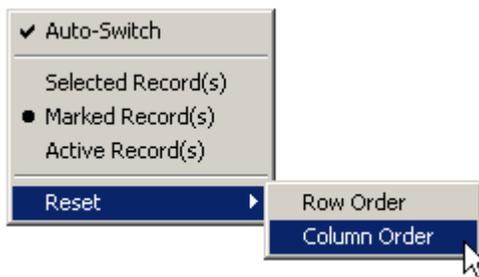


### Rearranging column order

The horizontal order of the Details-on-Demand columns can be rearranged.

► **To rearrange column order:**

1. Place the mouse pointer on a column heading.
2. Drag-and-drop the column heading to the left or right, to the desired place among the other column headings.
3. To revert to the original order, right-click in the Details-on-Demand window and select **Reset > Column Order** from the pop-up menu.



## 6.3 Locking the Details-on-Demand Window

The Details-on-Demand information can be locked to always show a certain category of records; Selected, Marked or Active. This "lock function" is controlled by the **Auto-Switch** option. (See Marking, Activating and Highlighting in the Visualizations chapter for more information.)

By turning Auto-Switch **on**, the Details-on-Demand window automatically updates the Details-on-Demand window if you mark new records or make one record active.

However, if you turn Auto-Switch **off**, the Details-on-Demand window will only show information about a certain category of your choice.

**Example:** You choose to display only *Selected* records by turning Auto-Switch off, and selecting the Selected Records option. Then you click on a record, which makes it *Active*. This will not cause the Details-on-Demand window to show information about that particular record, but instead it continues to display information about the currently *Selected* records.

► **To always show selected records:**

1. Right-click in the Details-on-Demand window. A pop-up menu appears.
2. Clear the Auto-Switch option. (No checkmark should be shown to the left of the option).



3. Select **Selected Records** from the same pop-up menu.

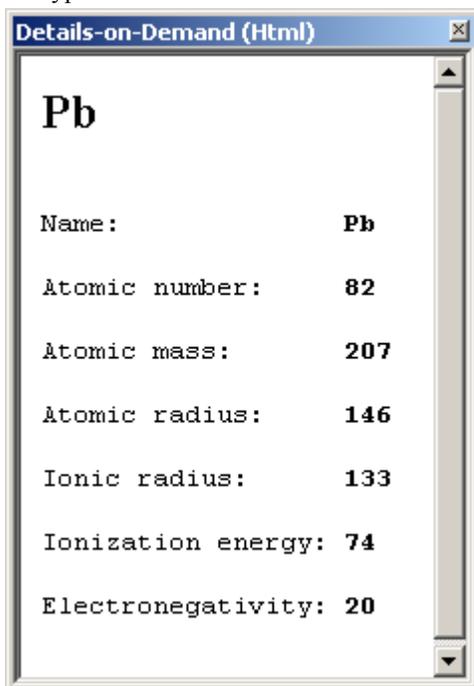
Making a record active in the visualization will now have no effect on the Details-on-Demand window. The Details-on-Demand window will always display information about the currently selected records. If you use the Query Devices or zoom bars to change the selected records, the information in the window will be updated.

**Note:** The **Limit maximum number of records shown** option that can be found in the Data and Background tab of the Properties dialog applies only to the HTML Details-on-Demand, not to the text Details-on-Demand.

## 6.4 HTML

Spotfire DecisionSite can display the data for active or marked records as an HTML formatted document in the details frame. This is initialized by selecting **View > Details on Demand (Html)**.

Spotfire DecisionSite uses the HTML template specified for the data set to lay out the information. If no template has been defined, the application will provide a default template for the type of visualization that is active.



It is also possible to launch an external browser, such as Netscape or Internet Explorer, to view the details of the data. To do so, select **View > Details on Demand (External Browser)**.

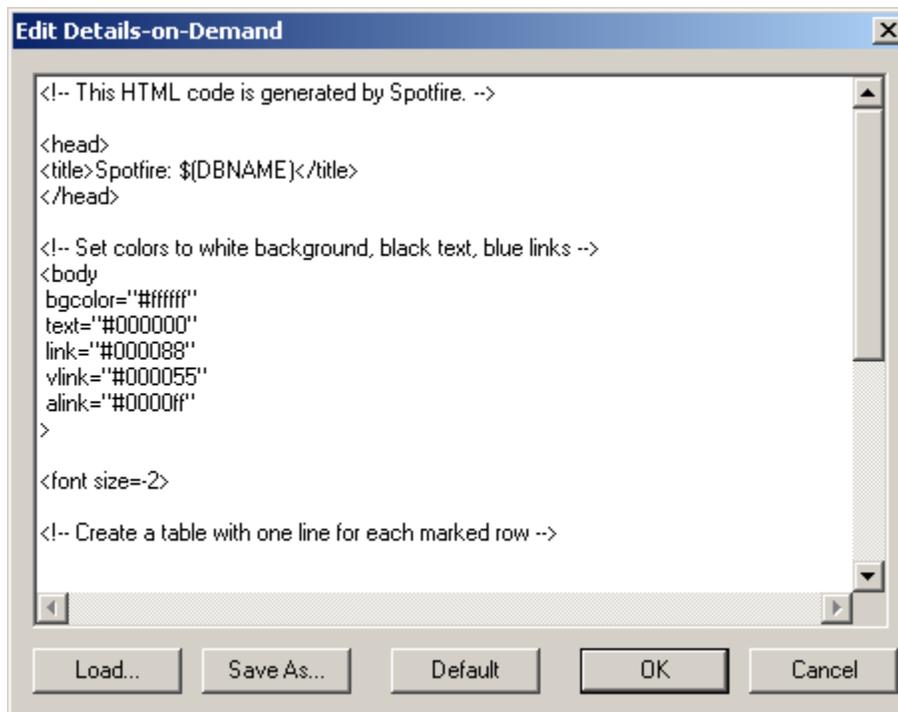
## 6.5 Editing HTML Templates

The HTML templates used for formatting record details are accessed and edited through the **Data and Background** tab of the **Properties** dialog box. There are six editable templates, one each for:

- Pie – highlighted pie details.
- Bar – highlighted bar details.
- Active Marker – these are individual records in scatter plots, profile charts, line charts, tables or heat maps that have been clicked on.
- Marked Records Header – the header part of the Details-on-Demand (DoD) shown for marked records in all types of plots.
- Marked Records Body – the body part of the DoD shown for marked records in all types of plots.
- Marked Records Footer – the footer part of the DoD shown for marked records in all types of plots.

When some records have been marked or activated, the details of those records are presented according to the three marked records templates.

The **Edit...** button brings up an edit box in which you can edit the selected template. In the HTML editing window you have several possibilities for creating and modifying the template.



*The HTML Edit window for the **Marked records Header**.*

The **Load** button allows you to browse for an external file and use it as the template. Here, you can also load a template file that you previously have edited for the current or for a different data set. The **Save As...** button saves the changes in an external HTML file that can be used to format information in other DecisionSite sessions. The **Default** button will revert to the default settings and remove any changes made to the open template. **OK** applies the editing changes to the Details-on Demand window. **Cancel** removes any changes you have made since opening the **Edit** window.

When a new data set is loaded into Spotfire DecisionSite, the program creates default HTML templates that can be edited to suit your needs.

**Tip:** The HTML templates made for another data set will also be applied to the presently loaded data set if you apply the previously created data set as a template (**File > Apply Template**). In this case, not only the HTML Details-on-Demand, but also any visualization settings, query device settings and general settings will be applied. See Applying Templates for more information. For a template file to work properly, it should only be applied to data with a structure similar to the one used to create the template.

#### **Variables**

In the HTML templates, variables that refer to the value of a specific column or to other information can be used, which will then be replaced with current values from any active or marked record:

<b>HTML variable</b>	<b>Refers to</b>
\$(Name)	Value of a particular record in column 'Name'.
\$(Format(Name))	Value of a particular record in column "Name", formatted according to the configured number formatting for the column and the Windows locale.
\$(DBDIR)	The full path to the location of the directory of the current database (file), including a trailing backslash.
\$(DBPATH)	The full path, including the file name, of the currently loaded database.

\$(DBFILE)	The name of the currently loaded database, including the file extension (.skv, .csv, etc.).
\$(DBNAME)	The name of the currently loaded database, excluding the file extension.

Additional variables for displaying descriptive statistics about the data set are described below.

## 6.6 Descriptive Statistics for HTML Templates

The following variables may be added into the HTML template to display information about the records.

Measurement	Variable	Explanation
VISIBLE	\$(VISIBLE)	# of visible points
MARKED	\$(MARKED)	# of marked points
SELECTED	\$(SELECTED)	# of selected points
ALL	\$(ALL)	# total

## 6.7 Editing HTML: An Example

There is a plethora of literature on HTML programming. This example is merely a short demonstration of changing the colors and typeface of the displayed details.

### ► To alter the appearance of the Details-on-Demand presentation:

1. Load a data set. In this example we will use the `periodic.csv` data set.
2. Select **Edit > Properties**, then click on the **Data and Background** tab.
3. From the **Template** drop-down list in the middle of the tab, select **Marked Records Header** and click on the **Edit...** button.
4. Add the following lines of code inside the header of the HTML page to present text in a straight typeface:

```
<style>
td {font: 10pt 'Helvetica'}
</style>
```

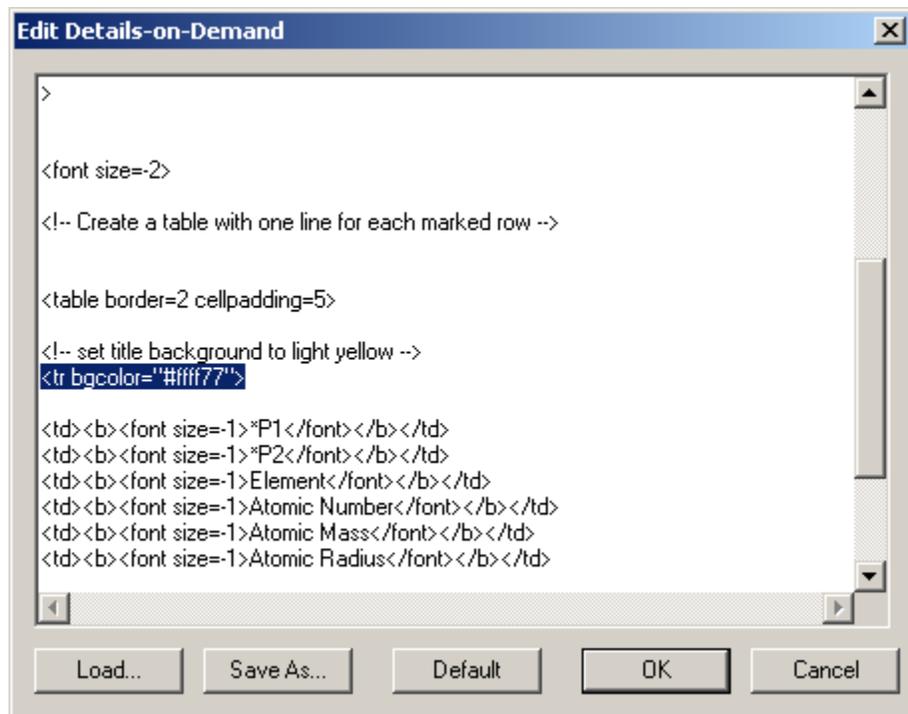
**Note:** This should be placed above the body of the template to affect the entire presentation. Notice also the use of 'curly brackets'.

5. Further down in the body, change the background color of the body to light blue by changing the color definition from `#ffffff` - white - to light blue:

```
bgcolor="#ddeeef"
```

6. Add the following line of code above the titles to make the title line appear with a light yellow background:

```
<tr bgcolor="#ffff77">
```



7. Click **OK**.

Select **View > Details-on-Demand (External Browser)**.

Each time you mark a number of records the details will be presented in a horizontal table in your web browser.

## 6.8 Information About the Data Set

The record meter in the status bar at the bottom of the Spotfire DecisionSite gives continuous information about visualization statistics. You can see at a glance what portion of all the data is currently visible, marked, etc. The same information is displayed as text.



Colors should be read as follows:

Green – Records that are selected and marked.

Yellow – Records that are selected and unmarked.

Gray – Records that are selected, but lack a value required for representation on the current axes, and hence are invisible.

The sum of the above makes up the set of selected records. The length of the record meter in relation to the box in which it sits is an indication of the relative size of the current selection.

To display or hide the status bar, use the **Status Bar** command in the **View** menu.

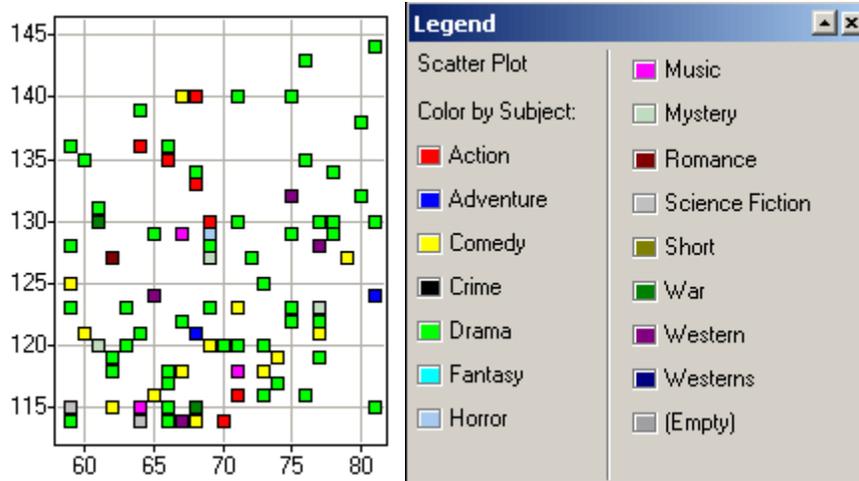
## 6.9 Legend

The markers of various plots can be colored to indicate a certain parameter. By showing the Legend window you can easily see what the color of a marker means. For Scatter Plots the

Legend also explains the significance of other visualization settings, that is, which columns are used for size, rotation, etc.

For other plots the Legend displays information about their relevant parameters. For example, in Bar Charts the Legend states what the height of the bars represents, and in Pie Charts the Legend states if the size of a pie corresponds to a certain parameter.

Also, if the plot has any active Statistical Measures, these will be described in the Legend.



► **To display the Legend window:**

Select **View > Legend**.

# 7 Working with the Data

## 7.1 Add Columns

### 7.1.1 Add Columns Overview

The Add Columns tool allows you to incorporate new columns into your current data set. Data can be added from a file, from the clipboard or by being opened and conditioned using advanced data import. The new columns are appended to the data set.

**Note:** When you are using the Add Columns tool, it is not possible to save the resulting data set as linked data. Only embedded data is supported. See Saving Spotfire files for more information.

### 7.1.2 Using Add Columns

#### 7.1.2.1 Adding Columns from a File

**Note:** The matching of values in the selected ID columns is case sensitive. If existing record IDs are missing in the file which is merged into the data set, the values in the new column will be empty for these records. Records with IDs that do not exist in the original data set will not be added at all.

► **To add columns from a file to an open data set:**

1. Select **Data > Add Columns...**  
Response: The Add Columns - Select Source dialog is opened.
2. Click the **File** radio button.
3. Click **Browse...** and open the file from which you want to add columns.  
Comment: You can also type the path and file name directly in the text box.  
Comment: Common formats like CSV, TXT, XLS, SKV, SFS, SFA or XSF can be opened.
4. Click to select a **Column match method**. (In this step instruction it is assumed that you select **Manual**.)  
Comment: If **Automatic** is selected, identifier columns with identical names (not case sensitive) must exist in both the old and the new data set. All columns with identical names will be used as identifier columns (implicit primary key matching). The new data set must also contain at least one new column. Clicking Finish in the first step of the wizard will add all columns with names that do not exist in the current data set. Clicking **Next >** will take you to the Add Columns - Select Columns dialog where you can select which columns to add.  
**Manual** allows you to select which columns to use in the matching of identifiers (explicit primary key matching). Use this option if you want to make sure that the matching is correct.
5. Click **Next >**.  
Response: The Add Columns - Select Matching Columns dialog is displayed.
6. If you have selected a Microsoft® Excel file, a second dialog is opened where you can choose the table or data sheet where the desired information is located. When you are done with your selections, click **OK** to reach the Add Columns - Select Matching Columns dialog.
7. Click to select a column from the **Columns in new data set** that you want to use to map against your current data.

Comment: This should be some kind of ID column (preferably containing unique identifiers). If a record in this column is missing in the current data set, the record will not be added to the data set. For information about how non-unique values are handled, see Details on how data are added.

Comment: If a column has already been used in a matching, it will not be available in the *Columns in new data set* list. Select a column pair in the *Matching columns* list and click on **Remove** to make the columns available in the two selection lists again.

8. Click to select a column from the **Columns in current data set**.

Comment: This should be some kind of ID column (preferably containing unique identifiers). For information about how non-unique values are handled, see Details on how data are added.

9. Click **Add Match**.

Comment: The selected column pair is moved to the *Matching columns* list box. If desired, it is possible to use multiple key pairs. In this case, only records that have identical values in all of the selected column pairs will be added to the data set. For more information, see Details on how data are added.

10. Click **Next >**.

Response: The Add Columns - Select Columns dialog is displayed.

Comment: Clicking Finish in the second step of the wizard will perform the addition of columns by adding all columns from the new data set that were not selected among the Matching columns above to the current data set.

11. Click to select the columns to actually include in your data set.

Comment: If a column to include has the same name as one of the columns already in the data set, it will be added with the suffix (1), (2), etc.

12. Click **Finish**.

Response: The new columns are added and query devices representing the new columns are shown in Spotfire DecisionSite. (You may have to scroll down in the Query Devices window to see the new query devices.)

### 7.1.2.2 Adding Columns from the Clipboard

**Note:** The matching of values in the selected ID columns is case sensitive. If existing record IDs are missing in the file which is merged into the data set, the values in the new column will be empty for these records. Records with IDs that do not exist in the original data set will not be added at all.

#### ► To add columns from the clipboard to an open data set:

1. Copy the columns that you want to add (e.g., from an Excel data sheet) together with one or more ID columns to be used in the matching against the current data set.
2. Select **Data > Add Columns...**

Response: The Add Columns - Select Source dialog is opened.

3. Click the **Clipboard** radio button.
4. Click to select a **Column match method**. (In this step instruction it is assumed that you select **Manual**.)

Comment: If **Automatic** is selected, identifier columns with identical names (not case sensitive) must exist in both the old and the new data set. All columns with identical names will be used as identifier columns (implicit primary key matching). The new data set must also contain at least one new column. Clicking **Finish** in the first step of the wizard will add all columns with names that do not exist in the current data set. Clicking **Next >** will take you to the Add Columns - Select Columns dialog where you can select which columns to add.

**Manual** allows you to select which columns to use in the matching of identifiers (explicit primary key matching). Use this option if you want to make sure that the matching is correct.

5. Click **Next** >.  
Response: The Add Columns - Select Matching Columns dialog is displayed.
6. Click to select a column from the **Columns in new data set** that you want to use to map against your current data.  
Comment: This should be some kind of ID column (preferably containing unique identifiers). If a record in this column is missing in the current data set, the record will not be added to the data set. For information about how non-unique values are handled, see Details on how data are added.  
Comment: If a column has already been used in a matching, it will not be available in the *Columns in new data set* list. Select a column pair in the *Matching columns* list and click on **Remove** to make the columns available in the two selection lists again.
7. Click to select a column from the **Columns in current data set**.  
Comment: This should be some kind of ID column (preferably containing unique identifiers). For information about how non-unique values are handled, see Details on how data are added.
8. Click **Add Match**.  
Comment: The selected column pair is moved to the *Matching columns* list box. If desired, it is possible to use multiple key pairs. In this case, only records that have identical values in all of the selected column pairs will be added to the data set. For more information, see Details on how data are added.
9. Click **Next** >.  
Response: The Add Columns - Select Columns dialog is displayed.  
Comment: Clicking Finish in the second step of the wizard will perform the addition of columns by adding all columns from the new data set that were not selected among the Matching columns above to the current data set.
10. Click to select the columns to actually include in your data set.  
Comment: If a column to include has the same name as one of the columns already in the data set, it will be added with the suffix (1), (2), etc.
11. Click **Finish**.  
Response: The new columns are added and query devices representing the new columns are shown in Spotfire DecisionSite. (You may have to scroll down in the Query Devices window to see the new query devices.)

### 7.1.2.3 Adding Columns using Advanced Data Import

The Advanced Data Import option in the Add Columns tool can be used to add columns to a data set from a different source than a file or the clipboard (e.g., from a database). It can also be used if the delimiter or data type must be modified to retrieve the data properly.

**Note:** The matching of values in the selected ID columns is case sensitive. If existing record IDs are missing in the file which is merged into the data set, the values in the new column will be empty for these records. Records with IDs that do not exist in the original data set will not be added at all.

#### ► To add columns using advanced data import:

1. Select **Data > Add Columns...**  
Response: The Add Columns - Select Source dialog is opened.
2. Click the **Advanced Data Import** radio button.
3. Click to select a **Column match method**. (In this step instruction it is assumed that you select **Manual**.)  
Comment: If **Automatic** is selected, identifier columns with identical names (not case sensitive) must exist in both the old and the new data set. All columns with identical names will be used as identifier columns (implicit primary key matching). The new data set must also contain at least one new column.

**Manual** allows you to select which columns to use in the matching of identifiers (explicit primary key matching). Use this option if you want to make sure that the matching is correct.

4. Click **Next >**.  
Response: The Import Data - Select Data Source dialog is displayed.
5. Click to select whether to add data from a **File**, a **Database** or the **Clipboard** or use one of the **Advanced** options.
6. Click **Next >**.  
Response: The Import Data - Data Conditioning dialog is displayed. (If you have selected one of the Advanced options you may be Guided through other wizards prior to reaching this dialog. See the online help for the wizard you are using for more information).
7. If desired, select a data conditioning method from the drop-down list.  
Comment: It is possible to pivot data using a Tall/Skinny => Short/Wide converter or to use the Case normalizer to remove duplicate strings based on case insensitive comparison. For more information about the conditioning methods, see Data Conditioning.
8. Click **Finish**.  
Response: The Add Columns - Select Matching Columns dialog is displayed.  
Comment: If you have selected Automatic as the Column Match method you will go straight to the Add Columns - Select Columns dialog where you can select which columns to add.
9. Click to select a column from the **Columns in new data set** that you want to use to map against your current data.  
Comment: This should be some kind of ID column (preferably containing unique identifiers). If a record in this column is missing in the current data set, the record will not be added to the data set. For information about how non-unique values are handled, see Details on how data are added.  
Comment: If a column has already been used in a matching, it will not be available in the *Columns in new data set* list. Select a column pair in the *Matching columns* list and click on **Remove** to make the columns available in the two selection lists again.
10. Click to select a column from the **Columns in current data set**.  
Comment: This should be some kind of ID column (preferably containing unique identifiers). For information about how non-unique values are handled, see Details on how data are added.
11. Click **Add Match**.  
Comment: The selected column pair is moved to the *Matching columns* list box. If desired, it is possible to use multiple key pairs. In this case, only records that have identical values in all of the selected column pairs will be added to the data set. For more information, see Details on how data are added.
12. Click **Next >**.  
Response: The Add Columns - Select Columns dialog is displayed.  
Comment: Clicking Finish here will perform the addition of columns by adding all columns from the new data set that were not selected among the Matching columns above to the current data set.
13. Click to select the columns to actually include in your data set.  
Comment: If a column to include has the same name as one of the columns already in the data set, it will be added with the suffix (1), (2), etc.
14. Click **Finish**.  
Response: The new columns are added and query devices representing the new columns are shown in Spotfire DecisionSite. (You may have to scroll down in the Query Devices window to see the new query devices.)

## 7.1.2.4 Adding Columns if Case Mismatches

Since the matching of values in the ID columns is based on a case-sensitive comparison, adding a column where the IDs are in lower case to a data set where the IDs are in upper case will not result in any values being added to the existing data. In this case, it can be useful to add a new column with all values expressed in lower case (or upper case) prior to the merge of new columns.

### ► To create an all lower case ID column in the current data set:

1. Select **Data > New Column > From Expression...** from the menu bar in Spotfire DecisionSite.

Response: The New Column from Expression - Enter Expression: Step 1(2) dialog is displayed.

2. Click to select the column you want to convert to lower case.
3. In the **Category** drop-down list on the right, select **Text Functions**.
4. In the **Function** list box, select **Lower**.
5. Click **Insert Function**.

Response: The function Lower () is inserted into the Expression box.

6. Click **Insert Columns** to use the column selected in step 1 as an argument to the function.
7. Click **Next >**.

Response: The New Column from Expression - Specify Column: Step 2(2) dialog is displayed.

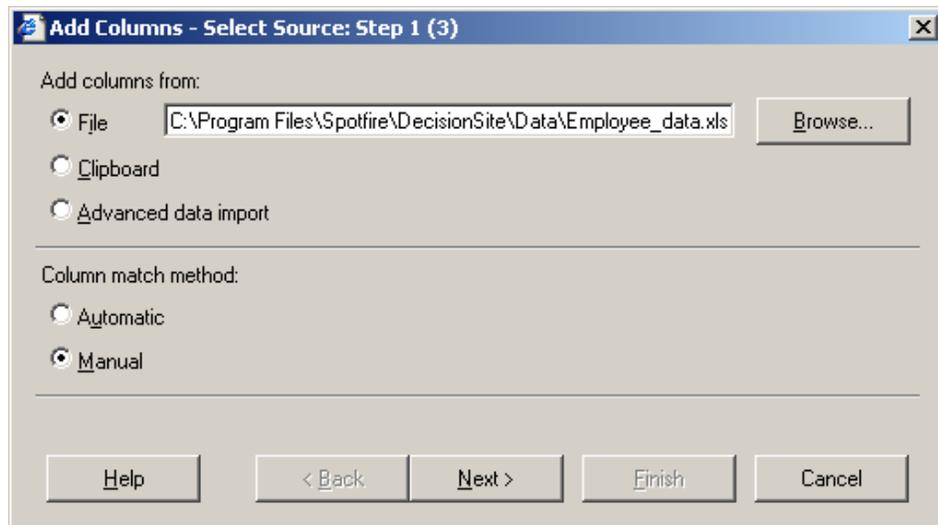
8. Type a suitable name for the new column.
9. Click **Finish**.

Response: The column is added to the data set.

10. Use this column to match against the ID column of the new data set in the Add Columns wizard.

## 7.1.3 User Interface

### 7.1.3.1 Add Columns - Select Source Dialog



Option	Description
File	Click this radio button and enter a path and a file name in the text box

	or click <b>Browse...</b> to locate a file containing the data that you want to add.
<b>Browse...</b>	Opens the Choose file dialog where you can select which file to open.
<b>Clipboard</b>	Click this radio button to add columns from a data set on the clipboard.
<b>Advanced Data Import</b>	Click this radio button to add data from a source other than a file or the clipboard (e.g., from a database). This option can also be used if the delimiter or data type must be modified to retrieve the data properly. Clicking <b>Next &gt;</b> will display the Import Data wizard. For more information about the Import Data wizard, see Importing Data.
<b>Automatic</b>	Spotfire DecisionSite will automatically match columns with identical names (implicit primary key matching). <b>Note:</b> If you have columns with identical names that do not contain the same identifiers, this option might result in that no data is added. In that case, it is probably better to use the Manual option (see below), and match on columns that contain correct identifiers.
<b>Manual</b>	Select this option if you want to be able to select which columns to use in the matching of IDs (explicit primary key matching). Use this option if you want to make sure that the matching is correct.
<b>Next &gt;</b>	Takes you on to the next step of the wizard. If Automatic has been selected as the Column match method you will go straight to the Add Columns - Select Source dialog. If Manual has been selected you will be Guided to the Add Columns - Select Matching Columns dialog.
<b>Finish</b>	Only available if the Automatic Column match method has been selected. All columns in the new and old data set that have identical names (not case sensitive) will be used as identifier columns. This means that all values in all of the identifier columns must match for the data to be added. All columns with names that do not exist in the current data set will be added.

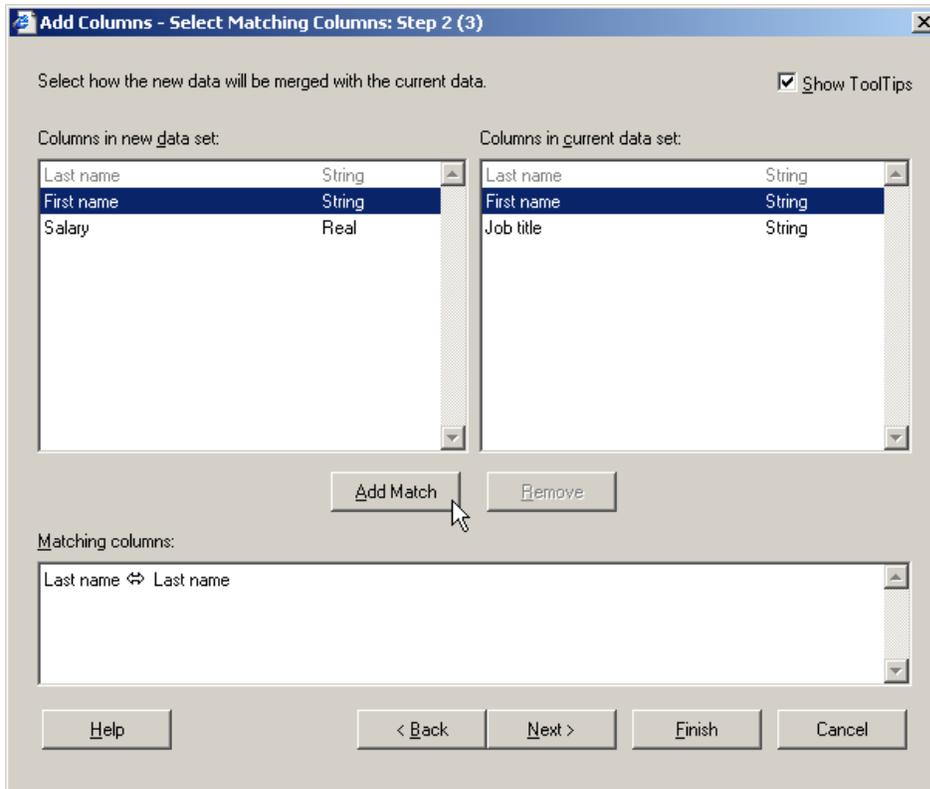
► **To reach the Add Columns - Select Source dialog:**

Select **Data > Add Columns...**

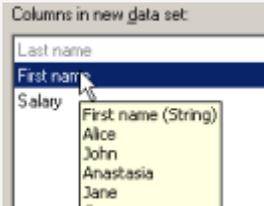
### 7.1.3.2 Add Columns - Select Matching Columns Dialog

This dialog is used to specify which columns should be used as keys in the merging of the new columns with the columns in the original data set. Normally, one column pair containing IDs is enough, but in some cases it may be necessary to use two or more column pairs to create unique mappings between the two data sets.

**Note:** If the data types of your ID columns mismatch, click < **Back** and use the *Advanced data import* option to specify your data types manually (or add a type definition row to your data set prior to using the Add Columns tool).



Option	Description
<b>Show ToolTips</b>	If selected, a ToolTip displaying the name and type of the column together with the content of the first five unique records is shown upon hovering over a column name with the mouse pointer.
<b>Columns in new data set</b>	Displays the columns in the new data set that are available for use in a matching columns pair. A column can only be used in a single column pair matching at a time and will therefore be grayed out in this list box after it has been included in the Matching columns list box.
<b>Columns in current data set</b>	Displays the columns in the current data set that are available for use in a column pair. A column can only be used in a single column pair matching at a time and will therefore be grayed out in this list box after it has been included in the Matching columns list box.
<b>Add Match</b>	Select an ID column in both list boxes above and click Add Match to add the pair to the Matching columns list box.

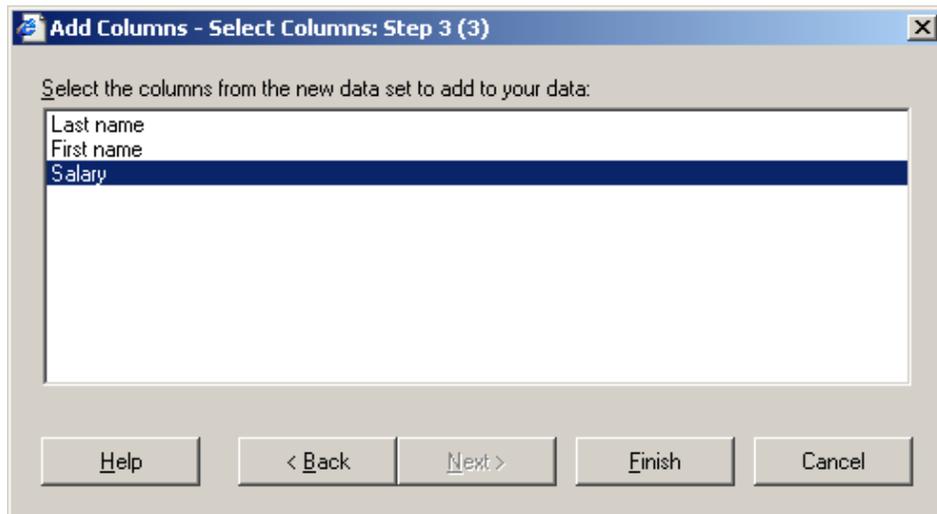


<b>Remove</b>	Select one or more column pairs in the Matching columns list box and click this button to remove the pairs from the list. This will return the columns to the list boxes of available columns above.
<b>Matching columns</b>	Displays the selected column pairs that specify how the merge between the two data sets will be made. If more than one pair is selected, only records that have identical values in all of the selected column pairs will be added to the data set. For more information, see Details on how data are added.
<b>Finish</b>	If Finish is clicked in the second step of the wizard, all columns in the new data set that are not used as identifiers in the Matching columns list will be added to the data set.

► **To reach the Add Columns - Select Matching Columns dialog:**

1. Select **Data > Add Columns...**
2. Make your choice in the Add Columns - Select Source dialog, make sure that you have selected **Manual** as the Column match method, and click **Next >**.

### 7.1.3.3 Add Columns - Select Columns Dialog



The list box shows the columns available for import. All columns in the new data set are listed. Per default, all new columns that are not included among the *Matching columns* in the previous dialog will be selected. Click the name of the column you want to add. For multiple selection, press **Ctrl** and click on the desired columns. You can also use **Shift** or drag the mouse over the desired columns.

► **To reach the Add Columns - Select Columns dialog:**

1. Select **Data > Add Columns...**
2. Make your choices in the Add Columns - Select Source dialog and click **Next >**.
3. Make your choices in the Add Columns - Select Matching Columns dialog and click **Next >**.

## 7.1.4 Theory and Methods

### 7.1.4.1 Details on How Data are Added

The merging is based on the selected ID fields of the current and the added data sets. The matching of names is case sensitive. If existing record IDs are missing in the data which are merged into the data set, the values in the new column will be empty for these records. Records with IDs that do not exist in the original data set will not be added at all.

If multiple IDs exist in the data to be added, the value in the added column will be the first record from the top in the data columns used for adding. See Example of adding columns with multiple IDs for more information.

If multiple IDs exist in the current data set, all of the entries will receive the value from the added column (the first in the column if there are multiple IDs in the column to be added (see above)).

If several matching column pairs are selected in the Add Columns - Select Matching Columns dialog, all values in the pairs must match for the data to be added. Multiple key pairs can be used to create unique identifiers from several ID columns with multiple IDs.

**Note:** Empty values work in the same way as other values. Hence, if empty values exist in the key column of the current data set and other records have empty values in the key for the columns to be added, there is a major risk that values are added to the wrong records. Therefore, it is advisable to not use columns containing empty values as key columns. See Example of adding columns with empty values for more information.

### 7.1.4.2 Example of Adding Columns with Multiple IDs

Imagine that you have a data set with the following columns and records loaded into Spotfire DecisionSite:

Last name	First name	Job title
Scott	Alice	Analyst
Ford	Henry	Analyst
Miller	John	Clerk
Smith	Jane	Clerk
Smith	George	Clerk

Note that there are two employees with the last name "Smith". Hence, the "Last name" column does not contain unique identifiers.

Now you want to add information about the salary of each employee which is located in a separate file or data sheet:

Last name	First name	Salary
Scott	Alice	3200
Miller	John	1300
Smith	Anastasia	4400
Smith	Jane	800
Smith	George	750

In this data set, the employee "Henry Ford" is missing and a person called "Anastasia Smith" is included who was not a part of the original data set.

The Add Columns tool can add the Salary column with the following results, depending on your selections in the Add Columns - Select Matching Columns dialog.

Matching columns:	Result:																								
Last name <-> Last name	<table border="1"> <thead> <tr> <th>Last name</th> <th>First name</th> <th>Job title</th> <th>Salary</th> </tr> </thead> <tbody> <tr> <td>Scott</td> <td>Alice</td> <td>Analyst</td> <td>3200</td> </tr> <tr> <td>Ford</td> <td>Henry</td> <td>Analyst</td> <td></td> </tr> <tr> <td>Miller</td> <td>John</td> <td>Clerk</td> <td>1300</td> </tr> <tr> <td>Smith</td> <td>Jane</td> <td>Clerk</td> <td>4400</td> </tr> <tr> <td>Smith</td> <td>George</td> <td>Clerk</td> <td>4400</td> </tr> </tbody> </table> <p>All employees with the last name Smith get the value 4400 in the Salary column, since that was the first record for the last name Smith in the new data set. Anastasia Smith will not be added to the data set. No value is added for Henry Ford (since he was not present in the new data set).</p>	Last name	First name	Job title	Salary	Scott	Alice	Analyst	3200	Ford	Henry	Analyst		Miller	John	Clerk	1300	Smith	Jane	Clerk	4400	Smith	George	Clerk	4400
Last name	First name	Job title	Salary																						
Scott	Alice	Analyst	3200																						
Ford	Henry	Analyst																							
Miller	John	Clerk	1300																						
Smith	Jane	Clerk	4400																						
Smith	George	Clerk	4400																						
Last name <-> Last name First name <-> First name	<table border="1"> <thead> <tr> <th>Last name</th> <th>First name</th> <th>Job title</th> <th>Salary</th> </tr> </thead> <tbody> <tr> <td>Scott</td> <td>Alice</td> <td>Analyst</td> <td>3200</td> </tr> <tr> <td>Ford</td> <td>Henry</td> <td>Analyst</td> <td></td> </tr> <tr> <td>Miller</td> <td>John</td> <td>Clerk</td> <td>1300</td> </tr> <tr> <td>Smith</td> <td>Jane</td> <td>Clerk</td> <td>800</td> </tr> <tr> <td>Smith</td> <td>George</td> <td>Clerk</td> <td>750</td> </tr> </tbody> </table> <p>With both last name and first name used as key pairs, the identification is unique and the correct salary is entered for Jane and George Smith. This would be the correct way of performing the merge.</p>	Last name	First name	Job title	Salary	Scott	Alice	Analyst	3200	Ford	Henry	Analyst		Miller	John	Clerk	1300	Smith	Jane	Clerk	800	Smith	George	Clerk	750
Last name	First name	Job title	Salary																						
Scott	Alice	Analyst	3200																						
Ford	Henry	Analyst																							
Miller	John	Clerk	1300																						
Smith	Jane	Clerk	800																						
Smith	George	Clerk	750																						

### 7.1.4.3 Example of Adding Columns with Empty Values

If you have empty values in the ID column of the current data set and other records have empty values in the ID column of the new data set, there is a major risk that values are added to the wrong records. Take a look at this simple example where the current data set contains an empty value:

Last name	First name	Job title
Scott	Alice	Analyst
Ford	Henry	Analyst
	John	Clerk
Smith	Jane	Clerk

Now you want to add information about the salary of each employee which is located in a separate file or data sheet:

Name	First name	Salary
	Alice	3200
Ford	Henry	2800
Miller	John	1300
Smith	Jane	800

Note that there is another record that contains the empty value in this data set.

Adding the column using *Last name* and *Name* as matching columns will produce the following result:

Last name	First name	Job title	Salary
Scott	Alice	Analyst	
Ford	Henry	Analyst	2800
	John	Clerk	3200
Smith	Jane	Clerk	800

The name Scott is missing in the new data set and Alice Scott will therefore not receive any value in the Salary column. The person in the original data set where no last name was entered (John) will be matched with the empty value in the new data set and, hence, receive the Salary 3200, even though this number has nothing to do with him. Selecting both last name and first name as key columns would have produced empty values for both Alice Scott and John X, which in this case would have been the correct procedure (unless it was possible to add the correct last names to the data sets prior to import).

## 7.2 New Column by Binning

### 7.2.1 Different Binning Methods

Depending on the type of values in the columns (numeric or alphanumeric, continuous or discrete) you may need to resort to different methods to rearrange the data. Spotfire DecisionSite provides a variety of binning methods:

#### Specific Limits

This option allows you to explicitly enter the values of the limits to use for each bin. Enter the value you wish to use for the limits of your bins and separate them with a semicolon. Do not use a space character after the semicolon.

#### Even Intervals

The subranges suggested are equal in scope. This is the default method, dividing the value range into equal intervals, and works for all data types except string. The current data range is divided up into the desired number of bins. Empty values will be empty in the new column, and when loading data sets from external sources (linked data) new values will be placed inside the bin, or in the upper and lower bin respectively.

#### Even Distribution

The suggested division works for all data types and is made so that the bins each contain an equal number of unique values. Extra values are placed in the final bins, so if you have four values and you want three bins with one value in each bin, your final value will be placed in the third bin. Empty values will be empty in the new column, and when loading data sets from external sources (linked data) the even distribution will be recalculated.

#### Cherry Picking

This method works for all data types and allows you to manually select which value to put in each bin. A list of all values in the column is shown. Cherry picking is useful when you want to be very specific with how you group your values. It is not recommended to use cherry picking when loading data sets from external sources (linked data) as the new values will become empty values.

#### ► To bin a column by Cherry Picking:

1. Select **Data > New Column > By Binning...**  
Response: The New Column by Binning dialog is launched.
2. Select a **Column** to bin.

3. Select **Cherry Picking** as method and click the **Settings...** button.  
Response: The Cherry Picking dialog is launched.
4. To create a new bin, click **New Bin**.
5. Select the desired values in the **Available values** field, and click **Add >>** to add the values to a bin.
6. Use the **Rename Bin** button (or **F2**) to rename bins.
7. When all values have been assigned a bin, click **OK**.
8. Type a **New column name** for the binned column or use the default name.
9. Click **OK**.

### Based on Standard Deviation

This method works for numeric columns. The range is divided into sections as described by the selected standard deviation multipliers. Bins are created using standard deviations +/- 0.5, 1, 2, 3, 6. In the example below, the range is divided into the following six subsections ( $\mu$  denoting the average value for the column and  $s$  the corresponding standard deviation):

lower limit ->  $(\mu - 3s)$

$(\mu - 3s)$  ->  $(\mu - s)$

$(\mu - s)$  ->  $\mu$

$\mu$  ->  $(\mu + s)$

$(\mu + s)$  ->  $(\mu + 3s)$

$(\mu + 3s)$  -> upper limit

Empty values will be empty in the new column, and when loading data sets from external sources (linked data) the standard deviation will be recalculated.

### Substring

This method works for all data types. It groups the records by the first or last characters of the values in the column to be binned – the exact number of characters to take into account must be supplied. Suppose the column to be binned contains family names, beginning with Adams and ending with Winter. To bin the records according to the first letter in the name, use Divide by Substring considering one character from the beginning. Bin names are generated from the substring, and if **Ignore case** is used, the bin names are all formatted as upper case.

#### ► To bin a column by substring:

1. Select **Data > New Column > By Binning...**  
Response: The New Column by Binning Dialog is launched.
2. Select a **Column** to bin.
3. Select the **Substring** radio button.
4. Decide whether to compare from the **Beginning** or **End** of the column value.
5. Set **Positions** to the number of characters that should be equal in each bin.
6. Select whether to **Ignore case**, that is whether "adams" and "Adams" would be considered the same or not.  
**Note:** If the Positions is three and Ignore case is selected, the bin name in this example would be ADA.
7. Type a **New column name** for the binned column or use the default name.
8. Click **OK**.  
Response: The Edit Bin Names dialog is launched.
9. Give the bins new names, if desired.
10. Click **OK**.

Empty values will be empty in the new column, and when loading data sets from external sources (linked data) the new values will be placed in new bins, taking the substrings into consideration.

## 7.2.2 Performing Binning

► **To perform binning:**

1. Select **Data > New Column > By Binning...**

Response: The New Column by Binning dialog is launched.

**Note:** You can also reach this dialog by right-clicking in the Query Device window and selecting **New Column > By Binning...**

2. From the drop-down list, select the name of the column that you want to bin.
3. Select the desired binning method and enter the respective values.
4. Type a **New column name** for the binned column or use the default name.
5. Click **OK**.

Response: The Edit Bin Names dialog is launched.

6. Enter the desired bin names and click **OK** to create the new column. This column can now be used as any other Spotfire DecisionSite column.

**Tip:** You can also show numerical values in a binned form on the X-axis of a bar chart by right-clicking on the X-axis selector and choosing **Use Binned Values**. The X-axis properties will then easily allow you to test a different number of bins.

## 7.2.3 User Interface

### 7.2.3.1 New Column by Binning Dialog

The dialog box is titled "New Column by Binning". It features a "Column:" dropdown menu with "MOLREGNO" selected. Below this is a "Bin method" section with several radio button options: "Specific limits (for example -1;0.5;10;40)", "Even intervals", "Even distribution", "Cherry picking", "Based on standard deviation", and "Substring". The "Specific limits" option is selected, and its corresponding text box contains the values "0;1250;3500;5250;6800". The "Even intervals" and "Even distribution" options each have a "Number of bins:" spinner set to 5. The "Based on standard deviation" option has five checkboxes labeled "+/- std dev to include:" with values 0.5, 1, 2, 3, and 6, all of which are checked. The "Cherry picking" option has a "Settings..." button. The "Substring" option has a "Compare from:" section with "Beginning" selected and "End" unselected, and a "Positions:" spinner set to 3. There is also an "Ignore case" checkbox which is unchecked. At the bottom, the "New column name:" field contains "Binned MOLREGNO". The dialog has "Help", "OK", and "Cancel" buttons.

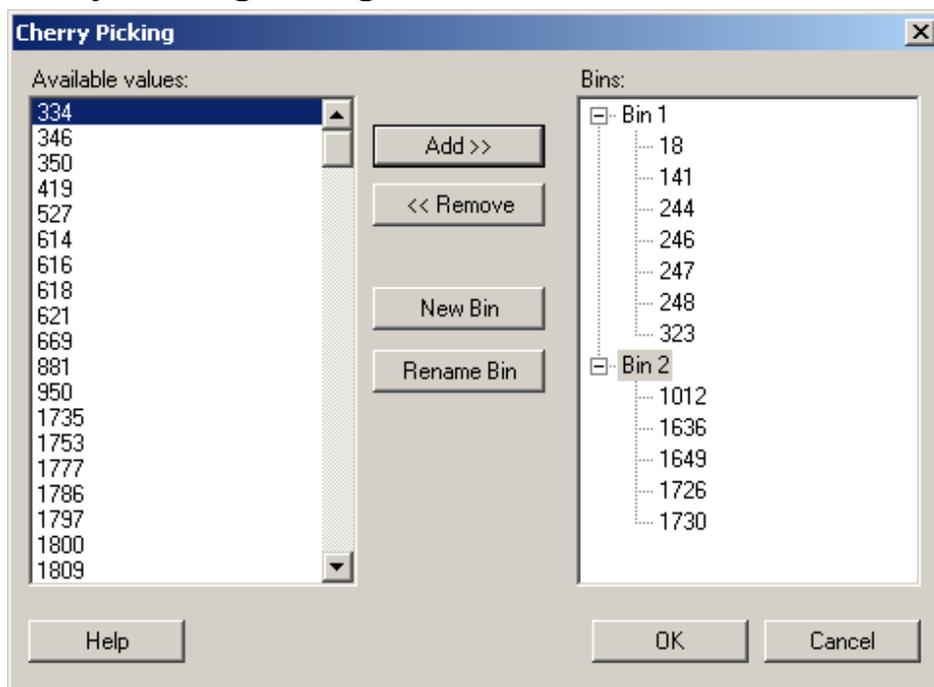
Option	Description
<b>Column</b>	Displays the available columns on which you can perform binning. The values from this column will be sorted into several bins or categories based on your selections.
<b>Specific limits</b>	Allows you to explicitly enter the desired values of the limits to use for each bin. Enter the value you wish to use for the limits of your bins and separate them with a semicolon.
<b>Even intervals</b>	Allows you to specify the desired number of bins and divides the value range into equal intervals.
<b>Even distribution</b>	Allows you to specify the desired number of bins and divides the bins so that each one contains an equal number of unique values.
<b>Cherry picking</b>	The Settings... button opens the Cherry Picking dialog where you can manually select which value to put in each bin.

<b>Based on standard deviation</b>	The range is divided into sections as described by the selected standard deviation multipliers.
<b>Substring</b>	Groups the records by the first or last characters of the values in the column to be binned. <b>Note:</b> The exact number of characters to take into account must be supplied.
<b>New column name</b>	Here you supply the binned column with an appropriate name.

► **To reach the New Column by Binning dialog:**

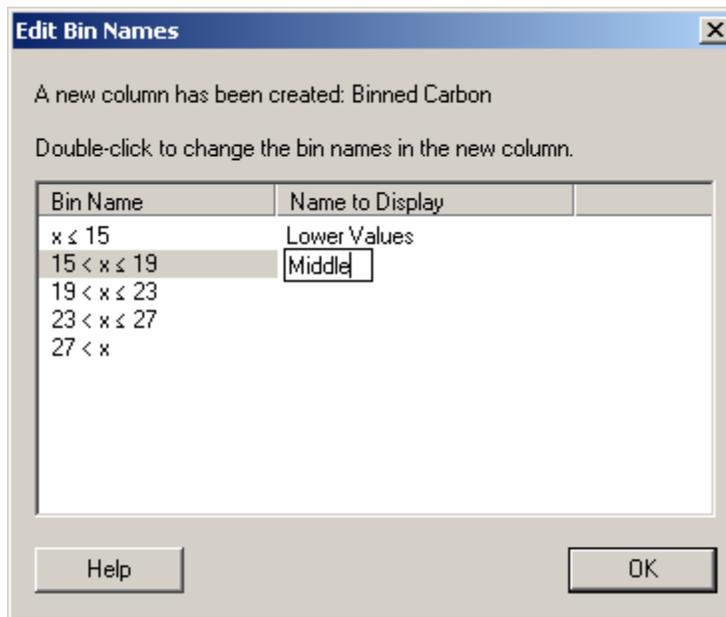
Select **Data > New Column > By Binning...** or right-click in the Query Device window and select **New Column > By Binning...**

### 7.2.3.2 Cherry Picking Dialog



Option	Description
<b>Available values</b>	The values available for use in the binning. Click a value in the list to select it. To select more than one value, press <b>Ctrl</b> and click the values in the list.
<b>Add &gt;&gt;</b>	Moves selected columns from the Available values field to the selected bin in the Bins field.
<b>&lt;&lt; Remove</b>	Removes a column and brings it back to the Available values field.
<b>New Bin</b>	Creates a new bin into which you can add values from the Available values field.
<b>Rename Bin</b>	Allows you to rename the bins with names of your choosing.

### 7.2.3.3 Edit Bin Names Dialog



Option	Description
<b>Bin name</b>	Displays the default names from the New Column by Binning dialog.
<b>New name</b>	Allows you to rename the bins with names of your own choosing. Double-click on a bin to change the name. <b>Note:</b> You are not required to change the names of the bins. If you feel the default names are sufficient, simply click <b>OK</b> .

## 7.3 New Column from Marked Records

### 7.3.1 New Column from Marked Records Dialog

When you have found an interesting subset in the data, you can mark these records and then create a new column indicating for each record whether it is part of the subset or not. By doing so, you will be able to toggle the subset, and also the records excluded from the subset.

**Note:** Columns created from marked records cannot be saved in templates (SFT files) and cannot be saved as linked data.



Option	Description
<b>Name</b>	Type a suitable name for the column to be created.
<b>Label for marked records</b>	Type a name for the value associated with marked records.
<b>Label for unmarked records</b>	Type a name for the value associated with unmarked records.

► **To reach the New Column from Marked Records dialog:**

Select **Data > New Column > From Marked Records...** or right-click in the Query Device window and select **New Column > From Marked Records...**

## 7.4 New Column from Expression

### 7.4.1 Calculating Columns

New columns can be computed from the current data set by using mathematical and logical expressions. This chapter describes how to create and evaluate such expressions using the New Column from Expression tool.

### 7.4.2 Workflow of the New Column from Expression Tool

Occasionally the columns included in a data set do not allow you to perform all necessary operations, or to create the visualizations needed to fully explore the data set. Still, in many cases the necessary information can be computed from existing columns. Spotfire DecisionSite provides the option to calculate new columns by applying mathematical and logical operators to existing values.

The following section explains the basic workflow of using the New Column from Expression tool. More detailed explanations on how to use the user interface and specifications of the various functions follows later in the chapter.

► **How to use the New Column from Expression tool:**

1. Start DecisionSite and load a data set.
2. Select **Data > New Column > From Expression...**

The first step of the wizard is displayed. You can also reach the tool by right-clicking a query device.

3. If you have previously created a suitable expression, you may select it from the **Recent Expressions** list and click the **Insert** button.
4. If you need to create a new expression, proceed to specify the expression by either typing it directly into the **Expression** text area or by selecting columns and functions from the lists.

By selecting columns and functions, and clicking the **Insert Columns** or **Insert Function** buttons, you can gradually build the expression you want. You can always modify the expression by editing the text in the Expression field, using cut&paste or typing text.

An example of an expression could be:  $[\text{Exports m\$}]/[\text{Population}]$

5. Verify that the result seems reasonable by looking at the **Sample result** field. This field will display the result of applying the expression to the first row of the data set.

If this field shows an error message, there is a problem with the expression. Moving the mouse pointer over the field or clicking on it, will display an explanation of what is wrong.

- When you are satisfied, press the **Next >** button.

The second step of the wizard is displayed.

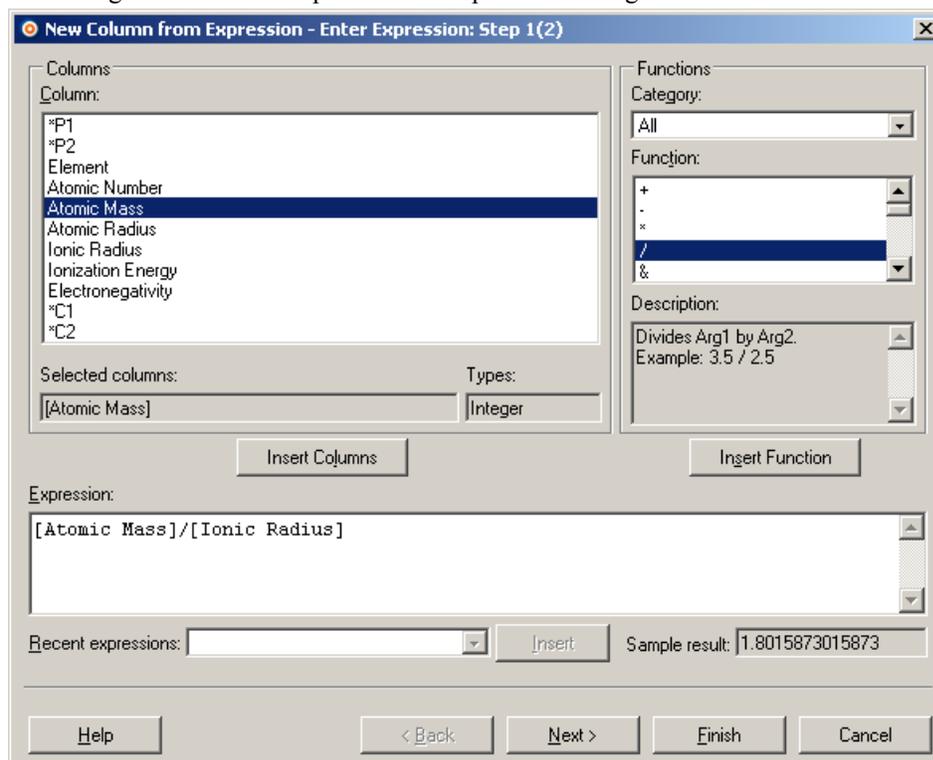
- Fill in the new **Column name** if the default name is not acceptable.
- Change the **Column type** if you want to.
- Watch the preview and verify that the result is what you want. If not, click on the **< Back** button to go back and modify the expression until the desired result is achieved.
- Click on the **Finish** button.
- The expression is now evaluated for each row in the data set and a new column is created. A new query device will appear with the name of the new column you created.

If the new column data still is not what you intended, delete the column from the **Properties** dialog, and invoke the **New Column from Expression...** tool again.

## 7.4.3 User Interface Description

### 7.4.3.1 Enter Expression Dialog

The dialog can be resized to provide more space for editing and for the lists.



#### Columns

Select a column by clicking on it, and click the **Insert Columns** button to insert it to the **Expression** field. You can also double-click on a column to insert it. You can select several columns by pressing **Ctrl** or **Shift**.

If you place the cursor at a specific location in the **Expression** field, the column will be inserted there.

If you have many columns you can use the scrollbar to find them, or click on any column and type in the first letter of the desired column name to jump to it.

You can see the Type of the selected column in the field below the list.

## Category

Select a category of functions to limit the choices in the **Function** list.

- All
- Operators
- Math Functions
- Statistical Functions
- Text Functions
- Logical Functions
- Date & Time Functions
- Conversion Functions

## Function

Select a function by clicking on it, and click the **Insert Function** button to insert it to the **Expression** field. You can also double-click on a function to insert it.

If you place the cursor at a specific location in the **Expression** field, the function will be inserted there.

If you have many columns you can use the scrollbar to find them, or click on any function and type in the first few letters of the desired function name to jump to it.

## Description

This field provides a brief description of the selected function. For more detailed descriptions, please see Spotfire Expression Language (SXL).

## Expression

This is the text field in which you build your expression. You can insert columns and functions to it from the lists, or enter text as in any standard text editor.

Cut/Copy/Paste works in the field using standard **Ctrl+X/Ctrl+C/Ctrl+V**.

Highlighting a section of the expression, and inserting a new function will cause that function to encompass the highlighted section within parenthesis.

Also, Undo/Redo functionality is available by pressing **Ctrl+Z/Ctrl+Y** respectively.

## Recent expressions

This list contains the twenty most recent expressions you have created. You can select one of these and click the Insert button to insert the expression into the **Expression** field. This will not replace the entire content of the field, only insert the selected expression at the cursor position.

## Sample result

This field displays the result of applying the current expression to the first row of the data set.

If this field shows an error message, there is a problem with the expression. Moving the mouse pointer over the field or clicking on it, will display an explanation of what is wrong. Pressing **F5** will also display the error description. Pressing **F4** will move the cursor to the position in the expression where the error lies.

There are three kinds of error messages:

#EXPR! – there is a problem with the syntax of the expression.

#NUM! – the row evaluates to infinity or other illegal number.

#ARG! – there is a problem with one or many arguments.

### 7.4.3.2 Specify Column Dialog

The dialog can be resized to provide more space for editing and for the lists.

**New Column from Expression - Specify Column: Step 2(2)**

Column name:

Column type:

Expression:

Preview:

Population	Pop.growthr.(ppm)	Calculated Column
3273131	19	3273150
3335044	18	3335062
3285224	11	3285235
3333839	12	3333851
7867541	7	7867548
7915145	5	7915150
10373881	5	10373886
10370269	3	10370272
9909285	1	9909286
9921910	1	9921911
10016623	30	10016653
...	...	...

Buttons:

#### Column name

Enter the name for the new column in this field.

#### Column type

This drop down box lets you select which Type the new column should have:

- String
- Integer
- Decimal
- Date
- Time
- DateTime

#### Expression

This field displays the expression which will be used to evaluate the new column. You cannot edit this field. Click the **< Back** button if you want to modify the expression.

#### Preview

This table provides a preview of how the first rows in the data set will be evaluated using the current expression. It displays the columns that are used in the expression and the resulting column. You can resize the window to show more rows.

Move the mouse pointer over the column headings to display a ToolTip stating the Type of the columns.

If the resulting column shows an error message, there is a problem with the expression for that row. Moving the mouse pointer over the field or clicking on it, will display an explanation of what is wrong.

There are three kinds of error messages:

#EXPR! – there is a problem with the syntax of the expression.

#NUM! – the row evaluates to infinity or other illegal number.

#ARG! – there is a problem with one or many arguments.

## 7.4.4 Spotfire Expression Language (SXL)

### 7.4.4.1 General Syntax

Spotfire DecisionSite uses an Expression Language which is described in this chapter. Some notes on the general syntax are:

Variables, functions and keywords are case insensitive:

SUM(C1) = Sum(C1) = sum(C1)

Column references are case sensitive.

The default null handling behavior is that operations on null return null.

### 7.4.4.2 Data Types

The data types with built in language support are:

- Integer
- Real
- Boolean
- String

#### Integer

Integer values are written as a sequence of digits, possibly prefixed by a + or - sign. If used where a decimal value was expected, they are automatically converted to a decimal value.

**Note:** Hexadecimal formatted values have a size limitation of 8 characters.

#### Examples:

```
0
101
-32768
+55
0xff      = 255
0x7ffffff = 2147483647
0x80000000 = -2147483648
```

#### Real

Real values are written as standard floating point numbers with a period for a decimal point and no thousands separator. The real values that can be specified range from

-1.79769313486231e+308 to 1.79769313486231e+308.

The exponent of real value constants may range from -307 to 308.

Math operations on real values that produce results that can't be represented by the real data type generate numeric errors. In the resulting data set, these special cases will be filtered out and replaced by null.

#### Examples:

0.0  
 0.1  
 10000.0  
 -1.23e-22  
 +1.23e+22  
 1E6

## Boolean

True or false. Booleans are used to represent true and false values returned by comparison operators and logical functions.

### Examples:

true  
 false  
 1 < 5

## String Literals

String literals are surrounded by double quotes or single quotes. A string literal can contain any sequence of UNICODE characters. A double quote can't be used within the string unless it is escaped. Backslash is used to escape special characters, so it must also be escaped.

The basic escaping rules are that only the characters defined below can be used after a \; everything else will generate an error.

Escape sequence	Result
\uHHHH	Any Unicode character expressed as four hexadecimal characters
\0ooo	A character in the range 0-255 expressed as three octal digits 0-7
\b	\u0008: backspace (BS)
\t	\u0009: horizontal tab (HT)
\n	\u000a: linefeed (LF)
\f	\u000c: form feed (FF)
\r	\u000d: carriage return (CR)
\"	\u0022: double quote "
\'	\u0027: single quote '
\\	\u005c: backslash \

### Examples:

"Hello world"  
 "25\"23"  
 "1\n2\n"  
 "C:\\TEMP\\image.png"

## Column References

Accessing columns are done by either simply writing the column name, or enclosing the column name in square brackets. The brackets are needed when the column name contains characters other than letters, digits or \_ (underscore), or if the column name begins with a digit. If a column name is bracketed; any end brackets and backslashes in the column name must be

escaped by \] or \\ respectively. The same backslash escaping rules as for strings are followed, except that double quotes (") may not be escaped.

**Examples:**

```
Column1
[Column1]
[Binned Column1]
[1]
[!@#$$%^&*()[]\]
```

**Time, Date, TimeStamp**

- Time – A time of day type, range 0:00 to 24:00.
- Date – Date type ranging from January 1st, 100 to December 31st, 9999.
- TimeStamp – A combination of Time and Date.

Mathematical operations on date, time and timestamp data types are supported in DecisionSite 9.0 and forward.

For example, it is possible to calculate how many days it differs between two date columns. When a date, time or timestamp column is subtracted from another date, time or timestamp column, the corresponding result column will show the number of days as a real (decimal) column. For example, "2006-10-10 7.00 AM minus 2006-10-10 1.00 AM" equals 0.25 since 6 hours is a quarter of a day.

**7.4.4.3 Operators**

**7.4.4.3.1 Operators Overview**

Please select which type of Operators you are interested in:

Unary Operators (Operators with only one argument)

Binary Operators (Operators with two arguments)

Trinary Operators (Operators with three arguments)

Operator Precedence

**7.4.4.3.2 Unary Operators**

A unary operator takes one argument following the operator.

Operator	Description
- Arg1	Negates the argument. The argument and the result are of type real.
! Arg1	Returns the logical Not of <i>Arg1</i> . The argument and the result are of type boolean. See also function Not.

**Example:**

!true -> false

!false -> true

**7.4.4.3.3 Binary Operators**

A binary operator takes two arguments, one preceding and one following the operator.

Operator	Description
Arg1 + Arg2	Adds the two arguments. The arguments and the result are of type real. See operator & for string concatenation.

$Arg1 - Arg2$	Subtracts <i>Arg2</i> from <i>Arg1</i> . The arguments and the result are of type real.
$Arg1 * Arg2$	Multiplies the two arguments. The arguments and the result are of type real.
$Arg1 / Arg2$	Divides <i>Arg1</i> by <i>Arg2</i> . The arguments and the result are of type real. Division by zero results in an error. Example: 7/2 -> 3.5 0/0 -> #NUM! -1/0 -> #NUM!
$Arg1 \& Arg2$	Appends <i>Arg2</i> to the end of <i>Arg1</i> . The arguments can be of any type, but are converted to strings. The result is of type string. See also function Concatenate. Example: "April " & (20+1) & "st" -> "April 21st" null & "Ape" -> #NULL!
$Arg1 < Arg2$	Returns true if <i>Arg1</i> is less than <i>Arg2</i> . The arguments are of type real and the result is of type boolean. The function is defined for comparing normal numbers to each other and to $\pm$ Infinity. It is also defined for comparing Infinity to -Infinity. Other combinations result in errors or null. Example: 1 < 2 -> true 1 < null -> #NULL! 1 < 1/0 -> true 1/0 < 1/0 -> #NUM! -1/0 < 1/0 -> true 1 < 0/0 -> #NUM!
$Arg1 > Arg2$	Returns true if <i>Arg1</i> is greater than <i>Arg2</i> . The arguments are of type real and the result is of type boolean. See operator < for the definition of valid arguments.
$Arg1 \leq Arg2$	Returns true if <i>Arg1</i> is less than or equal to <i>Arg2</i> . The arguments are of type real and the result is of type boolean. See operator < for the definition of valid arguments.
$Arg1 \geq Arg2$	Returns true if <i>Arg1</i> is greater than or equal to <i>Arg2</i> . The arguments are of type real and the result is of type boolean. See operator < for the definition of valid arguments.
$Arg1 = Arg2$	Returns true if <i>Arg1</i> is equal to <i>Arg2</i> . The arguments can be of any type, but must both be of the same type. The result is of type boolean. If any argument is null, the result is null. See function IsNull for comparing nulls. For arguments of type real, see operator < for the definition of valid arguments. Example: "Hello" = "hello" -> false "" = null -> #NULL! null = null -> #NULL!
$Arg1 \neq Arg2$	Returns true if <i>Arg1</i> is not equal to <i>Arg2</i> . The arguments can be of any type, but must both be of the same type. The result is of type boolean. If any argument is null, the result is null. See function IsNull for comparing nulls. For arguments of type real, see operator < for the definition of valid arguments.

Expr1, Expr2	Evaluates both expressions and returns <i>Expr2</i> . The expressions can be any valid expression, including expressions that evaluate to null.
--------------	---

### 7.4.4.3.4 Trinary Operators

A trinary operator takes three arguments.

Operator	Description
Arg1? Arg2: Arg3	Returns Arg2 if Arg1=true, and Arg3 if Arg1=false. Arg1 is of type boolean, usually the result of a comparison. Arg2 and Arg3 can be of any type, but must both be of the same type or null. If Arg1 is null, the result is also null. See also function If.

**Example:**

```
([Count] > 3)? "many": "few"
true? null: null -> #NULL!
true? 1: null -> 1
false? null: 2 -> 2
null? 1: 2 -> #NULL!
```

### 7.4.4.3.5 Operator Precedence

Below is a table showing the hierarchy of SXL operators with the highest precedence operator shown first.

Expressions inside parentheses are evaluated first; nested parentheses are evaluated from the innermost parentheses to the outer.

Operators in the same row in the chart have equal precedence

Operators	Type	Order of Evaluation
()	Parentheses	left to right
!	Not	right to left
- +	Unary minus and plus	right to left
* / %	Multiplicative	left to right
+ -	Additive	left to right
&	Concatenation	left to right
< > <= >=	Relational	left to right
= <>	Equality	left to right

### 7.4.4.4 Functions

#### 7.4.4.4.1 Math Functions

Function	Description
Abs(Arg1)	Returns the absolute value of <i>Arg1</i> . The argument and the result are of type real.
ACos(Arg1)	Returns the arccosine of <i>Arg1</i> as an angle expressed in radians in the interval $[0, \pi]$ . <i>Arg1</i> must be in the interval $[-1.0, 1.0]$ , otherwise NaN is returned. The

	argument and the result are of type real.
ASin(Arg1)	Returns the arcsine of <i>Arg1</i> as an angle expressed in radians in the interval $[-\pi/2, \pi/2]$ . <i>Arg1</i> must be in the interval $[-1.0, 1.0]$ , otherwise NaN is returned. The argument and the result are of type real.
ATan(Arg1)	Returns the arctangent of <i>Arg1</i> as an angle expressed in radians in the interval $[-\pi/2, \pi/2]$ . The argument and the result are of type real.
Ceiling(Arg1)	Rounds <i>Arg1</i> up to the nearest natural number. The argument and the result are of type real. Example: Ceiling(1.01) -> 2.0 Ceiling(-1.99) -> -1.0
Cos(Arg1)	Returns the cosine of <i>Arg1</i> where <i>Arg1</i> is an angle expressed in radians. The argument and the result are of type real.
Exp(Arg1)	Returns e (2.718281...) raised to the <i>Arg1</i> power. The argument and the result are of type real.
Floor(Arg1)	Rounds <i>Arg1</i> down to the nearest natural number. The argument and the result are of type real. Example: Floor(1.99) -> 1.0 Floor(-1.01) -> -2.0
Ln(Arg1)	Returns the natural logarithm of <i>Arg1</i> . The arguments and the result are of type real. If <i>Arg1</i> is negative, the result is a NaN error. If <i>Arg1</i> is zero, the result is Infinity error.
Log(Arg1, Arg2)	Returns the logarithm of <i>Arg1</i> expressed in the base specified by <i>Arg2</i> . Equivalent to $\text{Ln}(\text{Arg1})/\text{Ln}(\text{Arg2})$ . The arguments and the result are of type real. See function Ln for the definition of valid arguments.
Log10(Arg1)	Returns the 10-based logarithm of <i>Arg1</i> . Equivalent to $\text{Ln}(\text{Arg1})/\text{Ln}(10)$ . The arguments and the result are of type real. See function Ln for the definition of valid arguments.
Mod(Arg1, Arg2)	Returns the remainder of the division of <i>Arg1</i> by <i>Arg2</i> . The arguments and the result are of type real. If <i>Arg2</i> is 0, the result is NaN. $\text{Mod}(\text{Arg1}, \text{Arg2})$ is defined as: $\text{Arg1} - \text{Arg2} * \text{Floor}(\text{Arg1}/\text{Arg2})$
PI()	Returns the numerical constant $\pi$ . The result is of type real.
Power(Arg1, Arg2)	Returns <i>Arg1</i> raised to the <i>Arg2</i> power. The arguments and the result are of type real. Example: Power(10, 3) -> 1000 Power(10, -3) -> 0.001 Power(0, 0) -> 1

Product(Arg1, ...)	Returns the product of the arguments. The arguments and the result are of type real. Null arguments are ignored and do not contribute to the product. Example: Product(-1) -> -1 Product(1.5, -2, 3) -> -9 Product(1, null, 3) -> 3 Product(null) -> #NULL!
Round(Arg1, Arg2)	Rounds <i>Arg1</i> to the number of decimal places specified by <i>Arg2</i> . The arguments and the result are of type real, but for <i>Arg2</i> , only the integer part is used. Note that <i>Arg2</i> can be negative to round to even 10s, 100s etc. 0.5 is rounded upwards to a number with higher magnitude (ignoring the sign). Example: Round(PI(), 3) -> 3.142 Round(-0.5, 0) -> -1 Round(25, -1) -> 30
Sin(Arg1)	Returns the sine of <i>Arg1</i> where <i>Arg1</i> is an angle expressed in radians. The argument and the result are of type real.
Sqrt(Arg1)	Returns the square root of <i>Arg1</i> . The argument and the result are of type real. If <i>Arg1</i> is negative, the result is a NaN error.
Sum(Arg1, ...)	Returns the sum of the arguments. The arguments and the result are of type real. Null arguments are ignored and do not contribute to the sum. Example: Sum(-1) -> -1 Sum (1.5, -2, 3) -> 2.5 Sum (1, null, 3) -> 4 Sum (null) -> #NULL!
Tan(Arg1)	Returns the tangent of <i>Arg1</i> where <i>Arg1</i> is an angle expressed in radians. The argument and the result are of type real.

#### 7.4.4.4.2 Statistical Functions

Function	Description
Average(Arg1, ...)	Returns the average (arithmetic mean) of the arguments. The arguments and the result are of type real. Null arguments are ignored and do not contribute to the average. Example: Average(-1) -> -1 Average (1.5, -2, 3.5) -> 1 Average (1, null, 3) -> 2 Average (null) -> #NULL!
Max(Arg1, ...)	Returns the largest of the arguments. The argument and the result are of type real. Null arguments are ignored.

Min(Arg1, ...)	<p>Example:  Max(-1) -&gt; -1  Max (1.5, -2, 3) -&gt; 3  Max (1, null, 3) -&gt; 3  Max (null) -&gt; #NULL!</p> <p>Returns the smallest of the arguments. The argument and the result are of type real. Null arguments are ignored.</p> <p>Example:  Min(-1) -&gt; -1  Min (1.5, -2, 3) -&gt; -2  Min (1, null, 3) -&gt; 1  Min (null) -&gt; #NULL!</p>
----------------	--

### 7.4.4.4.3 Logical Functions

Function	Description
And(Arg1, ...)	<p>Returns the logical And of the arguments. If any argument is false, the result is false. Otherwise, if any argument is null, the result is null. If all arguments are true the result is true. The arguments and the result are of type boolean.</p> <p>Example:  And(true, false, true) -&gt; false  And(false, null) -&gt; false  And(true, null) -&gt; #NULL!</p>
If(Arg1, Arg2, Arg3)	<p>Returns <i>Arg2</i> if <i>Arg1</i>=true, and <i>Arg3</i> if <i>Arg1</i>=false. <i>Arg1</i> is of type boolean, usually the result of a comparison. <i>Arg2</i> and <i>Arg3</i> can be of any type, but must both be of the same type or null. If <i>Arg1</i> is null, the result is also null. See operator ? :</p> <p>Example:  If([Count] &gt; 3, "many", "few")  If(true, null, null) -&gt; #NULL!  If(true, 1, null) -&gt; 1  If(false, null, 2) -&gt; 2  If(null, 1, 2) -&gt; #NULL!</p>
IsError(Expr1)	<p>Returns true if <i>Expr1</i> evaluates to an error, and false if <i>Expr1</i> evaluates to a proper value or null. Errors are e.g. numeric errors (NaN, ±Infinity), conversion errors and indexing errors. <i>Expr1</i> can be of any type and the result is of type boolean.</p> <p>Example:  IsError(0/0) -&gt; true  IsError(null) -&gt; false  IsError(Left("A", -1)) -&gt; true  IsError(Real("Hello")) -&gt; true (conversion)</p>
IsNull(Arg1)	<p>Returns true if <i>Arg1</i> is null, false otherwise. <i>Arg1</i> can be of any type and the result is of type boolean.</p> <p>Example:</p>

	<p>IsNull(0) -&gt; false                  IsNull(null) -&gt; true                  IsNull(0/0) -&gt; #NUM!</p>
Not(Arg1)	<p>Returns the logical Not of <i>Arg1</i>. The argument and the result are of type boolean. See also unary operator !                  Example:                  Not(true) -&gt; false                  Not(false) -&gt; true</p>
Or(Arg1, ...)	<p>Returns the logical Or of the arguments. If any argument is true, the result is true. Otherwise, if any argument is null, the result is null. If all arguments are false the result is false. The arguments and the result are of type boolean.                  Example:                  Or(false, true, false) -&gt; true                  Or(true, null) -&gt; true                  Or(false, null) -&gt; #NULL!</p>
Xor(Arg1, Arg2)	<p>Returns the logical Xor of the arguments. If exactly one argument is true, the result is true, otherwise false. If any or both arguments are null, the result is null. The arguments and the result are of type boolean.                  Example:                  Xor(true, false) -&gt; true                  Xor(true, true) -&gt; false                  Xor(true, null) -&gt; #NULL!</p>

#### 7.4.4.4.4 Text Functions

Function	Description
Concatenate(Arg1, ...)	<p>Concatenates (appends) all the arguments into a string. The arguments can be of any type, but are converted to strings. The result is of type string. Null arguments are ignored.                  Example:                  Concatenate("April ", 20+1, "st") -&gt; "April 21st"                  Concatenate(null, "Ape") -&gt; "Ape"                  Concatenate (null, null) -&gt; #NULL!</p>
Find(Arg1, Arg2)	<p>Returns the 1-based index of the first occurrence of the string <i>Arg1</i> in <i>Arg2</i>. If not found, 0 is returned. The search is case-sensitive. The arguments are of type string and the result is of type integer. If <i>Arg1</i> is the empty string, 0 is returned.                  Example:                  Find("lo", "Hello") -&gt; 4                  Find("a", "Hello") -&gt; 0                  Find("", "Hello") -&gt; 0                  Find("", null) -&gt; #NULL!                  If(Find("Pri 1", [Col1])&gt;0, "Important", "Not important")</p>
Left(Arg1, Arg2)	<p>Returns the first <i>Arg2</i> characters of the string <i>Arg1</i>. <i>Arg1</i> and the result are of type string. <i>Arg2</i> is of type real, but only the integer part is used. If <i>Arg2</i> &gt; the length of <i>Arg1</i>, the whole string is returned. If <i>Arg2</i> is negative, an error is returned.                  Example:</p>

	<pre>Left("Daddy", 3.99) -&gt; "Dad" Left("Daddy", 386) -&gt; "Daddy" Left("Daddy", -1) -&gt; #ARG!</pre>
Len(Arg1)	<p>Returns the length of the string <i>Arg1</i>. <i>Arg1</i> is of type string and the result is of type integer.</p> <p>Example:  Len("Hello") -&gt; 5  Len(null) -&gt; #NULL!</p>
Lower(Arg1)	<p>Returns <i>Arg1</i> converted to lowercase. <i>Arg1</i> and the result are of type string.</p>
Mid(Arg1, Arg2, Arg3)	<p>Returns the substring of <i>Arg1</i> starting at index <i>Arg2</i> with a length of <i>Arg3</i> characters. <i>Arg1</i> and the result are of type string. <i>Arg2</i> and <i>Arg3</i> are of type real, but only the integer part is used. If <math>Arg2 &gt; Len(Arg1)</math>, an empty string is returned. Else, if <math>Arg2 + Arg3 &gt; Len(Arg1)</math>, <i>Arg3</i> is adjusted to <math>1 + Len(Arg1) - Arg2</math>. If either <i>Arg2</i> or <i>Arg3</i> is negative or if <i>Arg2</i> is zero, an error is returned.</p> <p>Example:  Mid("Daddy", 2, 3) -&gt; "add"  Mid("Daddy", 386, 4) -&gt; ""  Mid("Daddy", 4, 386) -&gt; "dy"  Mid("Daddy", -1, 2) -&gt; #ARG!  Mid("Daddy", 2, -1) -&gt; #ARG!</p>
Right(Arg1, Arg2)	<p>Returns the last <i>Arg2</i> characters of the string <i>Arg1</i>. <i>Arg1</i> and the result are of type string. <i>Arg2</i> is of type real, but only the integer part is used. If <math>Arg2 &gt;</math> the length of <i>Arg1</i>, the whole string is returned. If <i>Arg2</i> is negative, an error is returned.</p> <p>Example:  Right("Daddy", 3.99) -&gt; "ddy"  Right("Daddy", 386) -&gt; "Daddy"  Right("Daddy", -1) -&gt; #ARG!</p>
Upper(Arg1)	<p>Returns <i>Arg1</i> converted to uppercase. <i>Arg1</i> and the result are of type string.</p>

#### 7.4.4.4.5 Date and Time Functions

Function	Description
AddDays(Arg1, Arg2)	<p>Adds <i>Arg2</i> number of days to <i>Arg1</i>. <i>Arg2</i> is of type Real and <i>Arg1</i> is of type Date or TimeStamp. The result is of the same type as <i>Arg1</i>.</p> <p>Example:  AddDays(2002-03-04, -2) -&gt; 2002-03-02</p>
AddSeconds(Arg1, Arg2)	<p>Adds <i>Arg2</i> number of seconds to <i>Arg1</i>. <i>Arg2</i> is of type Real and <i>Arg1</i> is of type Time or TimeStamp. The result is of the same type as <i>Arg1</i>.</p> <p>Example:  AddSeconds([Time col], 30)  AddSeconds([Time col], 0.010)</p>
Date(Arg1, Arg2, Arg3)	<p>Creates a Date. The arguments are year, month and day and are of type Real. The year must be between 100</p>

	and 9999. The month must be between 1 and 12. The day must be between 1 and 31). See also conversion functions. Example: Date(2003, 4, 9) -> 2003-04-09 Date(2000, -1, 1) -> #ARG! (conversion error)
DateDiff(Arg1, Arg2)	Returns the difference in milliseconds in between two Date, Time or TimeStamp values. Example: DateDiff([Time col 1],[Time col 2])
Day(Arg1)	Extracts the day from a Date or TimeStamp. The result is of type Integer. Example: Day(2002-03-04) -> 4
Days(Arg1, Arg2)	Returns the number of days between two dates. The arguments can be either of type Date or of type TimeStamp. If the arguments are of type TimeStamp, the time part is ignored. The result is of type Integer. Example: Days(2002-03-04, 2002-03-02) -> 2
Hour(Arg1)	Extracts the hour from a Time or TimeStamp. The result is of type Integer. Example: Hour(11:38:02) -> 11
Millisecond(Arg1)	Extracts the millisecond part of a Time or TimeStamp. The result is of type Integer. Example: Millisecond([Time col])
Minute(Arg1)	Extracts the minute from a Time or TimeStamp. The result is of type Integer. Example: Minute(11:38:02) -> 38
Month(Arg1)	Extracts the month from a Date or TimeStamp. The result is of type Integer. Example: Month(2002-03-04) -> 3
Second(Arg1)	Extracts the second from a Time or TimeStamp. The result is of type Integer. Example: Second(11:38:02) -> 2
Seconds(Arg1, Arg2)	Returns the number of seconds between two times. The arguments can be either of type Time or of type TimeStamp. The result is of type Integer. Example: Seconds(11:38:02, 11:37:00) -> 62
Time(Arg1, Arg2, Arg3)	Creates a Time. The arguments are hours, minutes and seconds and are of type Real. The hours, minutes and seconds must be valid (0-23, 0-59, 0-59). See also conversion functions. Example: Time(14,4,0") -> 14:04:00

TimeStamp(Arg1, Arg2)	Time(10, -1, 1) -> #ARG! (conversion error) Creates a TimeStamp. The arguments are a Date and a Time. See also conversion functions. Example: TimeStamp([Date col], [Time col])
Year(Arg1)	Extracts the year from a Date or TimeStamp. The result is of type Integer. Example: Year(2002-03-04) -> 2002

#### 7.4.4.4.6 Conversion Functions

Function	Description
Date(Arg1)	Converts Arg1 to a date. If the conversion fails, an error is returned. Arg1 can be of type String or TimeStamp and the result is of type Date. If a TimeStamp is specified, the time part is removed. See also date & time functions. Example: Date("2003-03-21") -> 2003-03-21 Date("10") -> #ARG! (conversion error) Date(null) -> #NULL! Date(2003-03-21 11:37:00) -> 2003-03-21
Integer(Arg1)	Converts Arg1 to an integer number. If the conversion fails, an error is returned. Arg1 can be of types integer, real or string, and the result is of type integer. Real numbers are truncated, i.e., only the integer part is used. Example: Integer("-123") -> -123 Integer("-2.99") -> -2 Integer("0%") -> #ARG! (syntax error) Integer(1e20) -> #ARG! (overflow) Integer(null) -> #NULL!
Real(Arg1)	Converts Arg1 to a real number. If the conversion fails, an error is returned. Arg1 can be of types integer, real or string, and the result is of type real. Example: Real("1.23") -> 1.23 Real(2) -> 2.0 Real("0%") -> #ARG! (syntax error) Real(null) -> #NULL!
SE(Arg1, Arg2)	Substitutes errors. Returns Arg1 if it is not an error, Arg2 otherwise. Arg1 and Arg2 can be of any type, but must both be of the same type or null. The result is of the same type as the arguments. Example: SE(1, 2) -> 1 SE(null, 2) -> #NULL! SE(0/0, 2) -> 2
SN(Arg1, Arg2)	Substitutes null values. Returns Arg1 if it is not null,

	<p><i>Arg2</i> otherwise. <i>Arg1</i> and <i>Arg2</i> can be of any type, but must both be of the same type or null. The result is of the same type as the arguments.</p> <p>Example:  SN(1, 2) -&gt; 1  SN(null, 2) -&gt; 2  SN(0/0, 2) -&gt; #NUM!</p>
String( <i>Arg1</i> )	<p>Converts <i>Arg1</i> to a string. This conversion never fails except if <i>Arg1</i> is null. <i>Arg1</i> can be of any type and the result is of type string.</p> <p>Example:  String(1.23) -&gt; "1.23"  String(null) -&gt; #NULL!</p>
Time( <i>Arg1</i> )	<p>Converts <i>Arg1</i> to a time. If the conversion fails, an error is returned. <i>Arg1</i> can be of type String or TimeStamp and the result is of type Time. If a TimeStamp is specified, the date part is removed. See also date &amp; time functions.</p> <p>Example:  Time("11:37:00") -&gt; 11:37:00  Time("10") -&gt; #ARG! (conversion error)  Time (null) -&gt; #NULL!  Time(2003-03-21 11:37:00) -&gt; 11:37:00</p>
TimeStamp( <i>Arg1</i> )	<p>Converts <i>Arg1</i> to a time stamp. If the conversion fails, an error is returned. <i>Arg1</i> can be of type String or Date and the result is of type TimeStamp. If a Date is specified, the time part is set to 00:00:00. See also date &amp; time functions.</p> <p>Example:  TimeStamp("2003-03-21 11:37:00") -&gt; 2003-03-21 11:37:00  TimeStamp("10") -&gt; #ARG! (conversion error)  TimeStamp(null) -&gt; #NULL!  TimeStamp (2003-03-21) -&gt; 2003-03-21 00:00:00</p>

#### 7.4.4.5 Reserved Words

Import  
Result  
Template  
Type  
null  
true  
false

#### 7.4.4.6 Errors and Null

An expression is considered valid if it is syntactically correct and all function, operator and column references can be resolved. If an expression is not valid, it cannot be evaluated. This will be indicated in the SXL UI as:

**#EXPR!**

When evaluating an expression, some operations produce errors or null values. Each function and operator can choose how to handle arguments that are errors or null. The default behavior is to propagate the first error or null value that is encountered. So, if a function takes two arguments and the first is null and the second is an error, the default behavior is to return null. Functions that handle errors and null in other ways are explained in their Descriptions.

## Errors

For operations on arguments of type real, the result is sometimes not defined. This produces a **NaN** (Not a Number) error. If the result of an operation is greater than the maximum real number, an **Infinity** error (or **-Infinity** error) is produced. Many operations are well defined for +/- **Infinity** and will work as expected, e.g.,  $2.5 < 1/0$  returns true. When generated, these errors are grouped together as numeric errors, displayed as:

**#NUM!**

If the argument for a function (or operator) is invalid, an error is also produced. For example, functions expecting an index might produce an error because the index is negative and conversion functions produce an error if the argument cannot be converted. When generated, these errors are grouped together as argument errors displayed as:

**#ARG!**

The **IsError**(*Arg1*) function can be used to determine if a sub-expression results in an error. The **SE**(*Arg1*, *Arg2*) function can be used to substitute errors with a certain value, e.g. null or 0.

When generating a result data set from the expression, errors are converted to null. Wrap the expression with a call to the **SN**(*Arg1*, *Arg2*) function to override this behavior.

Error	Details	Example	Description
#NUM!	NaN	0/0 atan(2) sqrt(-1)	Not a Number, means that the result is undefined. All subsequent math operations on NaN produce NaN.
#NUM!	Infinity	1/0 1e200*1e200	Infinity, means that the number is too big to store in the real data type. Many math operations treat this as a "huge" number.
#NUM!	-Infinity	-1/0 -1e200*1e200	Negative infinity, means that the number is too big to store in the real data type. Many math operations treat this as a "huge" negative number.
#ARG!	Invalid Argument	Left("Hello", -1) Mid("Hello", 0, 1)	Invalid argument. In this case because length must be positive and position cannot be zero.
#ARG!	Conversion	Real("Hello")	Conversion failed.

## Null

Null values are usually only generated when retrieving a column value from the data set or by explicitly writing **null** in the expression. Results that are null, are displayed as:

**#NULL!**

The **IsNull**(*Arg1*) function can be used to determine if a sub-expression results in null. The **SN**(*Arg1*, *Arg2*) function can be used to substitute null with a certain value, e.g., 0.

### 7.4.4.7 Compatibility

The old expression language in DecisionSite Client 7.1.1 and earlier, had a different syntax and a different set of functions and operators. All the functionality of the old expression language is present in the new expression language and mapping the old onto the new is described here.

Quoted column names are now bracketed instead: "Column 1" is now [Column 1]

String literals can now contain escaped characters such as quotes, backslashes, new lines etc: "22\\", '22"', "1\n2\n", 'C:\\TEMP\\file.csv'

Constants are replaced by function calls: PI is now PI(), E is now EXP(1)

Concatenating strings is now supported via the & operator instead of +

Operator ^ is replaced by function POWER

Operator precedence is now correct: 1+2\*3 is now evaluated as 1+(2\*3) instead of (1+2)\*3

Function Compatibility

The old functions and their new counterparts are listed below:

Old Function	New Function	Description
ADD	SUM	Now sums any number of arguments. See also operator +
SUBTRACT		Now only available as an operator. See operator -
MULTIPLY	PRODUCT	Now multiplies any number of arguments. See also operator *
DIVIDE		Now only available as an operator. See operator /
MOD	MOD	
EXP	POWER	See also operator ^
	EXP	Equivalent to POWER(x, 2.718281...)
SQRT	SQRT	
ABS	ABS	
	LOG(num, base)	Now requires a base argument as well (not 10 by default). See function LOG10 below.
LOG	LOG10	10 logarithm, replaces old LOG(x) function
LN	LN	Natural logarithm
FLOOR	FLOOR	
CEIL	CEILING	
SIN	SIN	
COS	COS	
TAN	TAN	
NEG		No longer supported. See unary operator -
PI (constant)	PI()	Now a function like in Excel.

E (constant)		No longer supported. Use EXP(1) instead.
MAX	MAX	
MIN	MIN	
TOUPPERCASE	UPPER	
TOLOWERCASE	LOWER	

## Operator Compatibility

The old operators and their new counterparts are listed below:

### Binary:

Old Operator	New Operator	Description
+	+	Adds numeric values. See operator & for string concatenation.
-	-	Subtract numeric values.
*	*	Multiply numeric values.
/	/	Divide numeric values.
^		No longer supported. See function POWER.
+	&	Concatenate (append) strings or lists.

### Unary:

Old Operator	New Operator	Description
	-	Negates the argument.

## Examples

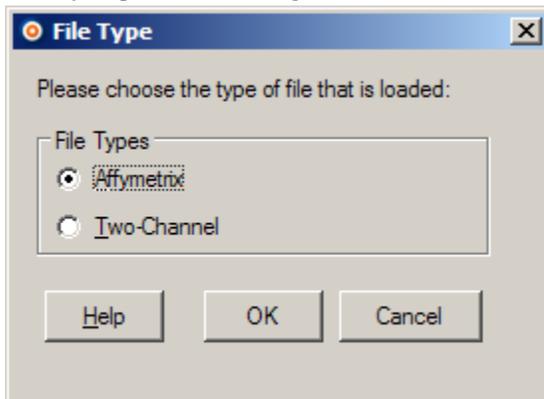
Here are some examples of how expressions would look using both the old and the new syntax. We assume a data set with string column "S1" and numeric columns "N1", "N2" and "Binned N1".

Old Expression	New Expression
$N1 + 2 / N2$	$(N1 + 2) / N2$
SUBTRACT(N1, "Binned N1")	$N1 - [\text{Binned N1}]$
$N1 ^ 3 + \text{EXP}(N2, 0.5)$	$\text{POWER}(N1, 3) + \text{POWER}(N2, 0.5)$
NEG(N1)	-N1
TOUPPERCASE(S1)	UPPER(S1)
'C:' + S1 + '\' + N1 + '.txt'	'C:\' & S1 & '\' & N1 & '.txt'

## 7.5 Set File Type Information

### 7.5.1 File Type Dialog

This dialog is used if you select to import data by methods other than the Import Affymetrix CEL/CHP Files tool or the Import Two Channel Array Files tool. Use this tool to assign a data type to your data set, so that the correct data specific prompts are launched when you run the Modify Experimental Design tool or the Multifactor ANOVA tool, etc.



Option	Description
<b>Affymetrix</b>	Select this option if you are analyzing Affymetrix CHP or CEL files.
<b>Two-Channel</b>	Select this option if you are analyzing two-channel files.

► **To reach the File Type dialog:**

- This dialog is automatically displayed when you run a Multifactor ANOVA (**Data > Differential Expression Testing > Multifactor ANOVA...**) if you have imported data by some other means than by using the Import Affymetrix CEL/CHP Files tool or the Import Two-Channel Array Files tool.
- The dialog can also be reached by selecting **Data > Set File Type Information...**

## 7.6 Modify Experimental Design

### 7.6.1 Specifying the Design for Affymetrix Files

This tool is used to define the experimental design needed in order to run multifactor ANOVA. Here, you need to associate the factors and levels (for example, Time and 0H, 1H, respectively) with the data columns in DecisionSite. This information is then used in making the comparisons between microarrays and determining the significance of differential expression.

► **To specify the design for Affymetrix files:**

1. If this tool has not been displayed automatically, select **Data > Modify Experimental Design...**
2. If data columns were imported by a method OTHER than by using the Import Affymetrix CEL/CHP Files tool, then select the appropriate file type (**Affymetrix**) from the File Type dialog.

Comment: If the data was imported using the Import Affymetrix CEL/CHP Files tool this information is already available and you will not be prompted to select the file type.

Response: The Affymetrix Design - Column Selection dialog is displayed.

3. Select the desired columns to be included in the design.
4. Click **OK**.  
Response: The Create/Modify Design dialog is displayed.
5. Make your input on experimental design information that includes number of arrays, factors, levels and naming in the Create/Modify Design dialog and click **OK**.  
Response: The Affymetrix Design dialog is displayed.
6. In the design dialog you are prompted to associate columns in DecisionSite with corresponding factors and levels. For example, a column named t0Tumor is assigned the Factor of Time and Level of 0 Hour, the second Factor is Sample type and the Level is Tumor.
7. Click **OK**.  
Response: The dialog is closed and the design information is saved in the SFS file.  
If applicable, proceed with step 3 in Performing Multifactor ANOVA.

## 7.6.2 Specifying the Design for Two Channel Files

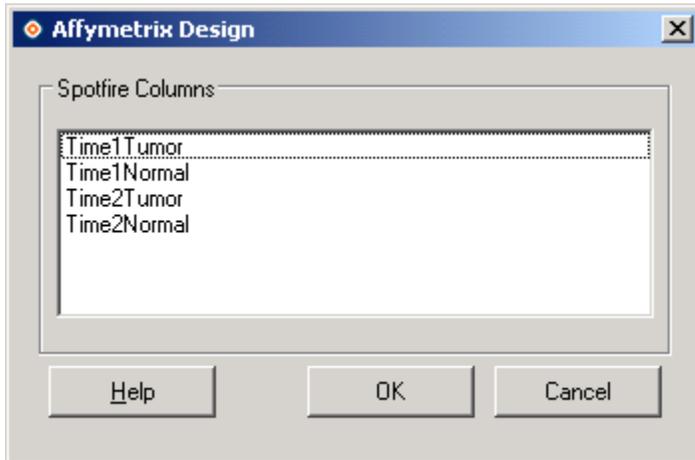
This tool is used to define the experimental design needed in order to run multifactor ANOVA. Here, you need to associate the factors and levels (for example, Time and 0H, 1H, respectively) with the data columns in DecisionSite. This information is then used in making the comparisons between microarrays and determining the significance of differential expression.

### ► To specify the design for two channel files:

1. If this tool has not been displayed automatically, select **Data > Modify Experimental Design....**
2. If data columns were imported by a method OTHER than by using the Import Two Channel Array Files tool, then select the appropriate file type (**Two-Channel**) from the File Type dialog.  
Comment: If the data was imported using the Import Two Channel Data tool this information is already available and you will not be prompted to select the file type.  
Response: The Two Channel Design - Column Selection dialog is displayed.
3. Choose the columns to be used in differential expression testing from the initial dialog. Both the M and A columns must be selected.
4. Click **OK**.  
Response: The Create/Modify Design dialog is displayed.
5. Make your input on experimental design information that includes number of arrays, factors, levels and naming in the Create/Modify Design dialog and click **OK**.  
Response: The Two Channel Design dialog is shown.
6. In the design dialog you are prompted to associate columns in DecisionSite with corresponding factors and levels. For example, a column named t0Tumor is assigned the Factor of Time and Level of 0 Hour, the second Factor is Sample type and the Level is Tumor.
7. Click **OK**.  
Response: The dialog is closed and the design information is saved in the SFS file.
8. If applicable, proceed with step 3 in Performing Multifactor ANOVA.

## 7.6.3 User Interface

### 7.6.3.1 Affymetrix Design - Column Selection Dialog

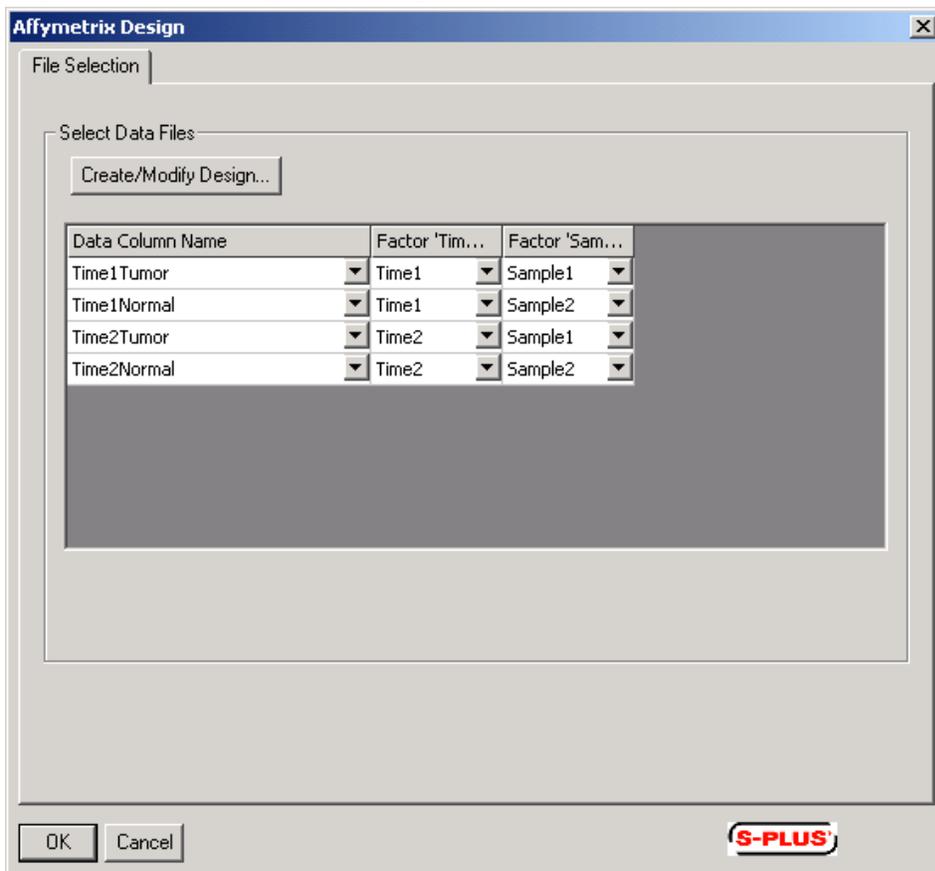


Option	Description
Spotfire Columns	Click to select the columns you want to use in the differential expression testing.

► **To reach the Affymetrix Design - Column Selection dialog:**

- This dialog is automatically displayed when you run a Multifactor ANOVA (**Data > Differential Expression Testing > Multifactor ANOVA...**) if no design has been previously specified.
- The dialog can also be reached by selecting **Data > Modify Experimental Design...**

### 7.6.3.2 Affymetrix Design Dialog



Option	Description
<b>File Selection tab</b>	Here you assign column names to factors and levels.
<b>Create/Modify Design...</b>	Allows you to return to the Create/Modify design dialog in order to change the factor names and levels which are used to generate the current dialog.
<b>Data Column Name</b>	Columns in DecisionSite to be associated with factors and levels. The Data Column Name can be selected from the drop-down list by double-clicking on the arrow.
<b>Factor "Name" Level (First factor column):</b>	Associate First Factor and level names to appropriate columns. The Factor "Name" Level can be selected from the drop-down list by double-clicking on the arrow.
<b>Factor "Name" Level (Second factor column):</b>	Associate Second Factor and level names to appropriate columns. The Factor "Name" Level can be selected from the drop-down list by double-clicking on the arrow.

► **To reach the Affymetrix Design dialog:**

Select **Data > Differential Expression Testing > Multifactor ANOVA...**

### 7.6.3.3 Create/Modify Design Dialog

#### Affymetrix

Factor	Name	# of Levels	Level Values
A	Time	2	Time1 Time2
B	Sample	2	Sample1 Sample2

Option	Description
<b>Number of Arrays</b>	Specify the number of arrays to be used in differential expression testing by using the arrow keys to scroll or by typing a value and pressing Enter.
<b>Number of Factors</b>	Specify one or two factors to be used in differential expression testing by using the arrow keys to scroll or by typing a value and pressing Enter.
<b>Factor</b>	Designation of first Factor as A and second Factor as B.
<b>Name</b>	The names specified here will automatically be used for your experimental factors in following dialogs. The factor names can be changed by double-clicking on a cell and typing the new value.
<b># of Levels</b>	Specify the number of levels (for example, 2 timepoints) by double-clicking on a cell and then scrolling with arrow keys or by typing a value and pressing Enter.
<b>Level Values</b>	Level values are automatically generated based on Name and # of levels entered in the previous columns.

## Two Channel

**Create / Modify Design**

Factors

Number of Arrays: 4      Number of Factors: 2

Factor	Name	# of Levels	Across Chip ?	Level Values
A	Time	2	No	Time1 Time2
B	Sample	2	Yes	Sample1 Sample2

Design Type

Two Sample

Dye Swap

Reference

Factor: Time

Ref Level: Time1

Ref Cy3    Ref Cy5    Dye Swap

Loop

Factor: Time

Dye Swap

Other

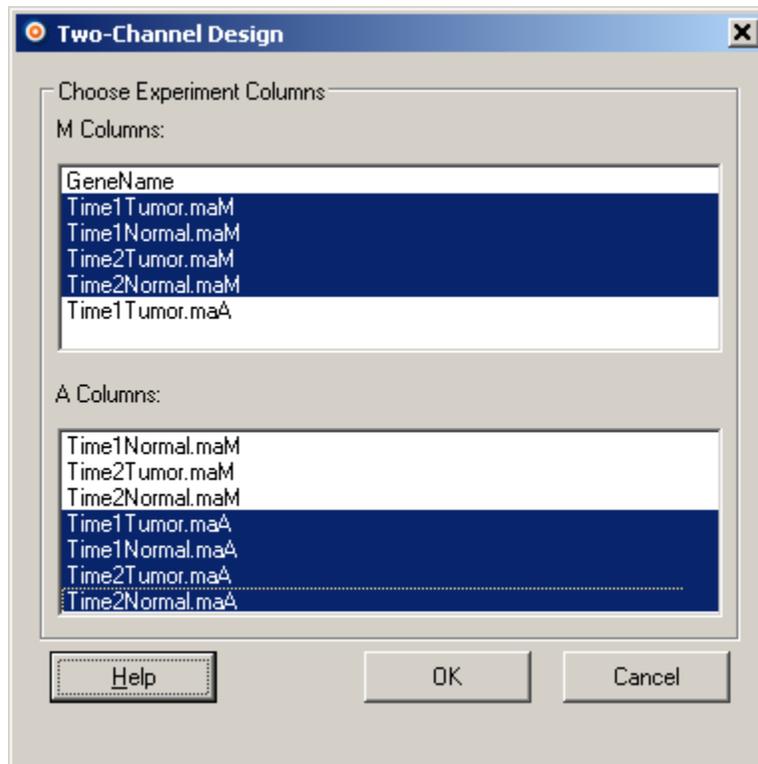
OK      Cancel

Option	Description
<b>Number of Arrays:</b>	Specify the number of arrays to be used in differential expression testing by using the arrow keys to scroll or by typing a value and pressing Enter.
<b>Number of Factors:</b>	Specify one or two factors to be used in differential expression testing by using the arrow keys to scroll or by typing a value and pressing Enter.
<b>Factor Name</b>	Designation of first Factor as A and second Factor as B. The names specified here will automatically be used for your experimental factors in following dialogs. The factor names can be changed by double-clicking on a cell and typing the new value.
<b># of Levels</b>	Specify the number of levels (for example, 2 timepoints) by double-clicking on a cell and then scrolling with arrow keys or by typing a value and pressing Enter.
<b>Level Values</b>	Level values are automatically generated based on Name and # of levels entered in the previous columns.
<b>Design Type</b>	Specify two sample, reference, loop or other design type and dye swap here.

► **To reach the Create/Modify Design dialog:**

Select **Data > Differential Expression Testing > Multifactor ANOVA...**

### 7.6.3.4 Two-Channel Design - Column Selection Dialog

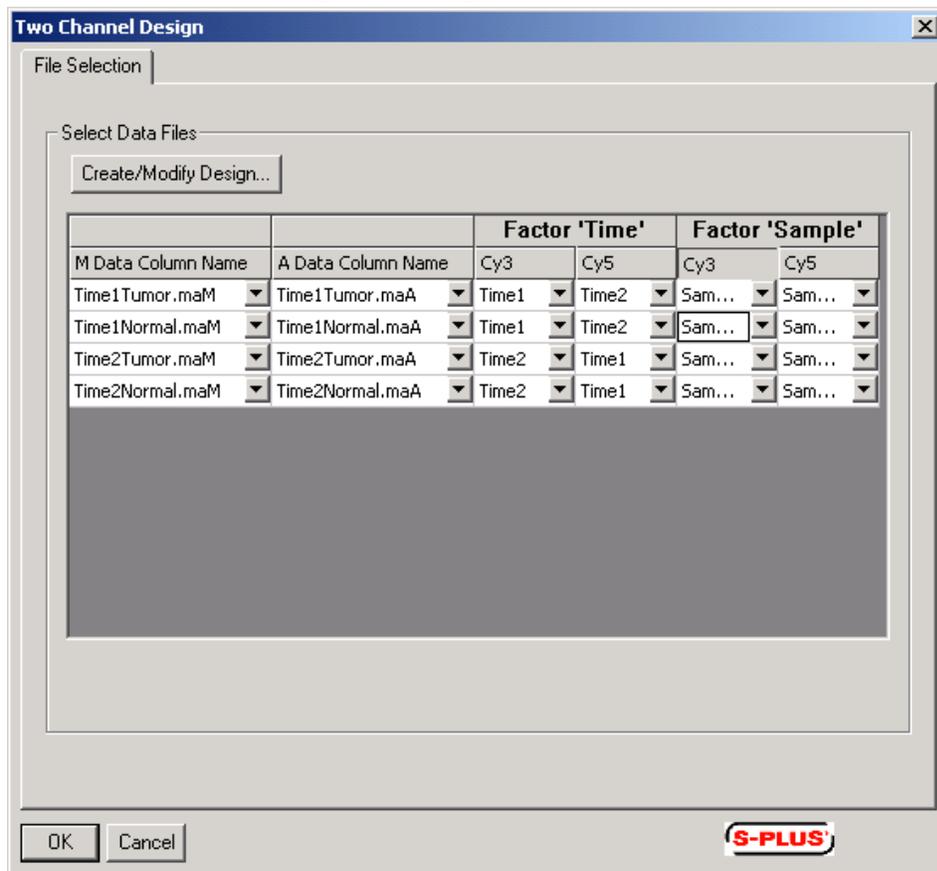


Option	Description
<b>Spotfire Columns</b>	Click to select the columns you want to use in the differential expression testing.
<b>M Columns</b>	Log-ratio of the intensities between channels.
<b>A Columns</b>	Average of the log intensities for the channels.

► **To reach the Two Channel Normalization Design dialog:**

- This dialog is automatically displayed when you run a Multifactor ANOVA (**Data > Differential Expression Testing > Multifactor ANOVA...**) if no design has been previously specified.
- The dialog can also be reached by selecting **Data > Modify Experimental Design...**

### 7.6.3.5 Two Channel Design Dialog



Option	Description
<b>File Selection tab</b>	Here you assign column names to factors and levels.
<b>Create/Modify Design...</b>	Allows you to return to the Create/Modify design dialog in order to change the factor names and levels which are used to generate the current dialog.
<b>M Data Column Name</b>	Columns in DecisionSite containing M values (Log-ratio of the intensities between channels) to be used in differential expression testing.
<b>A Data Column Name</b>	Columns in DecisionSite containing A values (Average of the log intensities for the channels) to be used in differential expression testing.
<b>Factor "Name" Level (First factor column):</b>	Associate First Factor and level names to appropriate columns. The Factor "Name" Level can be selected from the drop-down list by double-clicking on the arrow.
<b>Factor "Name" Level (Second factor column):</b>	Associate Second Factor and level names to appropriate columns. The Factor "Name" Level can be selected from the drop-down list by double-clicking on the arrow.
<b>Cy3</b>	Indicates which factor and level is associated with the Cy3 fluorescent dye intensity. Cy3 can be selected from the drop-down list by double-clicking on the arrow.

**Cy5**

Indicates which factor and level is associated with the Cy5 fluorescent dye intensity. Cy5 can be selected from the drop-down list by double-clicking on the arrow.

**► To reach the Two Channel Design dialog:**

Select **Data > Differential Expression Testing > Multifactor ANOVA...**

## 7.7 CHP Normalization

### 7.7.1 Performing CHP Normalization

The CHP Normalization tool can be used to perform additional normalization on data from Affymetrix CHP files or text files.

**► To perform CHP Normalization:**

1. Select **Data > CHP Normalization...**

Response: The CHP Normalization dialog is displayed.

2. Select the value columns on which to base the normalization from the **Available columns** list and click **Add >>**.

Comment: For multiple selection, press **Ctrl** and click on the desired columns in the Available columns list. Then click **Add >>** to move the columns to the Selected columns list. You can sort the columns in the list alphabetically by clicking on the Name bar.

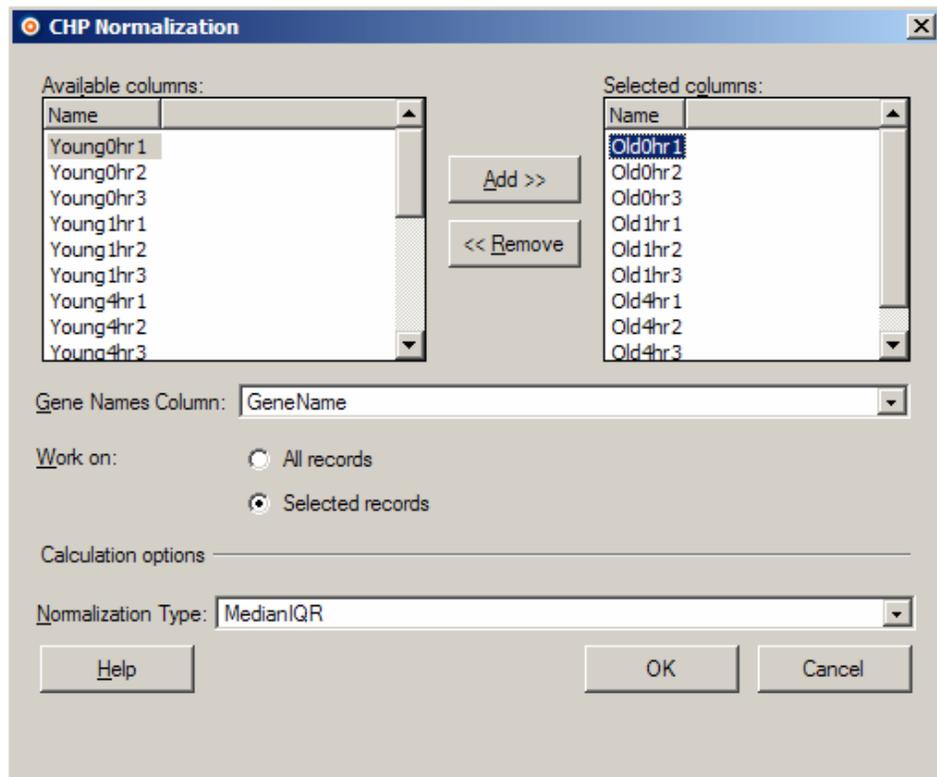
3. Select the Gene Names Column. This is the identifier column of the data set. It will be used to join the results to the data set.
4. Click a radio button to select whether to work on **All records** or **Selected records**. Select whether you want to **Work on Genes** or **Experiments**.

Comment: This determines the measure that is used to perform the calculation and how the output is handled. Selecting **Genes** causes the application to add a new column of data into DecisionSite. The data set has one row of clustering information per row of data clustered. Selecting **Experiments** causes the application to open a data set in a new session of DecisionSite. The data set has two columns and one row of data per column of data clustered.

5. Click **OK**.

Response: The CHP Normalization dialog is closed and the normalization is started. You see a graphical representation of the result in the visualizations created. The results of the normalization are added as new data columns to the data set.

## 7.7.2 CHP Normalization Dialog



Option	Description
<b>Available columns</b>	Displays all available data columns on which you can perform a normalization. Click a column name in the list and click <b>Add &gt;&gt;</b> to add it to the Selected columns list. To select more than one column, press <b>Ctrl</b> and click the column names in the list, then click Add >>.
<b>Selected columns</b>	Displays the currently selected data columns on which you want to perform a normalization.
<b>Add &gt;&gt;</b>	Adds the highlighted data column to the list of selected columns.
<b>&lt;&lt; Remove</b>	Removes the highlighted data column from the list of selected columns and places them back in the list of available columns.
<b>Gene Names Column</b>	The identifier column of the data set. This will be used to join the results to the data set.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Normalization Type</b>	<b>MedianIQR:</b> Adjusts the location and scale of the data so expression values on all arrays have equal medians and equal interquartile ranges (i.e., the spread between the 25th and 75th percentiles is the same). <b>AffyScaleValue:</b> Values are scaled according to Affymetrix

scaling protocol.

**VSN:** VSN is short for variance stabilization normalization. In the VSN normalization method, the intensities from each array are calibrated by a suitable affine transformation, then transformed by a variance stabilizing transformation. This is useful for subsequent analyses such as hypothesis tests, ANOVA modeling, clustering, or classification that assume that the variance is the same for all observations. Note that VSN only addresses the dependence of the variance on the mean intensity. There may be other factors influencing the variance, such as gene-inherent properties, or changes of the tightness of transcriptional control in different conditions. If necessary, these need to be addressed by other methods. For additional information on this method please refer to Huber (2002 and 2003).

**Quantiles:** Assuming an underlying common distribution, the set of chips are normalized so that their quantiles have the same value.

## References

Huber, W., Heydebreck, A., Sueltmann H., Poustka, A., Vingron, M. (2002). Variance stabilization applied to microarray data calibration and to the quantification of differential expression, *Bioinformatics* 18 Suppl.1 S96-S104.

### ► To reach the CHP Normalization dialog:

Select **Data > CHP Normalization...**

## 7.8 MIAME Annotation

### 7.8.1 Viewing and Editing MIAME Annotations

Minimum Information About Microarray Experiments (MIAME) can be entered upon import of Affymetrix CEL/CHP data files or import of two channel data, allowing you to specify experimental information to be permanently stored with the Spotfire analysis file (SFS). MIAME is used to label data and the tool can also be run separately to annotate any type of data set.

### ► To View or Edit MIAME Annotations:

1. Select **Tools > MIAME**.

Comment: If you are importing data via the Affymetrix CEL/CHP or Two Channel Import tools, MIAME is run automatically.

2. View or Edit the fields as you choose.

Comment: If the SFS file was annotated using the MIAME Annotation tool in another session those details are displayed. If the SFS file was not previously annotated, the tool shows the details supplied the last time the MIAME Annotation tool was run.

3. Click **OK**.

Response: When the SFS file is saved, the annotation details are added to the file.

## 7.8.2 MIAME Annotation Dialog

Option	Description
<b>Experimenter's Name</b>	Name of scientist running experiment.
<b>Laboratory</b>	Name of the laboratory.
<b>Contact Information</b>	Contact information for scientist running experiment.
<b>Experiment Title</b>	Descriptive title that reflects goal of the experiment (e.g., the title from the related publication).
<b>Experiment Description</b>	A brief description of the experiment (e.g., the abstract from the related publication).
<b>Existing Notes</b>	Link or path to document containing additional information. For example, keywords, experimental factors, design, quality control steps, links to publications or supplemental websites, samples used, extract preparation and labeling, hybridization procedures and parameters, image scanning and data extraction details, and array design.

► **To reach the MIAME Annotation dialog:**

Select **Tools > MIAME...**

## 7.9 Add Columns from NetAffx

### 7.9.1 Add Columns from NetAffx Overview

The Add Column from NetAffx tool allows you to easily add annotation data as new columns to your existing data set.

The tool allows you to download your most commonly used annotation files from Affymetrix's online Gene Chip Annotation repository NetAffx Analysis Center. Downloaded files are

automatically stored on your local computer. From the downloaded files, you can add the annotation data to your existing data set as new columns. The columns will be added based on a common ID field in your local data set and the annotation file from NetAffx, most commonly the “Probe Set ID” column.

**Note:** The Add Columns from NetAffx tool only supports comma separated annotation files (.csv) from the NetAffx site.

### **Software requirements for Add Columns From NetAffx**

To use the Add Column from NetAffx tool you must install the NetAffx SDK which is available to registered users of Affymetrix. More details can be found [here](#).

## **7.9.2 Using Add Columns from NetAffx**

### **7.9.2.1 Add Columns from Downloaded File**

The matching of values in the selected ID columns is case sensitive. If the existing record IDs are missing in the file which is to be merged with the current data set, the values in the new column will be empty for these records. Records with IDs that do not exist in the current data set will not be added at all.

#### **► To add columns from a downloaded file to an open data set:**

1. Select **Data > Add Columns from NetAffx...**  
Response: The Add Columns from NetAffx - Select Annotation File and Column Match Method Dialog is opened.
2. Select a file from the downloaded NetAffx annotation files list.  
**Note:** The first time you use this tool, or if there are no downloaded files available, you will be asked to download files with the Select Annotation Files to Download dialog.  
Comment: To ensure that the selected file is the latest available version from NetAffx, check the **Get latest version from NetAffx** check box.
3. Select the **Column match method**.  
**Note:** If **Automatic** is selected, identifier columns with identical names (not case sensitive) must exist in both old and new data set. All columns with identical names will be used as identifier columns (implicit primary key matching). The new data set must also contain at least one new column. If there are no matching columns found, the tool tries to match the NetAffx “Probe Set ID” with DecisionSite columns called “Probe Set Name” (case sensitive).  
**Manual** allows you to select which columns to use in the matching of identifiers (explicit primary key matching). Use this option if you want to make sure that the matching is correct.
4. Click **Next >**.  
Response: The Add Columns from NetAffx - Select Matching Columns Dialog is displayed.  
Comment: Clicking **Finish** in this step would add all columns with names that do not exist in the current data set.
5. Click to select a column from the **Columns in new data set** that you want to use to map against your current data.  
Comment: This should be an ID column (preferably containing unique identifiers). If a record in this column is missing in the current data set, the record will not be added to the data set.

Comment: If a column has already been used in a matching, it will not be available in the Columns in new data set list. Select a column pair in the Matching columns list and click on Remove to make the columns available in the two selection lists again.

6. Click to select a column from the **Columns in current data set**.

Comment: This should be an ID column (preferably containing unique identifiers).

7. Click **Add Match**.

Comment: The selected column pair is moved to the **Matching columns** list box. If desired, it is possible to use multiple key pairs. In this case, only records that have identical values in all the selected column pairs will be added to the data set.

8. Click **Next >**.

Response: The Add Columns from NetAffx - Select Columns Dialog is displayed.

Comment: Clicking **Finish** in this step would add all columns from the new data set that were not selected among the Matching columns above to the current data set.

9. Select the columns you wish to include in your data set.

Comment: If a column to include has the same name as one of the columns already in the data set, it will be added with the suffix (1), (2), etc.

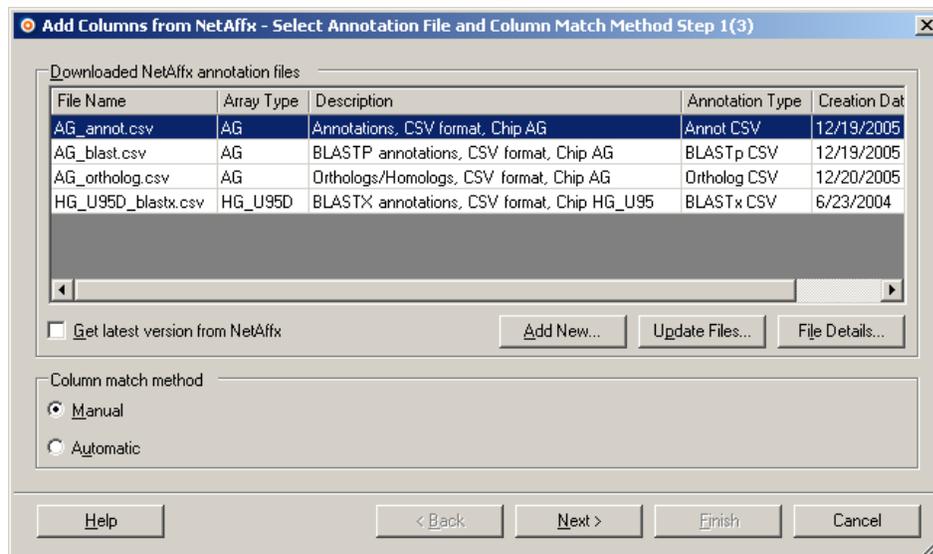
10. Click **Finish**.

Response: The new columns are added and Query Devices representing the new columns are shown in Spotfire DecisionSite. (You may have to scroll down in the Query Devices window to see the new query devices.)

**Note:** The matching of values in the selected ID columns is case sensitive. If the existing record IDs are missing in the file which is to be merged with the current data set, the values in the new column will be empty for these records. Records with IDs that do not exist in the current data set will not be added at all.

## 7.9.3 User Interface

### 7.9.3.1 Add Columns from NetAffx - Select Annotation File and Column Match Method Dialog



Option	Description
Downloaded	Displays the list of downloaded annotation files with information.

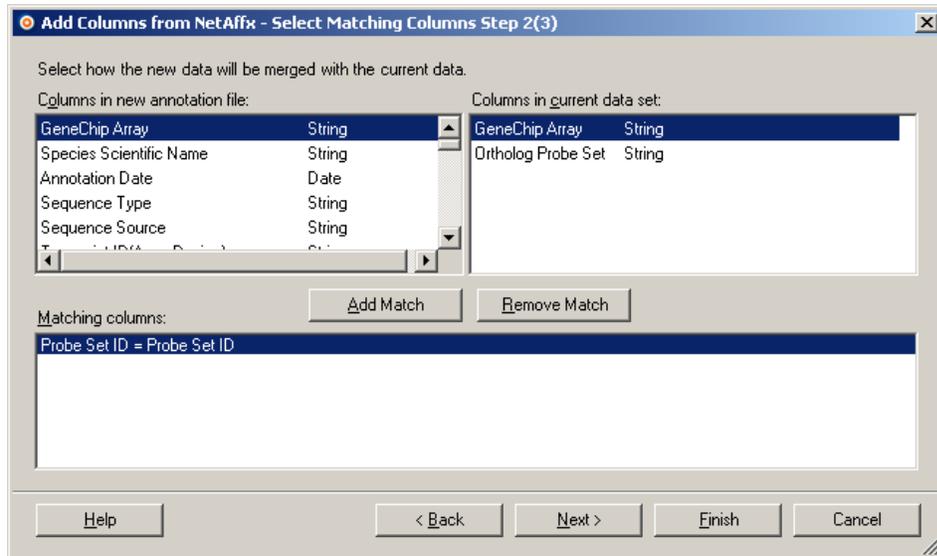
<b>NetAffx annotation files</b>	Select a file containing the data that you want to add.
<b>Get latest version from NetAffx</b>	If selected, this connects to the Affymetrix NetAffx server and downloads the latest selected file when you click <b>Next &gt;</b> .
<b>Add New...</b>	Opens the Select Annotation Files to Download Dialog where you can select new annotation file to download for future use.
<b>Update Files...</b>	Opens the Update Files Dialog where you can check for newer versions of the downloaded files available on the online NetAffx Analysis Center.
<b>File Details...</b>	Opens the File Details Dialog where you can see the details about the selected file.
<b>Manual</b>	Select this option if you want to manually select the columns to use in the matching of IDs (explicit primary key matching). Use this option if you want to make sure that the matching is correct.
<b>Automatic</b>	Spotfire DecisionSite will automatically match columns with identical names (implicit primary key matching). <b>Note:</b> If you have columns with identical names that do not contain the same identifiers, this option might not add any data.
<b>Next &gt;</b>	Takes you on to the next step of the wizard. If <b>Automatic</b> has been selected as the Column match method you will go straight to the Add Columns from NetAffx - Select Columns Dialog. If <b>Manual</b> has been selected you will be Guided to the Add Columns from NetAffx - Select Matching Columns Dialog.
<b>Finish</b>	Only available if the Automatic column match method has been selected. All columns in the new and old data set that have identical names (not case sensitive) will be used as identifier columns. This means that all values in all the identifier columns must match for the data to be added. All columns with names that do not exist in the current data set will be added.

► **To reach the Add Columns from NetAffx - Select Annotation File and Column Match Method Dialog:**

Select **Data > Add Columns from NetAffx...**

### 7.9.3.2 Add Columns from NetAffx - Select Matching Columns Dialog

This dialog specifies which columns should be used as keys in the merging of the new columns with the columns in the original data set. Normally, for NetAffx annotation files, one column pair containing IDs is enough, but in some cases it may be necessary to use two or more column pairs to create unique mappings between the two data sets.

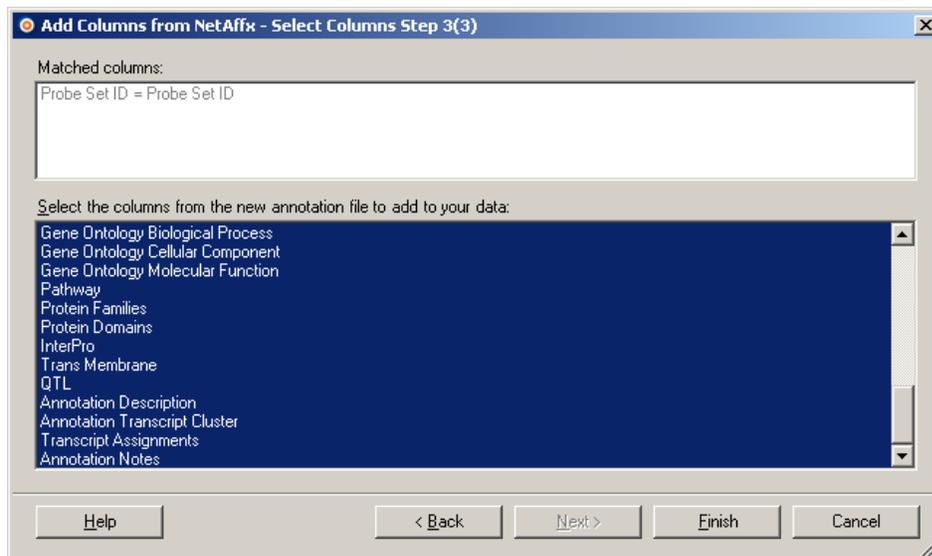


Option	Description
<b>Columns in new annotation file</b>	Displays the columns in the new annotation file that are available for use in a matching columns pair. A column can only be used in a single column pair matching at a time and will therefore be removed from this list box after it has been included in the Matching columns list box.
<b>Columns in current data set</b>	Displays the columns in the current data set that are available for use in a column pair. A column can only be used in a single column pair matching at a time and will therefore be removed from this list box after it has been included in the Matching columns list box.
<b>Add Match</b>	Select an ID column in both list boxes mentioned above and click Add Match to add the pair to the Matching columns list box.
<b>Remove</b>	Select one or more column pairs in the Matching columns list box and click this button to remove the pairs from the list. This will return the columns to the list boxes of available columns above.
<b>Matching columns</b>	Displays the selected column pairs that specify how the merge between the two data sets will be made. If more than one pair is selected, only records that have identical values in the entire selected column pairs will be added to the data set.
<b>Finish</b>	If Finish is clicked in the second step of the wizard, all columns in the new data set that are not used as identifiers in the Matching columns list, will be added to the data set.

► **To reach the Add Columns from NetAffx - Select Matching Columns dialog:**

1. Select **Data > Add Columns from NetAffx...**
2. Make your choice in the Add Columns from NetAffx - Select Annotation File and Column Match Method Dialog and select **Manual** as the Column match method.
3. Click **Next >**.

### 7.9.3.3 Add Columns from NetAffx - Select Columns Dialog



Option	Description
<b>Matched columns</b>	Lists the columns that are matched. This list is read-only and only for display purpose.
<b>Select the columns from the new annotation file to add your data</b>	Lists the columns available for adding as new columns. All columns in the new data set are listed. By default, all new columns that are not included among the Matching columns in the previous dialog will be selected. Click a column name in the list to select it. To select more than one column, press <b>Ctrl</b> and click the column names in the list.

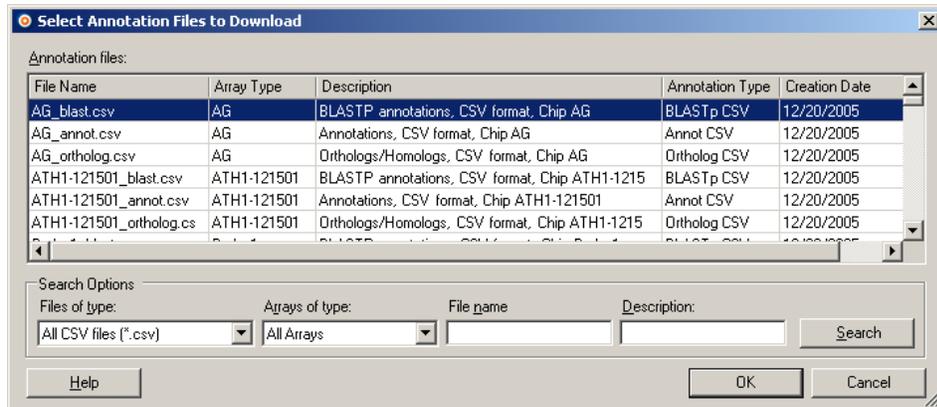
#### ► To reach the Add Columns from NetAffx - Select Columns Dialog:

1. Select **Data > Add Columns from NetAffx...**
2. Make your choices in the Add Columns from NetAffx - Select Annotation File and Column Match Method Dialog and click **Next >**.
3. Make your choices in the Add Columns from NetAffx - Select Matching Columns Dialog and click **Next >**.

### 7.9.3.4 Select Annotation Files to Download Dialog

This dialog lists all annotation files (.csv) present in the Affymetrix NetAffx server.

**Note:** If you are not already connected to the NetAffx server, the Affymetrix NetAffx Login Dialog will be displayed. If you do not have a username and password with Affymetrix, please visit the Affymetrix website where you can get more information on registration.



Option	Description
<b>Annotation files</b>	Lists all annotation files (.csv) present in the NetAffx server, along with their details and creation date. Click a column name in the list to select it. To select more than one column, press <b>Ctrl</b> and click the column names in the list or choose <b>Select All</b> from the right-click menu.
<b>Files of type</b>	Allows you to select the desired filter value to narrow down the list of annotation files to include only the .csv file category you are interested in.
<b>Arrays of type</b>	Lists arrays of type related to .csv files present in the NetAffx server. Here you can select the desired filter value to narrow down the list of annotation files to include only those array types you are interested in.
<b>File name</b>	Here you can enter the file name (or part of the file name) you are searching for.
<b>Description</b>	Here you can enter the file description (or part of the description) of the file you are searching for.
<b>Search</b>	Press <b>Search</b> when you have entered the desired search criteria to decrease the number of files shown in the Annotation files list based on those filter conditions you have entered.

► **To reach the Select Annotation Files to Download Dialog:**

1. Select **Data > Add Columns from NetAffx...**
2. Click **Add New...** in the Add Columns from NetAffx - Select Annotation File and Column Match Method Dialog.

### 7.9.3.5 Affymetrix NetAffx Login Dialog

This dialog is used to authenticate the NetAffx server with user ID and password. You need to supply NetAffx user ID and password here. If you are not registered with NetAffx server, see the Affymetrix website for more information.

**Note:** If you have already connected to the NetAffx server during your DecisionSite session, this dialog will not be displayed again.



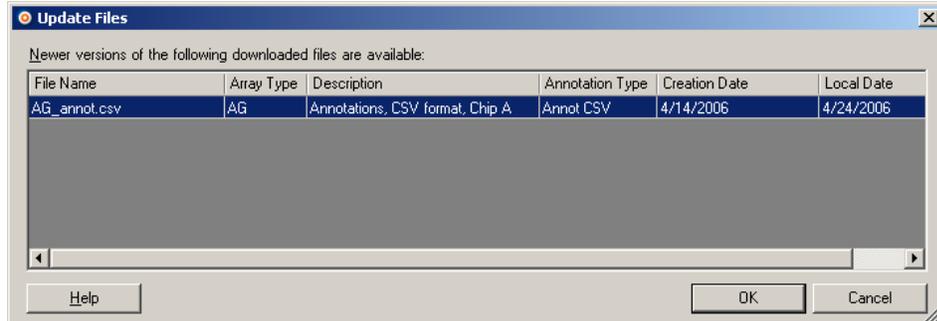
► **To reach the Affymetrix NetAffx Login Dialog:**

1. Select **Data > Add Columns from NetAffx...**
2. Click on either **Add New...** or **Update Files...** in the Add Columns from NetAffx - Select Annotation File and Column Match Method Dialog.
3. Alternatively, select either **Add New...** or **Update Files...** from the right-click menu in the Add Columns from NetAffx - Select Annotation File and Column Match Method Dialog.

### 7.9.3.6 Update Files Dialog

This dialog is used to check for newer versions of the downloaded files available on the online NetAffx Analysis Center to ensure that the downloaded annotation data is the most current. There are two column headers in the list, Creation Date and Local Date, that shows the differences between the files. If there are no newer versions of files present, this dialog will not be displayed.

**Note:** If you are not already connected to the NetAffx server, the Affymetrix NetAffx Login Dialog will be displayed. If you do not have a username and password with Affymetrix, please visit the Affymetrix website where you can get more information on registration.



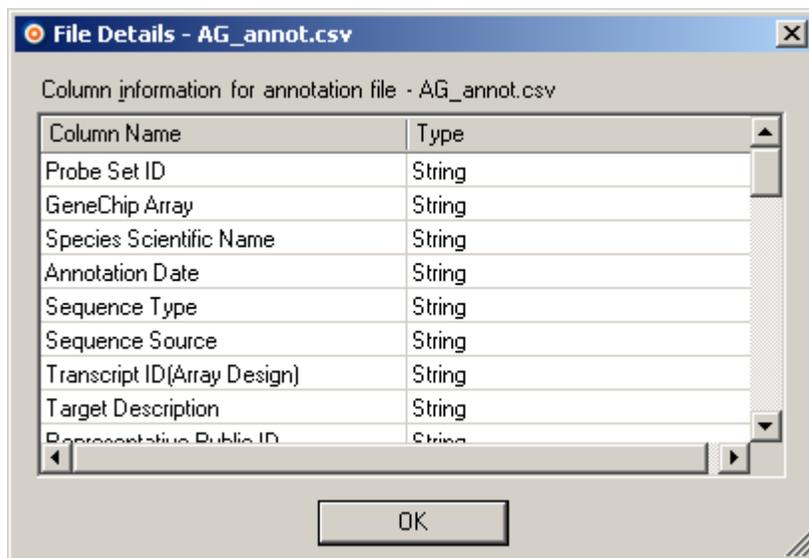
Option	Description
<b>Newer version of Annotation files</b>	Lists newer versions of annotation files (.csv) present in the NetAffx server along with their details, Creation Date and Local Date. Click a column name in the list to select it. To select more than one column, press <b>Ctrl</b> and click the column names in the list or choose <b>Select All</b> from the right-click menu.

► **To reach the Check for Updated Files Dialog:**

1. Select **Data > Add Columns from NetAffx...**
2. Click **Update Files...** in the Add Columns from NetAffx - Select Annotation File and Column Match Method Dialog.

### 7.9.3.7 File Details Dialog

This dialog is used to display the list of column information present in the selected annotation file.



► **To reach the File Details Dialog:**

1. Select **Data > Add Columns from NetAffx...**
2. Click **File Details...** in the Add Columns from NetAffx - Select Annotation File and Column Match Method Dialog.

## 7.10 Differential Expression Testing Multifactor ANOVA

### 7.10.1 Multifactor ANOVA Overview

This tool allows you to test hypotheses taking into account one to two experimental variables. Differential expression testing in DecisionSite for Microarray Analysis is defined as statistical testing of the difference in expression intensities between the treatment conditions under study. Effectively, this means that a separate hypothesis test is computed for each gene or probe on the chip. In two sample problems (e.g., two tissue types, treatment vs. control), this boils down to a t-test (or other two sample test) for each gene. When computing tests for chips with many probes, setting a usual Type I Error (false positive) rate for individual tests will result in many false positives. One key ingredient to good expression testing is controlling the family-wise error rate (FWER) or false discovery rate (FDR). The net effect of poor FWER control is wasted time and money in discovering many genes that really are not differentially expressed.

### 7.10.2 Using Multifactor ANOVA

#### 7.10.2.1 Performing Multifactor ANOVA

The Multifactor ANOVA tool can be used to test hypotheses where more than one experimental condition is being tested.

► **To perform Multifactor ANOVA:**

1. Select **Data > Differential Expression Testing > Multifactor ANOVA...**
2. If this is the first time that Multifactor ANOVA has been run on this data set, you will be prompted to enter design information. This information describes the setup of the experiment and is explained in the Specifying the Design for Affymetrix Files and Specifying the Design for Two Channel Files sections. The results from these tools are stored within the SFS file. Complete the steps in all design dialogs and click OK to continue.

Response: If you have Affymetrix data, the Multifactor ANOVA dialog is displayed. If you have Two Channel data, the Two-Channel Multifactor ANOVA dialog is displayed.

3. In the Multifactor ANOVA dialog choose the desired settings.  
The Options group contains the procedures for controlling the FWER and FDR. Select one and specify the family-wise error rate (for either an FWER or FDR procedure) in the FWER editable field.

The Contrasts group contains settings for selecting the types of comparisons done between the levels of the factors. The selected contrasts are 'orthogonal' and may be considered as independent sources of information extracted from the experimental data. The contrast factor is chosen first. There are three choices for the contrasts on this chosen factor: Baseline, Sequential, and Linear/Quadratic.

4. Click **OK**.

Response: The dialog is closed and the ANOVA is calculated. The results of the calculation are added as new data columns to the data set.

## 7.10.3 User Interface

### 7.10.3.1 Multifactor ANOVA Dialog

**Multifactor ANOVA**

**Options**

FWER/FDR: 0.05

Adjustment: Bonferroni

Gene Names Column: GeneName

**Contrasts**

First Factor: Age

Baseline

Level:

Sequential

Linear/Quadratic

Order: Old  
Young

None

Second Factor: Time

Apply Contrasts:  Within Second  
 Across Second

Help OK Cancel

Option	Description
<b>FWER/FDR</b>	Allows you to set the family-wise error rate (FWER) or false discovery rate (FDR) to maintain an overall Type I error rate (false positive rate) based on adjusting individual test p-values to account for multiple tests. For example, setting this to 0.05 will result in a 5% FWER or FDR in the returned data.
<b>Adjustment</b>	Error rate correction method used. For something other than the default BH correction with FWER/FDR = 0.05, select an adjustment procedure from the drop-down list and input the overall error rate in the FWER/FDR field above.
<b>Gene Names Column</b>	Select the column containing gene names from the drop-down list.
<b>First Factor</b>	Experimental condition having several levels, potentially in an ordered group with baseline. Example: time is the factor, t0, t1, t2, t3, t4 are the levels and they may be investigated in sequential

	<p>order with a baseline of t0.</p> <p>The first factor affecting the results of the experiment can be set to time, age, or other type of differentiating factors.</p>
<b>Baseline Level</b>	<p>Compares the levels of the chosen <b>Factor</b> to the <b>Baseline Level</b> selected. This is commonly used in a time course or concentration series experiment in which levels of a <b>Factor</b> representing the different time points are contrasted against the <b>Baseline Level</b> as the initial time point (or any other reference time point). For example, if a factor time had levels (t0, t1, t2, t3) and t0 was chosen as baseline level, the contrasts would be t1-t0, t2-t0, t3-t0, i.e., the differences between baseline and each subsequent time. The contrast analysis identifies genes that are differentially expressed at each particular time point compared to baseline. These differentially expressed genes for each contrast provide visibility into the biological sequence of events across the time course.</p>
<b>Sequential</b>	<p>Compares levels of the chosen factor in sequential ordered pairs. For example, if a factor time had levels (t0, t1, t2, t3), the contrasts would be t1-t0, t2-t1, t3-t2. These contrasts also provide systematic view of differential expression over the time course or factor levels. The choice of Sequential vs. Baseline may depend on whether a true baseline condition was run and/or the interpretive goals of the experiment.</p>
<b>Linear/Quadratic Order</b>	<p>Fits linear and quadratic contrasts across the (ordered) levels of the chosen factor. This analysis identifies genes that exhibit (a) a significant linear trend in either the positive (up) or negative (down) direction; and (b) a significant quadratic trend in either the positive (down in the middle) or negative (up in the middle) direction.</p>
<b>None</b>	<p>Select this option if you do not wish to use any second factor.</p>
<b>Second Factor</b>	<p>Second experimental condition to be used in testing, such as Sample type (Levels: Male and Female).</p>
<b>Apply Contrasts: Within Second</b>	<p>Contrasts may be applied either Within or Across the second factor. For example, if there are two sexes (M, F) tested at each of the 4 time points mentioned above, i.e., (t0, t1, t2, t3), testing the time contrasts vs. baseline Within the Sex factor would result in the comparisons (t1-t0, t2-t0, t3-t0) for each of the 2 sexes. Testing the time contrasts vs. baseline Across the Sex factor would result in just one set of comparisons (t1-t0, t2-t0, t3-t0) averaged across the 2 sexes. Similarly if Sex was chosen as the contrast factor, testing the Sex contrast Within the Time factor would result in the comparisons (M-F at t0, M-F at t1, M-F at t2, M-F at t3); and testing the Sex contrast Across the Time factor would result in a single sex comparison M-F.</p>
<b>Apply Contrasts: Across Second</b>	<p>See Apply Contrasts: Within Second above.</p>

► **To reach the Multifactor ANOVA dialog:**

Select **Data > Differential Expression Testing > Multifactor ANOVA...**

### 7.10.3.2 Two-Channel Multifactor ANOVA Dialog

Option	Description
<b>FWER/FDR</b>	Allows you to set the family-wise error rate (FWER) or false discovery rate (FDR) to maintain an overall Type I error rate (false positive rate) based on adjusting individual test p-values to account for multiple tests. For example, setting this to 0.05 will result in a 5% FWER or FDR in the returned data.
<b>Adjustment</b>	Error rate correction method used. For something other than the default BH correction with FWER/FDR = 0.05, select an adjustment procedure from the drop-down list and input the overall error rate in the FWER/FDR field above.
<b>Reference Design Response</b>	Here you can choose to analyze either the difference (M) or the average (A) of the two channels in a 2-channel experiment.
<b>Gene Names Column</b>	Select the column containing gene names from the drop-down list.
<b>First Factor</b>	Experimental condition having several levels, potentially in an ordered group with baseline. Example: time is the factor, t0, t1, t2,

	<p>t3, t4 are the levels and they may be investigated in sequential order with a baseline of t0.</p> <p>The first factor affecting the results of the experiment can be set to time or other type of differentiating factors.</p>
<b>Baseline Level</b>	<p>Compares the levels of the chosen <b>Factor</b> to the <b>Baseline Level</b> selected. This is commonly used in a time course or concentration series experiment in which levels of a <b>Factor</b> representing the different time points are contrasted against the <b>Baseline Level</b> as the initial time point (or any other reference time point). For example, if a factor time had levels (t0, t1, t2, t3) and t0 was chosen as baseline level, the contrasts would be t1-t0, t2-t0, t3-t0 i.e. the differences between baseline and each subsequent time. The contrast analysis identifies genes that are differentially expressed at each particular time point compared to baseline. These differentially expressed genes for each contrast provide visibility into the biological sequence of events across the time course.</p>
<b>Sequential</b>	<p>Compares levels of the chosen factor in sequential ordered pairs. For example, if a factor time had levels (t0, t1, t2, t3), the contrasts would be t1-t0, t2-t1, t3-t2. These contrasts also provide systematic view of differential expression over the time course or factor levels. The choice of Sequential vs. Baseline may depend on whether a true baseline condition was run and/or the interpretive goals of the experiment.</p>
<b>Linear/Quadratic Order</b>	<p>Fits linear and quadratic contrasts across the (ordered) levels of the chosen factor. This analysis identifies genes that exhibit (a) a significant linear trend in either the positive (up) or negative (down) direction; and (b) a significant quadratic trend in either the positive (down in the middle) or negative (up in the middle) direction.</p>
<b>None</b>	<p>Select this option if you do not wish to use any second factor.</p>
<b>Second Factor</b>	<p>Second experimental condition to be used in testing, such as Gender (Levels: Male and Female).</p>
<b>Apply Contrasts: Within Second</b>	<p>Contrasts may be applied either Within or Across the second factor. For example, if there are two sexes (M, F) tested at each of the 4 time points mentioned above, i.e., (t0, t1, t2, t3), testing the time contrasts vs. baseline Within the Sex factor would result in the comparisons (t1-t0, t2-t0, t3-t0) for each of the 2 sexes. Testing the time contrasts vs. baseline Across the Sex factor would result in just one set of comparisons (t1-t0, t2-t0, t3-t0) averaged across the 2 sexes. Similarly if Sex was chosen as the contrast factor, testing the Sex contrast Within the Time factor would result in the comparisons (M-F at t0, M-F at t1, M-F at t2, M-F at t3); and testing the Sex contrast Across the Time factor would result in a single sex comparison M-F.</p>
<b>Apply Contrasts: Across Second</b>	<p>See Apply Contrasts: Within Second above.</p>

► **To reach the Two-Channel Multifactor ANOVA dialog:**  
 Select **Data > Differential Expression Testing > Multifactor ANOVA...**

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## 7.11 Normalization

### 7.11.1 Normalization Overview

This tool allows you to normalize your data in various ways and to do fold change calculations. The normalized data are added as new columns to the data set. The original data columns are not affected.

### 7.11.2 Using Normalization

#### 7.11.2.1 Normalizing by Mean

► **To normalize by mean:**

1. Select **Data > Normalization...**  
Response: The Normalization: step 1(2) dialog is opened.
2. Click **Normalize by mean**.
3. Click **Next >**.  
Response: The Normalization: step 2(2) dialog is opened.
4. Select the **Value columns** on which to perform the calculations.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns or click one column and drag to select the following.
5. Click a radio button to select whether to work on **All records** or **Selected records**.
6. Select a method to **Replace empty values with** from the drop-down list.  
Comment: Constant allows you to replace the empty values by any constant (type a number in the text box). Row average replaces the value by the average value of the entire row. Row interpolation sets the missing value to the interpolated value between the two neighboring values in the row.
7. In the lower section of the dialog, select a **Baseline variable for rescaling**.  
Comment: You can specify one of the variables in the records as baseline variable. Select None if you do not want to use a baseline variable.
8. Select the **Overwrite existing columns** check box if you want to overwrite the last data columns added using this normalization method.  
Comment: Make sure Overwrite existing columns is cleared if you do not want to overwrite.
9. Click a radio button to select whether to Calculate mean from **All genes** or **Genes from Portfolio...**  
Comment: If you select Genes from Portfolio... this will open the Portfolio dialog where you can choose a number of records or lists to calculate mean from. Choose a list and click **OK** to go back to the Normalization dialog.
10. Click **Finish**.  
Response: Columns with normalized data are added to the data set. The number of new columns depends on the format of your original data.

#### 7.11.2.2 Normalizing by Percentile

► **To normalize by percentile:**

1. Select **Data > Normalization...**  
Response: The Normalization: step 1(2) dialog is opened.
2. Click **Normalize by percentile**.
3. Click **Next >**.

- Response: The Normalization: step 2(2) dialog is opened.
4. Select the **Value columns** on which to perform the calculations.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns or click one column and drag to select the following.
  5. Click a radio button to select whether to work on **All records** or **Selected records**.
  6. Select a method to **Replace empty values with** from the drop-down list.  
Comment: Constant allows you to replace the empty values by any constant (type a number in the text box). Row average replaces the value by the average value of the entire row. Row interpolation sets the missing value to the interpolated value between the two neighboring values in the row.
  7. Select a **Baseline variable for rescaling**.  
Comment: You can specify one of the variables in the records as baseline variable. Select None if you do not want to use a baseline variable.
  8. Enter a **Percentile**.  
Comment: For example, the 70-percentile (70th percentile) is the value that 70 % of all values are less than or equal to.
  9. Select the **Overwrite existing columns** check box if you want to overwrite the last data columns added using this normalization method.  
Comment: Make sure Overwrite existing columns is cleared if you do not want to overwrite.
  10. Click a radio button to select whether to Calculate percentile from **All genes** or **Genes from Portfolio...**  
Comment: If you select Genes from Portfolio... this will open the Portfolio dialog where you can choose a number of records or lists to calculate percentile from. Choose a list and click **OK** to go back to the Normalization dialog.
  11. Click **Finish**.  
Response: Columns with normalized data are added to the data set. The number of new columns depends on the format of your original data.

### 7.11.2.3 Normalizing by Trimmed Mean

#### ► To normalize by trimmed mean:

1. Select **Data > Normalization...**  
Response: The Normalization: step 1(2) dialog is opened.
2. Click **Normalize by trimmed mean**.
3. Click **Next >**.  
Response: The Normalization: step 2(2) dialog is opened.
4. Select the **Value columns** on which to perform the calculations.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns or click one column and drag to select the following.
5. Click a radio button to select whether to work on **All records** or **Selected records**.
6. Select a method to **Replace empty values with** from the drop-down list.  
Comment: Constant allows you to replace the empty values by any constant (type a number in the text box). Row average replaces the value by the average value of the entire row. Row interpolation sets the missing value to the interpolated value between the two neighboring values in the row.
7. In the lower section of the dialog, select a **Baseline variable for rescaling**.  
Comment: Select **None** if you do not want to use a baseline variable.
8. Enter a **Trim value**.  
Comment: If you enter a trim value of 20 %, the highest 10 % and the lowest 10 % of the values will be excluded when calculating the mean.

9. Select the **Overwrite existing columns** check box if you want to overwrite the last data columns added using this normalization method.  
Comment: Make sure Overwrite existing columns is cleared if you do not want to overwrite.
10. Click a radio button to select whether to Calculate trimmed mean from **All genes** or **Genes from Portfolio...**  
Comment: If you select Genes from Portfolio... this will open the Portfolio dialog where you can choose a number of records or lists to calculate trimmed mean from. Choose a list and click **OK** to go back to the Normalization dialog.
11. Click **Finish**.  
Response: Columns with normalized data are added to the data set. The number of new columns depends on the format of your original data.

### 7.11.2.4 Other Normalization Methods

This procedure describes how to normalize data by Scaling between 0 and 1, Subtracting the mean or Subtracting the median.

#### ► To normalize using other normalization measures:

1. Select **Data > Normalization...**  
Response: The Normalization: step 1(2) dialog is opened.
2. Select the corresponding radio button: **Scale between 0 and 1**, **Subtract the mean** or **Subtract the median**.  
Comment: For more information about the various methods, see Normalization methods overview.
3. Click **Next >**.  
Response: The Normalization: step 2(2) dialog is opened.
4. Select the **Value columns** on which to perform the calculations.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns or click one column and drag to select the following.
5. Click a radio button to select whether to work on **All records** or **Selected records**.
6. Select a method to **Replace empty values with** from the drop-down list.  
Comment: Constant allows you to replace the empty values by any constant (type a number in the text box). Row average replaces the value by the average value of the entire row. Row interpolation sets the missing value to the interpolated value between the two neighboring values in the row.
7. Select the **Overwrite existing columns** check box if you want to overwrite the last data columns added using the selected normalization method.  
Comment: Make sure Overwrite existing columns is cleared if you do not want to overwrite.
8. Click **Finish**.  
Response: Columns with normalized data are added to the data set. The number of new columns depends on the format of your original data.

### 7.11.2.5 Calculating Fold Change

This procedure shows you how to calculate fold change as *Signed ratio*, as *Log ratio* or as *Log ratio in standard deviation units*.

#### ► To calculate fold change:

1. Select **Data > Normalization...**  
Response: The Normalization: step 1(2) dialog is opened.

2. Select the corresponding radio button **Fold change as signed ratio**, **Fold change as log ratio** or **Fold change as log ratio in std dev units**.  
Comment: For more information about the various methods, see Normalization methods overview.
3. Click **Next >**.  
Response: The Normalization: step 2(2) dialog is opened.
4. Select the **Value columns** on which to perform the calculations.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns or click one column and drag to select the following.
5. Click a radio button to select whether to work on **All records** or **Selected records**.
6. Select a method to **Replace empty values with** from the drop-down list.  
Comment: **Constant** allows you to replace the empty values by any constant (type a number in the text box). **Row average** replaces the value by the average value of the entire row. **Row interpolation** sets the missing value to the interpolated value between the two neighboring values in the row.
7. In the lower part of the dialog, select a **Baseline variable for rescaling**.  
Comment: You can specify one of the variables in the profiles as baseline variable. Select *None* if you do not want to use a baseline variable.
8. Select the check box **Truncate values below** to set all values that lie below the entered truncation value to that specific value.  
Comment: The truncation takes place before any calculation is made and the truncated values are used for the computation.
9. Select the **Overwrite existing columns** check box if you want to overwrite the last data columns added using the selected method.  
Comment: Make sure Overwrite existing columns is cleared if you do not want to overwrite.
10. Click **Finish**.  
Response: Columns with normalized data are added to the data set. The number of new columns depends on the format of your original data.

### 7.11.2.6 Calculating Z-score

► **To calculate z-score:**

1. Select **Data > Normalization...**.  
Response: The Normalization: step 1(2) dialog is opened.
2. Click **Z-score calculation**.
3. Click **Next >**.  
Response: The Normalization: step 2(2) dialog is opened.
4. Select the **Value columns** on which to perform the calculations.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns or click one column and drag to select the following.
5. Click a radio button to select whether to work on **All records** or **Selected records**.
6. Select a method to **Replace empty values with** from the drop-down list.  
Comment: **Constant** allows you to replace the empty values by any constant (type a number in the text box). **Row average** replaces the value by the average value of the entire row. **Row interpolation** sets the missing value to the interpolated value between the two neighboring values in the row.
7. Select the **Overwrite existing columns** check box if you want to overwrite the last data columns added using the selected method.  
Comment: Make sure Overwrite existing columns is cleared if you do not want to overwrite.

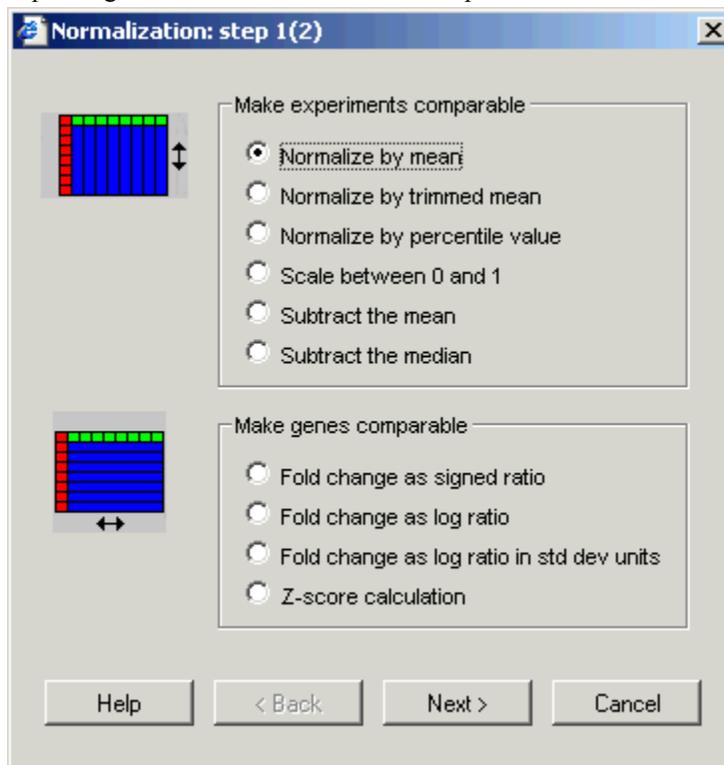
8. Select the **Add mean column** check box if you want to add a column with the mean of each record.
9. Select the **Add standard deviation column** check box if you want to add a column with the standard deviation of each record.
10. Select the **Add coef. of variation column** check box if you want to add a column with the coefficient of variation for each record.
11. Click **Finish**.

Response: Columns with normalized data are added to the data set. The number of new columns depends on the format of your original data.

## 7.11.3 User Interface

### 7.11.3.1 Normalization step 1(2): Dialog

In the first Normalization dialog the method of normalization is set. The second dialog varies depending on the chosen method in this step.



Option	Description
Next >	Opens the Normalization: step2(2) dialog. The user interface of that dialog will depend on what normalization method you choose here: Normalization by mean Normalization by trimmed mean Normalization by percentile value Normalization using other normalization methods Normalization by fold change (three different types) Normalization by z-score

► **To reach the Normalization dialog:**

Select **Data > Normalization...**

### 7.11.3.2 Normalization step 2(2): Fold Change

If **Fold change** (as signed ratio, as log ratio, or as log ratio in std dev units) was chosen in the first Normalization dialog, the following options become available.

The dialog options are identical for each of the three methods for calculating fold change: Signed ratio, Log ratio and Log ratio in standard deviation units. The picture shows the dialog for Signed ratio.

Option	Description
<b>Value columns</b>	The data columns that you want to normalize. Click a column name in the list to select it. To select more than one column, press <b>Ctrl</b> and click the column names in the list. You can choose from all columns that contain reals or integers.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.

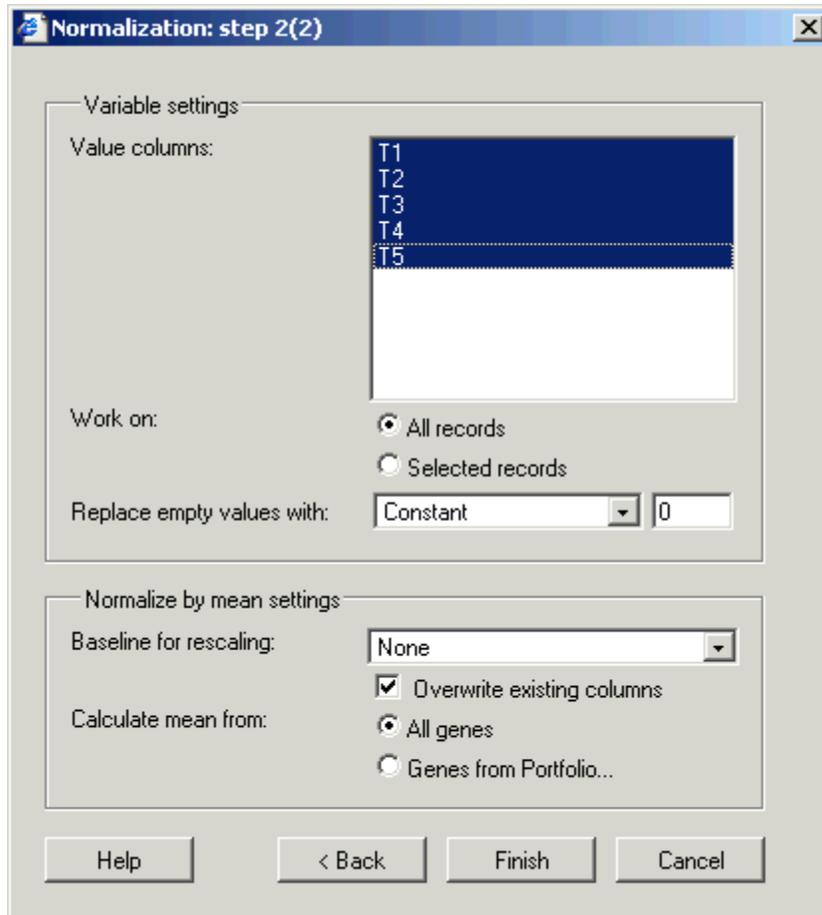
<b>Replace empty values with</b>	Defines how empty values in the data set should be replaced in the calculation. <b>Constant</b> allows you to replace the empty values by any constant (type a number in the text box). <b>Row average</b> replaces the value by the average value of the entire row. <b>Row interpolation</b> sets the missing value to the interpolated value between the two neighboring values in the row.
<b>Baseline variable</b>	You can specify one of the variables in the records as baseline variable. All values will then be multiplied with the mean of the baseline variable after they have been divided by their own mean. The values of the baseline variable are thereby unaltered.
<b>Truncate values below</b>	Select this check box to set all values that lie below the entered truncation value to that specific value. The truncation takes place before any calculation is made and the truncated values are used for the computation.
<b>Overwrite existing columns</b>	Select this check box if you want to replace previously added columns from this type of normalization. Clear the check box if you wish to keep the old column.
<b>Calculate Fold change from: All genes</b>	The only available option. Fold change is always calculated on all records.

► **To reach the Normalization: step2(2) dialog:**

Select **Data > Normalization...** This brings up the Normalization: step1(2) dialog. Then click the appropriate radio button and **Next >**.

### 7.11.3.3 Normalization step 2(2): Mean

If **Normalization by mean** was chosen in the first Normalization dialog, the following options become available.



Option	Description
<b>Value columns</b>	The data columns that you want to normalize. Click a column name in the list to select it. To select more than one column, press <b>Ctrl</b> and click the column names in the list. You can choose from any column that contains reals or integers.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Replace empty values with</b>	Defines how empty values in the data set should be replaced in the calculation. <b>Constant</b> allows you to replace the empty values by any constant (type a number in the text box). <b>Row average</b> replaces the value by the average value of the entire row. <b>Row interpolation</b> sets the missing value to the interpolated value between the two neighboring values in the row.
<b>Baseline for rescaling</b>	You can specify one of the variables in the records as baseline variable. All values will then be multiplied with the mean of the baseline variable after they have been divided by their own mean. The values of the baseline variable are thereby unaltered.
<b>Overwrite</b>	Select this check box if you want to replace previously added columns

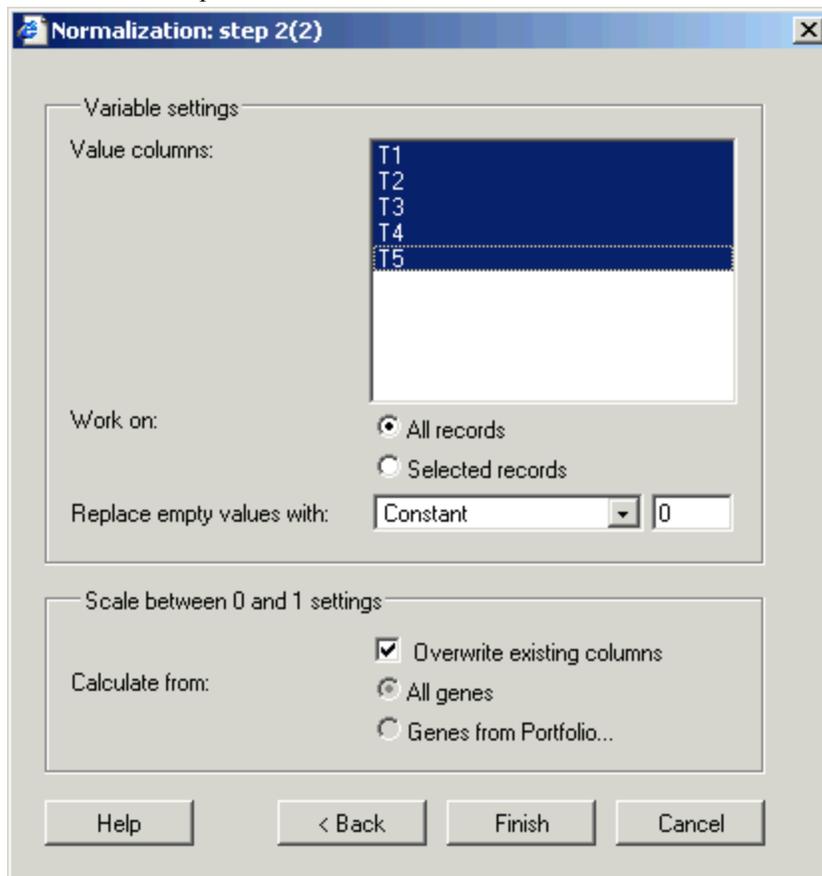
<b>existing columns</b>	from this type of normalization. Clear the check box if you wish to keep the old column.
<b>Calculate mean from: All genes</b>	Click this radio button to use the mean of all records in the normalization.
<b>Calculate mean from: Genes from Portfolio...</b>	Click this radio button to bring up the Portfolio dialog with the current content of the Portfolio. Select the records to use from any portfolio list.

► **To reach the Normalization: step2(2) mean dialog:**

Select **Data > Normalization...** This brings up the Normalization: step1(2) dialog. Then click the **Normalize by mean** radio button and **Next >**.

### 7.11.3.4 Normalization step 2(2): Other Normalization Methods

If **Scale between 0 and 1**, **Subtract the mean** or **Subtract the median** was chosen in the first Normalization dialog, the following options become available. In the picture below, the **Scale between 0 and 1** option has been selected.



Option	Description
<b>Value columns</b>	The data columns that you want to normalize. Click a column name in the list to select it. To select more than one column, press <b>Ctrl</b> and click the column names in the list. You can choose from all columns that contain reals or integers.
<b>Work on: All</b>	All records in the value columns are included in the calculations.

**records**

**Work on: Selected records** Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.

**Replace empty values with** Defines how empty values in the data set should be replaced in the calculation. **Constant** allows you to replace the empty values by any constant (type a number in the text box). **Row average** replaces the value by the average value of the entire row. **Row interpolation** sets the missing value to the interpolated value between the two neighboring values in the row.

**Overwrite existing columns** Select this check box if you want to replace previously added columns from this type of normalization. Clear the check box if you wish to keep the old column.

**Calculate from: All genes** The only available option.

► **To reach the Normalization: step2(2) dialog:**

Select **Data > Normalization...** This brings up the Normalization: step1(2) dialog. Then click the appropriate radio button and **Next >**.

### 7.11.3.5 Normalization step 2(2): Percentile

If **Normalize by percentile value** was chosen in the first Normalization dialog, the following options become available.

Option	Description
<b>Value columns</b>	The data columns that you want to normalize. Click a column name in the list to select it. To select more than one column, press <b>Ctrl</b> and click the column names in the list. You can choose from all columns that contain reals or integers.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Replace empty values with</b>	Defines how empty values in the data set should be replaced in the calculation. <b>Constant</b> allows you to replace the empty values by any constant (type a number in the text box). <b>Row average</b> replaces the value by the average value of the entire row. <b>Row interpolation</b> sets the missing value to the interpolated value between the two neighboring values in the row.
<b>Baseline for rescaling</b>	You can specify one of the value columns as baseline variable. All values will then be multiplied with the percentile value of the baseline variable after they have been divided by their own percentile value. The values of the baseline variable are thereby unaltered.

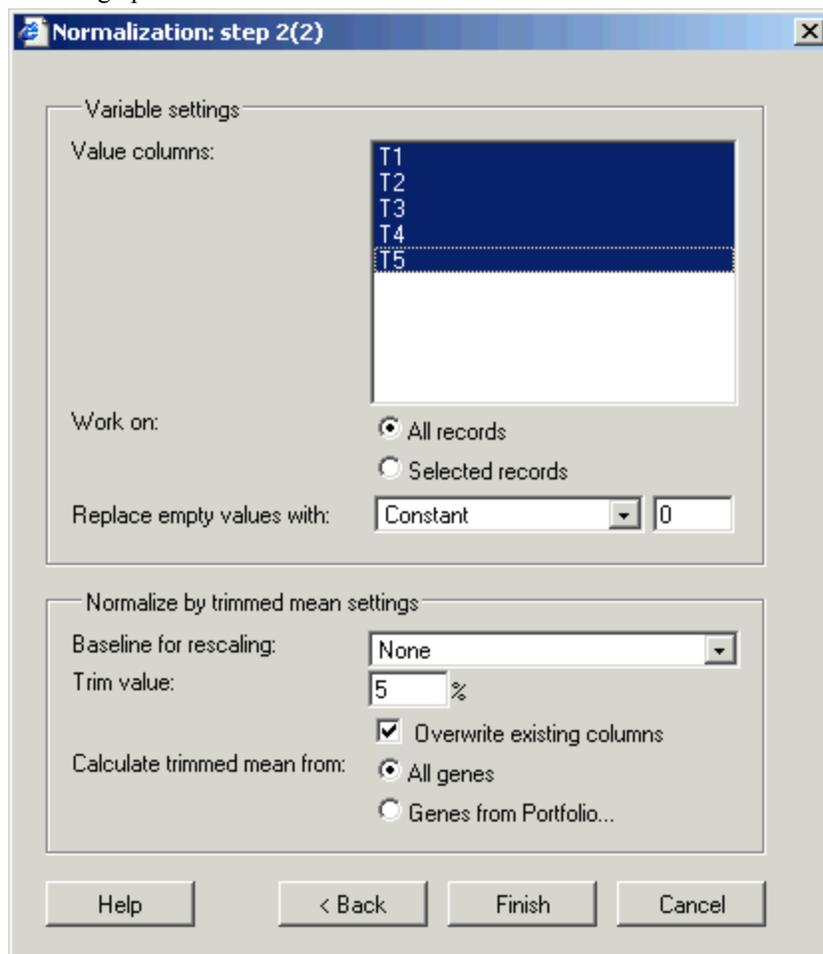
<b>Percentile</b>	The percentile to use. 75 % means that you select the value that 75 % of the values for each variable are less than or equal to.
<b>Overwrite existing columns</b>	Select this check box if you want to replace previously added columns from this type of normalization. Clear the check box if you wish to keep the old column.
<b>Calculate percentile value from: All genes</b>	Click this radio button to use the percentile value of all records in the normalization.
<b>Calculate percentile value from: Genes from Portfolio...</b>	Click this radio button to bring up the Portfolio dialog with the current content of the Portfolio. Select the records to use from any portfolio list.

► **To reach the Normalization: step2(2) percentile dialog:**

Select **Data > Normalization...**. This brings up the Normalization: step1(2) dialog. Then click the **Normalize by percentile** radio button and **Next >**.

### 7.11.3.6 Normalization step 2(2): Trimmed Mean

If **Normalization by trimmed mean** was chosen in the first Normalization dialog, the following options become available.



Option	Description
<b>Value columns</b>	The data columns that you want to normalize. Click a column name in

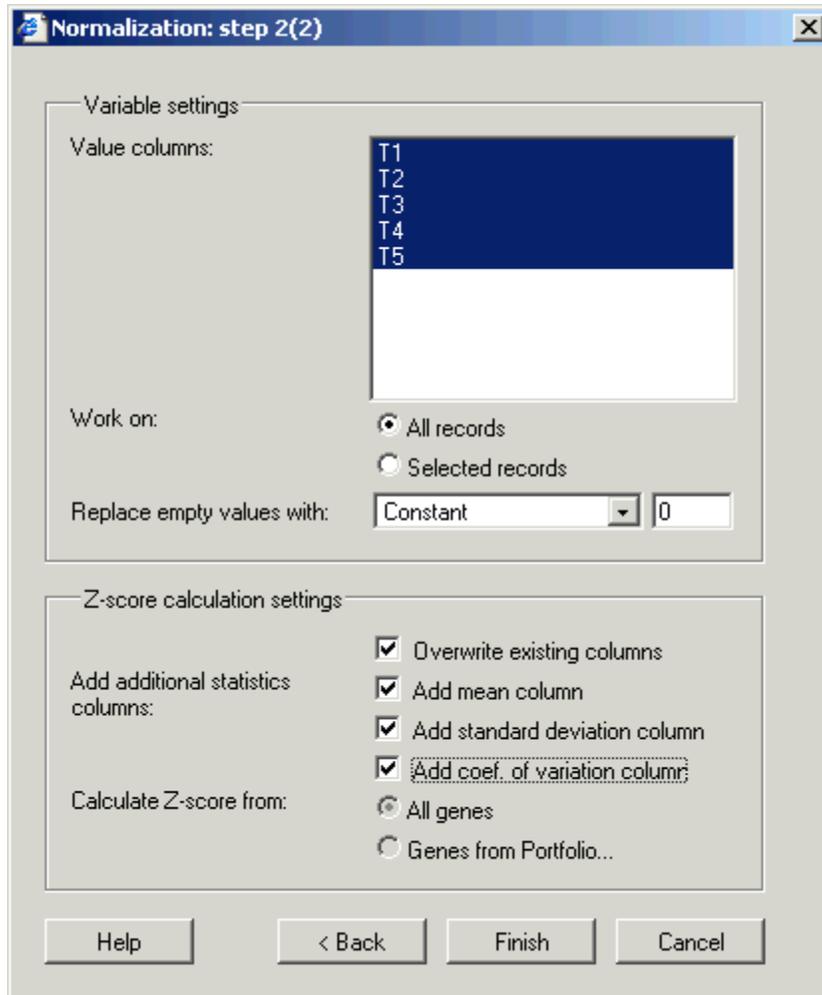
	the list to select it. To select more than one column, press <b>Ctrl</b> and click the column names in the list. You can choose from all columns that contain reals or integers.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Replace empty values with</b>	Defines how empty values in the data set should be replaced in the calculation. <b>Constant</b> allows you to replace the empty values by any constant (type a number in the text box). <b>Row average</b> replaces the value by the average value of the entire row. <b>Row interpolation</b> sets the missing value to the interpolated value between the two neighboring values in the row.
<b>Baseline for rescaling</b>	You can specify one of the value columns as baseline variable. All values will then be multiplied with the trimmed mean of the baseline variable after they have been divided by their own trimmed mean. The values of the baseline variable are thereby unaltered.
<b>Trim value</b>	This percentage of the profiles is removed before the mean is calculated. 10 % means that the highest 5 % of the values and the lowest 5 % of the values are excluded from the calculated mean.
<b>Overwrite existing columns</b>	Select this check box if you want to replace previously added columns from this type of normalization. Clear the check box if you wish to keep the old column.
<b>Calculate trimmed mean from: All genes</b>	Click this radio button to use the trimmed mean of all records in the normalization.
<b>Calculate trimmed mean from: Genes from Portfolio...</b>	Click this radio button to bring up the Portfolio dialog with the current content of the Portfolio. Select the records to use from any portfolio list.

► **To reach the Normalization: step2(2) trimmed mean dialog:**

Select **Data > Normalization...** This brings up the Normalization: step1(2) dialog. Then click the **Normalize by trimmed mean** radio button and **Next >**.

### 7.11.3.7 Normalization step 2(2): Z-score

If **Z-score calculation** was chosen in the first Normalization dialog, the following options become available.



Option	Description
<b>Value columns</b>	The data columns that you want to normalize. Click a column name in the list to select it. To select more than one column, press <b>Ctrl</b> and click the column names in the list. You can choose from all columns that contain reals or integers.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Replace empty values with</b>	Defines how empty values in the data set should be replaced in the calculation. <b>Constant</b> allows you to replace the empty values by any constant (type a number in the text box). <b>Row average</b> replaces the value by the average value of the entire row. <b>Row interpolation</b> sets the missing value to the interpolated value between the two neighboring values in the row.
<b>Overwrite existing columns</b>	Select this check box if you want to replace previously added columns from this type of normalization. Clear the check box if you wish to keep the old column.

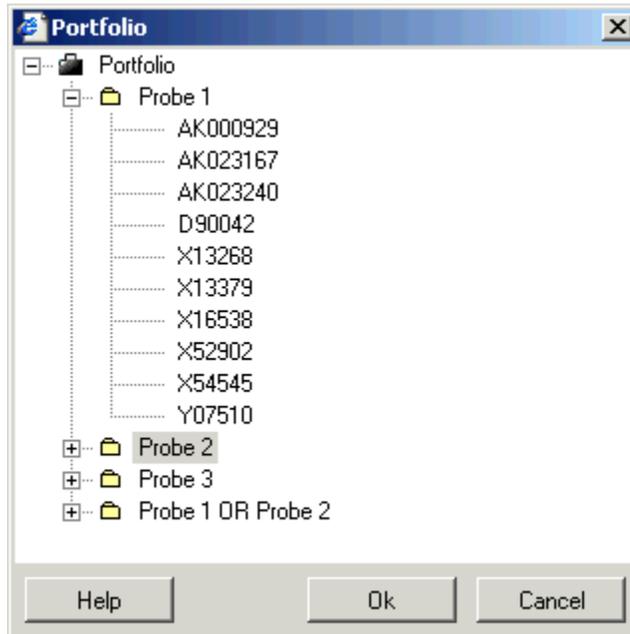
<b>Add mean column</b>	Adds a column with the mean of each record to the data set.
<b>Add standard deviation column</b>	Adds a column with the standard deviation of each record to the data set.
<b>Add coef. of variation column</b>	Adds a column with the coefficient of variation (the standard deviation divided by the mean) for each record to the data set.
<b>Calculate Z-score from: All genes</b>	The only available option. Z-score is always calculated using all records.

► **To reach the Normalization: step2(2) z-score dialog:**

Select **Data > Normalization...**. This brings up the Normalization: step1(2) dialog. Then click the **Z-score calculation** radio button and **Next >**.

### 7.11.3.8 Normalization Portfolio Dialog

It is possible to use the means of genes (records) from a selected list in your current Portfolio in the normalization calculation. This is done by clicking the Calculate mean from: Genes in Portfolio...radio button and selecting a list from the Portfolio.



Option	Description
<b>Portfolio</b>	Click to select the list or records that you are interested in. For multiple selection, press <b>Ctrl</b> and click on the desired records. You can toggle the display of subtrees in the Portfolio by clicking the plus (+) and minus (-) signs to the left of any list icon.

► **To reach the Portfolio dialog:**

Select **Data > Normalization...**. In step 2 of the Normalization procedure, when the records to calculate mean from are chosen, click **Genes from Portfolio...**

## 7.11.4 Theory and Methods

### 7.11.4.1 Normalization Methods Overview

The following normalization methods are available in the Normalization module:

- Normalize by mean
- Normalize by trimmed mean
- Normalize by percentile
- Scale between 0 and 1
- Subtract the mean
- Subtract the median
- Fold change as signed ratio
- Fold change as log ratio
- Fold change as log ratio in standard deviation units
- Z-score calculation

### 7.11.4.2 Normalization by Log Ratio

Assume that there are  $n$  records with seven variables, A, B, C, D, E, F and G, in the data view. We use variable E as an example in the expressions. All target variables are normalized in the same way.

If we select A as baseline variable the normalized value of  $e_i$  for variable E in the  $i^{\text{th}}$  record is calculated as

$$\text{Normalized } (e_i) = \log \frac{e_i}{a_i}$$

where

$a_i$  = the value for variable A in the  $i^{\text{th}}$  record

### 7.11.4.3 Normalization by Log Ratio in Standard Deviation Units

Assume that there are  $n$  records with  $k$  variables, A, B, C, D, E, F and G, in the data view. We use variable E as an example in the expressions. All target variables are normalized in the same way.

If we select A as baseline variable the normalized value of  $e_i$  for variable E in the  $i^{\text{th}}$  record is calculated as

$$\text{Normalized } (e_i) = \frac{1}{\text{std}(x)} \log \frac{e_i}{a_i}$$

where

$$\text{std}(x) = \sqrt{\frac{1}{n} \frac{1}{(k-1)} \sum_{i=1}^n \sum_{j=1}^{k-1} (x_{ij} - \bar{x})^2}$$

$$\bar{x} = \frac{1}{n} \frac{1}{(k-1)} \sum_{i=1}^n \sum_{j=1}^{k-1} x_{ij}$$

$x$  = a matrix that consists of the logarithm of the ratio of all original values and the baseline variable for the corresponding record. In other words the value for variable E in the  $i^{\text{th}}$  record in the matrix is equal to  $\log(e_i/a_i)$ . The matrix includes all variables except the baseline variable and therefore has the dimension  $n$  records times  $(k-1)$  variables.

### 7.11.4.4 Normalization by Mean

Assume that there are  $n$  records with seven variables, A, B, C, D, E, F and G, in the data view. We use variable E as an example in the expressions. The remaining variables in the records are normalized in the same way.

#### Without rescaling (Baseline variable = None)

The normalized value of  $e_i$  for variable E in the  $i^{\text{th}}$  record is calculated as

$$\text{Normalized } (e_i) = \frac{e_i}{\frac{1}{p} \sum_{j=1}^p e_j}$$

where

$p$  = the number of records that are used to calculate the mean

#### Rescaling by a baseline variable

If we select variable A as baseline variable, the normalized value of  $e_i$  for variable E in the  $i^{\text{th}}$  record is calculated as

$$\text{Normalized } (e_i) = \frac{e_i \cdot \frac{1}{p} \sum_{j=1}^p a_j}{\frac{1}{p} \sum_{j=1}^p e_j}$$

where

$p$  = the number of records that are used to calculate the mean

$a_j$  = the value for variable A in the  $j^{\text{th}}$  record

#### Which records are used to calculate the mean?

In the *Normalization: step 2(2)* dialog you select which records to use for calculating the mean. This choice determines the value of  $p$  in the expressions above. There are two options: *All genes* or *Genes from Portfolio*. In the second option, all records whose ID is present in a specified Portfolio list is used in the calculation.

### 7.11.4.5 Normalization by Percentile

The X-percentile is the value in a data set that X % of the data is less than or equal to. To understand how it is computed in this tool, consider the following two examples:

- Consider a data set with four values [1,3,5,7]. Let  $N$  be the number of values, in this case 4. The index of the 75% percentile is computed as  $0.75 N = 3$ , which means that the 75% percentile is 5.
- Consider a data set with five values [1,3,5,7,9]. The index of the 75% percentile in this case would be 3.75. This is rounded to 4, so that the 75% percentile value in this case is 7.

Assume that there are  $n$  records with seven variables, A, B, C, D, E, F and G, in the data view. We use variable E as an example in the expressions. The remaining variables in the records are normalized in the same way.

#### Without rescaling (Baseline variable = None)

The normalized value of  $e_i$  for variable E in the  $i^{\text{th}}$  record is calculated as

$$\text{Normalized } (e_i) = \frac{e_i}{q_{E,X\%}}$$

where

$q_{E,X\%}$  = the value that X % of the values for variable E, among the selected records, are less than or equal to

X = the percentile value that you specify when you normalize the data

### Rescaling by a baseline variable

If we select variable A as baseline variable, the normalized value of  $e_i$  for variable E in the  $i^{\text{th}}$  record is calculated as

$$\text{Normalized } (e_i) = \frac{e_i \cdot q_{A,X\%}}{q_{E,X\%}}$$

where

$q_{A,X\%}$  = the value that X % of the values for variable A, among the selected records, are less than or equal to

$q_{E,X\%}$  = the value that X % of the values for variable E, among the selected records, are less than or equal to

X = the percentile value that you specify when you normalize the data

### Which records are used to derive the percentile?

In the Normalization: step 2(2) dialog you decide which records to use when deriving the percentile. There are two options: All genes or Genes from Portfolio. In the second option, all records whose ID is present in a specified Portfolio list is used in the calculation.

## 7.11.4.6 Normalization by Trimmed Mean

The trimmed mean for a variable is based on all values except a certain percentage of the lowest and highest values for that variable. This removes the effect of outliers during the normalization. If the trim value is set to 10 % then the highest 5 % of the values and the lowest 5 % of the values are excluded from the calculated mean.

Assume that there are  $n$  records with seven variables, A, B, C, D, E, F and G, in the data view. We use variable E as an example in the expressions. The remaining variables in the records are normalized in the same way.

### Without rescaling (Baseline variable = None)

The normalized value of  $e_i$  for variable E in the  $i^{\text{th}}$  record is calculated as

$$\text{Normalized } (e_i) = \frac{e_i}{\frac{1}{p} \sum_{j \in T} e_j}$$

where

T = the set of records that are left after trimming

p = the number of records in T

### Rescaling by a baseline variable

If we select variable A as baseline variable, the normalized value of  $e_i$  for variable E in the  $i^{\text{th}}$  record is calculated as

$$\text{Normalized } (e_i) = \frac{e_i \cdot \frac{1}{p} \sum_{j \in T} a_j}{\frac{1}{p} \sum_{j \in T} e_j}$$

where

T = the set of records that are left after trimming

p = the number of records in T

$a_j$  = the value for variable A in the  $j^{\text{th}}$  record

### Which records are used to calculate the trimmed mean?

In the Normalization: step 2(2) dialog you select which records to use for calculating the trimmed mean. There are two options: All genes or Genes from Portfolio. In the second option, all records whose ID is present in a specified Portfolio list is used in the calculation. The selected set of records is then trimmed and the remaining set of records is used in the expressions above.

#### 7.11.4.7 Normalization by Scaling Between 0 and 1

Assume that there are  $n$  records with seven variables, A, B, C, D, E, F and G, in the data view. We use variable E as an example in the expressions. The remaining variables in the records are normalized in the same way.

The normalized value of  $e_i$  for variable E in the  $i^{\text{th}}$  record is calculated as

$$\text{Normalized } (e_i) = \frac{e_i - E_{\min}}{E_{\max} - E_{\min}}$$

where

$E_{\min}$  = the minimum value for variable E

$E_{\max}$  = the maximum value for variable E

If all values for variable E are identical, so  $E_{\min}$  is equal to  $E_{\max}$ , then all values for variable E are set to zero.

#### 7.11.4.8 Normalization by Signed Ratio

Assume that there are  $n$  records with seven variables, A, B, C, D, E, F and G, in the data view. We use variable E as an example in the expressions. All target variables are normalized in the same way.

If we select A as baseline variable, the normalized value of  $e_i$  for variable E in the  $i^{\text{th}}$  record is calculated as

$$\text{Normalized } (e_i) = \frac{e_i}{a_i} \quad \text{if } e_i > a_i$$

$$\text{Normalized } (e_i) = -\frac{a_i}{e_i} \quad \text{if } e_i < a_i$$

where

$a_i$  = the value for variable A in the  $i^{\text{th}}$  record

#### 7.11.4.9 Normalization by Subtracting the Mean

Assume that there are  $n$  records with seven variables, A, B, C, D, E, F and G, in the data view. We use variable E as an example in the expressions. The remaining variables in the records are normalized in the same way.

The normalized value of  $e_i$  for variable E in the  $i^{\text{th}}$  record is calculated as

$$\text{Normalized } (e_i) = e_i - \frac{1}{n} \sum_{j=1}^n e_j$$

where

$n$  = the total number of records in the data view

#### 7.11.4.10 Normalization by Subtracting the Median

Assume that there are  $n$  records with seven variables, A, B, C, D, E, F and G, in the data view. We use variable E as an example in the expressions. The remaining variables in the records are normalized in the same way.

The normalized value of  $e_i$  for variable E in the  $i^{\text{th}}$  record is calculated as

$$\text{Normalized } (e_i) = e_i - E_{\text{median}}$$

where

$E_{\text{median}}$  = the median of variable E

The median of a set of values is the middle value when the values are sorted from lowest to highest. If the number of values is even, the median is the average of the two middle values.

### 7.11.4.11 Normalization by Z-score

Assume that there are five records with the IDs A, B, C, D and E, each record containing  $n$  different variables (columns). We use record E as an example in the expressions. The remaining records are normalized in the same way.

The normalized value of  $e_i$  for record E in the  $i^{\text{th}}$  column is calculated as

$$\text{Normalized } (e_i) = \frac{e_i - \bar{E}}{\text{std}(E)}$$

where

$$\text{std}(E) = \sqrt{\frac{1}{n-1} \sum_{i=1}^n (e_i - \bar{E})^2}$$

$$\bar{E} = \frac{1}{n} \sum_{i=1}^n e_i$$

If all values for record E are identical — so the standard deviation of E ( $\text{std}(E)$ ) is equal to zero — then all values for record E are set to zero.

## 7.12 Pivot Data

### 7.12.1 Pivot Data Overview

Pivoting, in its simplest form, means rotating a table. Mostly, though, it also includes performing some form of aggregation, so that the new table is more compact than the original. To better understand how the pivoting tool works, study one of the examples.

### 7.12.2 Using Pivot Data

#### 7.12.2.1 Pivoting the Data Set

► **To pivot the current data set:**

1. Select **Data > Pivot Data...**

Response: The Tall/Skinny => Short/Wide dialog is opened.

2. In the **Identity** list, select one or more columns.

Comment: Each unique value in the chosen column produces a row in the generated table. You can choose more than one column. Doing so means that the new table will have a separate row for *each unique combination* of values in the chosen columns.

3. In the **Category** list, select one or more columns.

Comment: Each unique value in the chosen column produces a new column in the generated table. Selecting more than one column means that the new table will have a separate column for *each unique combination* of values in the chosen columns.

4. In the **Values** list, select one or more columns.

Comment: The column selected under **Values** is the column from which the data is pulled. It is possible to select more than one Value column. The values in the generated table are always computed as the average of values in the original table, unless the original values are strings. If so, values in the generated table will consist of

concatenated strings. To change the way the values are calculated, right-click on the Method and select a different method from the list, or use Ctrl+click to select multiple methods.

- In the **Other Columns** list, select one or more columns.

Comment: This option allows you to include an overall average of a particular measurement, for each row in the generated table. For each column selected here, one new column will be created in the new table. To change the way the measurements are calculated, right-click on the Method and select a different method from the list, or use Ctrl+click to select multiple methods.

- Click **OK**.

### 7.12.2.2 Example of Pivoting

Pivoting a data set means changing it from a tall/skinny format to a short/wide format. Consider the following tall/skinny table, based on a series of temperature measurements:

City	Month	Temp
London	February	4
New York	February	6
London	May	16
New York	May	19
London	August	28
New York	August	26
London	November	13
New York	November	11

As we add more observations, the table grows taller, but remains three columns wide. While useful during data collection, this format may not be appropriate for certain types of calculations or visualizations. For example, the entities that interest us are the different cities, so we may want a representation with a single record for each city.

Tall/Skinny=>Short/Wide conversion lets us pivot this table, producing the following (note that avg(Temp) is the average of a single cell):

City	avg(Temp) for February	avg(Temp) for May	avg(Temp) for August	avg(Temp) for November
London	4	16	28	13
New York	6	19	26	11

Each city is now represented by a single record, which makes this format very suitable for Spotfire DecisionSite profile charts. This example demonstrates three steps:

- Creating a row for each unique value in City.
- Creating a column for each unique value in Month.
- Entering a value from Temp for each cell in the resulting grid.

In the Tall/Skinny => Short/Wide dialog, the following settings would be made:

- Identity: City
- Category: Month

- Values: Temp

### 7.12.2.3 Example of Pivoting with Aggregation

**Note:** To understand this example, it is recommended to read Example of Pivoting first. Apart from changing format from tall/skinny to short/wide, pivoting can be used to create a more compact table. Consider the following table, based on a series of temperature measurements:

City	Month	Day	Temp
London	February	1	5
London	February	15	8
London	May	1	15
London	May	15	22
New York	February	1	9
New York	February	15	7
New York	May	1	18
New York	May	15	24

Tall/Skinny=>Short/Wide conversion lets us pivot and aggregate this table, producing the following:

City	avg(Temp) for February	avg(Temp) for May
London	6.5	18.5
New York	8	21

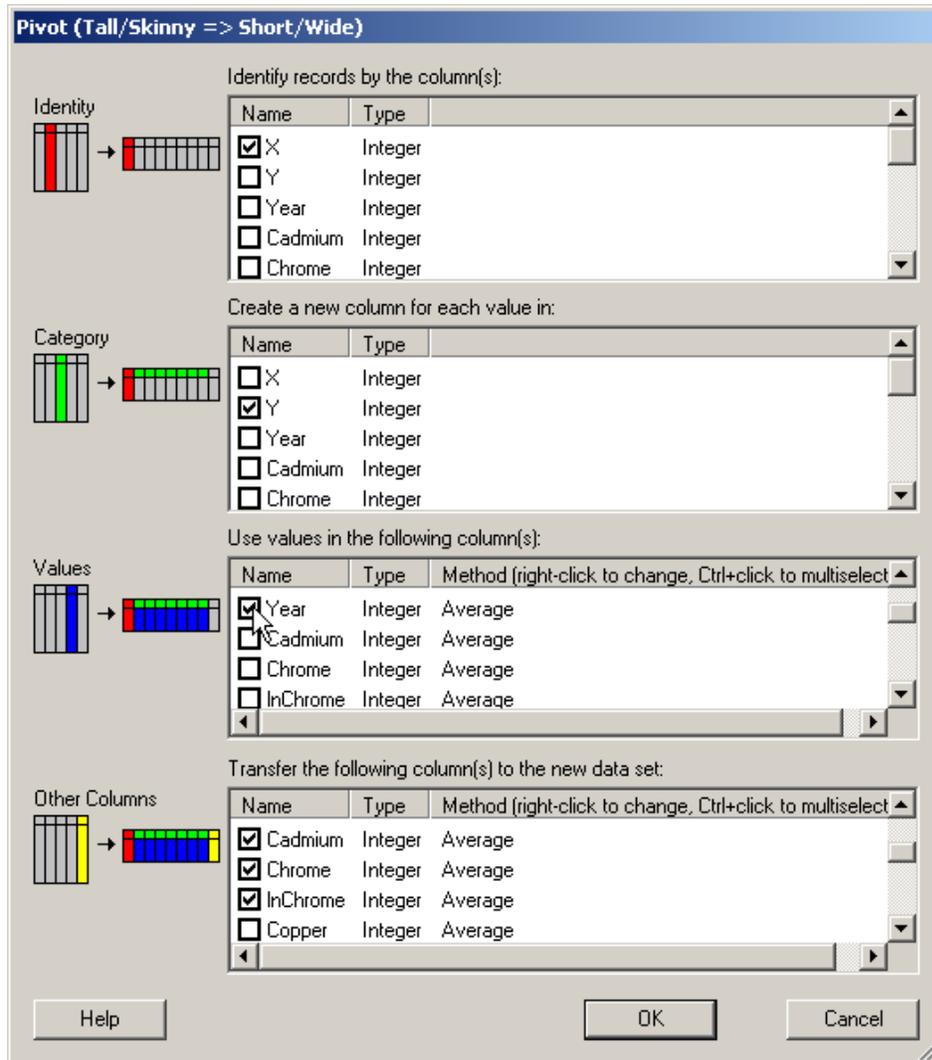
A smaller table has been created, summarizing the original table. In the Tall/Skinny => Short/Wide dialog, the following settings would be made:

- Identity: City
- Category: Month
- Values: Temp

## 7.12.3 User Interface

### 7.12.3.1 The Tall/Skinny => Short/Wide Dialog

This dialog allows you to configure how pivoting is performed.



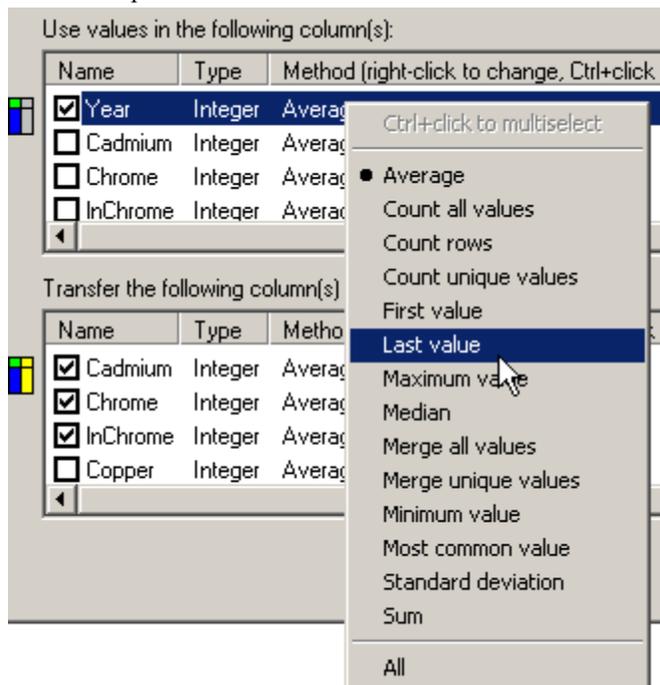
Option	Description
<b>Identity</b>	<p>Each unique value in the chosen column produces a row in the generated table.</p> <p>You can choose more than one column. Doing so means that the new table will have a separate row for <i>each unique combination</i> of values in the chosen columns.</p>
<b>Category</b>	<p>Each unique value in the chosen column produces a new column in the generated table.</p> <p>Selecting more than one column means that the new table will have a separate column for <i>each unique combination</i> of values in the chosen columns.</p>
<b>Values</b>	<p>The column selected under Values is the column from which the data is pulled. It is possible to select more than one Value column.</p> <p>The values in the generated table are always computed as the average of values in the original table, unless the original values are strings. If so, values in the generated table will consist of concatenated strings. To change the way the values are calculated, right-click on the Method and select a different method from the list, or use Ctrl+click to select</p>

multiple methods.

**Other Columns** This option allows you to include an overall average of a particular measurement, for each row in the generated table. For each column selected here, one new column will be created in the new table. To change the way the measurements are calculated, right-click on the Method and select a different method from the list, or use Ctrl+click to select multiple methods.

### Method Selection List

Right-click on the Method to change the method of calculation for your column. Ctrl+click to select multiple methods.



► To reach the Tall/Skinny => Short/Wide dialog:

Select Data > Pivot Data...

## 7.13 Depivot Data

### 7.13.1 Depivot Data Overview

Pivoting, in its simplest form, means rotating a table. While the Pivot Data tool transforms a table from the tall/skinny variant to the short/wide form, the Depivot Data tool does the opposite. While most tools in DecisionSite require that data is short and wide, there may be occasions when you want to view data in a different form, such as a bar chart visualization showing different years on the x-axis.

## 7.13.2 Using Depivot Data

### 7.13.2.1 Depivoting the Data Set

► **To depivot the current data set:**

1. Select **Data > Depivot Data...**  
Response: The Depivot (Short/Wide => Tall/Skinny) dialog is opened.
2. In the **Available columns** list, click to select the columns that you want to transform.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns in the Available columns list. You can sort the columns in the list alphabetically by clicking on the Name bar.
3. Click on the **Add >>** button to send the selected columns to the **Columns to transform** list.  
Comment: These columns should be the ones that contain the actual values and that you want to combine into a new value column. For example, "Sales 2005", "Sales 2004" and "Sales 2003".
4. In the **Available columns** list, click to select the columns that you want to pass through the depivoting process without any transformation.
5. Click on the **Add >>** button to send the selected columns to the **Columns to pass through** list.  
Comment: These columns can contain other categorical information, IDs, etc. For example, "Region", "Name" or "Priority".
6. Type a new **Category column name** in the provided text field.  
Comment: For instance, "Year" could be used when sales figures for several different years are to be combined to a single column.  
Select the data **Type** for the new column from the drop-down list.  
Type a new **Value column name** in the provided text field.  
Comment: For instance, "Sales" containing sales figures for several different years.  
Select the data **Type** for the new column from the drop-down list.
7. Click **OK**.

### 7.13.2.2 Example of Depivoting

Depivoting a data set means changing it from a short/wide format to a tall/skinny format. Consider the following short/wide table, containing sales data for a fictive company:

Name	Region	Sales 2003	Sales 2004	Sales 2005
Connelly	New Jersey	23	22	25
Fallon	New Jersey	34	37	38
Smiths	New York	21	30	32
Bergman	New York	35	35	35
Taylor	Texas	24	23	24
Roberts	Texas	31	30	29
Miller	Texas	29	32	33
Hanegan	Florida	24	26	25

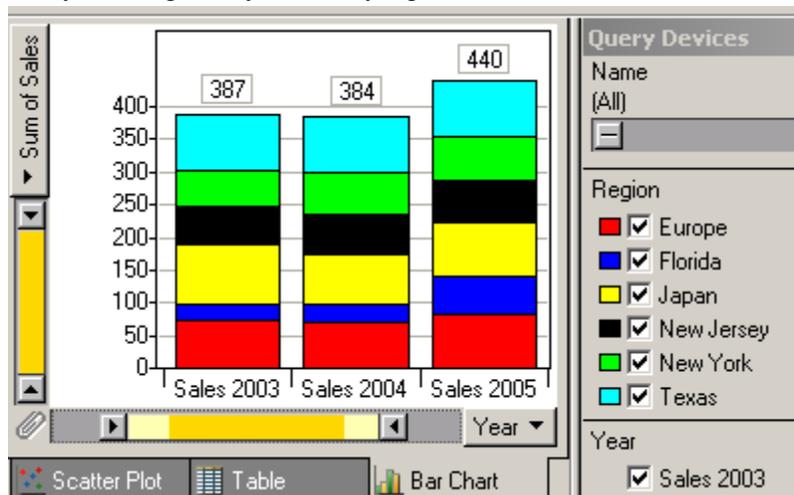
Suzuki	Japan	45	38	39
Takahashi	Japan	47	40	45
Olsen	Europe	26	25	29
Ottosson	Europe	25	24	26
Olsson	Europe	23	22	28
James	Florida			32

If you want to view how the sales figures from the different regions vary during the years in a bar chart, the current format is not always optimal. By depivoting the data set to a tall/skinny format with all sales figures in a single column, you will be able to create a suitable bar chart with minimal effort.

Name	Region	Year	Sales
Connelly	New Jersey	Sales 2003	23
Connelly	New Jersey	Sales 2004	22
Connelly	New Jersey	Sales 2005	25
Fallon	New Jersey	Sales 2003	34
Fallon	New Jersey	Sales 2004	37
Fallon	New Jersey	Sales 2005	38
Smiths	New York	Sales 2003	21
Smiths	New York	Sales 2004	30
Smiths	New York	Sales 2005	32
Bergman	New York	Sales 2003	35
Bergman	New York	Sales 2004	35
Bergman	New York	Sales 2005	35
Taylor	Texas	Sales 2003	24
Taylor	Texas	Sales 2004	23
Taylor	Texas	Sales 2005	24
Roberts	Texas	Sales 2003	31
Roberts	Texas	Sales 2004	30
Roberts	Texas	Sales 2005	29
Miller	Texas	Sales 2003	29
Miller	Texas	Sales 2004	32
Miller	Texas	Sales 2005	33
Hanegan	Florida	Sales 2003	24
Hanegan	Florida	Sales 2004	26

Hanegan	Florida	Sales 2005	25
Suzuki	Japan	Sales 2003	45
Suzuki	Japan	Sales 2004	38
Suzuki	Japan	Sales 2005	39
Takahashi	Japan	Sales 2003	47
Takahashi	Japan	Sales 2004	40
Takahashi	Japan	Sales 2005	45
Olsen	Europe	Sales 2003	26
Olsen	Europe	Sales 2004	25
Olsen	Europe	Sales 2005	29
Ottosson	Europe	Sales 2003	25
Ottosson	Europe	Sales 2004	24
Ottosson	Europe	Sales 2005	26
Olsson	Europe	Sales 2003	23
Olsson	Europe	Sales 2004	22
Olsson	Europe	Sales 2005	28
James	Florida	Sales 2003	
James	Florida	Sales 2004	
James	Florida	Sales 2005	32

The resulting data set can easily be displayed as a bar chart showing the total sum of sales for each year, categorically colored by region:



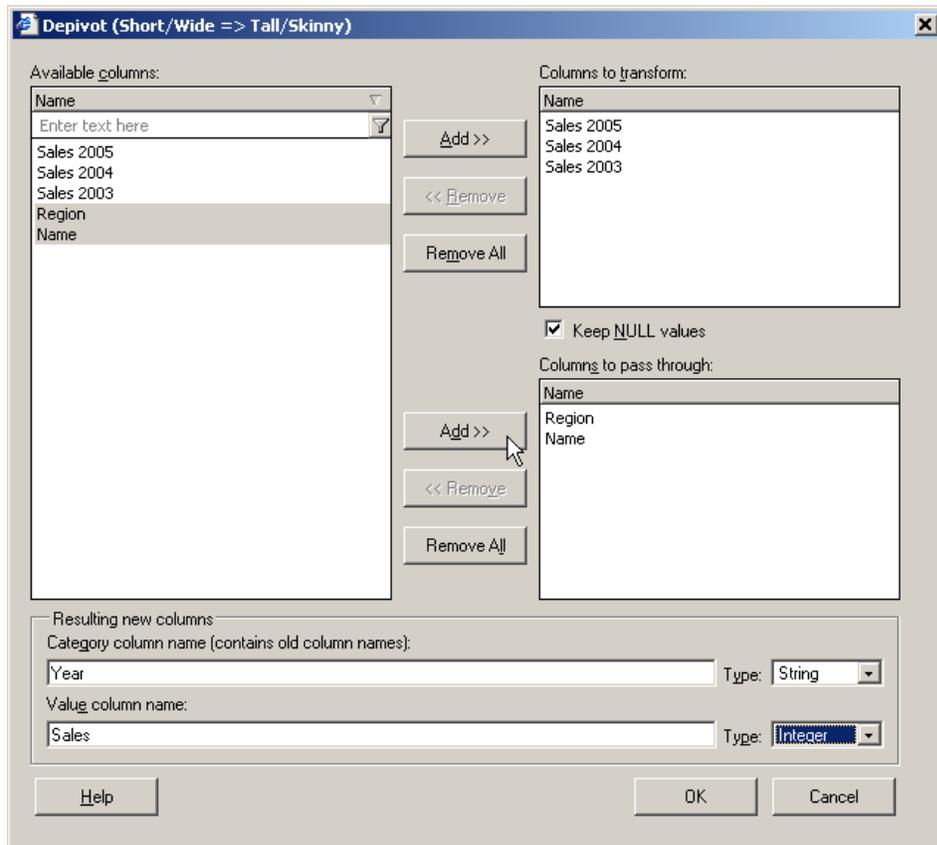
► **How to do it:**

1. Select **Sales 2005**, **Sales 2004** and **Sales 2003** as Columns to transform.
2. Select **Region** and **Name** as Columns to pass through.

3. Type **Year** as the Category column name and make sure String is the selected data type.
4. Type **Sales** as the Value column name and select the data type Integer.
5. Click **OK**.

## 7.13.3 User Interface

### 7.13.3.1 Depivot (Short/Wide => Tall/Skinny) Dialog



Option	Description
<b>Available columns</b>	The columns available for use in the depivot operation. Click a column name in the list to select it. To select more than one column, press <b>Ctrl</b> and click the column names in the list. Use one of the Add >> buttons to send the selected column to either the Columns to transform or Columns to pass through field, see below.
<b>Enter text here</b> 	If you have a data set with many columns, you can right-click on the header of the columns in the Available columns list box and select <b>Show Search Field</b> from the pop-up menu. This will display a search field where you can type a search string and limit the number of items in the list. It is possible to use the wildcard characters * and ? in the search.
<b>Add &gt;&gt;</b>	Moves selected columns from the Available columns field to the field next to the button.

<b>&lt;&lt; Remove</b>	Removes a column and brings it back to the Available columns field.
<b>Remove All</b>	Removes all columns from the selected columns fields.
<b>Columns to transform</b>	The selected columns containing the values that you wish to combine into a single column. The column names of these columns will be used as category values in the resulting new category column. Typically, this might be a number of columns containing the same type of data. For example, sales figures for different years.
<b>Keep NULL values</b>	Select this check box to transfer empty values to the depivoted data view. If the check box is cleared, all records containing empty values will be discarded.
<b>Columns to pass through</b>	The selected columns containing information that should be transferred to the depivoted data set without any transformation. This could be ID columns, categorical information such as Region, Priority etc.
<b>Category column name (contains old column names)</b>	Type a column name that summarize the information provided in the columns that you have selected to transform. For instance, "Year" could be used when sales figures for several different years are to be combined to a single column.
<b>Value column name</b>	Type a column name that shows what type of information is included in the new value column. For instance, "Sales" would be a good name for a column containing sales figures for several different years.
<b>Type</b>	Specify the data type for the respective column. A column containing names should be set to string, whereas a column containing figures should be decimal or integer.

► **To reach the Depivot (Short/Wide => Tall/Skinny) dialog:**

Select **Data > Depivot Data...**

## 7.14 Transpose Data

### 7.14.1 Transpose Data Overview

The Transpose Data tool is used to rotate a data set, so that columns become records and vice versa. Transposing may be necessary if you want to be able to use your data in a certain type of visualization or if you just want to get a better overlook the data.

### 7.14.2 Using Transpose Data

#### 7.14.2.1 Transposing Columns

Transposing a data set means rotating it, so that columns become records and vice versa.

► **To transpose columns:**

1. Select **Data > Transpose Data...**  
Response: The Transpose Data wizard step 1 is opened.
2. Select an identifier column from the drop-down list.  
Comment: Each value in the selected column will become a column name in the transposed data set
3. Select whether to create columns from **All records** or just **Selected records**.

Comment: The transposed data set will have the same number of columns as the number of records selected. The upper limit is 5000.

4. Click **Next** >.
 

Response: Step 2 of the wizard is shown.
5. Select the columns you want to include in the transposed data set, and click **Add** >> .
 

Comment: Each selected column will become a separate record in the transposed data set.
6. Click **Next** >.
 

Response: Step 3 of the wizard is shown.
7. If required, select annotation columns.
 

Comment: Each transposed column will be annotated with the value of this column.
8. Click **Finish**.
 

Response: A message box appears, prompting you to save your previous data set.
9. Click **Yes** to save the previous data set.
 

Response: The new, transposed data set replaces the original data set.

### 7.14.2.2 Example of Transposing

Transposing a data set means rotating it, so that columns become records and vice versa. Consider the following table, describing a series of meteorological observations:

Day	Temperature	Wind	Humidity
Monday	16	5	75
Tuesday	19	8	70
Wednesday	17	10	70
Thursday	24	9	65
Friday	26	2	75
Saturday	27	2	80
Sunday	25	4	80

As we add more observations, the table grows taller, but remains four columns wide. While useful during data collection, this format may not be appropriate for certain types of calculations or visualizations. By transposing this table, the following can be produced:

Transposed columns	Tuesday	Wednesday	Thursday	Friday
Temperature	19	17	24	26
Humidity	70	70	65	75

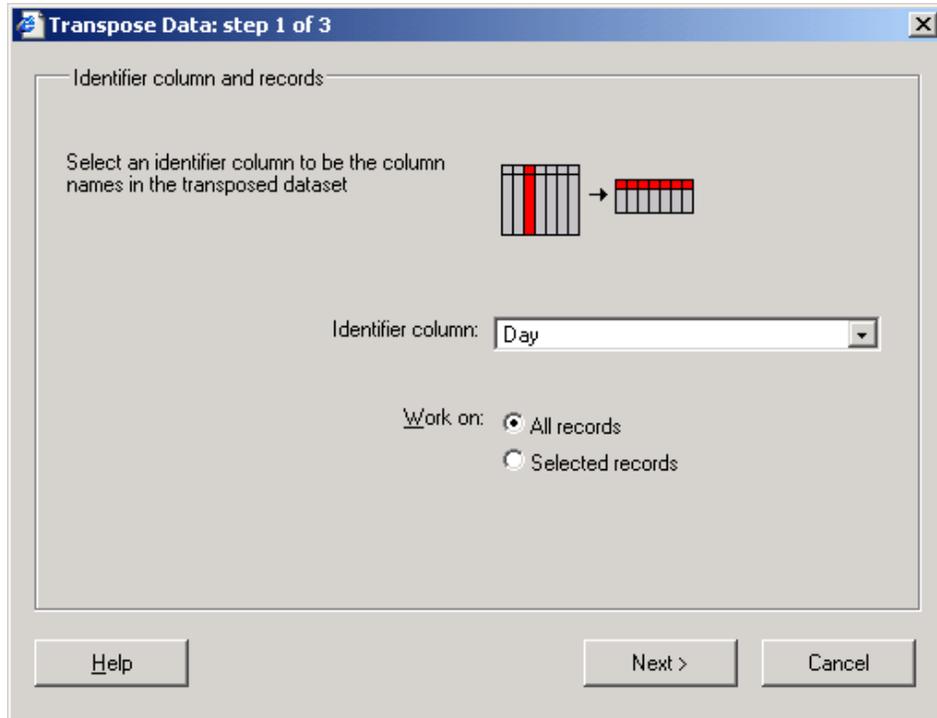
#### ► To produce this result:

1. In a visualization, select (using the query devices) the records Tuesday, Wednesday, Thursday and Friday.
2. Launch the Transpose Data tool.
3. Select **Day** as identifier column.
4. Select **Work on: Selected records**.

5. Select **Temperature** and **Humidity** as value columns.

## 7.14.3 User Interface

### 7.14.3.1 Transpose Data Wizard Step 1

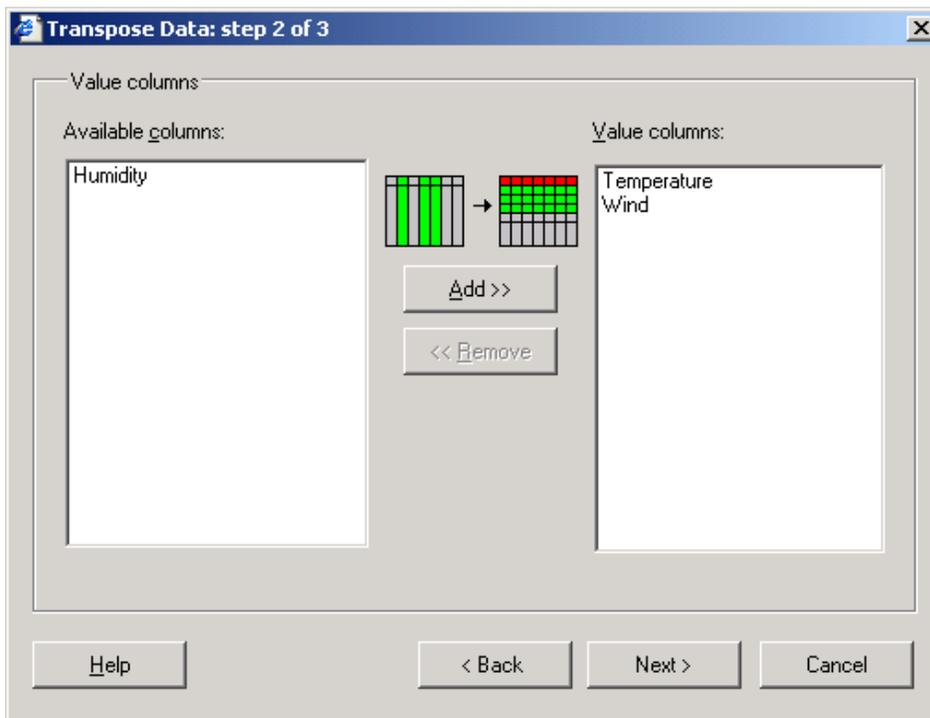


Option	Description
<b>Identifier column</b>	Each value in the selected identifier column will become a column name in the transposed data set.
<b>Work on: All records</b>	Creates a column for each record in the data set. Note that this may result in a very large number of columns.
<b>Work on: Selected records</b>	Creates a column for each record selected in the data set.

#### ► To reach the Transpose Data wizard:

Select **Data > Transpose Data...**

### 7.14.3.2 Transpose Data Wizard Step 2

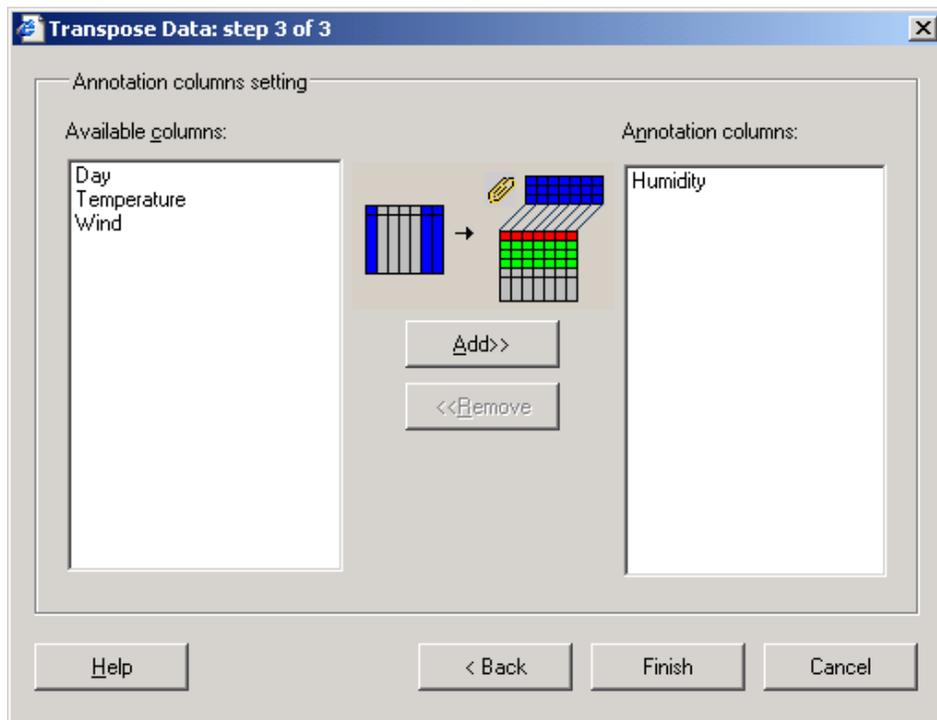


Option	Description
<b>Available columns</b>	The columns available for transposing. Only numerical columns are displayed.
<b>Value columns</b>	The columns selected for transposing.
<b>Add &gt;&gt;</b>	Moves a column to the Value columns field.
<b>&lt;&lt; Remove</b>	Removes a column from the Value columns field.

► **To reach the Transpose Data wizard:**

Select **Data > Transpose Data...**

### 7.14.3.3 Transpose Data Wizard Step 3



Option	Description
<b>Available columns</b>	The columns available for annotation.
<b>Annotation columns</b>	The columns selected for annotation.
<b>Add &gt;&gt;</b>	Moves a column to the Annotation columns field.
<b>&lt;&lt; Remove</b>	Removes a column from the Annotation columns field.

► **To reach the Transpose Data wizard:**

Select **Data > Transpose Data...**

## 7.15 PAM Clustering

### 7.15.1 Performing PAM Clustering

The PAM Clustering tool can be used to group similar genes or experiments.

The partitioning around medoids (PAM) algorithm is similar to k-means clustering but uses medoids rather than centroids. Medoids are the median in multiple dimensions and here represent a real gene in the data set, not a mean as in k-means. This lessens the effect of rare outlying observations upon the final cluster membership. The method PAM is fully described in Chapter 2 of Kaufman and Rousseeuw (1990). Compared to k-means clustering, PAM has the following features:

- It accepts a dissimilarity matrix.
- It is more robust because it minimizes a sum of dissimilarities instead of a sum of squared Euclidean distances.

Partitioning methods are appropriate when distinct sets of subpopulations are hypothesized.

**Note:** PAM clustering is limited to 1000 genes. Prior to running, filter the data set using query devices down to 1000 genes or less, based on p-value, QC parameters, or intensity values.

► **To perform PAM Clustering:**

1. Select **Data > Clustering > PAM Clustering...**  
Response: The PAM Clustering dialog is displayed.
2. Select the value columns on which to base the clustering from the **Available columns** list and click **Add >>**.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns in the Available columns list. Then click Add >> to move the columns to the Selected columns list. You can sort the columns in the list alphabetically by clicking on the Name bar.
3. Select the Gene Names Column. This is the identifier column of the data set. It will be used to join the results to the data set.
4. Click a radio button to select whether to work on **All records** or **Selected records**.  
Comment: To limit a data set having greater than 1000 genes (rows), filtering should be performed as noted above and **Selected records** MUST always be selected.
5. Select the **Number of Clusters** from the drop-down list.  
Comment: Choosing **Auto** will result in the method determining the optimal number of clusters.  
Select whether you want to **Cluster On Genes** or **Experiments**.  
Comment: This determines the measure that is used to perform the calculation and how the output is handled. Selecting **Genes** causes the application to add a new column of data into DecisionSite. The data set has one row of clustering information per row of data clustered. Selecting **Experiments** causes the application to open a data set in a new session of DecisionSite. The data set has two columns and one row of data per column of data clustered.
6. Click **OK**.  
Response: The PAM Clustering dialog is closed and the clustering is started. You see a graphical representation of the result in the visualizations created. The results of the clustering are added as new data columns to the data set.

## References

Kaufman, L., Rousseeuw, P.J. (1990). Finding Groups in Data: An Introduction to Cluster Analysis. John Wiley & Sons: New York.

## 7.15.2 PAM Clustering Dialog

Option	Description
<b>Available columns</b>	Displays all available data columns on which you can perform a clustering. Click a column name in the list and click <b>Add &gt;&gt;</b> to add it to the Selected columns list. To select more than one column, press <b>Ctrl</b> and click the column names in the list, then click Add >>.
<b>Selected columns</b>	Displays the currently selected data columns on which you want to perform a clustering.
<b>Add &gt;&gt;</b>	Adds the highlighted data column to the list of selected columns.
<b>&lt;&lt; Remove</b>	Removes the highlighted data column from the list of selected columns and places them back in the list of available columns.
<b>Gene Names Column</b>	The identifier column of the data set. This will be used to join the results to the data set.
<b>Work on: All Records</b>	All records in the value columns are included in the calculations. This option is not available if there are more than 1000 records in the data set.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.

	<b>Note:</b> This option must be selected if the data set is larger than 1000 genes (rows) and filtering must have been applied in order to reduce the selected records in the visualization to less than 1000 genes. This is necessary to run this clustering method.
<b>Number of Clusters</b>	Any value is acceptable. Choosing <b>Auto</b> will result in the system determining the optimal number of clusters.
<b>Column Name</b>	Specify the column name of the new column containing cluster information to be added to the data set.
<b>Overwrite</b>	Select this option to overwrite a previously added column with the same name.
<b>Cluster On: Genes</b>	Causes a new column of data to be added into DecisionSite.
<b>Cluster On: Experiments</b>	Causes a new data set to be opened in a new session of DecisionSite. The resulting data set has two columns and one row of data per column of data clustered.

► **To reach the PAM Clustering dialog:**

Select **Data > Clustering > PAM Clustering...**

## 7.16 PCA on Experiments or Genes

### 7.16.1 Performing PCA on Experiments or Genes

The PCA on Experiments or Genes tool can be used to transform a set of correlated variables into a smaller set of uncorrelated variables called principal components. It is therefore most useful for screening multivariate data in order to

- reduce the dimensionality of the data set,
- identify new, meaningful underlying variables,
- verify clustering.

► **To perform PCA on Experiments or Genes:**

1. Select **Data > Clustering > PCA on Experiments or Genes...**

Response: The PCA on Experiments or Genes dialog is displayed.

2. Select the value columns on which to base the clustering from the **Available columns** list and click **Add >>**.

Comment: For multiple selection, press **Ctrl** and click on the desired columns in the Available columns list. Then click **Add >>** to move the columns to the Selected columns list. You can sort the columns in the list alphabetically by clicking on the Name bar.

3. Select the **Gene Names Column**. This is the identifier column of the data set. It will be used to join the results to the data set.

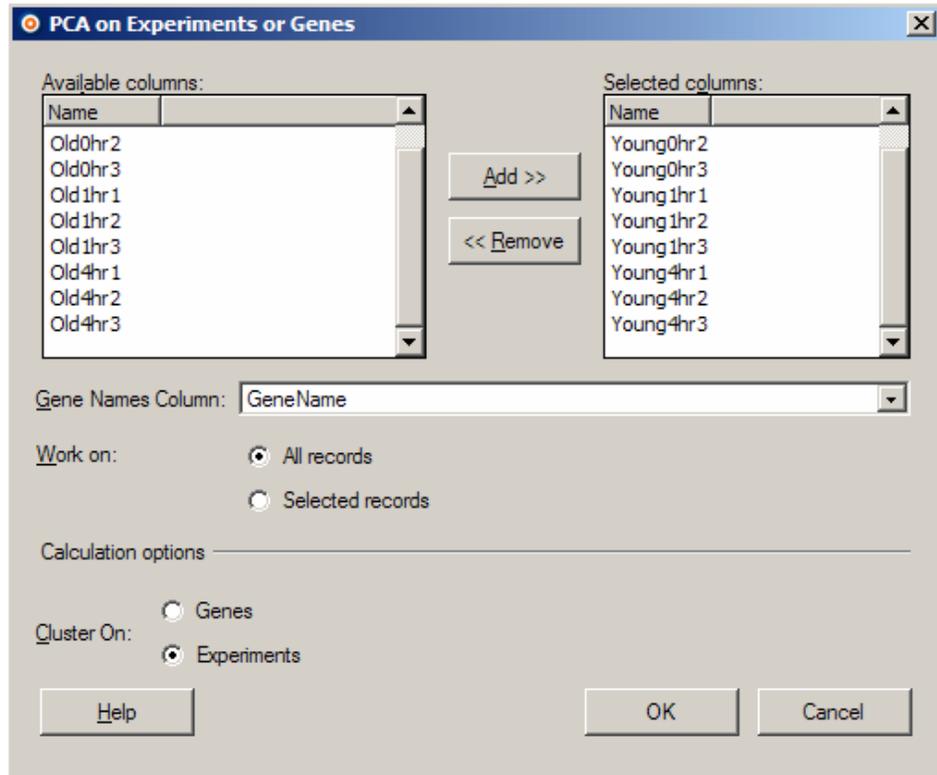
4. Click a radio button to select whether to work on **All records** or **Selected records**. Select whether you want to cluster on **Genes** or **Experiments**.

Comment: This determines the measure that is used to perform the calculation and how the output is handled. Selecting **Genes** causes the application to add a new column of data into DecisionSite. The data set has one row of clustering information per row of data clustered. Selecting **Experiments** causes the application to open a data set in a new session of DecisionSite. The data set has two columns and one row of data per column of data clustered.

5. Click **OK**.

Response: The PCA on Experiments or Genes dialog is closed and the PCA is performed. You see a graphical representation of the result in the visualizations created.

## 7.16.2 PCA on Experiments or Genes Dialog



Option	Description
<b>Available columns</b>	Displays all available data columns which you can use in a calculation. Click a column name in the list and click <b>Add &gt;&gt;</b> to add it to the Selected columns list. To select more than one column, press <b>Ctrl</b> and click the column names in the list, then click <b>Add &gt;&gt;</b> .
<b>Selected columns</b>	Displays the currently selected data columns that you want to use in the calculation.
<b>Add &gt;&gt;</b>	Adds the highlighted data column to the list of selected columns.
<b>&lt;&lt; Remove</b>	Removes the highlighted data column from the list of selected columns and places them back in the list of available columns.
<b>Gene Names Column</b>	The identifier column of the data set. This will be used to join the results to the data set.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.

<b>Cluster On: Genes</b>	Causes a new column of data to be added into DecisionSite.
<b>Cluster On: Experiments</b>	Causes a new data set to be opened in a new session of DecisionSite. The resulting data set has two columns and one row of data per column of data clustered.

► **To reach the PCA on Experiments or Genes dialog:**

Select **Data > Clustering > PCA on Experiments or Genes...**

## 7.17 Hierarchical Clustering

### 7.17.1 Hierarchical Clustering Overview

The Hierarchical Clustering tool groups records and arranges them in a dendrogram (a tree graph) based on the similarity between them.

### 7.17.2 Using Hierarchical Clustering

#### 7.17.2.1 Initiating a Hierarchical Clustering

► **To start a clustering:**

1. Select **Data > Clustering > Hierarchical Clustering...**  
Response: The Hierarchical Clustering dialog is displayed.
2. Select the value columns on which to base the clustering from the **Available columns** list and click **Add >>**.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns in the Available columns list. Then click **Add >>** to move the selected columns to the Selected columns list. You can sort the columns in the list alphabetically by clicking on the Name bar.
3. Click a radio button to select whether to work on **All records** or **Selected records**.
4. Select a method to **Replace empty values with** from the drop-down list.
5. Select which **Clustering method** to use for calculating the similarity between clusters.  
Comment: Click for information about available clustering methods.
6. Select which **Similarity measure** to use in the calculations.  
Comment: Click for information about available similarity measures.
7. Select which **Ordering function** to use for displaying the results.  
Comment: Click for information about available ordering functions.
8. Type a new **Column name** in the text box or use the default name.  
Comment: Select the **Overwrite** check box if you want to overwrite a previously added column using the same name. Clear the check box to keep old columns.
9. Select the **Calculate column dendrogram** check box if you want to create a column dendrogram.
10. Click **OK**.  
Response: The Hierarchical Clustering dialog is closed and the clustering is started. The result is displayed according to your settings in the dialog.

#### 7.17.2.2 Hierarchical Clustering on Keys

A *structure key* is a string that lists the substructures which form a compound. Clustering on keys, then means grouping compounds with similar sets of substructures.

Clustering on keys is based only on the values within the key column, and not all the columns. The key column should contain comma separated string values for all or some of the records in the data set.

The procedure below only shows you how to cluster records based on a specific key column.

► **To cluster on keys:**

1. If you have not already done it, you should first import the keys that you want to cluster on into Spotfire DecisionSite.
2. Select **Data > Clustering > Hierarchical Clustering on Keys...**  
Response: The Hierarchical Clustering on Keys dialog is displayed.
3. Select the **Key column** on which to base the calculations.  
Comment: The key column could be any string column in the data set.
4. Click a radio button to select whether to work on **All records** or **Selected records**.
5. Select which **Clustering method** to use for calculating the similarity between clusters.  
Comment: Click for information about available clustering methods.
6. Select which **Similarity measure** to use in the calculations.  
Comment: Click for information about available similarity measures.
7. Select which **Ordering function** to use for displaying the results.  
Comment: Click for information about available ordering functions.
8. Type a new **Column name** in the text box or use the default name.  
Comment: Select the **Overwrite** check box if you want to overwrite a previously added column using the same name. Clear the check box to keep old columns.
9. Click **OK**.  
Response: The *Hierarchical Clustering on Keys* dialog is closed and the clustering is started. A heat map and a row dendrogram visualization is created and information about the clustering is added to the visualization as an annotation.

### 7.17.2.3 Adding a Column from Hierarchical Clustering

The ordering column which is added to the data set upon performing a hierarchical clustering is used only to display the row dendrogram and to connect it to the heat map. In order to compare the hierarchical clustering results to those of a K-means clustering, you must first add a clustering column to your data set.

A clustering column contains information about which cluster each record belongs to, and can be used to create a trellis plot.

► **To add a clustering column:**

1. Perform a hierarchical clustering and locate the Row dendrogram which can be found to the left of the heat map.  
Comment: For more information on how to create the row dendrogram, see Initiating a hierarchical clustering.
2. If the cluster line is not visible (a dotted red line in the row dendrogram), right-click and select **View > Cluster scale** from the pop-up menu to display it.  
Comment: The cluster line will enable you to see how many clusters you are selecting in the dendrogram.
3. Click on the red circle on the cluster slider above the dendrogram and drag it to control how many clusters you want to include in the data column. You can also use the left and right keyboard arrow keys to step through the different number of clusters.  
Response: All clusters for the current position on the cluster slider are shown as small, red circles in the dendrogram.  
Comment: If you position the red circle at its rightmost position on the cluster slider, you get one cluster for each record. If you position it at its leftmost position, you get a

single cluster that includes all records. The number of clusters is displayed as a ToolTip which is shown when clicking and holding the left mouse-button on the red circle on the cluster slider.

4. Select **Add Cluster Column** from the row dendrogram menu.

Response: A column with information about which cluster each record belongs to, is added to the data set.

Comment: Records in the data set that are not included in the row dendrogram will have empty values in the new clustering column.

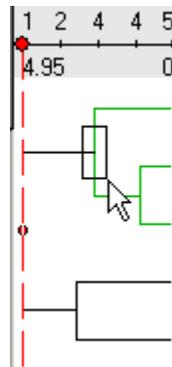
**Tip:** You can also click on the **Add Clustering Column** button, , to add a clustering column from the last row dendrogram.

## 7.17.2.4 Marking and Activating Nodes in the Dendrogram

### Marking nodes

To mark a node, click just outside it and drag to enclose the node within the frame that appears and then release. You can also press **Ctrl** and click on the node to mark it. To mark more than one node, press **Ctrl** and click on all the nodes you want to mark. To unmark all nodes, drag to select an area outside the dendrogram.

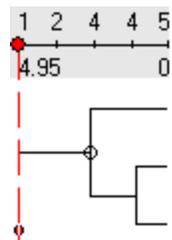
When you mark a node or a number of nodes, the marked parts of the dendrogram are shaded in the color used for marked records, by default green as shown below. The corresponding records are also marked in the heat map and other visualizations.



**Note:** It is only possible to mark nodes in the row dendrogram, not in the column dendrogram.

### Activating nodes

To activate a node, click on it in the dendrogram. The node gets a black ring around it. Only one node can be active at a time. The node remains active until another node is activated. It is possible to zoom in on the active node in the dendrogram by selecting **Zoom to Active** from the Hierarchical Clustering menu or from the dendrogram pop-up menu.



### Highlighting nodes

Highlighting nodes in the dendrogram does not have any effect on the visualizations.

### 7.17.2.5 Zooming in the Dendrogram

You can zoom to a subtree in the row dendrogram, either by using the visualization zoom bar or the **Zoom to Active** command in the pop-up menu. The pop-up menu is brought up by right-clicking in the dendrogram.

Double-clicking on a node will give the same results as the Zoom to Active command. Double-clicking a white surface in the dendrogram (no node) will take back the zooming one step, unlike the Reset Zoom command which takes you all the way back to the original zooming position.

The dendrogram can also be shown in log scale. This only affects the display of the dendrogram. The numbers in the cluster slider are not transformed into log values. Select **View > Log Scale** from the pop-up menu to view the dendrogram this way.

### 7.17.2.6 Resizing the Dendrogram

It is possible to adjust how much of the space in the visualization will be occupied by the dendrogram. This can be especially useful if the heat map contains a single column and the dendrogram structure is complex.

#### ► To resize the dendrogram:

First click on the dendrogram to make sure it is in focus. Then, press **Ctrl** and use the left or right arrow key on the keyboard to make the dendrogram slimmer or wider.

Comment: You cannot make the dendrogram or the heat map completely disappear by resizing them in the visualization.

### 7.17.2.7 Exporting a Dendrogram

**Note:** The Hierarchical Clustering tool allows the dendrograms to be saved with the Analysis. However, it is also possible to export the dendrograms separately and import them again via the Hierarchical Clustering: Dendrogram Import dialog.

#### ► To export a dendrogram:

1. Perform a hierarchical clustering.  
Comment: For more information, see Initiating a hierarchical clustering.
2. Locate the dendrogram(s) in the created heat map visualization.
3. Select **Export > Row Dendrogram** or **Column Dendrogram** from the menu in the top left of the heat map visualization.

Comment: The command **Export > Column Dendrogram** is only available if you selected to create a column dendrogram during the calculation.

Response: A Save As dialog is displayed.

4. Type a **File name** and save the file as a DND file.

Comment: The entire tree structure is saved even if only part of it is visible at the moment of saving.

**Tip:** To save the dendrogram and heat map as an image, use one of the Reporting tools of Spotfire DecisionSite: PowerPoint® Presentation, Word Presentation or Export as Web Page.

### 7.17.2.8 Importing a Dendrogram

**Note:** The Hierarchical Clustering tool allows the dendrograms to be saved with the Analysis. However, it is still possible to save the dendrograms separately and import them again via the Hierarchical Clustering: Dendrogram Import dialog.

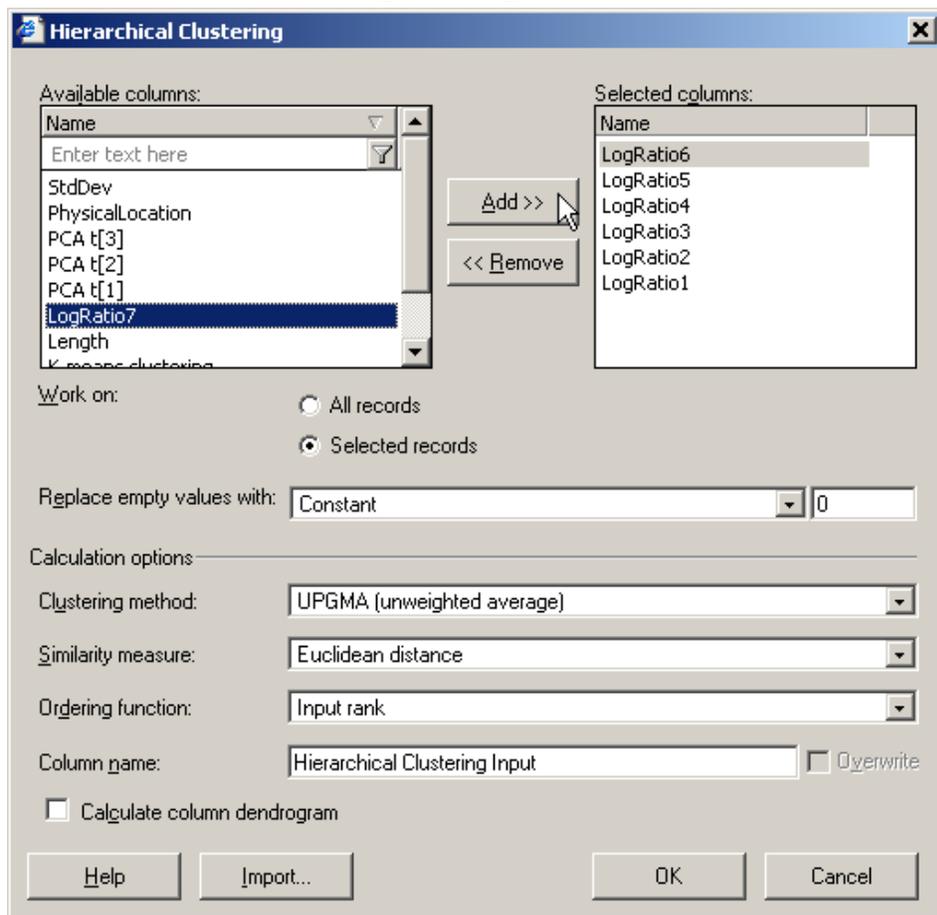
#### ► To import a saved dendrogram:

1. Select **Data > Clustering > Hierarchical Clustering...**  
Response: The Hierarchical Clustering dialog is displayed.

2. Click **Import...**  
Response: The Hierarchical Clustering: Dendrogram Import dialog is displayed.
3. Click the **Browse...** button by the **Row dendrogram** field.  
Response: An Open File dialog is displayed.
4. Locate the previously exported **Row dendrogram** file (\*.dnd) and click **Open**.  
Comment: Only dendrograms associated with the active data set can be opened. If there is a column missing in the data set, or if the names of the columns in the data set have been changed since the dendrogram was saved, an error message will appear and no dendrogram can be displayed.
5. Decide if you want to open a corresponding column dendrogram or not. Browse to locate the **Column dendrogram** file similarly to steps 3-4 above.
6. Type a **Column name** or use the default one.  
Comment: Select the **Overwrite** check box to overwrite a column with the same name in the data set.
7. Click **OK**.  
Comment: The column containing the hierarchical clustering order of the dendrogram is added to the data set. A heat map visualization is created with the dendrogram(s) displayed on the side(s).

## 7.17.3 User Interface

### 7.17.3.1 Hierarchical Clustering Dialog



Option	Description
<b>Available columns</b>	Displays all available data columns on which you can perform a clustering. Click a column name in the list and click <b>Add &gt;&gt;</b> to move it to the Selected columns list. To select more than one column, press <b>Ctrl</b> and click the column names in the list, then click Add >>. You can choose from all columns that contain real numbers or integers. <b>Note:</b> You can right-click on the Name header to get a pop-up menu where you can select other attributes you would like to be visible.
<b>Enter text here</b> 	If you have a data set with many columns, you can right-click on the header of the columns in the Available columns list box and select <b>Show Search Field</b> from the pop-up menu. This will display a search field where you can type a search string and limit the number of items in the list. It is possible to use the wildcard characters * and ? in the search.
<b>Selected columns</b>	Displays the currently selected data columns on which you want to perform a clustering.
<b>Add &gt;&gt;</b>	Adds the highlighted data column to the list of selected columns.
<b>&lt;&lt; Remove</b>	Removes the highlighted data column from the list of selected columns and places them back in the list of available columns.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Replace empty values with</b>	Defines how empty values in the data set should be replaced in the clustering. <b>Constant</b> allows you to replace the empty values by any constant (type a number in the text box). <b>Row average</b> replaces the value by the average value of the entire row. <b>Row interpolation</b> sets the missing value to the interpolated value between the two neighboring values in the row. <b>Column average</b> returns the average of the corresponding column values.
<b>Clustering method</b>	The clustering method to use for calculating the similarity between clusters. Click here for a description of the available methods.
<b>Similarity measure</b>	The similarity measure to use for the clustering. Click here for a description of the available similarity measures.
<b>Ordering function</b>	The ordering function to use for the clustering. Click here for a description of the available ordering functions.
<b>Column name</b>	The name of the new columns containing the results from the hierarchical clustering.
<b>Overwrite</b>	Select this check box if you want to replace a previously added column and plot (with the same name as the one typed in the Column name text box) when you add a new column. Clear the check box if you wish to keep the old column and plot.
<b>Calculate column dendrogram</b>	Select this check box to calculate a column dendrogram during the clustering.
<b>Import...</b>	Opens the Hierarchical Clustering: Dendrogram Import dialog where you

can import row and column dendrogram files.

► **To reach the Hierarchical Clustering dialog:**

Select **Data > Clustering > Hierarchical Clustering...**

### 7.17.3.2 Hierarchical Clustering on Keys Dialog

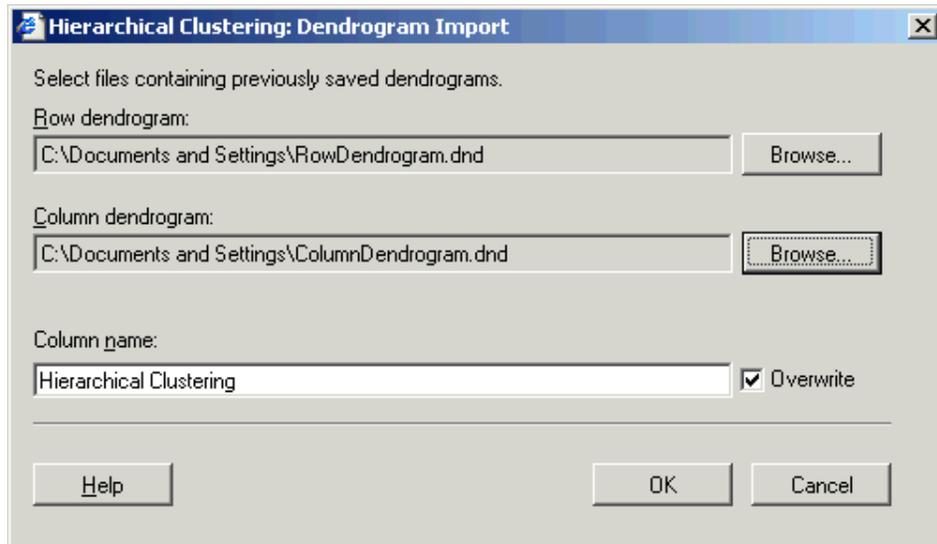
Option	Description
<b>Key column</b>	The data column on which to base the calculations. The key column should contain comma separated string values for all or some of the records in the data set.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Clustering method</b>	The clustering method to use for calculating the similarity between clusters. Click here for a description of the available methods.
<b>Similarity measure</b>	The similarity measure to use for the clustering. Click here for a description of the available similarity measures.
<b>Ordering function</b>	The ordering function to use for the clustering. Click here for a description of the available ordering functions.
<b>Column name</b>	The name of the new columns containing the results from the hierarchical clustering.
<b>Overwrite</b>	Select this check box if you want to replace a previously added column and plot (with the same name as the one typed in the Column name text box) when you add a new column. Clear the check box if you wish to

	keep the old column and plot.
<b>Open...</b>	Opens the Hierarchical Clustering: Dendrogram Import dialog where you can open row dendrogram files. Column dendrograms are not available when you are clustering on keys.

► **To reach the Hierarchical Clustering on Keys dialog:**

Select **Data > Clustering > Hierarchical Clustering...**

### 7.17.3.3 Hierarchical Clustering Dendrogram Import Dialog



Option	Description
<b>Row dendrogram</b>	Click on the <b>Browse...</b> button to display an Open File dialog, where you can select the row dendrogram to open. Only row dendrograms directly associated with the open data set can be opened.
<b>Column dendrogram</b>	Click on the corresponding <b>Browse...</b> button to display an Open File dialog, where you can select the column dendrogram to open. The column dendrogram option is not available when you are accessing this dialog from the Hierarchical Clustering on Keys dialog.
<b>Column name</b>	The name of the new columns containing the results from the hierarchical clustering.
<b>Overwrite</b>	Select this check box if you want to replace a previously added column (with the same name as the one typed in the Column name text box) when you add a new column. Clear the check box if you wish to keep the old column.

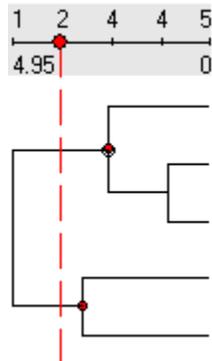
► **To reach the Hierarchical Clustering: Dendrogram Import dialog:**

1. Select **Data > Clustering > Hierarchical Clustering...**
2. Click on the **Open...** button in the lower left part of the dialog to display the **Hierarchical Clustering: Dendrogram Import** dialog.

### 7.17.3.4 The Row Dendrogram

The row dendrogram shows the similarity between rows and shows which nodes each record belongs to as a result of the clustering. An example of part of a row dendrogram is shown below.

The vertical axis of the row dendrogram consists of the individual records, and the horizontal axis represents the clustering level.

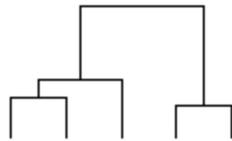


The individual records in the clustered data set are represented by the rightmost nodes in the row dendrogram. Each remaining node in the dendrogram represents a cluster of all records that lie to the right of it in the dendrogram. The leftmost node in the dendrogram is thus a cluster that contains all records.

The row dendrogram is automatically displayed next to the heat map which is created upon clustering. It can, however, be hidden or displayed by selecting **View > Row dendrogram** from the Hierarchical Clustering menu.

### 7.17.3.5 The Column Dendrogram

The column dendrogram is drawn in the same way as the row dendrogram but shows the similarity between the variables (the selected value columns). The variables in the clustered data set are represented by the nodes at the lowest part of the column dendrogram.



To display the column dendrogram (if one has been calculated), select **View > Column Dendrogram** from the Hierarchical Clustering menu. The column dendrogram can only be displayed if it has been calculated (select this in the Hierarchical Clustering dialog).

#### Restricted functionality

The column dendrogram offers less interactivity than the row dendrogram. You cannot add the results from the column dendrogram to the data set and so you cannot create visualizations based on it. There is no cluster slider above the column dendrogram, no cluster line and no horizontal zooming.

### 7.17.3.6 Row Dendrogram Menu and Toolbar

#### Toolbar



The row dendrogram toolbar is located directly above the row dendrogram. The row dendrogram is automatically created upon clustering and it is located to the left of the heat map. Click on the buttons in the toolbar to activate the corresponding functions.



Displays the Hierarchical Clustering menu.



Adds a new column to the data set with information about which cluster each record belongs to. The position of the red circle on the cluster slider above the dendrogram controls the number of clusters. The column can be used to create a trellis plot of the clusters.

## Hierarchical Clustering menu

Option	Description
<b>Zoom to Active</b>	Zooms to the selected subtree so that the active node in the row dendrogram is displayed to the far left of the visualization.
<b>Reset Zoom</b>	Resets the horizontal zooming to its original size so the full width of the row dendrogram is visible.
<b>View &gt;</b>	
<b>&gt; Log Scale</b>	Displays the dendrogram in log scale. Affects only the display of the dendrogram and not the actual numbers of the calculated similarity measures.
<b>&gt; Toolbar</b>	Displays or hides the row dendrogram toolbar. If the toolbar has been hidden, right-click on the row dendrogram and select <b>View &gt; Toolbar</b> from the pop-up menu to display it again.
<b>&gt; Cluster Scale</b>	Displays or hides the cluster scale (and cluster line) above the row dendrogram. The cluster scale must be displayed if you want to select the number of clusters to be included in the added cluster column.
<b>&gt; Column Dendrogram</b>	Displays or hides the column dendrogram (if one has been created).
<b>&gt; Row Dendrogram</b>	Displays or hides the row dendrogram.
<b>&gt; Include Empty</b>	Relevant only when you have performed a clustering using selected records. This produces a Hierarchical Clustering (order) column with empty values for all of the remaining records. By marking or clearing the Include Empty option you can determine whether or not to display the records that were not a part of the clustering calculation in the heat map. Obviously, no dendrogram can be displayed for these rows.
<b>Remove Dendrograms</b>	Removes the dendrograms permanently from the visualization.
<b>Add Cluster Column</b>	Adds a new column to the data set with information about which cluster each record belongs to. The position of the red circle on the cluster slider above the dendrogram controls the number of clusters. The column can be used to create a trellis plot of the clusters.
<b>Overwrite</b>	Selects whether or not to overwrite a Hierarchical Clustering (cluster) column, when using the Add cluster column function.
<b>Export &gt;</b>	
<b>&gt; Row Dendrogram</b>	Opens a dialog where you can select a file name and save your row dendrogram.

<b>&gt; Column dendrogram</b>	Opens a dialog where you can select a file name and save your column dendrogram.
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**Note:** The Hierarchical Clustering tool allows the dendrograms to be saved with the Analysis. However, it is still possible to export the dendrograms separately and then import them from within the Hierarchical Clustering: Dendrogram Import dialog.

### 7.17.3.7 Dendrogram Pop-up Menus

Right-click in the dendrogram to bring up the pop-up menu.

#### Row dendrogram pop-up menu:

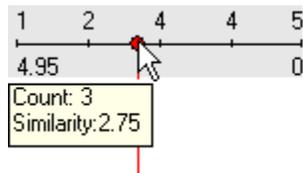
Option	Description
<b>Zoom to Active</b>	Zooms horizontally so that the active node in the row dendrogram is displayed to the far left of the visualization.
<b>Reset Zoom</b>	Resets the horizontal zooming to its original size so the full width of the row dendrogram is visible.
<b>View &gt;</b>	
<b>&gt; Log Scale</b>	Displays the dendrogram in log scale. Affects only the horizontal distances in the dendrogram and not the actual numbers of the calculated similarity measures.
<b>&gt; Toolbar</b>	Displays or hides the row dendrogram toolbar. If the toolbar has been hidden, right-click on the row dendrogram and select <b>View &gt; Toolbar</b> from the pop-up menu to display it again.
<b>&gt; Cluster Scale</b>	Displays or hides the cluster scale (and cluster line) above the row dendrogram. The cluster scale must be displayed if you want to select the number of clusters to be included in the added cluster column.
<b>&gt; Column Dendrogram</b>	Displays or hides the column dendrogram (if one has been created).
<b>&gt; Row Dendrogram</b>	Displays or hides the row dendrogram.
<b>&gt; Include Empty</b>	Relevant only when you have performed a clustering using selected records. This produces a Hierarchical Clustering (order) column with empty values for all of the remaining records. By marking or clearing the Include Empty option you can determine whether or not to display the records that were not a part of the clustering calculation in the heat map. Obviously, no dendrogram can be displayed for these rows.
<b>Remove Dendrograms</b>	Removes the dendrograms permanently from the visualization.
<b>Add Cluster Column</b>	Adds a new column to the data set with information about which cluster each record belongs to. The position of the red circle on the cluster slider above the dendrogram controls the number of clusters. The column can be used to create a trellis plot of the clusters.
<b>Overwrite</b>	Selects whether or not to overwrite a Hierarchical Clustering (cluster) column, when using the Add cluster column function.

**Column dendrogram pop-up menu:**

Option	Description
<b>Zoom to Active</b>	Zooms so that the active node in the column dendrogram is displayed at the top of the visualization.
<b>Reset Zoom</b>	Resets the zooming to its original size so the full width of the row dendrogram is visible.
<b>View &gt;</b>	
<b>&gt; Log Scale</b>	Displays the dendrogram in log scale. Affects only the horizontal distances in the dendrogram and not the actual numbers of the calculated similarity measures.

**7.17.3.8 Cluster Slider in Dendrogram**

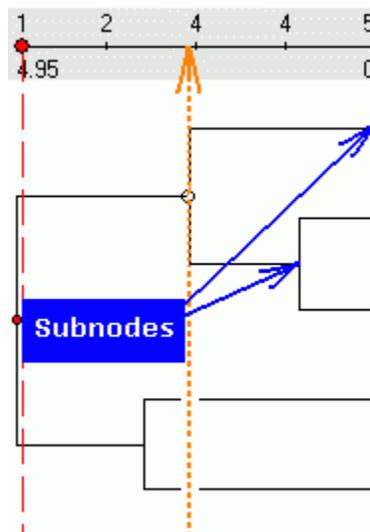
The scale above the row dendrogram is the cluster slider. The numbers above the scale refer to the number of clusters at different positions in the dendrogram. The numbers below the scale refer to the calculated similarity measures. When you move the cursor over the scale, the number of clusters and the similarity measure at that position are given in a ToolTip.

**Upper scale**

The upper scale assists you in selecting the number of clusters before creating a new clustering column. Click on the red circle on the cluster slider and drag it to the horizontal position you want. The selected clusters are indicated as red circles in the dendrogram. The total number of clusters is shown in a ToolTip as long as you hold down the mouse button.

**Lower scale**

The lower scale shows the calculated similarity measure in the dendrogram. The position of a node along the scale represents the similarity measure between the two subnodes in that node (there are always exactly two subnodes in each node). In the figure below, the similarity measure between the two subnodes in the active node is indicated by the dotted orange arrow.



The vertical distance has no mathematical meaning in the dendrogram.

**Note:** There is no cluster slider above the column dendrogram. You cannot create clusters in a column dendrogram and you cannot export information about the column dendrogram as a new column.

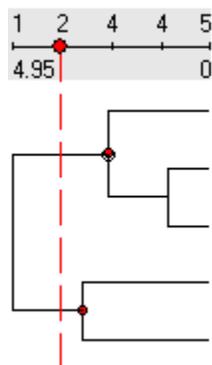
**Tip:** The cluster slider can also be moved by using the left and right arrows on the keyboard. This increases or decreases the number of clusters in a stepwise fashion.

## 7.17.4 Theory and Methods

### 7.17.4.1 Hierarchical Clustering Method Overview

Hierarchical clustering arranges objects in a hierarchy with a treelike structure based on the similarity between them.

The graphical representation of the resulting hierarchy is called a dendrogram, or a tree graph. This figure shows a small part of a dendrogram.



In Spotfire DecisionSite, the vertical axis of the dendrogram consists of the individual records and the horizontal axis represents the clustering level. The individual records in the clustered data set are represented by the rightmost nodes in the row dendrogram. Each remaining node in the dendrogram represents a cluster of all records that lie below it to the right in the dendrogram, thus making the leftmost node in the dendrogram a cluster that contains all records.

#### Misapplication of clustering

Clustering is a very useful data reduction technique. However, it can easily be misapplied. The clustering results are highly affected by your choice of similarity measure and other input parameters. You should bear this in mind when you evaluate the results. If possible, you should replicate the clustering analysis using different methods. Apply cluster analysis with care and it can serve as a powerful tool for identifying patterns within a data set.

### 7.17.4.2 Hierarchical Clustering Algorithm

The algorithm used in the Hierarchical Clustering tool is a hierarchical agglomerative method. This means that the cluster analysis begins with each record in a separate cluster, and in subsequent steps the two clusters that are the most similar are combined to a new aggregate cluster. The number of clusters is thereby reduced by one in each iteration step. Eventually, all records are grouped into one large cluster.

#### ► This is how it works:

1. The similarity between all possible combinations of two records is calculated using a selected similarity measure.
2. Each record is placed in a separate cluster.
3. The two most similar clusters are grouped together and form a new cluster.

4. The similarity between the new cluster and all remaining clusters is recalculated using a selected clustering method.
5. Steps 3 and 4 are repeated until all records eventually end up in one large cluster.

### 7.17.4.3 Required Input for Hierarchical Clustering

When you start a clustering you need to specify a number of parameters.

The parameters are set in the Hierarchical Clustering dialog that you reach by selecting **Clustering > Hierarchical Clustering** from the **Data** menu.

**You need to answer the following questions:**

- Which clustering method should be used to calculate the similarity between clusters?
- Which similarity measure should be used to calculate the similarity between records?
- Which ordering function should be used for drawing the dendrogram?

### 7.17.4.4 Hierarchical Clustering Ordering Function

The ordering function controls in what vertical order the records (rows) are plotted in the row dendrogram. The two subclusters within a cluster (there are always exactly two subclusters) are weighted and the cluster with the lower weight is placed above the other cluster. The weight can be any one of the following:

- **Input rank** of the records. This is the order of the records during import to DecisionSite.
- **Average value** of the rows. For example, a record  $a$  with 5 dimensions would have the average  $(a_1+a_2+a_3+a_4+a_5)/5$ . The average for a record  $a$  with  $k$  dimensions is calculated as

$$\bar{a} = \frac{1}{k} \sum_{j=1}^k a_j$$

#### Calculating the weight of a cluster

To calculate the weight  $w_3$  of a new cluster  $C_3$  formed from two subclusters  $C_1$  and  $C_2$  with a weight of  $w_1$  and  $w_2$ , and each containing  $n_1$  and  $n_2$  records, you use the following expression:

$$w_3 = \frac{n_1 \cdot w_1 + n_2 \cdot w_2}{(n_1 + n_2)}$$

### 7.17.4.5 Hierarchical Clustering References

#### Hierarchical clustering

Mirkin, B. (1996) *Mathematical Classification and Clustering, Nonconvex Optimization and Its Applications* Volume 11, Pardalos, P. and Horst, R., editors, Kluwer Academic Publishers, The Netherlands.

Sneath, P., Sokal, R. R. (1973) *Numerical taxonomy, Second Edition*, W. H. Freeman, San Francisco.

#### General information about clustering

Hair, J.F.Jr., Anderson, R.E., Tatham, R.L., Black, W.C. (1995) *Multivariate Data Analysis, Fourth Edition*, Prentice Hall, Englewood Cliffs, New Jersey.

## 7.17.4.6 Similarity Measures

### 7.17.4.6.1 Similarity Measures Overview

Spotfire DecisionSite contains several tools which calculate the similarity between different records (e.g., Hierarchical Clustering, K-means Clustering and Profile Search). Calculating similarities can be useful if you want to create lists of similar records which may possibly be treated as a group or if you want to find the record that is most similar to another record. The following similarity measures can be used to calculate the resemblance between records:

- Euclidean distance
- Correlation
- Cosine correlation
- City block distance
- Tanimoto coefficient (only available for Profile Search and Hierarchical Clustering)
- Half square Euclidean distance (only available for Hierarchical Clustering)

**Note:** When used in clustering, some of the similarity measures may be transformed so that they are always greater than or equal to zero (using  $1 - \text{calculated similarity value}$ ).

#### Dimensions

The term *dimension* is used in all similarity measures. The concept of dimension is simple if we are describing the physical position of a point in three dimensional space when the positions on the x, y and z axes refer to the different dimensions of the point. However, the data in a dimension can be of any type. If, for example, you describe a group of people by their height, their age and their nationality, then this is also a three dimensional system. For a record, the number of dimensions is equal to the number of variables in the record.

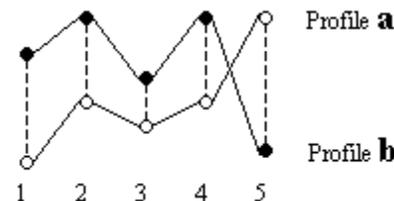
### 7.17.4.6.2 Euclidean Distance

The *Euclidean distance* between two profiles,  $a$  and  $b$ , with  $k$  dimensions is calculated as

$$\sqrt{\sum_{j=1}^k (a_j - b_j)^2}$$

The Euclidean distance is always greater than or equal to zero. The measurement would be zero for identical profiles and high for profiles that show little similarity.

The figure below shows an example of two profiles called  $a$  and  $b$ . Each profile is described by five values. The dotted lines in the figure are the distances  $(a_1 - b_1)$ ,  $(a_2 - b_2)$ ,  $(a_3 - b_3)$ ,  $(a_4 - b_4)$  and  $(a_5 - b_5)$  which are entered in the equation above.



### 7.17.4.6.3 Correlation

The *Correlation* between two profiles,  $a$  and  $b$ , with  $k$  dimensions is calculated as

$$\frac{\text{cov}(a, b)}{\text{std}(a) \cdot \text{std}(b)}$$

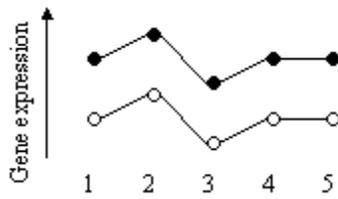
where

$$\text{cov}(a, b) = \frac{1}{k} \sum_{j=1}^k (a_j - \bar{a}) \cdot (b_j - \bar{b})$$

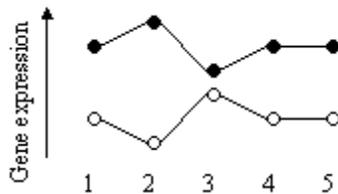
$$\text{std}(a) = \sqrt{\frac{1}{k} \sum_{j=1}^k (a_j - \bar{a})^2}$$

$$\bar{a} = \frac{1}{k} \sum_{j=1}^k a_j$$

This correlation is called *Pearson Product Momentum Correlation*, simply referred to as *Pearson's correlation* or *Pearson's r*. It ranges from +1 to -1 where +1 is the highest correlation. Complete opposite profiles have correlation -1.



Profiles with identical shape have maximum correlation.



Perfectly mirrored profiles have the maximum negative correlation.

#### 7.17.4.6.4 Cosine Correlation

The *Cosine correlation* between two profiles,  $a$  and  $b$ , with  $k$  dimensions is calculated as

$$\frac{\sum_{j=1}^k a_j \cdot b_j}{\text{norm}(a) \cdot \text{norm}(b)}$$

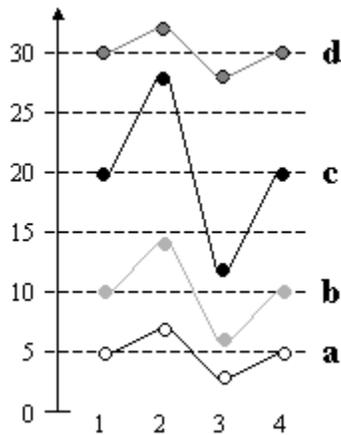
where

$$\text{norm}(a) = \sqrt{\sum_{j=1}^k a_j^2}$$

The cosine correlation ranges from +1 to -1 where +1 is the highest correlation. Complete opposite profiles have correlation -1.

#### Comparison between Cosine correlation and Correlation

The difference between Cosine correlation and Correlation is that the average value is subtracted in Correlation. In the example below, the Cosine correlation will be +1 between any combination of profiles  $a$ ,  $b$ , and  $c$ , but it will be slightly less than that between profile  $d$  and any of the other profiles (+0.974). However, the regular Correlation will be +1 between any of the profiles, including profile  $d$ .



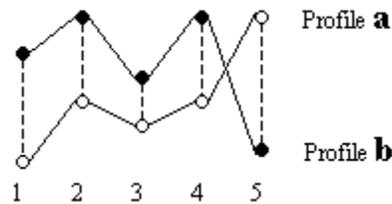
### 7.17.4.6.5 City Block Distance

The City block distance between two profiles,  $a$  and  $b$ , with  $k$  dimensions is calculated as

$$\sum_{j=1}^k |a_j - b_j|$$

The City Block distance is always greater than or equal to zero. The measurement would be zero for identical profiles and high for profiles that show little similarity.

The figure below shows an example of two profiles called  $a$  and  $b$ . Each profile is described by five values. The dotted lines in the figure are the distances  $(a_1-b_1)$ ,  $(a_2-b_2)$ ,  $(a_3-b_3)$ ,  $(a_4-b_4)$  and  $(a_5-b_5)$  which are entered in the equation above.



In most cases, this similarity measure yields results similar to the Euclidean distance. Note, however, that with City block distance, the effect of a large difference in a single dimension is dampened (since the distances are not squared).

The name *City block distance* (also referred to as *Manhattan distance*) is explained if you consider two points in the  $xy$ -plane. The shortest distance between the two points is along the hypotenuse, which is the *Euclidean distance*. The *City block distance* is instead calculated as the distance in  $x$  plus the distance in  $y$ , which is similar to the way you move in a city (like Manhattan) where you have to move around the buildings instead of going straight through.

### 7.17.4.6.6 Tanimoto Coefficient

The *Tanimoto coefficient* between two rows,  $a$  and  $b$ , with  $k$  dimensions is calculated as

$$\frac{\sum_{j=1}^k a_j \cdot b_j}{\left( \sum_{j=1}^k a_j^2 + \sum_{j=1}^k b_j^2 - \sum_{j=1}^k a_j \cdot b_j \right)}$$

The Tanimoto similarity measure is only applicable for a binary variable, and for binary variables the Tanimoto coefficient ranges from 0 to +1 (where +1 is the highest similarity).

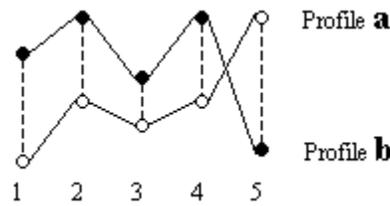
### 7.17.4.6.7 Half Square Euclidean Distance

The *Half square Euclidean distance* between two profiles,  $a$  and  $b$ , with  $k$  dimensions is calculated as

$$\frac{1}{2} \sum_{j=1}^k (a_j - b_j)^2$$

The Half square Euclidean distance is always greater than or equal to zero. The measurement would be zero for identical profiles and high for profiles that show little similarity.

The figure below shows an example of two profiles called  $a$  and  $b$ . Each profile is described by five values. The dotted lines in the figure are the distances  $(a_1-b_1)$ ,  $(a_2-b_2)$ ,  $(a_3-b_3)$ ,  $(a_4-b_4)$  and  $(a_5-b_5)$  which are entered in the equation above.



## 7.17.4.7 Cluster similarity methods

### 7.17.4.7.1 Cluster Similarity Methods

A hierarchical clustering starts by calculating the similarity between all possible combinations of two records using a selected similarity measure. These calculated similarities are then used to derive the similarity between all clusters that are formed from the records during the clustering. You select one of the following clustering methods:

- UPGMA
- WPGMA
- Single linkage
- Complete linkage
- Ward's method

### 7.17.4.7.2 UPGMA

UPGMA stands for Unweighted Pair-Group Method with Arithmetic mean.

Assume that there are three clusters called  $C_1$ ,  $C_2$  and  $C_3$  including  $n_1$ ,  $n_2$  and  $n_3$  number of records. Clusters  $C_2$  and  $C_3$  are aggregated to form a new single cluster called  $C_4$ .

The similarity between cluster  $C_1$  and the new cluster  $C_4$  in the example above is calculated as

$$\text{sim}_{C_1, C_4} = a \cdot \text{sim}_{C_1, C_2} + b \cdot \text{sim}_{C_1, C_3}$$

where

$\text{sim}$  = the similarity between the two indexed clusters and

$$a = \frac{n_2}{(n_2 + n_3)}$$

$$b = \frac{n_3}{(n_2 + n_3)}$$

### 7.17.4.7.3 WPGMA

WPGMA stands for Weighted Pair-Group Method with Arithmetic mean.

Assume that there are three clusters called  $C_1$ ,  $C_2$  and  $C_3$  including  $n_1$ ,  $n_2$  and  $n_3$  number of records. Clusters  $C_2$  and  $C_3$  are aggregated to form a new single cluster called  $C_4$ .

The similarity between cluster  $C_1$  and the new cluster  $C_4$  in the example above is calculated as

$$\text{sim}_{C_1, C_4} = \frac{1}{2} (\text{sim}_{C_1, C_2} + \text{sim}_{C_1, C_3})$$

where

sim = the similarity between the two indexed clusters.

#### 7.17.4.7.4 Single Linkage

This method is based on minimum distance. To calculate the similarity between two clusters, each possible combination of two records between the two clusters is compared. The similarity between the clusters is the same as the similarity between the two records in the clusters that are most similar.

#### 7.17.4.7.5 Complete Linkage

This method is based on maximum distance and can be thought of as the opposite of *Single linkage*. To calculate the similarity between two clusters, each possible combination of two records between the two clusters is compared. The similarity between the two clusters is the same as the similarity between the two records in the clusters that are least similar.

#### 7.17.4.7.6 Ward's Method

Ward's method means calculating the incremental sum of squares. The similarity measure is automatically set to *Half square Euclidean distance* when using Ward's method. This is not configurable.

Assume that there are three clusters called  $C_1$ ,  $C_2$  and  $C_3$  including  $n_1$ ,  $n_2$  and  $n_3$  number of records. Clusters  $C_2$  and  $C_3$  are aggregated to form a new single cluster called  $C_4$ .

The similarity between cluster  $C_1$  and the new cluster  $C_4$  in the example above is calculated as

$$\text{sim}_{C_1, C_4} = a \cdot \text{sim}_{C_1, C_2} + b \cdot \text{sim}_{C_1, C_3} - c \cdot \text{sim}_{C_2, C_3}$$

where

sim = the similarity between the two indexed clusters

$$a = \frac{n_1 + n_2}{(n_1 + n_2 + n_3)}$$

$$b = \frac{n_1 + n_3}{(n_1 + n_2 + n_3)}$$

$$c = \frac{n_1}{(n_1 + n_2 + n_3)}$$

## 7.18 Self-Organizing Maps

### 7.18.1 Self-Organizing Maps Overview

A Self-Organizing Map (SOM) is a type of clustering algorithm based on neural networks. The algorithm produces a Trellis profile chart, in which similar records appear close to each other, and less similar records appear more distant. From this map it is possible to visually investigate how records are related.

### 7.18.2 Using Self-Organizing Maps

#### 7.18.2.1 Performing Clustering using Self-Organizing Maps

► **To perform clustering:**

1. Select **Data > Clustering > Self-Organizing Maps...**

Response: The Self-Organizing Maps dialog is displayed.

2. Select the value columns on which to base the clustering from the **Available columns** list and click **Add >>**.

Comment: For multiple selection, press **Ctrl** and click on the desired columns in the Available columns list. Then click Add >> to move the columns to the Selected columns list. You can sort the columns in the list alphabetically by clicking on the Name bar.

3. Click a radio button to select whether to work on **All records** or **Selected records**.
4. Select a method to **Replace empty values with** from the drop-down list.
5. Select a **Normalization method** from the drop-down list.

Comment: Self Organizing Maps offers three different Normalization methods: Z-score (subtract the mean and divide by standard deviation), Divide by standard deviation, and Scale between 0 and 1. Each of these three methods apply normalization to columns, but not to rows.

6. Enter the **Grid size** width and height.

Comment: This is the number of separate maps to be calculated. Entering large values gives the map a better resolution, but makes the calculation slower. Entering small values may result in dissimilar records being assigned to the same node.

7. If desired, click **Advanced...** to modify the calculation settings. If you do not want to change the calculation settings, continue to step 14.
8. Select a **Neighborhood function** from the drop-down list.

Comment: For more information about the available methods, see Neighborhood function.

9. Modify the **Begin radius** and the **End radius** according to your choice.

10. Select a **Learning function**.

Comment: For more information about the available methods, see Learning function.

11. Modify the **Initial rate**.

Comment: If you receive the message "Calculation error: Overflow in floating numbers" upon calculation, you may have set the initial training rate too high. Try a lower value.

12. Enter a **Number of training steps** or use the default setting.

13. Click **OK**.

14. Type a new **Column name**, or use the default name.

Comment: Select the **Overwrite** check box if you want to overwrite a previously added column with the same name.

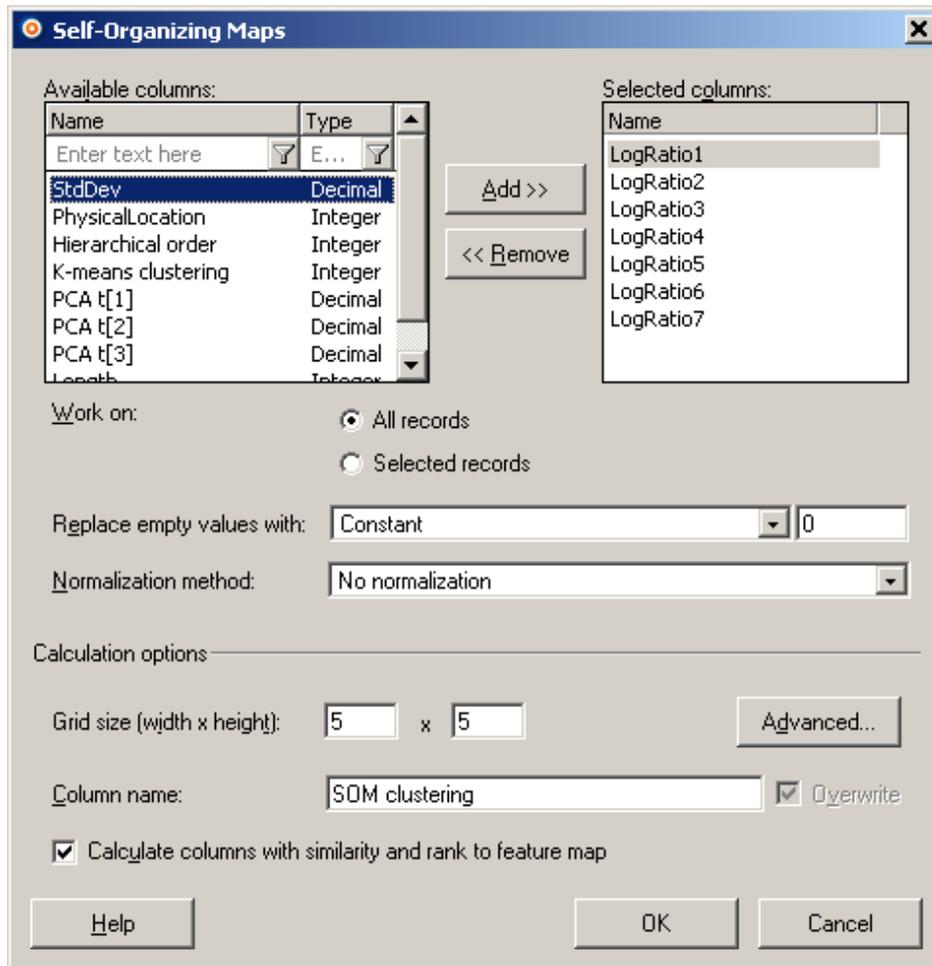
15. Select or clear the **Calculate columns with similarity and rank to feature map** check box.

16. Click **OK**.

Response: The dialog is closed and the algorithm is started. The results of the clustering are added as new data columns to the data set. You see a graphical representation of the result in the trellised profile charts. Each profile chart represents a node in the SOM.

## 7.18.3 User Interface

### 7.18.3.1 Self-Organizing Maps Dialog



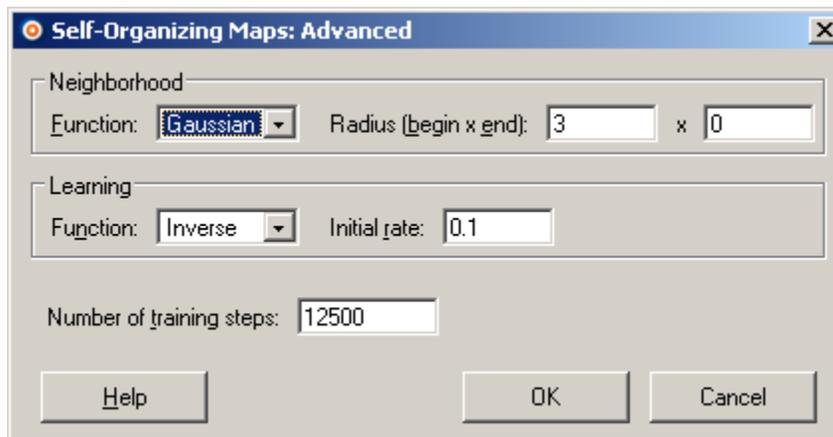
Option	Description
<b>Available columns</b>	<p>Lists all columns available for clustering. Click to select a column to be used in the Self-Organizing Maps, then click Add &gt;&gt;. To select more than one column at a time, press <b>Ctrl</b> and click the column names in the list. All numerical columns in the data set are available as value columns.</p> <p>You can sort the columns in the list alphabetically by clicking on the Name bar. Click again to reverse sorting and once more to reset the sort order.</p> <p><b>Note:</b> You can right-click on the Name header to get a pop-up menu where you can select other attributes you would like to be visible.</p>
<b>Enter text here</b> 	<p>If you have a data set with many columns, you can right-click on the header of the columns in the Available columns list box and select <b>Show Search Field</b> from the pop-up menu. This will display a search field where you can type a search string and limit the number of items in the list. It is possible to use the wildcard characters * and ? in the search.</p>

<b>Selected columns</b>	Lists the selected columns to be used in the calculation.
<b>Add &gt;&gt;</b>	Adds the columns selected in the Available columns list to the Selected columns list.
<b>&lt;&lt; Remove</b>	Removes the selected columns from the Selected columns list.
<b>Work on: All records</b>	All records are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Replace empty values with</b>	Defines how empty values in the data set should be replaced in the clustering. <b>Constant</b> allows you to replace the empty values by any constant (type a number in the text box). <b>Row average</b> replaces the value by the average value of the entire row. <b>Row interpolation</b> sets the missing value to the interpolated value between the two neighboring values in the row. <b>Column average</b> replaces the value by the average value of the entire column.
<b>Normalization method</b>	Defines which normalization method to use in the calculation.
<b>Grid size (width x height)</b>	The width and height of the map. Entering large values gives the map a better resolution, but makes the calculation slower. Entering small values may result in dissimilar records being assigned to the same node.
<b>Advanced...</b>	Displays the Self-Organizing Maps: Advanced dialog.
<b>Column name</b>	The main name of the columns added to the data set. The columns identifying the row and column index of the node to which each record has been assigned are appended with (x value) and (y value).
<b>Overwrite</b>	Select the check box to overwrite previously added columns with the same name.
<b>Calculate columns with similarity and rank to feature map</b>	Select this check box to add extra columns to the data set. The first column will contain the rank of the calculated similarity to centroid values. This means that the rank column contains a numbered list where 1 represents the record that is the most similar to its centroid. The name of the added column will be the same as the one entered under Column name, followed by (rank). The second column will contain the calculated similarity of each record to its centroid. The name of the added column will be the same as the one entered under <i>Column name</i> , followed by (similarity).

► **To reach the Self-Organizing Maps dialog:**

Select **Data > Clustering > Self-Organizing Maps...**

### 7.18.3.2 Self-Organizing Maps Advanced Dialog



Option	Description
<b>Neighborhood Function</b>	The method used to compute how the weight vector of a node should be updated in each iteration. For more information about the available methods, see Neighborhood function.
<b>Radius (begin x end)</b>	The neighborhood radius begin and end values. For more information, see Neighborhood function. The default value of the begin radius is 1/2 of the longer side of the grid. The end radius default value is 0.
<b>Learning Function</b>	The function which controls how learning decreases over time. Usually, the Inverse is more efficient than Linear. For more information about the available methods, see Learning function.
<b>Initial rate</b>	The initial learning-rate, see Learning function. Higher values are recommended for coarse-adjustment and lower values for fine-adjustments. The default value is 0.05. <b>Tip:</b> If you receive the message "Calculation error: Overflow in floating numbers" upon calculation, you may have set the initial learning rate too high. Try a lower value.
<b>Number of training steps</b>	The number of iterations of the algorithm. The default value is 500 times the number of nodes in the map.

► **To reach the Self-Organizing Maps: Advanced dialog:**

1. Select **Data > Clustering > Self-Organizing Maps...**
2. Click **Advanced...** in the Self-Organizing Maps dialog.

## 7.18.4 Theory and Methods

### 7.18.4.1 Self-Organizing Maps Theory Overview

Self-Organizing Maps (SOMs) are a special class of *artificial neural networks* based on *competitive learning*. The algorithm produces a two-dimensional grid, in which similar records appear close to each other, and less similar records appear more distant. From this map it is possible to visually investigate how records are related. In this sense, SOMs provide a form of clustering.

## Misapplication of clustering

Clustering is a very useful data reduction technique. However, it can easily be misapplied. The clustering results are highly affected by your choice of similarity measure and clustering algorithm. You should bear this in mind when you evaluate the results. If possible, you should replicate the clustering analysis using different methods. Apply cluster analysis with care and it can serve as a powerful tool for identifying patterns within a data set.

### 7.18.4.2 Self-Organizing Maps Algorithm

The following is a non-mathematical introduction to Self-Organizing Maps (SOMs). For the mathematical details, see Update Formula, and References.

The goal of the algorithm is to distribute records in a two-dimensional grid, such that similar records appear close to each other, and less similar records appear more distant.

#### ► This is how it works:

1. **Initialization.** A two-dimensional rectangular grid is set up. Each node in the grid is assigned an initial weight vector. This vector has the same number of dimensions as the input data.
2. **Sampling.** A record is picked from the data set by random. This record is called the *input vector*.
3. **Similarity matching.** The input vector is compared to the weight vector of each node, and the node whose weight vector is most similar to the input vector is declared the *winner*.
4. **Updating.** The weight vector of each node is modified.  
Comment: Nodes close to the winner (in terms of their position in the grid, not their weight vectors) have their weight vectors modified to approach the input vector, while nodes far from the winner are less affected, or not affected at all. See Update formula.
5. **Iteration.** The algorithm is repeated from step 2.
6. **Best match.** After a number of iterations, the training ends. Each record in the data set is assigned to the node whose weight vector most closely resembles it, using Euclidean distance.
7. **Visualization.** Two new columns are automatically added to the data set, and a Trellis profile chart is created.

Comment: In the SOM, a node is represented by an X and Y index denoting its position in the grid. After the algorithm has been executed, each record in the data set is given the indices of the node to which it was assigned (see step 6 above). This means that two new columns are added to the data set. The result is visualized as a number of profile charts, trellised by the two new columns such that each chart represents a SOM node and the records assigned to it.

### 7.18.4.3 Self-Organizing Maps - Update Formula

The SOM algorithm is an iterative process (see Self-Organizing Maps algorithm). Each time an input vector (a record picked by random from the original data set) has been selected and a winning node appointed, the weight vectors of all the nodes in the grid are updated.

The new weight vector of a node  $w_j$  is given by the equation:

$$w_j(t+1) = w_j(t) + a(t) * h_{j,i(x)}(t) * (x(t) - w_j(t))$$

where

t = time, number of iterations so far

a = learning-rate factor

$h$	= neighborhood function
$\mathbf{x}$	= input vector (a record from the original data set)
$\mathbf{w}_j$	= weight vector of a node with index $j$
$i(\mathbf{x})$	= winning node for input vector $\mathbf{x}$

In other words, the new weight vector is given by the old vector plus the product of learning-rate factor, neighborhood function and distance to input vector.

#### 7.18.4.4 Self-Organizing Maps - Initial Weight Vectors

In the initialization step of the SOM algorithm, each node is assigned an *initial weight vector*. This vector has the same number of dimensions as the input vector, supplying a starting configuration for the SOM.

By default, *linear initialization* is used. Under certain conditions this will fail, and in this case *random initialization* will be used. If so, the algorithm is conducted in two phases: a rough phase and a fine-tune phase.

##### Linear initialization

Linear initialization creates the most effective starting configuration, reducing the number of iterations needed to reach a meaningful result.

Determine the two eigenvectors of the autocorrelation matrix of the training data  $\mathbf{x}$  that have the largest eigenvalues, and then let these eigenvectors span a two dimensional linear subspace. A rectangular lattice is defined along this subspace, its centroid coinciding with that of the mean of the  $\mathbf{x}(t)$ , and the main dimensions being the same as the two largest eigenvalues.

##### Random initialization

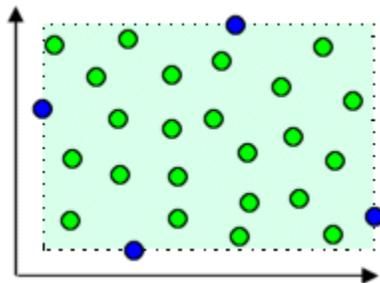
In random initialization, each weight vector  $\mathbf{w}$  is populated with random values, such that for dimension  $i$ :

$$\mathbf{w}_i = r_i((\max(x_i) - \min(x_i)) + \min(x_i))$$

where

$\mathbf{w}$	= weight vector
$r$	= random value and $0 \leq r \leq 1$
$i$	= dimension (column)
$\mathbf{x}$	= data set

Less formally, this means that the initial weight vectors are uniformly distributed within a space bounded by the extreme values in the data set:



Random initialization is not considered as effective as linear initialization. This is compensated for by introducing a *rough phase* before the normal training. This means that the first 20% of the assigned training length is carried out with an initial learning rate that is 10 times higher

than that which has been defined. The remaining 80% of the training is then carried out with normal parameters.

### 7.18.4.5 Self-Organizing Maps - Similarity Matching

In the similarity matching step of the SOM algorithm, a winning node is selected by finding the weight vector most similar to the input vector. Similarity is measured as Euclidean distance.

The winning node  $i(\mathbf{x})$  is selected using the following formula:

$$i(\mathbf{x}) = \arg \min_j \|\mathbf{x}(t) - \mathbf{w}_j\|_{j=1}^{j=t}$$

where

- $t$  = time, number of iterations
- $\mathbf{w}_j$  = weight vector of a node  $j$
- $\mathbf{x}(t)$  = input vector at time  $t$

### 7.18.4.6 Self-Organizing Maps - Neighborhood Function

The equation (see Update formula) for calculating how the weight vector of a node is modified in each iteration includes a *neighborhood function*. This function takes into account the Euclidean distance between a node and the winning node, as well as the time passed.

The tool provides two alternatives: the Bubble function and the Gaussian function. Both include a parameter called *effective radius* which varies with time.

#### Effective Radius

The radius at step  $t$  is given by:

$$r(t) = r(\text{begin}) + \Delta r \cdot t$$

where

$$\Delta r = \frac{r(\text{end}) - r(\text{begin})}{k}$$

- $t$  = time, number of iterations so far
- $k$  = training length (set by user)
- $r(\text{end})$  = end radius (set by user)
- $r(\text{begin})$  = initial radius (set by user)

Less formally this means that as the training progresses, the radius goes from the initial value down to the end value.

#### Bubble neighborhood function

The Bubble function affects all surrounding nodes equally up to a threshold radius. Beyond this radius, nodes are unaffected.

The Bubble function for a node  $j$  and a winning node  $i(\mathbf{x})$  is defined as follows:

$$h_{j,i(\mathbf{x})} = \begin{cases} 1 & \text{if } d_{i,j} \leq r(t) \\ 0 & \end{cases}$$

where

$d_{i,j}$  = Euclidean distance between node and winning node

#### Gaussian neighborhood function

The Gaussian function is defined as follows:

$$h_{j,i(\mathbf{x})} = -\exp\left(\frac{d_{i,j}^2}{2r(t)}\right)$$

### 7.18.4.7 Self-Organizing Maps - Learning Function

The Update formula includes a factor called the *learning-rate factor*. This parameter decreases over time in accordance with a *learning function*. Two options are available: an inverse function, and a linear function (the names describe how learning decreases with time). Which function to use is selected in the Self-Organizing Maps: Advanced dialog.

Both functions initially take the value of the user-specified initial learning-rate. As the training progresses, the functions approach zero.

#### Inverse learning function

The learning-rate factor at step  $t$  is given by:

$$\alpha(t) = \alpha(0) \frac{b}{t + b}$$

where

- $t$  = time, number of iterations
- $b$  = training length / 100
- $\alpha(0)$  = initial learning-rate (set by user)

#### Linear learning function

The learning-rate factor at step  $t$  is given by:

$$\alpha(t) = \alpha(0) \left( 1 - \left( 1 - \frac{\alpha(0)}{100} \right) \cdot \frac{t}{trainlen} \right)$$

where

- $t$  = time, number of iterations
- $trainlen$  = training length (set by user)
- $\alpha(0)$  = initial learning-rate (set by user)

### 7.18.4.8 Map Quality Measures

The quality of the created Self-Organizing Maps can be evaluated based on the mapping precision and the topology preservation. This information is included as a plot annotation after running the tool.

#### Mapping Precision

The average quantization error is calculated as follows:

$$\epsilon_q = \frac{1}{N} \sum_{i=1}^N \|x_i - w_c\|$$

where  $c$  is the best matching unit for the actual  $x$ .

#### Topology Preservation

The topographic error is calculated as follows:

$$\epsilon_t = \frac{1}{N} \sum_{i=1}^N u(x_k)$$

where  $u$  is 1 if the first and second best matching units are not in the near vicinity of each other, otherwise  $u$  is 0.

### 7.18.4.9 Self-Organizing Maps References

Mirkin, B. (1996) *Mathematical Classification and Clustering, Nonconvex Optimization and Its Applications Volume 11*, Pardalos, P. and Horst, R., editors, Kluwer Academic Publishers, The Netherlands.

MacQueen, J. (1967). Some methods for classification and analysis of multivariate observations. In Le Cam, L. M. and Neyman, J., editors, *Proceedings of the Fifth Berkeley Symposium on Mathematical Statistics and Probability. Volume I: Statistics*, pages 281-297. University of California Press, Berkeley and Los Angeles, CA.

## 7.19 K-means Clustering

### 7.19.1 K-means Clustering Overview

K-means clustering is a form of non-hierarchical clustering, which groups records into a defined number of clusters based on their similarity.

### 7.19.2 Using K-means Clustering

#### 7.19.2.1 Performing K-means Clustering

##### ► To initiate a K-means clustering:

1. Select **Data > Clustering > K-means Clustering...**  
Response: The K-means Clustering dialog is displayed.
2. Select the value columns on which to base the clustering from the **Available columns** list and click **Add >>**.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns in the Available columns list. Then click Add >> to move the columns to the Selected columns list. You can sort the columns in the list alphabetically by clicking on the Name bar.
3. Click a radio button to select whether to work on **All records** or **Selected records**.
4. Select a method to **Replace empty values with** from the drop-down list.
5. Enter the **Maximum number of clusters**.  
Comment: Since empty clusters are discarded at the calculation, the resulting number of clusters may be less than what is specified in this text box.
6. Select a **Cluster initialization** method from the drop-down menu.  
Comment: For more information about the available methods, see Initializing K-means cluster centroids.
7. Select which **Similarity measure** to use for the clustering.  
Comment: Click for information about the available similarity measures.
8. Type a new **Column name** in the text box or use the default name.  
Comment: Select the **Overwrite** check box if you want to overwrite a previously added column with the same name.
9. Click **OK**.  
Response: The K-means Clustering dialog is closed and the clustering is started. You see a graphical representation of the result in the visualizations created. The results of the clustering are added as new data columns to the data set.

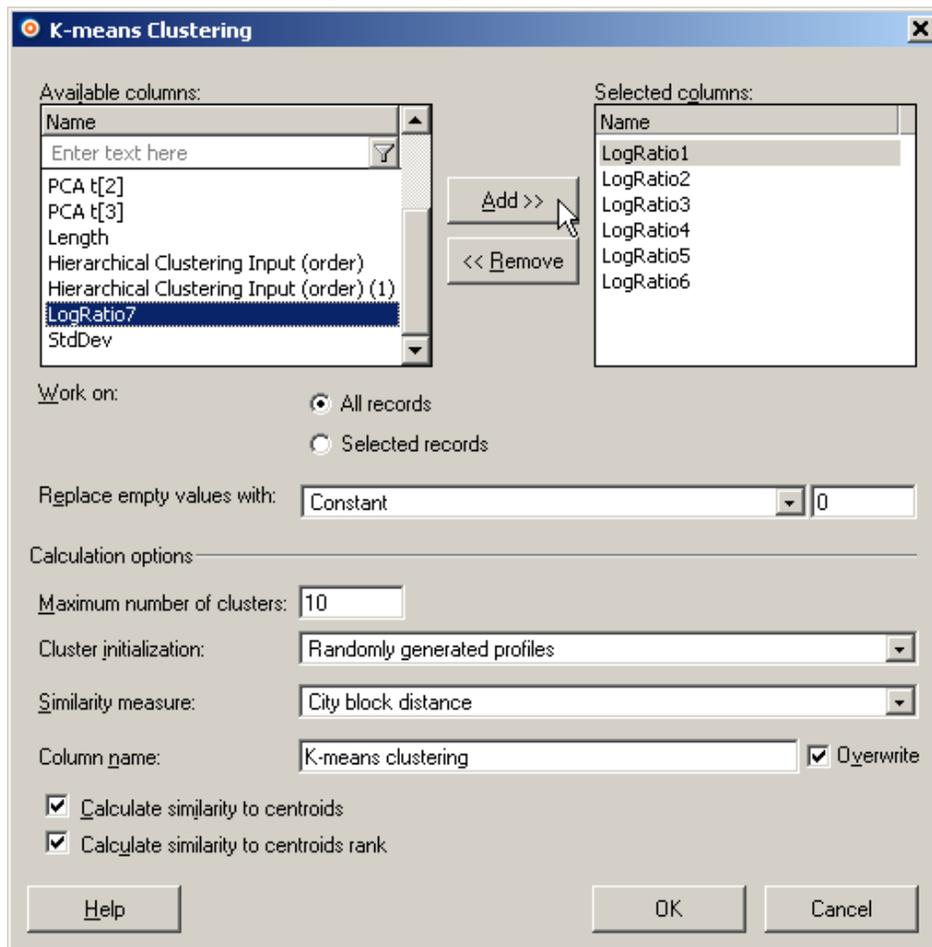
## 7.19.2.2 K-means Clustering - Finding Out Cluster Belonging

### ► To find out which cluster a record belongs to:

1. Perform a K-means clustering.
2. In any visualization (for example, a scatter plot or profile chart), click to activate the record that you are interested in.
3. Look in the Details-on-Demand window and locate the number in the K-means clustering column.

## 7.19.3 User Interface

### 7.19.3.1 K-means Clustering Dialog



Option	Description
<b>Available columns</b>	Displays all available data columns on which you can perform a clustering. Click a column name in the list and click <b>Add &gt;&gt;</b> to add it to the Selected columns list. To select more than one column, press <b>Ctrl</b> and click the column names in the list, then click <b>Add &gt;&gt;</b> . You can choose from all columns that contain real numbers or integers. <b>Note:</b> You can right-click on the Name header to get a pop-up menu where you can select other attributes you would like to be visible.
<b>Enter text here</b>	If you have a data set with many columns, you can right-click on the

	header of the columns in the Available columns list box and select <b>Show Search Field</b> from the pop-up menu. This will display a search field where you can type a search string and limit the number of items in the list. It is possible to use the wildcard characters * and ? in the search.
<b>Selected columns</b>	Displays the currently selected data columns on which you want to perform a clustering.
<b>Add &gt;&gt;</b>	Adds the highlighted data column to the list of selected columns.
<b>&lt;&lt; Remove</b>	Removes the highlighted data column from the list of selected columns and places them back in the list of available columns.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Replace empty values with</b>	Defines how empty values in the data set should be replaced in the clustering. <b>Constant</b> allows you to replace the empty values by any constant (type a number in the text box). <b>Row average</b> replaces the value by the average value of the entire row. <b>Row interpolation</b> sets the missing value to the interpolated value between the two neighboring values in the row. <b>Column average</b> returns the average of the corresponding column values.
<b>Maximum number of clusters</b>	The maximum number of clusters that you want to calculate (some may turn out empty and will in that case not be displayed).
<b>Cluster initialization</b>	Determines which method to use when initializing the clusters. For more information about the available methods, see Initializing K-means cluster centroids.
<b>Similarity measure</b>	The similarity measure that you want to use for the K-means clustering. For more information about the available measures, see Similarity measures.
<b>Column name</b>	The name for the new columns containing the results from the K-means clustering.
<b>Overwrite</b>	Select this check box if you want to replace a previously added column (with the same name as the one typed in the <i>Column name</i> text box) when you add a new column. Clear the check box if you wish to keep the old column.
<b>Calculate similarity to centroids</b>	Select this check box to add an extra column to the data set. This column will contain the calculated similarity of each record to its centroid. The name of the added column will be the same as the one entered under <i>Column name</i> , followed by (similarity).
<b>Calculate similarity to centroids rank</b>	Select this check box to add an extra column to the data set. This column will contain the rank of the calculated similarity to centroid values. This means that the rank column contains a numbered list where 1 represents the record that is the most similar to its centroid. The name of the added column will be the same as the one entered under <i>Column name</i> , followed by (rank).
<b>OK</b>	Saves all your settings, launches the K-means clustering calculation and

closes the K-means Clustering dialog. A new bar chart visualization is created with the bars colored according to which cluster they belong to. A trellis profile chart visualization is also displayed. Clustering statistics are added as an annotation connected to the visualizations. The clustering statistics contains information about the clustering initialization and results.

► **To reach the K-means Clustering dialog:**

Select **Data > Clustering > K-means Clustering...**

## 7.19.4 Theory and Methods

### 7.19.4.1 K-means Clustering Method Overview

K-means clustering is a method used for grouping data points into a predetermined number of clusters based on their similarity. Before you start the clustering you must decide how many clusters you want and how the centroids (the center points of these clusters) should be initialized.

K-means clustering is a type of non-hierarchical clustering. It is an iterative process in which each record is assigned to the closest centroid. The centroid for each cluster is then recomputed. These steps are repeated until a steady state has been reached.

#### Misapplication of clustering

Clustering is a very useful data reduction technique. However, it can easily be misapplied. The clustering results are highly affected by your choice of similarity measure and clustering algorithm. You should bear this in mind when you evaluate the results. If possible, you should replicate the clustering analysis using different methods. Apply cluster analysis with care and it can serve as a powerful tool for identifying patterns within a data set.

### 7.19.4.2 K-means Clustering Algorithm

The K-means clustering algorithm is an iterative process. Each record is assigned to the closest centroid. New centroids are calculated for the resulting clusters and the records are reassigned to the closest centroid. The process automatically stops once a steady state has been reached.

► **This is how it works:**

1. The similarity between each record and all centroids is calculated using a selected similarity measure.
2. All records are assigned to the centroid that is most similar to them.
3. The new centroids for the resulting clusters are calculated according to a method defined by the choice of similarity measure.
4. Steps 1 - 3 are repeated until a steady state is reached, or in other words when no records any longer change cluster between two steps and the centroids no longer vary.

**Note:** If you are using Data centroid based search then the algorithm is slightly different.

### 7.19.4.3 Required Input for K-means Clustering

You have to specify the following before you can start a K-means clustering:

- Which similarity measure should be used?
- How many clusters do you want?
- How should the cluster centroids be initialized?

## Similarity measures

Several different similarity measures are available to the K-means clustering tool. Similarity measures express the similarity between records or profiles as numbers and thus make it possible to rank the records according to their similarity. For information about the various measures, go to the section called Similarity measures.

## Initializing cluster centroids

When you start a K-means clustering, you have to decide how many clusters you want to use and how the centroids of these clusters should be initialized.

The number of clusters should be based on a reasonable hypothesis of the distribution of the data. If you have too few clusters, you may miss important details and if you have too many clusters, you may end up with many empty clusters or clusters with only one record in them. Click for information about the available methods for Initializing cluster centroids.

## Calculating resulting cluster centroids

The centroids for the resulting clusters from each step in a K-means clustering are calculated differently depending on which similarity measure you use. Click for information about calculating resulting cluster centroids.

### 7.19.4.4 Initializing K-means Cluster Centroids

To initiate a K-means clustering, you have to decide which initial centroids to use. The following methods are available:

- Data centroid based search
- Evenly spaced profiles
- Randomly generated profiles
- Randomly selected profiles
- From marked records

#### Data centroid based search

This method for initializing the centroids uses a slightly different algorithm compared to other methods.

##### ► This is how it works:

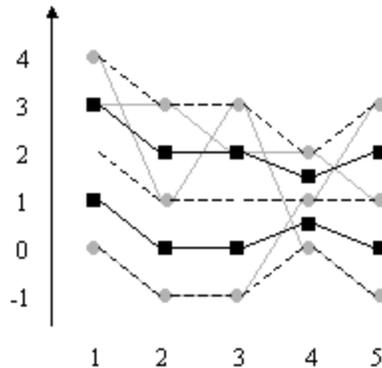
1. The first centroid is calculated as the average of all profiles.
2. The similarity between the centroid and all profiles is calculated using a selected similarity measure.
3. The profile that is least similar to the first centroid is picked to be the second centroid.
4. The similarity between the second centroid and all remaining profiles is calculated.
5. The profiles that are more similar to the second centroid than the first centroid are assigned to the second centroid and are then not investigated further.
6. Of the remaining profiles, the profile that is least similar to the first centroid is picked to be the third centroid.
7. Steps 4 through 6 are repeated until the specified number of clusters is reached, or until there are no more profiles left to assign.

If you run out of profiles before the specified number of clusters has been created, the procedure is automatically repeated but with an adjusted requirement for assigning profiles to the second centroid instead of the first centroid. In the first round, the requirement is that the second centroid must be more similar to the profile than the first centroid. In the second round we sharpen this requirement so that fewer profiles are assigned to the second centroid. If you again run out of profiles before the specified number of clusters has been created, the requirement is again adjusted using the same method.

## Evenly spaced profiles

This method generates profiles to be used as centroids that are evenly distributed between the minimum and maximum value for each variable in the profiles in your data set.

The example below shows how the initial centroids are derived. We have a total of three profiles in the data set (the gray circles connected with lines). We have specified that we want two clusters. The distance between the minimum and maximum value for each variable in the profiles has therefore been divided into two parts (separated by the dashed black lines). The centroids are the average values of each part between the minimum and maximum values (the black squares connected with black lines).

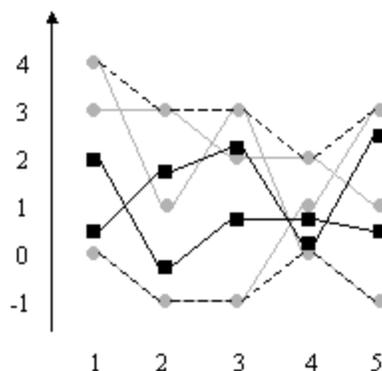


In reality you would have many more than three profiles in your data set, but the example shows the principle of how centroids are derived using the evenly spaced method.

## Randomly generated profiles

In this method you generate new profiles to use as centroids from random values based on your data set. Each value in the centroids is randomly selected as any value between the minimum and maximum for each variable in the profiles in your data set.

The example below shows how the initial centroids are derived. We have a total of three profiles in the data set (the gray circles connected with lines). The minimum and maximum values are connected with the dashed black lines. Two examples of randomly generated profiles are shown as the black squares connected with black lines. As can be seen from the figure, each variable in the randomly generated profiles can assume any value between the minimum and maximum value for that variable.



In reality you would have much more than three profiles in your data set, but the example shows the principle of how centroids are randomly generated.

## Randomly selected profiles

With this method, you use existing profiles that are randomly selected from your data set as centroids.

### From marked records

You import the currently marked profiles in your visualizations and use them as centroids. This option is only available if there are any records marked when starting the tool.

## 7.19.4.5 Calculating Resulting K-means Cluster Centroids

After each step in a K-means clustering, the resulting centroid of each cluster is calculated. The centroids are calculated differently depending on the similarity measure used for the clustering.

The new centroid  $c_{new}$  for a K-means cluster  $C$  with  $n$  records  $\{a_i\}_{i=1}^n$  and  $k$  dimensions is calculated as shown below for the various similarity measures.

### Correlation

$$c_{new}(C) = c_{new}\left(\left\{\frac{\bar{a}_i - \bar{a}_i}{std(\bar{a}_i)}\right\}_{i=1}^n\right) = \left(\frac{1}{n} \sum_{i=1}^n \frac{(\bar{a}_{ij} - \bar{a}_i)}{std(\bar{a}_i)}\right)_{j=1}^k$$

where

$$std(\bar{a}_i) = \sqrt{\frac{1}{k} \sum_{j=1}^k (\bar{a}_{ij} - \bar{a}_i)^2}$$

$$\bar{a}_i = \frac{1}{k} \sum_{j=1}^k \bar{a}_{ij}$$

### Cosine correlation

$$c_{new}(C) = c_{new}\left(\left\{\frac{\bar{a}_i}{norm(\bar{a}_i)}\right\}_{i=1}^n\right) = \left(\frac{1}{n} \sum_{i=1}^n \frac{\bar{a}_{ij}}{norm(\bar{a}_i)}\right)_{j=1}^k$$

where

$$norm(\bar{a}_i) = \sqrt{\frac{1}{k} \sum_{j=1}^k \bar{a}_{ij}^2}$$

### Euclidean distance and City block distance

$$c_{new}(C) = c_{new}\left(\{\bar{a}_i\}_{i=1}^n\right) = \left(\frac{1}{n} \sum_{i=1}^n \bar{a}_{ij}\right)_{j=1}^k$$

## 7.19.4.6 K-means Clustering References

### K-means clustering

Mirkin, B. (1996) Mathematical Classification and Clustering, Nonconvex Optimization and Its Applications Volume 11, Pardalos, P. and Horst, R., editors, Kluwer Academic Publishers, The Netherlands.

MacQueen, J. (1967). Some methods for classification and analysis of multivariate observations. In Le Cam, L. M. and Neyman, J., editors, Proceedings of the Fifth Berkeley Symposium on Mathematical Statistics and Probability. Volume I: Statistics, pages 281-297. University of California Press, Berkeley and Los Angeles, CA.

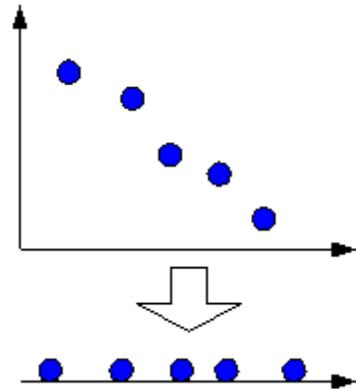
## General information about clustering

Hair, J.F.Jr., Anderson, R.E., Tatham, R.L., Black, W.C. (1995) *Multivariate Data Analysis*, Fourth Edition, Prentice Hall, Englewood Cliffs, New Jersey.

## 7.20 Principal Component Analysis

### 7.20.1 Principal Component Analysis Overview

Spotfire DecisionSite Statistics provides a simple but powerful data reduction tool called Principal Component Analysis (PCA). The goal of PCA is to reduce the dimensionality of a data set (describe the data set using fewer variables) without significant loss of information.



The PCA algorithm takes a high-dimensional data set as input, and produces a new data set consisting of fewer variables. These variables are linear combinations of the original variables, so it is often possible to ascribe meaning to what they represent.

### 7.20.2 Using Principal Component Analysis

#### 7.20.2.1 Initiating a PCA Calculation

##### ► To initiate a PCA calculation:

1. Select **Data > Clustering > Principal Component Analysis...**  
Response: The Principal Component Analysis dialog is opened.
2. Select the value columns on which to base the clustering from the **Available columns** list and click **Add >>**.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns in the Available columns list. Then click **Add >>** to move the columns to the Selected columns list. You can sort the columns in the list alphabetically by clicking on the Name bar.
3. Click a radio button to select whether to work on **All records** or **Selected records**.
4. Select a method to **Replace empty values with** from the drop-down list.
5. Type the number of **Principal components** that you want to calculate.  
Comment: The number of principal components is the number of dimensions to which you wish to reduce the original data. The PCA tool calculates the  $n$  best components, where  $n$  is the same as the number of dimensions to which you are projecting.
6. Type a **Column name** for the resulting column or use the default name.  
Comment: Select the **Overwrite** check box to overwrite an old column with the same name.
7. Select whether to create a **2D** or a **3D** scatter plot showing the principal components.

Comment: Clear the Create Scatter Plot check box if you want to perform the calculation without creating any new visualizations.

8. Decide if you want to **Generate HTML report** or not, by selecting or clearing the check box.

Comment: The PCA HTML report contains information about the calculation presented as an HTML page.

9. Decide if you want to **Launch DecisionSite with PCA report** or not, by selecting or clearing the check box.

Response: This launches a new session of DecisionSite containing a plot with the PCA results. For more information on the results, see PCA HTML Report.

10. Click **OK**.

Response: The principal components are calculated and new columns containing the results are added to the data set. If **Create Scatter Plot** has been selected, a new scatter plot is created according to your settings (2D or 3D). If **Generate HTML report** has been selected, then the PCA Result report is displayed in your default web browser.

### 7.20.2.2 Interpreting PCA Results

When the PCA tool is executed, a Principal Component Analysis is performed on the current data set. The result can be regarded as a new data set with fewer variables.

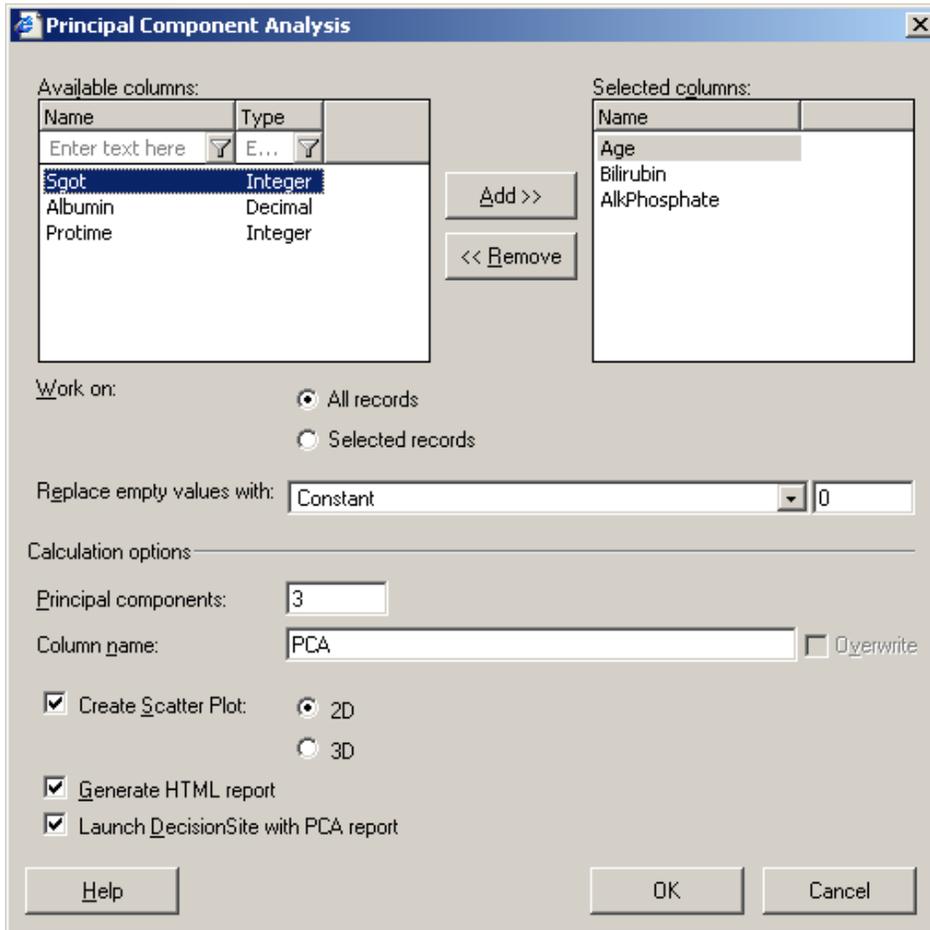
The results of a PCA calculation are often displayed in a scatter plot (scores plot) mapping the principal component score of each projected record. Each point in the plot represents a record in the original data set. The position along a certain axis represents the score of the record on that principal component.

The PCA tool generates one or more principal components depending on the settings in the Principal Component Analysis dialog.

An alternative way of studying the results of PCA is by showing to what extent each original dimension (value column) has contributed to a certain principal component. If desired, you can generate either a new DecisionSite session or a PCA HTML report containing an eigenvector plot where you can directly see which column has contributed the most to a certain principal component.

## 7.20.3 User Interface

### 7.20.3.1 Principal Component Analysis Dialog



Option	Description
<b>Available columns</b>	Displays all available data columns which you can use in a calculation. Click a column name in the list and click <b>Add &gt;&gt;</b> to add it to the Selected columns list. To select more than one column, press <b>Ctrl</b> and click the column names in the list, then click <b>Add &gt;&gt;</b> . You can choose from all columns that contain decimal numbers or integers. <b>Note:</b> You can right-click on the Name header to get a pop-up menu where you can select other attributes you would like to be visible.
<b>Enter text here</b> 	If you have a data set with many columns, you can right-click on the header of the columns in the Available columns list box and select <b>Show Search Field</b> from the pop-up menu. This will display a search field where you can type a search string and limit the number of items in the list. It is possible to use the wildcard characters * and ? in the search.
<b>Selected columns</b>	Displays the currently selected data columns that you want to use in the calculation.
<b>Add &gt;&gt;</b>	Adds the highlighted data column to the list of selected columns.
<b>&lt;&lt; Remove</b>	Removes the highlighted data column from the list of selected columns

	and places them back in the list of available columns.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Replace empty values with</b>	Defines how empty values in the data set should be replaced. <b>Constant</b> allows you to replace the empty values by any constant (type a number in the text box). <b>Row average</b> replaces the value by the average value of the entire row. <b>Row interpolation</b> sets the missing value to the interpolated value between the two neighboring values in the row. <b>Column average</b> returns the average of the corresponding column values.
<b>Principal components</b>	Enter the number of dimensions to which you wish to reduce the original data. This is directly linked to preserved variability. This is also the number of columns that will be exported to the data set.
<b>Column name</b>	The name of the columns containing the results from the principal component analysis.
<b>Overwrite</b>	Select this check box if you want to replace a previously added column (with the same name as the one typed in the <b>Column name</b> text box) when you add a new column. Clear the check box if you wish to keep the old column.
<b>Create Scatter Plot</b>	Select whether to create a 2D or 3D plot showing the result of the principal component analysis. Clear the check box if you do not want to create a plot.
<b>Generate HTML report</b>	Select this check box to generate an HTML report with the PCA results. Note that the report is not saved automatically.
<b>Launch DecisionSite with PCA report</b>	Select this check box to start a new DecisionSite session containing a plot with the PCA results. For more information on the results, see PCA HTML Report.

► **To reach the Principal Component Analysis dialog:**

Select **Data > Clustering > Principal Component Analysis...**

### 7.20.3.2 PCA HTML Report

The PCA Result report contains all information about the calculation and results. It is displayed as an HTML page in your default web browser. You decide whether or not you want to create a PCA report by selecting or clearing the **Generate HTML report** check box in the Principal Component Analysis dialog.

**Note:** The PCA Result report is not saved automatically. To keep the report, you have to save it manually.

Option	Description
<b>Number of principal components</b>	The number of components that you selected to project your data to.

<b>Variability preserved</b>	This is directly linked to the number of dimensions to project to (see above). A value of 100% indicates that all variability of the original data is preserved. See also Preserving variability.
<b>Added scored columns</b>	Displays the names of the result columns added to the data set.
<b>Value columns included</b>	Displays the names of the value columns that were included in the calculation.
<b>Eigenvalues</b>	<p>The Eigenvalues table presents the output of the PCA in a numerical format. Each row is associated with a principal component. The columns represent the following:</p> <p><b>Principal Component:</b> Identifies the principal component.</p> <p><b>Eigenvalue:</b> Informally, a measure of the amount of information contained in that component.</p> <p><b>Eigenvalue (%):</b> Displays the eigenvalue as a percentage of the total of all eigenvalues.</p> <p><b>Cumulative Eigenvalue (%):</b> The sum of the eigenvalues of this and previous components, as a percentage of the total of all eigenvalues. The cumulative eigenvalue of the N<sup>th</sup> principal component is the same as the variability preserved when projecting to N dimensions.</p>
<b>Eigenvalue plot</b>	<p>The Eigenvalues plot, found beside the Eigenvalues table, plots the relative eigenvalue of each principal component, ordered by magnitude. It is useful for rapidly discerning the number of components required for preserving a reasonable amount of variability.</p> <p>A sharp drop followed by a sequence of lower values indicates that the first few components contain a large proportion of the information:</p>
<b>Eigenvectors</b>	These figures indicate to what extent each column in the original data set contributes to each principal component.

## 7.20.4 Theory and Methods

### 7.20.4.1 PCA Methods Overview

PCA transforms a set of correlated variables into a smaller set of uncorrelated variables called principal components. It is therefore most useful for screening multivariate data in order to

- reduce the dimensionality of the data set
- identify new, meaningful underlying variables
- verify clustering

#### Reducing dimensionality

Strictly speaking, PCA does not *reduce* dimensionality, but reveals the *true* dimensionality of the original data. Even though  $n$  variables have been measured, data can sometimes be plotted in less than  $n$  dimensions without losing any significant information. PCA tells us if this is the case, and which the principal components are.

#### Identifying new variables

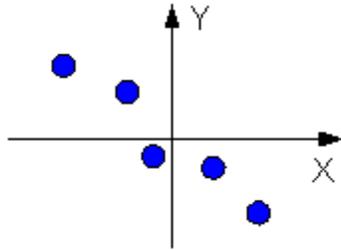
PCA will always identify new variables - principal components. These are linear combinations of the original variables, but are not necessarily *meaningful*. In some cases they can be interpreted as parameters that can be measured experimentally, but usually they cannot. Even so, principal components are often *useful*, for data screening, assumption checking, and cluster verification.

## Verifying clustering

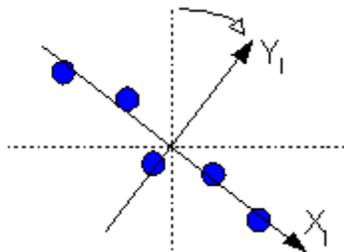
Clustering algorithms are not without drawbacks. Several parameters, such as initial centroid layout and distribution, affect the results of clustering. This means that we need an independent mechanism for evaluating our results. Because we cannot look at a multi-dimensional ( $> 3D$ ) data set visually, PCA can be used to reduce the dimensionality of the data set. We can then inspect it visually, and see if observable clusters correspond to the structure suggested by the clustering algorithm.

### 7.20.4.2 Understanding PCA

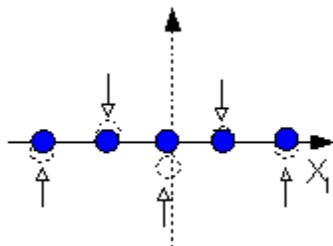
PCA works on the assumption that the data is distributed in such a way that it can be reduced to fewer dimensions. Consider the following:



The data set has two dimensions, and we cannot ignore one axis without losing a lot of important information. However, the data seems to be linear. We therefore rotate the coordinate system so as to maximize variation along one axis:



Seen in reference to the new coordinate system, we have a set of points that vary significantly only along  $X_1$ . We can therefore project the points onto this new axis, and ignore the comparatively small variation along  $Y_1$ :



The vectors that define the remaining dimensions (in this case only  $X_1$ ) are what we mean by **principal components**. The position of a point along a given principal component is referred to as its **score**.

This example deals with the trivial case of two dimensions being reduced to one, in which case data reduction is actually redundant. PCA becomes truly useful only with data sets that are comprised of a large number of variables.

### 7.20.4.3 PCA Preserving Variability

When performing PCA, we can choose the number of dimensions to project the data to. We want fewer variables than the original data set, but we also want to preserve as much of the

information as possible. The question is how many dimensions to include in order to find a balance between these two requirements.

### Total variability

If we add up the variance along each axis in the original data set, we get the **total variability**. Informally, this is an estimate of the amount of information in the data set.

$$V_T = [V_1 + V_2 + \dots + V_n]$$

When the PCA algorithm rotates the coordinate system, variability remains unchanged. However, when we select a subset of dimensions on which to project the data, we typically reduce the total variability.

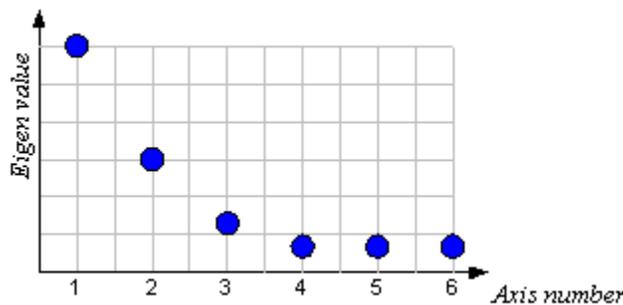
### Preserved variability

When a coordinate system has been rotated, the new axes are ranked according to the variance of the data along each new axis (which corresponds to the eigenvalue).

If we choose to project to one dimension, in other words the one with the highest variance, this dimension will correspond to a certain proportion of the total variability, for instance 60%. The second best dimension might contribute another 20%. This adds up to 80% **preserved variability**. By including more dimensions, we can improve this value.

$$V_P = \frac{[V_1 + V_2 + \dots + V_d]}{V_T}$$

Eventually, due to the nature of the PCA algorithm, adding more dimensions will have little or no effect on the preserved variability.



### How many dimensions should I use?

It is common to set a limit for the acceptable preserved variability (for example 95%), however, the limit depends largely on the type of data being analyzed. In most cases, it is desirable to reduce the dimensionality to two or three axes, so that these can be investigated visually.

#### 7.20.4.4 PCA References

For detailed accounts of the PCA methods and algorithms used in the Principal Component Analysis tool, the following book is recommended:

Jolliffe, I., T., *Principal Component Analysis*, Springer Series in Statistics, New York, Springer-Verlag, 1986.

## 7.21 Treatment Comparison

### 7.21.1 Treatment Comparison Overview

The Treatment Comparison tool provides methods for distinguishing between different treatments for an individual record. An example of when this could be useful would be a case where a cell has access to sugar for a certain number of timepoints ("first treatment") and then

has not for the remaining timepoints ("second treatment"). There are two types of treatment comparisons: t-test/Anova and Distinction/Multiple distinction.

The *t-test* is a commonly used method to evaluate the differences in means between two groups. *Anova* means **A**nalysis of **V**ariance and is similar to the t-test but can be used on multiple groups.

In the Distinction calculation the variables (columns) within a row are divided into two groups. A distinction value is calculated for each row based on the two groups of values. The distinction value is a measure of how distinct the difference in expression level is between the two parts of the row (e.g., access to sugar or no access).

## 7.21.2 Using Treatment Comparison

### 7.21.2.1 Calculating Distinction Values

The distinction value is a measure of how distinct the difference is between different parts of a profile.

#### ► To calculate distinction values:

1. Select **Data > Pattern Detection > Treatment Comparison...**  
Response: The Treatment Comparison dialog is displayed and all available columns are listed in the Value columns field. If the tool has been opened previously, the earlier grouping will remain.
2. Move and organize the desired columns into groups in the Grouped value columns field.  
Comment: Select columns and click on the **Add >>** button. The column will end up in the group that was selected in the Grouped value columns field. Click **New Group** to add a group, click **Delete Group** to delete a selected group. The tool requires at least two columns in each group to be able to perform the calculations.
3. Select a group and click on **Rename Group** to edit the group name.  
Comment: The names of the result columns will be the group names followed by (Distinction). Therefore, using meaningful group names will prove valuable when interpreting the results later on.
4. Click a radio button to select whether to work on **All records** or **Selected records**.
5. Select a method to **Replace empty values with** from the drop-down list.
6. Select **Distinction/Multiple distinction** from the **Comparison measure** list box.
7. Click **OK**.

Response: New columns that contain distinction values are added to the data set. A new visualization of the profiles is created, ordered by group with the range slider set to the lowest value (=the highest distinction). An annotation may also be added.

### 7.21.2.2 Calculating T-test/Anova P-values

The t-test/Anova is used to determine if there are any differences between the values of different groups in a row. A t-test is performed when comparing two groups while the Anova is used for three groups or more. The result is presented as a p-value, where a low p-value represents a large difference.

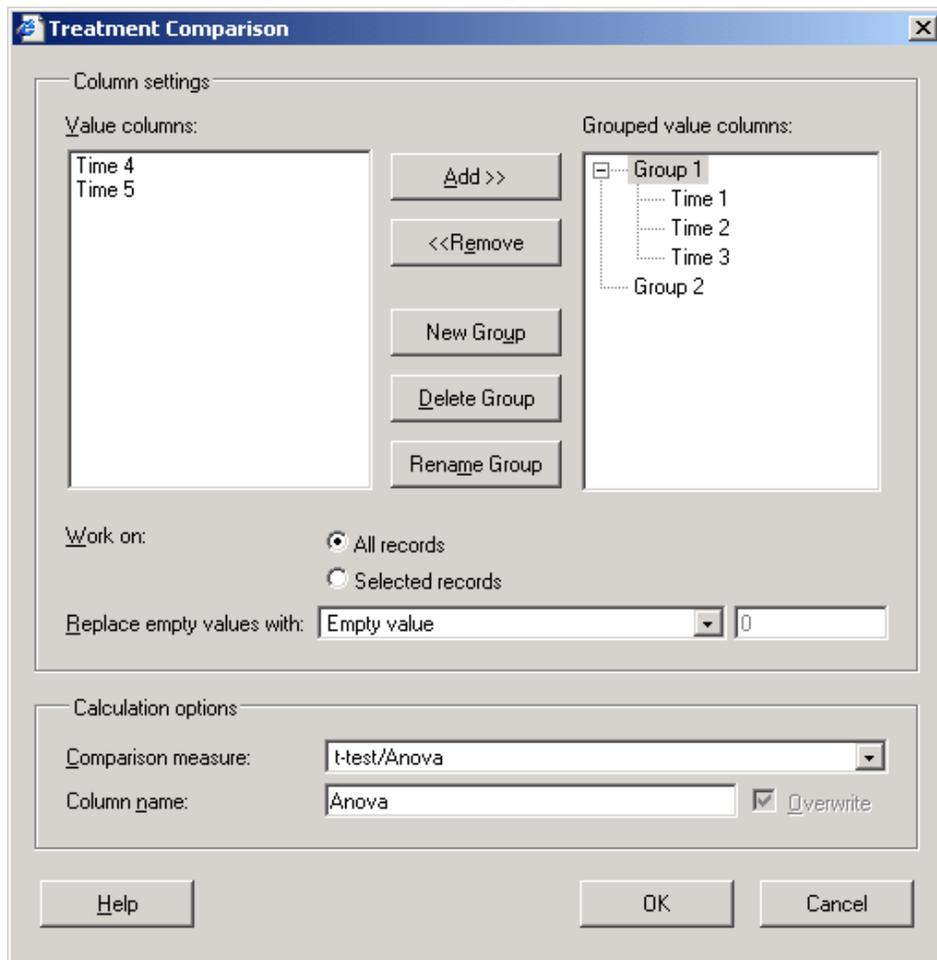
#### ► To calculate t-test/Anova p-values:

1. Select **Data > Pattern Detection > Treatment Comparison...**  
Response: The Treatment Comparison dialog is displayed and all available columns are listed in the Value columns field. If the tool has been opened previously, the earlier grouping will remain.

2. Move and organize the desired value columns into groups in the Grouped value columns field.  
 Comment: Select columns and click on the **Add >>** button. The column will end up in the selected group of the Grouped value columns field. Click **New Group** to add a group, click **Delete Group** to delete a selected group. The tool requires at least two columns in each group to be able to perform the calculations.
3. Click a radio button to select whether to work on **All records** or **Selected records**.
4. Select a method to **Replace empty values with** from the drop-down list.
5. Select **t-test/Anova** from the **Comparison measure** list box.
6. Type a new **Column name** in the text box or use the default name.  
 Comment: Select the **Overwrite** check box if you want to overwrite a previously added column with the same name. If you do not want to overwrite, make sure Overwrite is cleared or type a unique name in the Column name text box.
7. Click **OK**.  
 Response: A new column that contains the p-values (log-scaled) is added to the data set. A new visualization of the records is created, ordered by group with the range slider set to the lowest value (= the largest difference between the groups). An annotation containing information about which group each variable belongs to may also be added.

## 7.21.3 User Interface

### 7.21.3.1 Treatment Comparison Dialog



Option	Description
<b>Value columns</b>	The data columns that you want to use in the calculation. Click a column name in the list to select it. To select more than one column, press <b>Ctrl</b> and click the column names in the list. You can choose from any column that contains reals or integers.
<b>Grouped value columns</b>	Displays the groups on which the calculation is performed. You can add, delete or rename groups from the field by clicking on the corresponding buttons to the left of the field. You move value columns between the fields using the Add >> and << Remove buttons.
<b>Add &gt;&gt;</b>	Moves selected columns from the Value columns field to a selected group in the Grouped value columns field. Click to select the desired columns and the group that you want to add the columns to, then click on Add >>.
<b>&lt;&lt; Remove</b>	Removes all columns from a selected group and brings them back to the Value Columns field.
<b>New Group</b>	Adds a new group to the Grouped value columns field.
<b>Delete Group</b>	Deletes a selected group from the Grouped value columns field. If the group contained any value columns they are moved back to the Value columns field.
<b>Rename Group</b>	Opens the Edit Group Name dialog, where you can change the name of the selected group. Since the names of the result columns from a distinction calculation will be the group names followed by (Distinction), using meaningful group names will prove valuable when interpreting the results later on.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Replace empty values with</b>	Defines how empty values in the data set should be replaced. <b>Empty value</b> simply ignores empty values. <b>Constant</b> allows you to replace the empty values by any constant (type a number in the text box). <b>Row average</b> replaces the value by the average value of the entire row. <b>Row interpolation</b> sets the missing value to the interpolated value between the two neighboring values in the row.
<b>Comparison measure</b>	Select whether to perform a <b>t-test/Anova</b> or a <b>Distinction/Multiple distinction</b> calculation.
<b>Column name</b>	The name of the new column containing the results from the t-test/Anova calculation. The Column name text box is not available when performing Distinction/Multiple distinction calculations, since the names of the result columns are then based on the group names.
<b>Overwrite</b>	Select this check box if you want to replace previously added columns (with the same group names or the same name as the one typed in the <b>Column name</b> text box) when you add new columns. Clear the check box if you wish to keep the old columns.

► **To reach the Treatment Comparison dialog:**

Select **Data > Pattern Detection > Treatment Comparison....**

## 7.21.4 Theory and Methods

### 7.21.4.1 Distinction Calculation Method Overview

The distinction value is a measure of how distinct the difference in expression level is between different parts of a profile. This could be useful, e.g., when looking for genetic markers. An example would be a gene that shows high expression for a certain type of tumor cells but not for healthy cells.

You start by dividing the variables in your profiles into groups (based on factors such as type of tissue, pH, etc.). We are looking for genes that show a distinct difference in expression between the groups. While there should be a large difference in expression between the groups there should also be as little variation as possible within the groups. The profiles are compared to an idealized expression pattern in which the expression level is uniformly high in the first group and uniformly low in the second group, etc. The calculated distinction values are a measure of how similar each profile is with this ideal profile.

Group 1                      Group 2                      Group 3



Profiles with high positive distinction values have high expression values in the first group and low expression values in the second group. Profiles with high negative distinction values have low expression values in the first group and high expression values in the second group.

### 7.21.4.2 Distinction Calculation Algorithm

The distinction value for a profile  $y$  with  $n_1$  number of values in the first group and  $n_2$  number of values in the second group is calculated as:

$$\text{Dist.value}(y) = \frac{\bar{y}_1 - \bar{y}_2}{\text{std}(y_1) + \text{std}(y_2)}$$

where

$y_{1i}$  is the  $i$ th value in the first group and

$$\text{std}(y_1) = \sqrt{\frac{1}{n_1 - 1} \sum_{i=1}^{n_1} (y_{1i} - \bar{y}_1)^2}$$

$$\text{std}(y_2) = \sqrt{\frac{1}{n_2 - 1} \sum_{i=1}^{n_2} (y_{2i} - \bar{y}_2)^2}$$

$$\bar{y}_1 = \frac{1}{n_1} \sum_{i=1}^{n_1} y_{1i}$$

$$\bar{y}_2 = \frac{1}{n_2} \sum_{i=1}^{n_2} y_{2i}$$

### 7.21.4.3 T-test/Anova Method Overview

A t-test is performed in order to verify whether or not observed differences between two groups are real. If more than two groups are investigated, an Anova is the proper way to test whether the mean of a variable differs among the groups. An Anova on two groups is equivalent to a t-

test using two-sample equal variance. The Treatment Comparison tool will use the suitable calculation depending of the number of groups selected. In this version of the tool, a one-way layout of Anovas has been employed. This means that the experimental design should be of the type where the outcome of a single continuous variable is compared between different groups (such as cells exposed to different dosage of a growth factor). The tool cannot be used to analyze experiments where two or more variables vary together.

The t-test/Anova comparison assumes the following:

- The data is approximately normally distributed.
- The variances of the separate groups are approximately equal.

If the data do not fulfill these conditions, the t-test/Anova comparison will produce unreliable results.

#### 7.21.4.4 T-test/Anova Algorithm

The t-test/Anova calculation basically compares the difference between groups by comparing the mean values of the data. The results are obtained by testing the null hypothesis, e.g., the hypothesis that all the mean values of the different groups are equal.

The Anova tool calculates the mean values of the variable, both the total mean value and the means within the groups. Then, the difference between each of the values and the average value for the group is calculated and squared. This is done in order to obtain a positive number indicating how big the difference between the value and the average is.

Finally, the sum of the squared difference values is calculated. Now, we have a value that relates to the total deviation of the actual outcome of each record from the mean of each group. This value is referred to as the sum of squares within groups, or  $S2Wthn$ . To compare the groups, we also need to know the deviation of the group mean from the total mean value for all of the data. The required value, the sum of squares between groups, or  $S2Btwn$ , is calculated as the number of values in the groups times the squared difference sum between the group means and the total mean:

$$S2Btwn = N_1(\bar{x}_1 - \bar{x}_{tot})^2 + N_2(\bar{x}_2 - \bar{x}_{tot})^2 + \dots + N_N(\bar{x}_N - \bar{x}_{tot})^2$$

$$\bar{x}_{tot} = \frac{1}{n} \sum_{i=1}^n x_i$$

The two sums of squares can then be used to obtain a statistic for testing the null hypothesis, the so called F-statistic. The F-statistic is calculated as:

$$F = \frac{S2Btwn/dfB}{S2Wthn/dfW}$$

The degree of freedom between groups,  $dfB$ , equals the number of groups minus 1.

The degree of freedom within groups,  $dfW$ , equals the total number of values minus the number of groups.

If the null-hypothesis is true, there should be no difference between within and between groups variability and their ratio should be equal to 1. The F-value is distributed according to the F-distribution, which is commonly presented in mathematical tables/handbooks. The F-value, in combination with the degrees of freedom and an F-distribution table can give you the p-value.

The p-value is the observed significance level, or probability of a *Type I error* concluding that a difference between population means exists when in fact there is no difference. If the p-value is below a certain level (usually 0.05) it is assumed that there is a significant difference between the group means. The lower the p-value, the larger the difference.

#### 7.21.4.5 Treatment Comparison References

##### References for distinction calculation

This method was introduced for the analysis of transcript profiling data in Golub, T.R. et al. (1999), *Science*, 286, pp 531-537.

## 7.22 Profile Search

### 7.22.1 Profile Search Overview

The Profile Search tool calculates the similarity to a selected profile for all records in the data set and adds the result as a new column. The records are then ranked according to their similarity to the master profile.

You can use an existing record from your data set or create an average profile from several marked records. The built in profile editor makes it possible to edit the master profile.

### 7.22.2 Using Profile Search

#### 7.22.2.1 Initiating a Profile Search

► **To initiate a profile search:**

1. Click to activate the profile that you want to use as master profile in one of the visualizations or mark a number of profiles on which to base the master profile.  
Comment: You can always edit the active or marked profile to obtain a master profile entirely by your choice.
2. Select **Data > Pattern Detection > Profile Search...**  
Response: The Profile Search dialog is opened.
3. Select the value columns on which to base the clustering from the **Available columns** list and click **Add >>**.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns in the Available columns list. Then click Add >> to move the columns to the Selected columns list. You can sort the columns in the list alphabetically by clicking on the Name bar.
4. Click a radio button to select whether to work on **All records** or **Selected records**.
5. Select a method to **Replace empty values with** from the drop-down list.
6. Select whether to use profile from: **Active record** or **Average from marked records**. This is only an option if you have both marked records and an active record to begin with.  
Response: The selected profile is displayed in the profile editor and the name of the profile is displayed to the left above the profile in the editor.  
Comment: You can edit the profile in the editor and type a new name for the edited profile, if desired.
7. Select which **Similarity measure** you want to use for the profile search.  
Comment: Click for information about the available similarity measures.
8. Type a **Column name** for the resulting column or use the default name.  
Comment: Select the **Overwrite** check box to overwrite an old column with the same name.
9. Click **OK**.  
Response: The search is performed using the master profile displayed in the editor, and the results are added to the data set as a new column. A new scatter plot is created displaying the rank vs. the similarity, and an annotation containing information about the calculation settings is added to the visualization.

#### 7.22.2.2 Changing a Value in a Master Profile

**Note:** The starting profile does not restrict you in any way. You can easily change or delete existing values in the profile to create any master profile of your choice.

► **To change a value in a master profile:**

1. Select the profile that you want to edit by activating a record in a visualization.
2. Select **Data > Pattern Detection > Profile Search...**  
Response: The Profile Search dialog is opened. The active profile is displayed in the profile editor.
3. Select the value columns on which to base the clustering from the **Available columns** list and click **Add >>**.  
Comment: For multiple selection, press **Ctrl** and click on the desired columns in the Available columns list. Then click Add >> to move the columns to the Selected columns list. You can sort the columns in the list alphabetically by clicking on the Name bar.
4. Click **Edit...**  
Response: The Profile Search: Edit dialog is opened.
5. Click directly in the editor to activate the variable that you want to change and drag the value to obtain a suitable look on the profile.  
Response: The new value is immediately displayed in the editor.  
Comment: To set a value for a variable with a missing value, select the variable from the Active column list and type a number in the Value text box.
6. Type a **Profile name** in the text box or use the default name.
7. Click **OK**.  
Response: The Profile Search: Edit dialog is closed and the edited profile is shown in the Profile Search dialog. The **Edited** radio button has been selected by default, but you can return to the old profile by clicking Use profile from: **Active record**.

**Tip:** You can also use the fields below the editor to select an **Active column** in the profile and edit its **Value**.

### 7.22.2.3 Removing a Value from Profile Search

► **To remove a value from a master profile:**

1. Activate the profile that you want to edit in a visualization.
2. Select **Data > Pattern Detection > Profile Search...**  
Response: The Profile Search dialog is opened. The active profile is displayed in the profile editor.
3. Click **Edit...**  
Response: The Profile Search: Edit dialog is opened.
4. Click on the value that you want to remove and press **Delete**.  
Response: The value for the variable is removed in the display.

**Tip:** You can also use the fields below the editor to select an **Active column** in the profile and remove its **Value** by pressing **Delete**.

### 7.22.2.4 Interpreting the Results of Profile Search

When a profile search has been performed, the selected profiles or records in the data set have been ranked according to their similarity to the selected master profile. The value of the selected similarity measure is added to the data set as a new column.

A new scatter plot can be created (optionally) displaying the Similarity plotted against the Similarity rank. This means that the record that is most similar to the master profile will be displayed in the lower, left corner of the visualization.

## 7.22.2.5 Adjusting the Scale of the Profile Editor

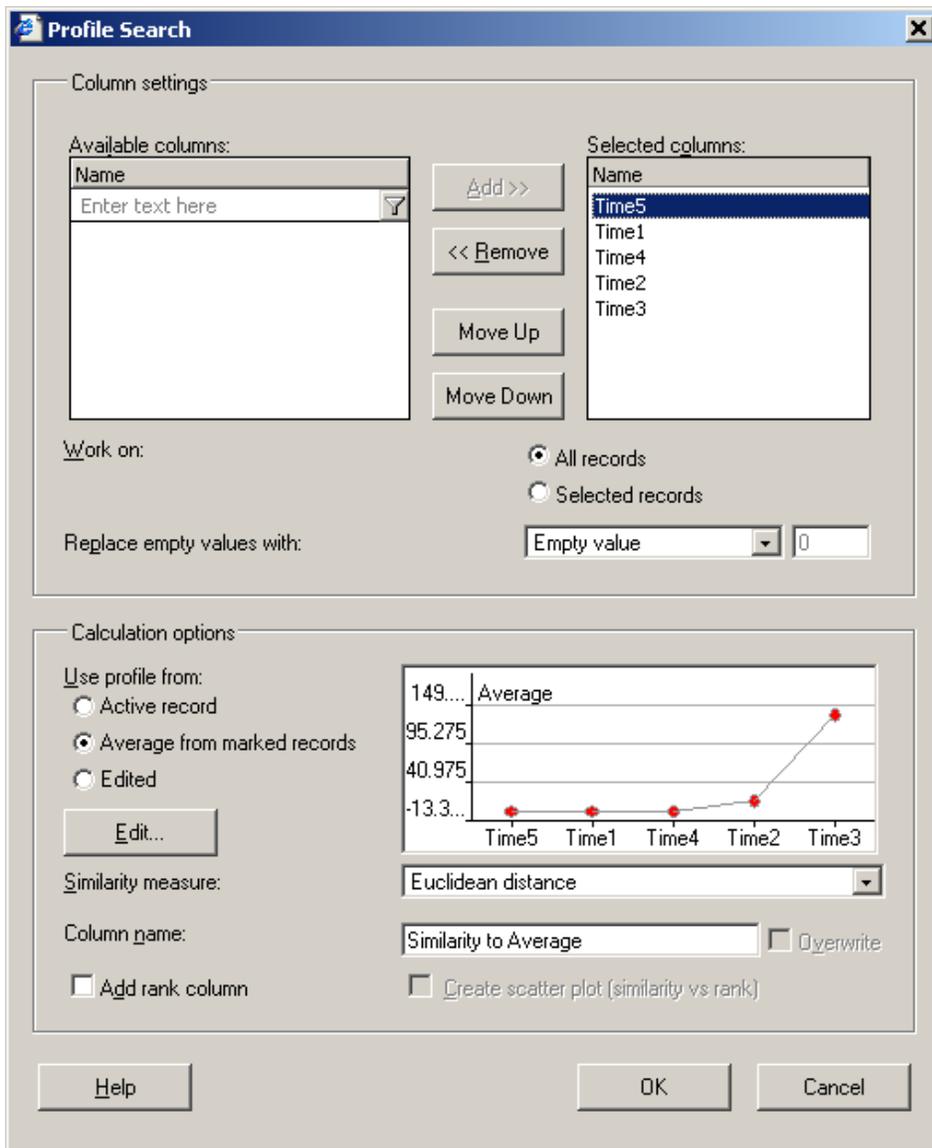
### ► To adjust the scale of the editor:

1. Click on the **Fit profile to screen** button, , in the Profile Search: Edit toolbar.
2. Click on the **Reset original profile scale** button, , to reset the scale.

**Tip:** You can also select **Fit to screen** or **Reset original scale** from the pop-up menu which is displayed by right-clicking in the edit window.

## 7.22.3 User Interface

### 7.22.3.1 Profile Search Dialog



**Profile Search**

Column settings

Available columns:

Name  
Enter text here

Add >>

<< Remove

Move Up

Move Down

Selected columns:

Name  
Time5  
Time1  
Time4  
Time2  
Time3

Work on:

All records  
 Selected records

Replace empty values with: Empty value 0

Calculation options

Use profile from:

Active record  
 Average from marked records  
 Edited

Edit...

Similarity measure: Euclidean distance

Column name: Similarity to Average  Overwrite

Add rank column  Create scatter plot (similarity vs rank)

Help OK Cancel

Line graph showing Average values for Time5, Time1, Time4, Time2, and Time3. The y-axis ranges from -13.3 to 149. The x-axis labels are Time5, Time1, Time4, Time2, and Time3.

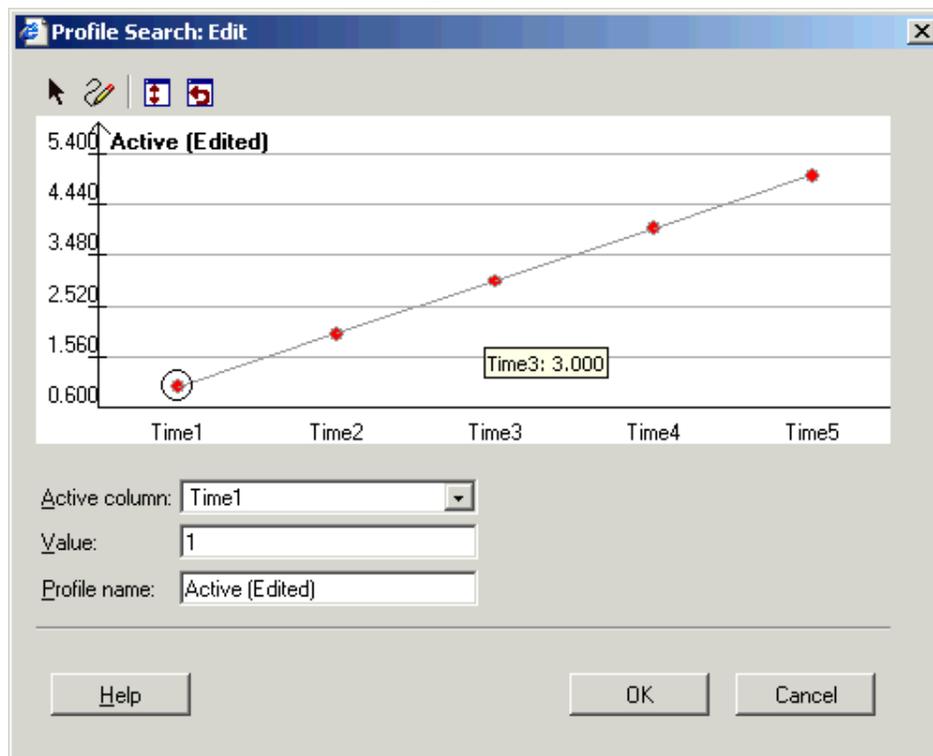
Option	Description
<b>Available columns</b>	The data columns that you can include in the search. Click a column name in the list to select it, then click <b>Add &gt;&gt;</b> to move it to the Selected columns list. To select more than one column, press <b>Ctrl</b> and click the column names in the list. You can choose from any column that contains decimal numbers or integers. <b>Note:</b> You can right-click on the Name header to get a pop-up menu where you can select other attributes you would like to be visible.
<b>Enter text here</b> 	If you have a data set with many columns, you can right-click on the header of the columns in the Available columns list box and select <b>Show Search Field</b> from the pop-up menu. This will display a search field where you can type a search string and limit the number of items in the list. It is possible to use the wildcard characters * and ? in the search.
<b>Selected columns</b>	Displays the currently selected data columns that you want to include in the search.
<b>Add &gt;&gt;</b>	Moves selected columns from the Available columns list to the Selected columns list.
<b>&lt;&lt; Remove</b>	Removes the selected columns and brings them back to the Available columns field.
<b>Move Up</b>	Moves the selected columns up in the Selected columns list and restructures the profile.
<b>Move Down</b>	Moves the selected columns down in the Selected columns list and restructures the profile.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.
<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Replace empty values with</b>	Defines how empty values in the data set should be replaced. <b>Empty value</b> calculates the similarity between the two profiles based only on the remaining part of the profile. The result is the same as if the missing value in the profile had been identical with the value for that variable in the master profile. <b>Constant</b> allows you to replace the empty values by any constant (type a number in the text box). <b>Row average</b> replaces the value by the average value of the entire profile. <b>Row interpolation</b> sets the missing value to the interpolated value between the two neighboring values in the profile.
<b>Use profile from: Active record</b>	Click this radio button to use an active record as the master profile.
<b>Use profile from: Average from marked records</b>	Click this radio button to use an average calculated from marked profiles as the master profile.
<b>Use profile from: Edited</b>	Click this radio button to use an edited profile as the master profile.
<b>Edit...</b>	Opens the Profile Search: Edit dialog.

<b>Similarity measure</b>	The similarity measure that you want to use when performing the search.
<b>Column name</b>	The name of the new columns containing the results from the profile search.
<b>Overwrite</b>	Select this check box if you want to replace a previously added column (with the same name as the one typed in the <b>Column name</b> text box) when you add a new column. Clear the check box if you wish to keep the old column.
<b>Add rank column</b>	Select this check box to add a column containing the similarity rank to the data set. In this column, the profile that is most similar to the master profile is given the number 1, the second profile is given number 2, etc.
<b>Create scatter plot (similarity vs rank)</b>	A new scatter plot can be created (optionally) displaying the Similarity plotted against the Similarity rank. This means that the record that is most similar to the master profile will be displayed in the lower, left corner of the visualization.

► **To reach the Profile Search dialog:**

Select **Data > Pattern Detection > Profile Search...**

### 7.22.3.2 Profile Search Edit Dialog



-  Edit profile. Allows you to manually edit a single value in the active column by clicking the value and dragging to the desired level.
-  Free hand drawing. Allows you to manually edit the values in the master profile by clicking and dragging the values using the mouse pointer as a free hand drawing tool.
-  Fit profile to screen. Automatically adjusts the scale to show the entire profile in the

edit window.



Reset original profile scale. Resets the scale to the original value range. Variables outside the range will no longer be visible in the editor.

Option	Description
<b>Active column</b>	Displays all columns available in the profile search.
<b>Value</b>	Displays the value of the active column. To change the value, type a new number in the box.
<b>Profile name</b>	The name of the edited profile. The name is displayed in the top left corner of the editorial window and it is also used in the default column name for the result of the search.

► **To reach the Profile Search: Edit dialog:**

1. Select **Data > Pattern Detection > Profile Search...**
2. Click **Edit...** below the displayed profile.

### 7.22.3.3 Profile Search Edit Pop-up Menu

The pop-up menu in the profile search editor includes the following options:

Option	Description
<b>Delete</b>	Deletes the value in the active column from the master profile.
<b>Insert</b>	Inserts a new value in the active column at the point of the right-click. This option is only available if there is a missing value in the master profile.
<b>Fit to screen</b>	Automatically adjusts the scale to show the entire profile in the edit window.
<b>Reset original scale</b>	Resets the scale to the original value range. Variables outside the range will no longer be visible in the editor.

► **To reach the Profile Search Edit pop-up menu:**

Right-click in the profile editor.

## 7.22.4 Theory and Methods

### 7.22.4.1 Profile Search Method Overview

In a profile search, all profiles (data points or table rows) are ranked according to their similarity to a master profile. The similarity between each of the profiles and the master profile is calculated using one of the available similarity measures. A new data column with the value of the selected similarity measure for each individual profile is added to the original data set as well as a similarity to master profile rank column.

### 7.22.4.2 Required Input for Profile Search

You have to specify the following before you can start a profile search:

- Which master profile do you want to use?

- Which similarity measure should be used?
- Should empty values be excluded from the search?

### **Master profile**

You can use an existing (active) profile as master profile or construct a new master profile as the average of several marked profiles. It is possible to edit the master profile using the built in editor before you start the search.

### **Similarity measures**

The Profile Search tool can use a variety of similarity measures. Similarity measures express the similarity between profiles as numbers, thus making it possible to rank the profiles according to their similarity. For information about the various measures, go to the section Similarity measures.

### **Excluding empty values**

The Profile Search tool can exclude empty values from the calculations. See Excluding empty values for more information.

## **7.22.4.3 Excluding Empty Values in Profile Search**

The Profile Search tool can exclude empty values from the calculations. When you calculate the similarity between the master profile and a profile that has a missing value, the variable with a missing value is excluded from the comparison. The calculated similarity between the two profiles is then based only on the remaining part of the profile. The result is the same as if the missing value in the profile had been identical with the value for that variable in the master profile.

### **Similarity measures based on the profile gradient**

If you are using a similarity measure that compares the gradients of the profiles, a missing value means that two gradients are excluded from the comparison. If we take an extreme example of a profile where every other value is missing, then there would be no gradients left in the profile to base the comparison on. Since excluding a missing value has the same effect as setting the value of the profile to the same value as in the master profile, the profile in this extreme example would then have the highest possible similarity with the master profile.

### **Missing values in the master profile**

Any missing values in the master profile are always excluded from the search. If, for example, the second variable in the master profile has no value then this variable is always excluded in the comparison with the other profiles, even if you have not specified that you want to exclude empty values.

## **7.23 Coincidence Testing**

### **7.23.1 Coincidence Testing Overview**

The Coincidence Testing tool can be used to investigate if values within two columns seem to coincide or not. The results are presented using probability p-values.

### **7.23.2 Using Coincidence Testing**

#### **7.23.2.1 Testing if Groups of Identifiers Have Overlap**

The coincidence testing can be used to assess whether or not different groups of identifiers have a significant overlap. This is useful for comparing different clustering methods.

► **To test if similarity is a coincidence:**

1. Select **Data > Pattern Detection > Coincidence Testing...**

Response: The Coincidence Testing dialog is displayed.

**Note:** If you cannot find this tool in the Data menu, you probably need to acquire another license.

2. Select the **First category column**.

Comment: If you are comparing clustering methods, then choose the results of the first clustering tool here.

3. Select the **Second category column**.

Comment: If you are comparing clustering methods, then choose the results of the second clustering tool here.

4. Select whether to work on **All records** or **Selected records**.

5. Type a **Column name** for the resulting column or use the default name.

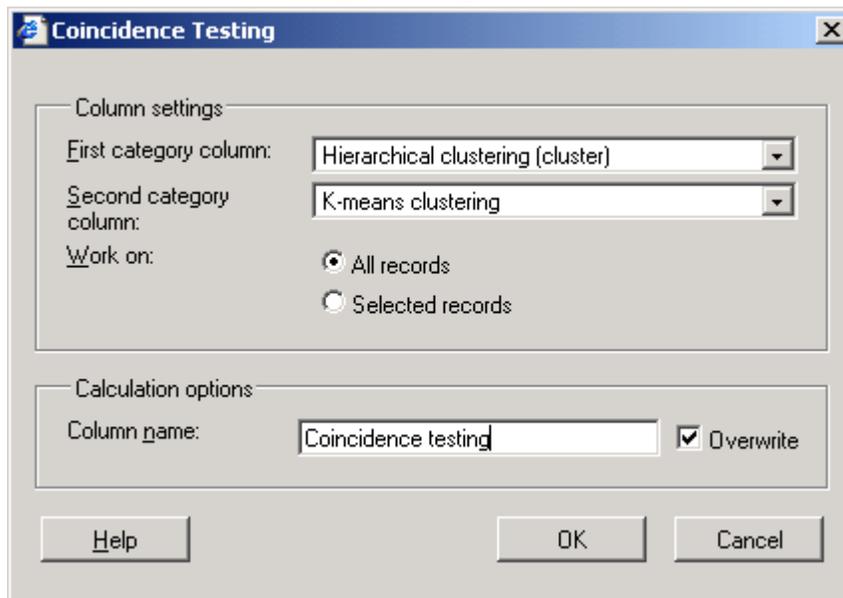
Comment: Select the **Overwrite** check box to overwrite an old column with the same name.

6. Click **OK**.

Response: A result column with p-values is added to the data set. An annotation may also be added.

## 7.23.3 User Interface

### 7.23.3.1 Coincidence Testing Dialog



Option	Description
<b>First category column</b>	The first data column that you want to test.
<b>Second category column</b>	The second data column that you want to test.
<b>Work on: All records</b>	All records in the value columns are included in the calculations.

<b>Work on: Selected records</b>	Only the selected records are included in the calculations. This lets you filter out any records that you do not want to include in the calculations, using the query devices and zooming.
<b>Column name</b>	The name of the new column containing the results from the calculation.
<b>Overwrite</b>	Select this check box if you want to replace a previously added column (with the same name as the one in the Column name text box).

► **To reach the Coincidence Testing dialog:**

Select **Data > Pattern Detection > Coincidence Testing...**

## 7.23.4 Theory and Methods

### 7.23.4.1 Coincidence Testing Methods Overview

The Coincidence Testing tool calculates the probability of getting an outcome at least as extreme as the particular outcome under the null hypothesis.

**Example:**

You have performed clustering using two different methods. You want to know how well the two methods agree on the classification of each record. The table below shows the identifiers and cluster classifications for some records. Performing a coincidence test on the two clustering columns produces the Coincidence column:

Identifier	Hierarchical clustering	K-means clustering	Coincidence	Interpretation
A	1	3	0.2	Good match
B	1	3	0.2	Good match
C	1	2	0.95	Worst match
D	2	2	0.2	Good match
E	2	2	0.2	Good match
F	3	1	0.166666...	Best match

The records for which the highest number of cluster classifications is similar will get the lowest p-value in the coincidence test. This means that in this example the "group" with only record F got the best match, but since there was only one record in the "group" this is rather irrelevant. The group with records A and B and the group with records D and E showed quite good matching. C received a low score since the clusterings disagree about the classification.

### 7.23.4.2 Description of the Coincidence Testing Algorithm

For any data set loaded into Spotfire DecisionSite, the Coincidence Testing algorithm may be applied to any two columns A and B. The algorithm will calculate a "probability value" (p-value) for each unique pair of values in A and B. The p-values can be used to identify value pairs that are over represented in the data set, i.e., occur more frequently than could be expected by pure chance, assuming no relationship between A and B. This information can be used to discover interesting facts and create hypotheses about the actual relationship between A and B.

**The algorithm:**

In order to describe the algorithm, the following definitions will be used:

$R$  = number of rows in the data set  $D$

$G$  = number of groups, i.e., unique value pairs, in columns  $A$  and  $B$

If the groups are numbered from 1 to  $G$ , the following definitions will be used for the group with index  $i$ :

$K_i$  = number of rows belonging to group  $i$

$M_i$  = number of rows in  $D$  where the  $A$  value = the  $A$  value in group  $i$

$N_i$  = number of rows in  $D$  where the  $B$  value = the  $B$  value in group  $i$

The  $p$ -value for the group with index  $i$  can then be calculated as follows:

$$P_i = P(X \geq K_i | R, N_i, M_i) = \sum P(X = x | R, N_i, M_i); x = K_i, \dots, \min(N_i, M_i)$$

where  $X$  is a random variable with a hypergeometric distribution. In probability theory, this distribution describes the number of successes in a sequence of a certain number of draws from a finite population without replacement.

This means that the probability formula can be written as follows:

$$P(X = x | R, N_i, M_i) = \binom{N_i}{x} \cdot \binom{R - N_i}{M_i - x} / \binom{R}{M_i}$$

where

$$\binom{n}{k} = \frac{n!}{k! (n-k)!} \text{ if } n \geq k \geq 0$$

$$\binom{n}{k} = 0 \text{ if } k < 0 \text{ or } k > n$$

is the binomial coefficient of  $n$  and  $k$ .

### Example:

Let us consider a data set  $D$  which contains information about the country of origin and the number of cylinders for 18 different cars:

Model	Origin	Cylinders
VW 1131	EU	4
Saab 99	EU	4
Chevrolet Impala	USA	8
Pontiac Catalina	USA	8
Plymouth Fury	USA	8
Mercury Monarch	USA	6
Buick Century	USA	6
Audi 100	EU	4
Renault 12	EU	4
Mercedes 280	EU	6
Chevrolet Caprice	USA	8

Oldsmobile Cutlass	USA	8
Peugeot 604	EU	6
Pontiac Lemans	USA	6
Peugeot 504	EU	4
Dodge Colt	USA	4
VW Rabbit	EU	4
Ford Galaxie	USA	8

If we apply the Coincidence Testing algorithm described above to Origin and Cylinders, we find that:

$$R = 18$$

$$G = 5$$

The 5 groups (unique value pairs for Origin and Cylinders) are:

Group 1: Origin = EU; Cylinders = 4

Group 2: Origin = EU; Cylinders = 6

Group 3: Origin = USA; Cylinders = 4

Group 4: Origin = USA; Cylinders = 6

Group 5: Origin = USA; Cylinders = 8

Furthermore, for group 1 (Origin = EU; Cylinders = 4), we find that:

$K_1 = 6$  (VW 1131, Sabb 99, Audi 100, Renault 12, Peugeot 504, VW Rabbit)

$M_1 = 8$  (number of rows where Origin = EU, regardless of Cylinders)

$N_1 = 7$  (number of rows where Cylinders = 4, regardless of Origin)

The p-value for this group of cars can be calculated as follows:

$$P_1 = P(X \geq 6 \mid 18, 7, 8) = 0.009049\dots$$

To find the most over represented groups of cars in the data set, we calculate the p-values for all groups and sort the groups by ascending p-value:

$$P_1 = 0.009049\dots$$

$$P_5 = 0.011312\dots$$

$$P_4 = 0.617647\dots$$

$$P_2 = 0.774509\dots$$

$$P_3 = 0.999748\dots$$

It should be noted that the largest groups are not necessarily the most over represented ones.

However, the low p-values for groups 1 and 5 show that, from a statistical point of view, European cars with 4 cylinders and American cars with 8 cylinders are strongly over represented in the data set. This information could perhaps be used to draw further conclusions about the relationship between Origin and Cylinders.

### 7.23.4.3 Coincidence Testing References

Tavazoie, S., Hughes, J.D., Campbell, M.J., Cho, R.J., Church, G.M., Systematic determination of genetic network architecture, *Nature Genetics*, 22 (3), 1999, pp 281-285

## 8 Tools

### 8.1 Create Venn Diagram

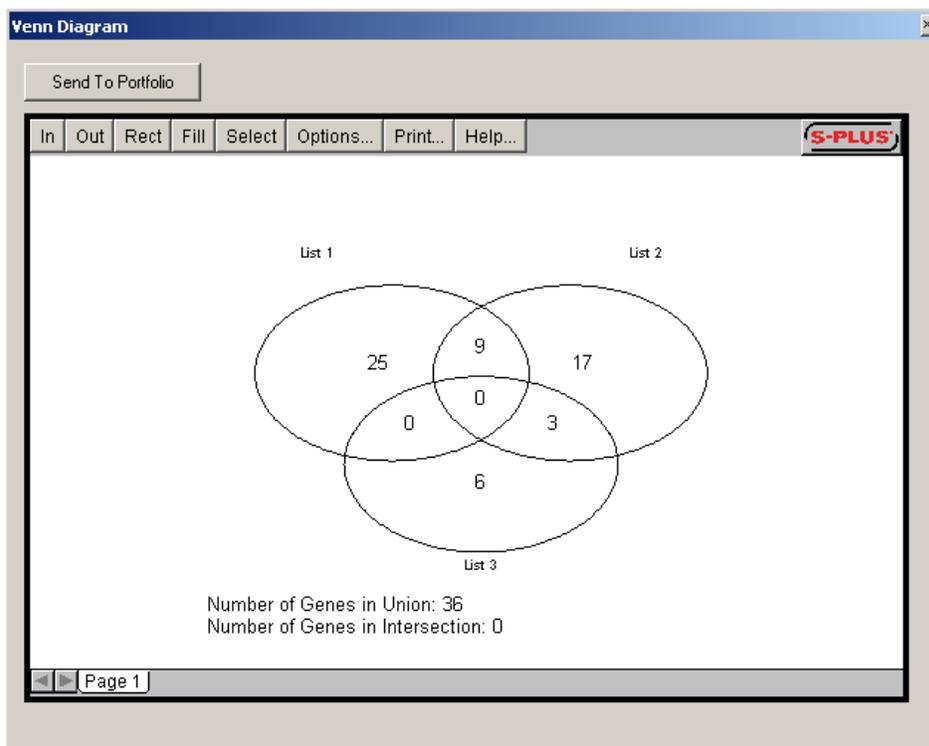
#### 8.1.1 Creating a Venn Diagram

The Create Venn Diagram tool can be used to create a Venn diagram representing selected Portfolio list logic. The interactive Venn diagram can also be used to create new Portfolio lists.

► **To create a Venn Diagram:**

1. If the Portfolio is not already open, select **Tools > Portfolio**.  
Comment: The Venn Diagram tool uses the Portfolio tool, which manages gene lists, to display list comparisons and create new Portfolio lists. Two or more lists must be created in the Portfolio before the tool can be run.
2. Make sure you have created all lists that you want to compare in the Portfolio.
3. Select **Tools > Create Venn Diagram**.  
Response: The Create Venn Diagram dialog is now displayed.
4. Select two or three Portfolio lists to use and press **OK**.  
Response: The Venn Diagram dialog is displayed.
5. To create new lists from the Venn diagram, click on a number associated with the relationship and click **Send To Portfolio**. Press Ctrl+click to select more than one region in the Venn diagram.
6. In the dialog that appears, supply the new list with a name.  
Your new list should now appear in the Portfolio.

#### 8.1.2 Venn Diagram Dialog

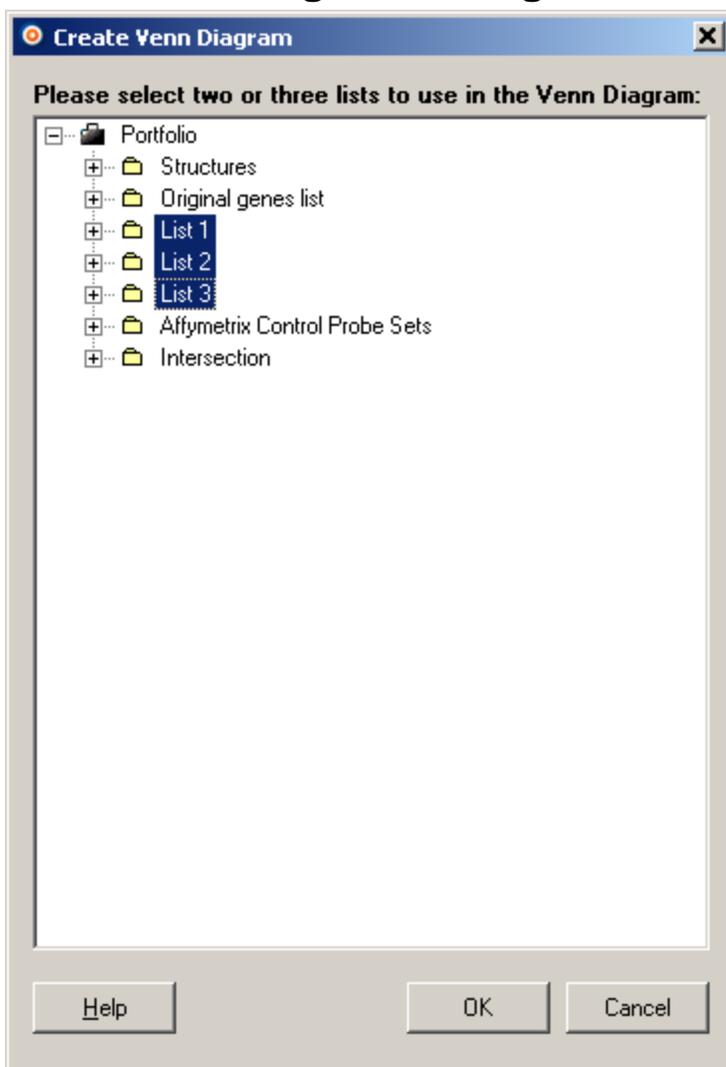


Option	Description
<b>Send To Portfolio</b>	Creates a new list based on the interactions between the lists. To do this, click to select a number associated with the interesting relationship and click <b>Send To Portfolio</b> .
<b>In</b>	Zooms in closer in the graph.
<b>Out</b>	Zooms out further in the graph.
<b>Rect</b>	Allows zooming in on a particular region. Press and drag left mouse button to define a rectangle, then press “Rect” to zoom in on it.
<b>Fill</b>	Resizes the graph to fill the window.
<b>Options...</b>	Brings up a window for modifying graphlet options: “Display mouse position” specifies whether or not the mouse graph coordinates should be displayed in the top left. “Mouse position digits” specifies the number of fraction digits in the mouse graph coordinates. “Enable active regions” specifies whether active regions should be highlighted. “Display page tabs” specifies whether to show tabs along the bottom of the pages.
<b>Help...</b>	Graphlet help.
<b>S-PLUS</b>	Link to Insightful webpage describing graphlet.

► **To reach the Venn Diagram dialog:**

1. Select **Tools > Create Venn Diagram**.
2. Select the desired Portfolio lists on which to create a Venn Diagram and click **OK**.

## 8.1.3 Create Venn Diagram Dialog



Option	Description
Please select two...	Displays the available Portfolio lists that you can use to create a Venn Diagram. Click on a list to select it.

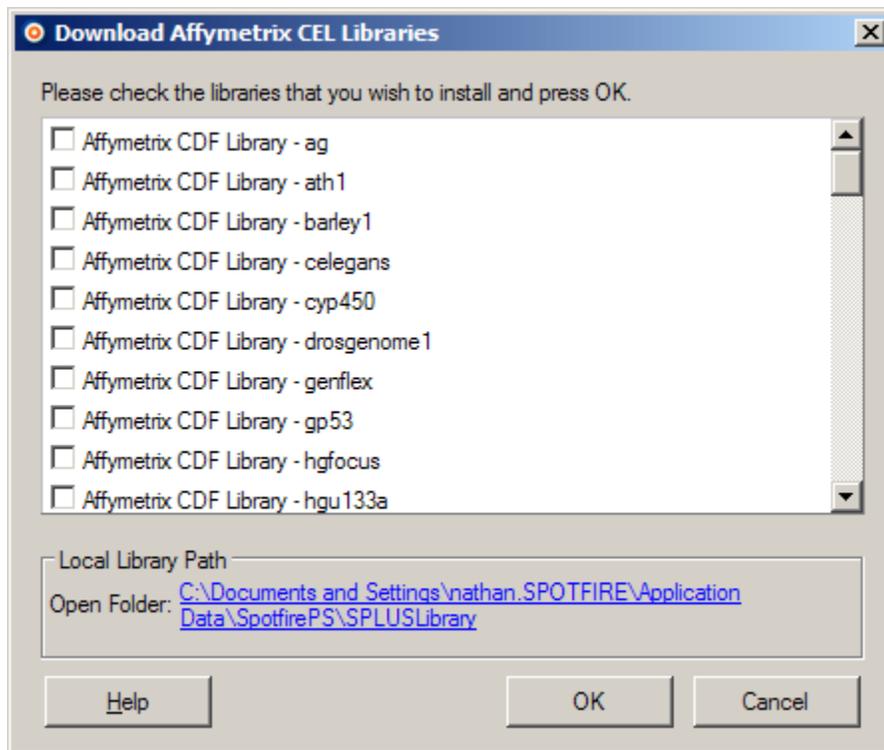
### ► To reach the Create Venn Diagram dialog:

Select **Tools > Create Venn Diagram**.

## 8.2 Download Affymetrix CEL Libraries

### 8.2.1 Download Affymetrix CEL Libraries Dialog

If you do not have the required libraries available for a set of CEL files, you can download annotation libraries from the Insightful web site using this tool.



Option	Description
Please check the libraries...	Select the check boxes for the libraries that you wish to install.
Local Library Path	This is the path to where the selected libraries are downloaded. The libraries must be located in the folder %USER_PROFILE%\Application Data\SpotfirePS\SPLUSLibrary for the tools of DecisionSite for Microarray Analysis to find them. You may click on the link to see what libraries you have currently installed.

► **To reach the Download Affymetrix CEL Libraries dialog:**  
 Select **Tools > Download Affymetrix CEL Libraries...**

## 8.3 Gene Ontology Browser

### 8.3.1 Gene Ontology Browser Overview

The Gene Ontology Browser is used to see where the records in your data set are located in a gene ontology hierarchy. With this tool, you can see subsets of genes from the visualizations appear in the ontology hierarchy and vice versa. It is also possible to perform searches in the gene ontology hierarchy.

You link your active data set in DecisionSite to the selected gene ontology file or files by using a matching annotation file.

**Note:** You have to make sure that you are using an annotation file that includes the same IDs as the ones in your data set in order to obtain any hits using this tool.

---

## 8.3.2 Using Gene Ontology Browser

### 8.3.2.1 Starting the Gene Ontology Browser

► **To display Gene Ontology files in DecisionSite:**

1. Select **Tools > Gene Ontology Browser**.  
Response: The Gene Ontology: Settings dialog is displayed.
2. Select the column from the drop-down list that you want to be the **Gene identifier column (Spotfire)**.  
Comment: All columns containing strings will be displayed in this list.
3. Select a Gene annotation file **Name** from the drop-down list.  
Comment: The annotation file is what links the gene or gene product IDs in your data set to the IDs in the gene ontology files. An annotation file is necessary in order to use this tool. Currently, the following annotation file formats are supported: tab separated text file, Affymetrix or Gene Ontology Consortium.
4. If this is your first time using the tool, click on the **Gene Ontology Files...** button to select gene ontology files. If you have already retrieved the interesting files for the tool, go to step 7.  
Response: The Gene Ontology: Gene Ontology Files dialog is displayed.
5. Choose whether to **Use default files from the server** or **Local files**.  
Comment: If you have access to a server, the first choice is normally preferred. If you select Local files, click **Add File...** and select the desired gene ontology file. To select more than one file, press **Ctrl** and click the files in the list. Click **Open** to add the files to the list. Note that if you use local files you should probably download/update the files at least once a month.
6. Click **OK** to close the Gene Ontology: Gene Ontology Files dialog.
7. Click **OK**.  
Response: The Gene Ontology window is displayed and the gene ontology hierarchy is loaded.
8. Normally, you would continue by retrieving records to the gene ontology hierarchy.

### 8.3.2.2 Retrieving Records to Gene Ontology Hierarchy

For any interaction to occur between the Gene Ontology Browser and your data set in DecisionSite, records must be retrieved into the Gene Ontology Browser.

Depending on what you want to do, you can retrieve all records, marked records or selected records. Automatic interaction options are also available in the Gene Ontology: Properties dialog.

► **To retrieve marked records:**

1. If the Gene Ontology Browser is not already open, see Starting the Gene Ontology Browser for more information.
2. Mark those records in the visualizations you want to retrieve to the gene ontology hierarchy.
3. Select **Retrieve Marked Records** from the Gene Ontology menu.  
Response: The marked records from the visualizations are now displayed in the gene ontology hierarchy. Records that are not annotated will be found in the bottom node called No (or no valid) Annotation.

**Tip:** You can also use the **Automatically retrieve marked records from visualizations** option in the Gene Ontology: Properties dialog to retrieve marked records to the gene ontology hierarchy.

► **To retrieve all records:**

1. If the Gene Ontology Browser is not already open, see Starting the Gene Ontology Browser for more information.
2. Select **Retrieve All Records** from the Gene Ontology menu.  
Response: All records from the visualization are now displayed in the gene ontology hierarchy. Records that are not annotated will be found in the bottom node called No (or no valid) Annotation.

► **To retrieve selected records:**

1. If the Gene Ontology Browser is not already open, see Starting the Gene Ontology Browser for more information.
2. Select those records in the data set you want to retrieve to the gene ontology hierarchy by using the query devices and zooming.
3. Select **Retrieve Selected Records** from the Gene Ontology menu.  
Response: The selected records from the visualizations are now displayed in the gene ontology hierarchy. Records that are not annotated will be found in the bottom node called No (or no valid) Annotation.

### 8.3.2.3 Marking Gene Ontology Nodes in Visualization

**Note:** Only the records that have been retrieved to the Gene Ontology Browser will be affected by the *Mark in Visualization* commands.

► **To mark gene ontology hierarchy nodes in the visualizations:**

1. If the Gene Ontology Browser is not already open, see Starting the Gene Ontology Browser for more information.
2. Retrieve the records in which you are interested into Gene Ontology Browser.
3. Click to select the node in the gene ontology hierarchy that you want to mark in the visualization.
4. Select **Mark in Visualization** from the Gene Ontology menu.  
Response: The selected nodes from the gene ontology hierarchy are now marked in the visualization.

**Tip:** You can also use the **Automatically mark in visualization** option in the Gene Ontology: Properties dialog, to make selected gene ontology hierarchy nodes marked in the visualization.

**Tip:** Pressing down the SHIFT key on the keyboard and clicking on a node simultaneously will mark all genes that are annotated by this specific term or any of the term's children.

► **Example workflow:**

1. Find some interesting genes in your data set and mark them in a DecisionSite visualization.
2. Use p-value search to find a highly significant GO term (node) in the hierarchy, select that node and see the explicit behavior of those genes that were in your original selection and in the node.
3. To see how similar the genes in the node that were not in your original selection are to the genes in your original selection, press SHIFT on the keyboard and click on the node. This will mark all genes that are indirectly annotated by this specific term.

### 8.3.2.4 Searching the Gene Ontology Hierarchy

► **To search the gene ontology hierarchy:**

1. If the Gene Ontology Browser is not already open, see Starting the Gene Ontology Browser for more information.

2. Select **Search** from the Gene Ontology Browser menu.  
Response: The Search field is displayed.
3. Enter the string, ID or p-value to search for in the text box.  
Comment: When searching for ID, it is recommended that the ID be written as: GO:0007049 or 0007049 (seven digits). Wildcards (\*) are not supported. Searching for p-values can be specified using the symbols <, >, <=, >= or =. See Gene Ontology search field for more details.
4. Select whether to perform a **Substring, ID, Exact match or p-values** search.  
Comment: Substring searches all the information in the tree for strings that contain the specified substring, ID searches the tree for the specified ID number, and Exact match searches the tree for only those items that match the specified string exactly. The search is not case sensitive. Note that blank spaces are valid search characters in substring and exact match searches.
5. Click **OK**.  
Response: Each found occurrence of the search string is highlighted in gray in the gene ontology hierarchy.
6. Use the << or >> arrow buttons to step through the search results.  
Comment: The active term is highlighted in yellow

**Tip:** You can also click on the **Search** button, , to show or hide the search pane and search the gene ontology hierarchy.

### 8.3.2.5 Displaying More Information for a Selected Node

More information regarding interesting terms, gene names or GOIDs can be found in the Gene Ontology: Node Information dialog.

#### ► To use the Node Information dialog:

1. Make sure that you have retrieved some records to the gene ontology hierarchy.  
Comment: See Retrieving records to the gene ontology hierarchy for more information.
2. Click to select the term (node) of interest in the hierarchy.
3. Select **Show Node Information** from the gene ontology menu, or click on the  button.  
Response: The Gene Ontology: Node Information dialog is displayed.
4. Look at the information in the window.  
Comment: You can select the text in the Node Information dialog and copy it to the clipboard.
5. If desired, you can use the Web Links function at the bottom of the window to search an external web page for more information. Select a Web Link from the drop-down list.  
Comment: The different web links can be edited using the Web Links tool.
6. Click on a link with GOID, term or gene name in the node information window, to execute a search against the selected web site using the GOID, term or gene name as search parameter.  
Response: The query is sent to the selected web site and the results are displayed in a new web browser.  
Comment: Some of the predefined web links may require that you log in before the search results are displayed.

### 8.3.2.6 Gene Annotation File Formats

The annotation file is used to link the gene or gene product IDs in your data set to the IDs in the gene ontology files. An annotation file is necessary in order to use the Gene Ontology Browser. Three different formats of annotation files are supported in the current version of the Gene Ontology Browser:

- Tab separated text file
- Affymetrix
- Gene Ontology

You will never use more than one annotation file at a time, and since it is only used to link the ontology and your data set together, the only columns needed in the annotation file are the ID column of your data set and the gene ontology ID.

#### Tab separated text file

The most simple form of annotation file is a text file with two columns containing GeneID and GOID (no column names are needed). This type of annotation file can be created by hand.

Example:

```
143820_at GO:0005886
143820_at GO:0007269
143820_at GO:0016192
143820_at GO:0030122
143820_at GO:0030122
154527_at GO:0003779
154527_at GO:0007016
154527_at GO:0008092
154652_at GO:0004091
143821_at GO:0004091
152623_at GO:0004091
```

#### Affymetrix

The NetAffx Analysis Center download center provides annotation data in a comma-separated values (CSV) tabular format. Each row is terminated by a new-line character and data in separate fields are enclosed in quotation marks and separated by commas.

There is one annotation file per GeneChip array. Spotfire supports both the new and previous version of NetAffx annotation file formats (column names appearing in the following paragraph).

The first row of each file contains the titles of the fields (columns). Probe Set ID is the probe set identifier and gene ontology (GO) data are displayed under the three columns Gene Ontology Biological Process, Gene Ontology Cellular Component, and Gene Ontology Molecular Function (the previous version of the NetAffx annotation files' columns are named Biological Process (GO), Cellular Component (GO), and Molecular Function (GO)). Each annotation consists of three parts: "Accession Number // Description // Evidence" (e.g., "7155 // cell adhesion // predicted/computed"). The accession number equals the GOID and is what links the probe set IDs to the ontology. All columns other than those mentioned above are unused by the Gene Ontology Browser tool.

See Add Columns from NetAffx Overview for more information regarding the download and use of NetAffx annotation files.

#### Gene Ontology

The Gene Ontology Consortium (GO) provides gene association files that are tab-delimited files with 15 fields. The DB\_Object\_ID field contains the identifier of the database object and

the GOid field contains the GO identifier for the term attributed to the DB\_Object\_ID. The DB\_Object\_Symbol field contains a unique symbol to which DB\_Object\_ID is matched. The DB\_Object\_Symbol field can use ORF name, a gene product symbol if available, or many gene product annotation entries can share a gene symbol. This is the field that is used to match the annotation to the data set in DecisionSite. For a thorough description of the other fields, see the annotations sections on <http://www.geneontology.org>.

GO recommends that GO terms are associated with gene products (RNA or protein products encoded by a gene) rather than genes. Annotations from GO are attributed to a source (a literature reference, another database or a computational analysis) and each annotation indicates the evidence on which it is based.

#### ► Downloading annotation files from Gene Ontology Consortium:

1. Go to the **Gene Ontology Consortium** web page for Current Annotations: <http://www.geneontology.org/GO.current.annotations.shtml>.
2. Right-click on the **Download** link of the species of interest and select **Save Target As...**
3. Browse to a suitable location on your hard-drive and save the file.

#### ► Using the annotation file

1. In the Gene Ontology: Settings dialog, under Gene annotation file, click **Browse...**
2. Select the previously downloaded file and click **Open**.

### 8.3.2.7 Gene Ontology File Formats

The gene ontology files are structured, controlled vocabularies that describe gene products in terms of their associated biological processes, cellular components and molecular functions in a species-independent manner.

Gene Ontology files in the GO flat file format are supported in the current version of the DecisionSite Gene Ontology Browser. Even though the GO format is deprecated, the files are still updated weekly from the newer OBO format files. More information about the GO flat file format can be found in the File Format Guide on the Gene Ontology Consortium's website at <http://www.geneontology.org>.

In the GO flat files the individual ontologies are held in separate files and the definitions are kept in a further separate file. The structure described below holds true for each of the ontology flat files:

- Biological Process (process.ontology)
- Molecular Function (function.ontology)
- Cellular Component (component.ontology)

#### Front matter

The beginning of each file contains comments (lines that begin with a !) about how and when the file was generated. The first lines always carry information about the version, the date of last update, (optionally) the source of the file, the name of the database, the domain of the file and the editors of the file (except HTML files).

Lines in which the first non-space character is a \$ either reflect the domain and aspect of the ontology (i.e., \$text) or the end of file (i.e., the \$ character on a line by itself).

Here is an example of the front matter of a GO flat file:

```
!autogenerated-by: DAG-Edit version 1.315
!date: Fri Jan 03 17:14:37 GMT 2003
!version: $Revision: 1.1 $
!type: % ISA Is a
!type: < PARTOF Part of
$Gene_Ontology ; GO:0003673
```

## Relationships between terms

In the GO flat files, the symbol % is used to represent an is-a relationship and the symbol < a part-of relationship. For more information on these relationships between terms, see the GO Editorial Style Guide. Parent-child relationships between terms are represented by indentation:

```
parent_term
  child_term
```

- **Is-a relationships**

```
%term0
  %term1 % term2
```

means that term1 is a subclass of term0 and also a subclass of term2.

- **Part-of relationships**

```
%term0
  %term1 < term2 < term3
```

means that term1 is a subclass of term0 and also a part-of of term2 and term3.

## Line syntax

The order in which items appear on a line (where [] indicates an optional item) is as follows:

```
< | % term [; db cross ref]* [; synonym:text]* [ < | % term]*
```

Here's a real example from the molecular function ontology (it would appear on a single line in the actual file):

```
%UDPsulfoquinovose synthase ; GO:0046507 ; EC:3.13.1.1 ;
synonym:sulfite\ :UDP-glucose sulfotransferase
```

### 8.3.2.8 Gene Ontology Browser Troubleshooting

This topic lists some known trouble situations when working with Gene Ontology Browser and explains how to solve or work around the problems.

#### Nothing happens in the Gene Ontology Browser when I mark records in the data set.

**Problem:** I have started the Gene Ontology Browser and set up the tool with an annotation file and an ontology file, but still nothing happens when I mark records in my visualizations.

**Explanation:** There may be a number of reasons why nothing happens. See below.

**Solution:**

You may have turned off the "Automatically retrieve marked records from visualization" option in the Gene Ontology: Properties dialog. Select **Retrieve Marked Records** from the menu or enable the option mentioned above to retrieve records into the gene ontology hierarchy.

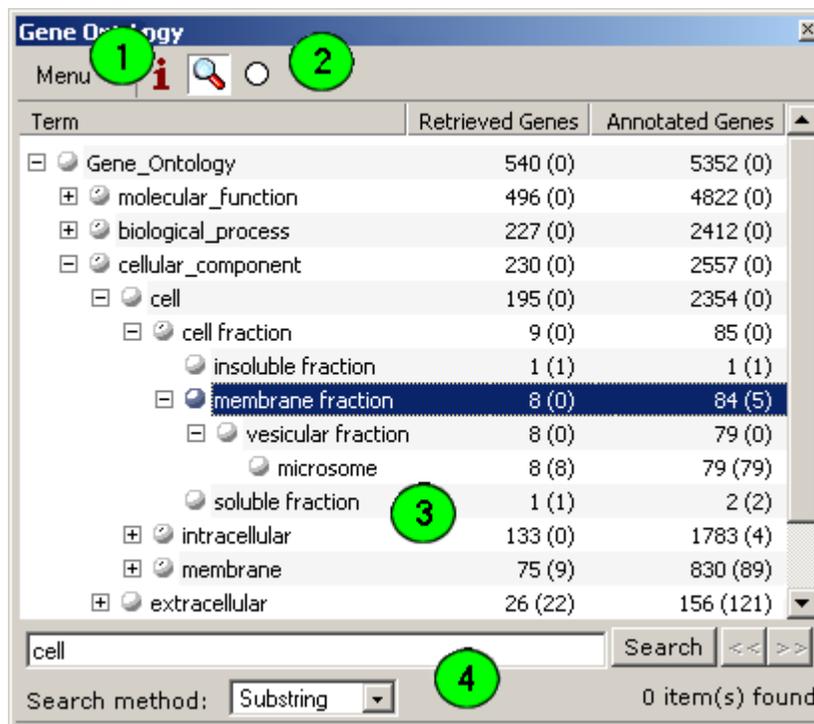
If the Retrieved Genes column is empty, except for the No (or no valid) Annotation node, either the genes are not annotated at all or you may have selected a Gene identifier column that does not match the IDs in the annotation file. Choose a different identifier column or switch to a new annotation file with matching IDs.

If the Annotated Genes column is empty, the annotation file is probably invalid or does not match the used ontology files. Switch to a different annotation file which matches the IDs in your data set. For more information see Gene annotation file formats.

## 8.3.3 User Interface

### 8.3.3.1 Gene Ontology Browser User Interface Overview

This is the Gene Ontology Browser main window:



1. Menu
2. Toolbar
3. Hierarchy window
4. Search field

#### 1. Gene Ontology menu



The Gene Ontology menu contains all menu commands required to work with the Gene Ontology Browser.

#### 2. Gene Ontology toolbar



Includes shortcuts for some of the most common commands in the Gene Ontology menu. Click [here](#) for a description of the buttons.

#### 3. Gene Ontology hierarchy window

The hierarchy window is where the gene ontology terms are displayed. The root level of the hierarchy tree is Gene\_Ontology and the sublevels are the selected ontologies specified in the Gene Ontology: Gene Ontology Files dialog and their terms (nodes).

Columns:

**Retrieved Genes** You can select to return a subset of records to the Gene Ontology Browser. These are the Retrieved Genes. The numbers not enclosed in parentheses under the Retrieved Genes column are the total number of unique genes from the selected term and all terms below it (its children). These numbers cannot be summed since a single gene often falls into multiple terms. The numbers enclosed within parentheses are the total number of unique genes in the data set that are retrieved to the Gene Ontology Browser and are at that specific

level or GO term.

<b>Annotated Genes</b>	Displays the <b>total number of unique genes in the annotation file</b> that are annotated with the selected term or any of the terms below it. The number within parenthesis is the total number of unique genes that are included in the annotation file and annotated with the specific term.
<b>p-value</b>	<p>Optionally, it is possible to display a column showing p-values for the different terms. P-values are calculated on the numbers for the selected term and its children. This value reflects the probability (a lower value is a higher probability) that the genes grouped within a term do NOT fall into that term by chance alone. To provide an extreme example, if you choose a subset of genes and map them to the browser and 30 out of 100 fall into apoptosis, this may not be significant if 30% of the genes that are annotated are classified under apoptosis. To put this another way, the analysis compares the overrepresentation of each annotation (e.g., "apoptosis") in a gene list to the overrepresentation of that annotation on the entire array. Say that 30% of the genes on an array are annotated with the term "apoptosis" and 30% of the genes in an important subset of genes derived from that array (e.g., selected based of their differential expression) are also annotated with the term "apoptosis". Then enrichment analysis would not flag apoptosis as a significant annotation for the gene list, because the percentage of selected genes having the annotation is about the same as the percentage of genes from a randomly selected subset of the microarray having that annotation.</p> <p>Results are given in the form of p-values. For each annotation, enrichment analysis computes the probability that the number of genes in the list having that annotation would occur in a list selected randomly from the same array. If the list-percentage is much higher than the array-percentage, then the annotation gets a low p-value, and we conclude that the gene list is "enriched" with the annotation. If the percentages are similar, then the p-value is high, indicating an insignificant result.</p> <p>The p-value is calculated using hypergeometric distribution. See P-values for Gene Ontologies for more information.</p>

The icons in the hierarchy window have the following meaning.

-  The term *is a part of* its parent. For example, the term "cell fraction" is a part of a "cell".
-  The term *is* its parent. For example, a "microsome" is a "membrane fraction".

You can toggle the display of subtrees in the Gene Ontology Browser by clicking the plus (+) or minus (-) sign beside a term. The left and right arrow keys on the keyboard can also be used to collapse or expand a node. All subnodes can be expanded/collapsed simultaneously by standing on the top node, e.g., Gene\_Ontology, and pressing the multiplication sign (\* or x) or the minus sign (-) on the numeric keypad.

#### 4. Search field

The search field is displayed or hidden by selecting Search from the gene ontology menu. Here, you can search for nodes that contain the specified Substring, ID, Exact match or p-values. You can use the Back (<<) and Forward (>>) buttons to browse the result from the search in the gene ontology hierarchy. The number of hits from the search are displayed to the right, below the field.

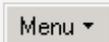
### 8.3.3.2 Gene Ontology Menu

The Gene Ontology menu is displayed by clicking  and contains all commands necessary for working with the Gene Ontology Browser.

Option	Description
<b>Retrieve All Records</b>	Retrieves all records from the data set and displays them in the gene ontology hierarchy.
<b>Retrieve Selected Records</b>	Retrieves currently selected records from the data set and displays them in the gene ontology hierarchy.
<b>Retrieve Marked Records</b>	Retrieves currently marked records from the data set and displays them in the gene ontology hierarchy.
<b>Mark in Visualization</b>	Marks the records that belong to the selected node of the gene ontology hierarchy in the DecisionSite data set and visualizations.
<b>Show Node Information</b>	Displays the Gene Ontology: Node Information dialog which contains information about GOID, Term, Genes, Synonyms, References and Parents for the selected node. The dialog is automatically updated once the selected node is changed.
<b>Search</b>	Displays or hides the Search pane, where you can perform a free text search of the contents of the gene ontology hierarchy.
<b>Show Empty Nodes</b>	Displays or hides the nodes in the gene ontology hierarchy that contain no records.
<b>Gene Ontology Settings...</b>	Launches the Gene Ontology: Settings dialog.
<b>Copy Visualization</b>	Copies the currently visible part of the Gene Ontology hierarchy to the clipboard as an enhanced metafile. The visualization may then be pasted into any other application (e.g., Microsoft Word or PowerPoint).
<b>Properties</b>	Launches the Gene Ontology: Properties dialog.

### 8.3.3.3 Gene Ontology Toolbar

The Gene Ontology toolbar includes shortcuts for some of the most common commands in the Gene Ontology menu. Click on the buttons on the toolbar to activate the corresponding functions.

	Displays the Gene Ontology menu.
	Displays the Gene Ontology: Node Information dialog which contains information about GOID, Term, Genes, Synonyms, References and Parents for the selected node. The information selected in the dialog can be copied by right-clicking in the dialog and selecting Copy from the pop-up menu.
	Shows or hides the Search pane where you can perform searches in the gene ontology hierarchy.
	Shows or hides the nodes in the gene ontology hierarchy that contain no records.
	Copies the currently visible part of the Gene Ontology hierarchy to the clipboard as an enhanced metafile. The visualization may then be pasted into any other application (e.g., Microsoft Word or PowerPoint).

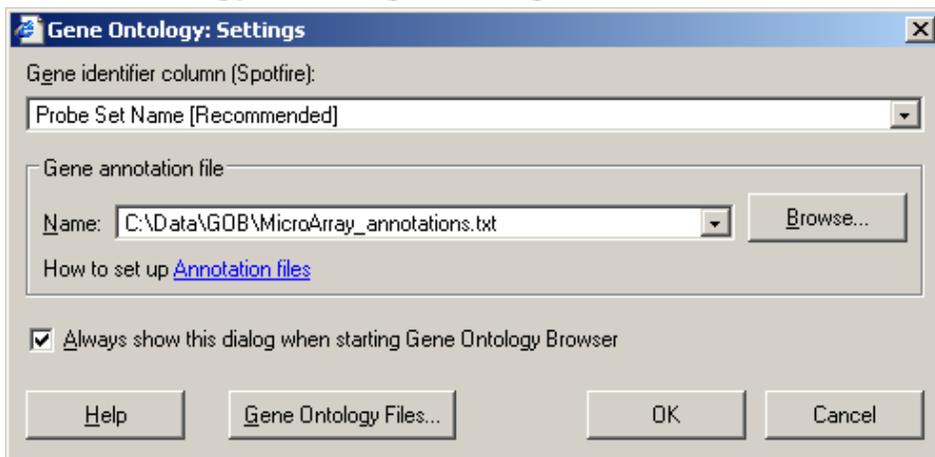
### 8.3.3.4 Gene Ontology Search Field

The search field is displayed or hidden by selecting **Search** from the gene ontology menu. Here, you can search for nodes that contain the specified Substring, ID, Exact match or p-values:

- Substring** Searches all the information in the hierarchy for strings that contain the specified substring. The search is not case sensitive. Note that blank spaces are valid search characters in a substring search.
- ID** Searches the hierarchy for the specified gene ontology ID. It is recommended that the ID be written as: GO:0007049 or 0007049 (seven digits). Wildcards (\*) are not supported.
- Exact match** Searches the hierarchy for only those items that match the specified string exactly. The search is not case sensitive. Note that blank spaces are valid search characters in an exact match search.
- p-values** Searches the hierarchy for the p-values lower than the specified number (real type number ( $0 \leq x \leq 1$ )). This means that if "0.05" is entered in the search box, all p-values lower than or equal to 0.05 will be displayed as the search result.
- It is also possible to use the symbols <, >, <=, >= and = before the number, to search for p-values that are lower than, higher than, lower than or equal to, higher than or equal to, and exactly equal to the specified number.
- If an integer larger than or equal to one is entered into the search box, the search will present the specified number of terms with the lowest p-values. This means that if "3" is entered in the search box, the three lowest p-values will be displayed as the search result.

You can use the Back (<<) and Forward (>>) buttons to browse the result from the search in the gene ontology hierarchy. The number of hits from the search are displayed to the right, below the field.

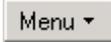
### 8.3.3.5 Gene Ontology: Settings Dialog



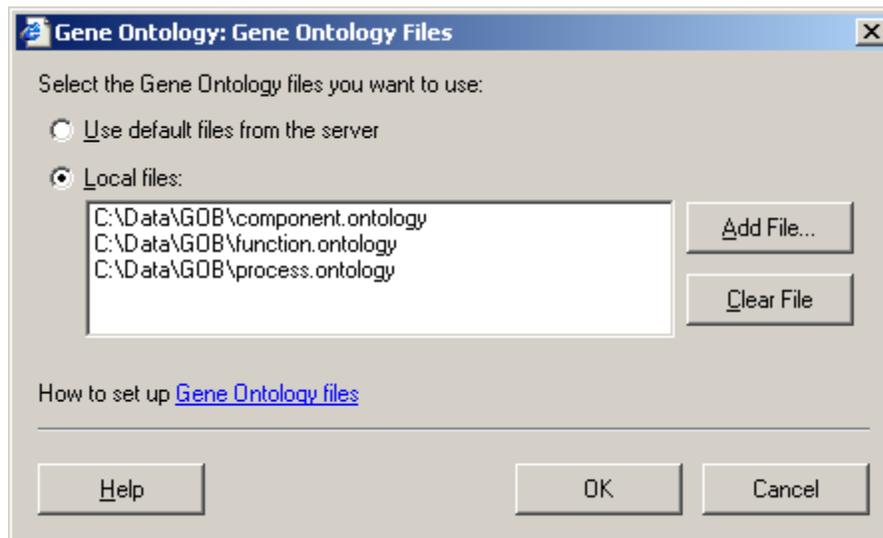
Option	Description
<b>Gene identifier column (Spotfire)</b>	Select the column in your current data set that uniquely identifies the genes or gene products. You can select the identifier from any column in the data set that contains strings. Normally, this is a column containing ORFs or Probe Set Names.

<b>Name</b>	Specify the path to the annotation file that links the gene or gene product IDs in your data set to the IDs in the gene ontology files. An annotation file is necessary in order to use this tool. Three different types of annotation files are currently supported. Choose from tab separated text file, Affymetrix or Gene Ontology formats. See Gene annotation file formats for more information. <b>Note:</b> If your administrator has set up annotation files on the DecisionSite Analytics Server, these will appear in this field automatically. For more information on how to add annotation files to the server, please consult the chapter Configuring DecisionSite for Functional Genomics in the Spotfire DecisionSite Analytics Server manual.
<b>How to set up Annotation files</b>	Opens this help file to a page with information about how to download and use annotation files.
<b>Always show this dialog when starting Gene Ontology Browser</b>	Select the check box to launch this dialog each time the Gene Ontology Browser is started. Clear the check box to start the Gene Ontology Browser using default settings the next time.
<b>Gene Ontology Files...</b>	Launches the Gene Ontology: Gene Ontology Files dialog where you can select which ontology files to work on.

► **To reach the Gene Ontology: Settings dialog:**

1. Select **Tools > Gene Ontology Browser**.
2. Click the Menu  button on the Gene Ontology toolbar.
3. Select **Settings...**

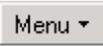
### 8.3.3.6 Gene Ontology: Gene Ontology Files Dialog



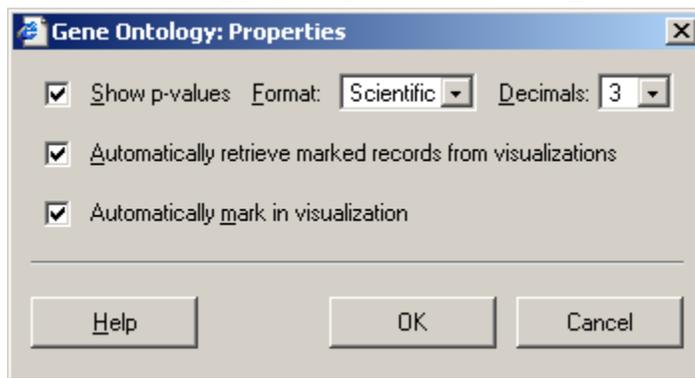
Option	Description
<b>Use default files from the server</b>	If you have access to a server where your Spotfire Administrator provides you with updated gene ontology files, this is probably the preferred selection.

<b>Local files</b>	If you do not have access to centrally updated gene ontology files, use this option to specify your own path to a local <i>Function</i> , <i>Process</i> , and/or <i>Subcellular location</i> file. Note that if you are running the Gene Ontology Browser against local files, you should probably download/update the files at least once a month. See the link below for more information on how this is done.
<b>Add...</b>	Opens a dialog where you can select local gene ontology files to add to the list.
<b>Remove</b>	Removes the selected file from the list.
<b>How to set up Gene Ontology Files</b>	Opens this help file to a page with information about how to download and use ontology files from the Gene Ontology Consortium.

► **To reach the Gene Ontology: Gene Ontology Files dialog:**

1. Select **Tools > Gene Ontology Browser**.
2. Click the Menu  button on the Gene Ontology toolbar.
3. Select **Settings...**
4. Click **Gene Ontology Files...** in the Gene Ontology: Settings dialog.

### 8.3.3.7 Gene Ontology: Properties Dialog

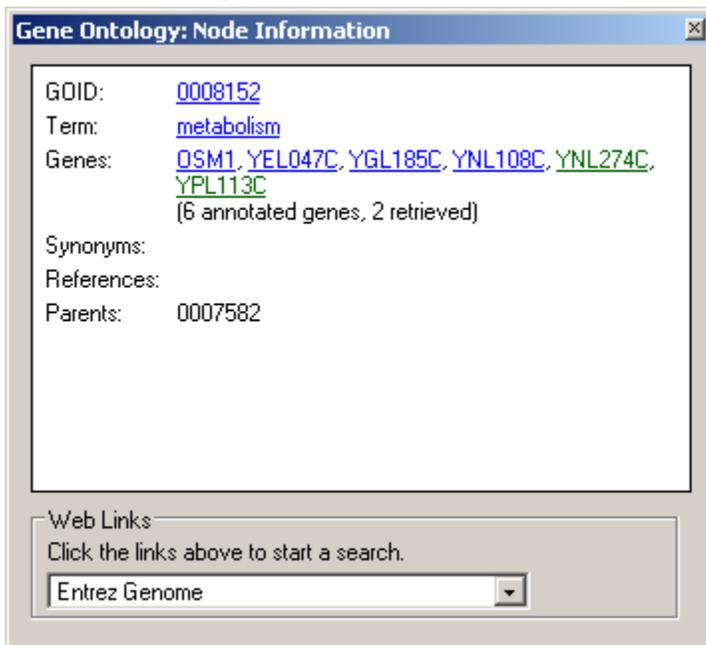


Option	Description
<b>Show p-values</b>	Select the check box to display p-values in the Gene Ontology window.
<b>Format</b>	Sets the format of the p-values to either <b>General</b> (displays the values on a decimal format), <b>Fixed</b> (displays a fixed number of decimals) or <b>Scientific</b> (displays a fixed number of decimals of the type: 1.1e-002).
<b>Digits/Decimals</b>	Select the number of significant digits or decimals that should be displayed.
<b>Automatically retrieve marked records from visualizations</b>	If this option is selected, the retrieved genes for all nodes in the Gene Ontology Browser will be updated each time a new set of records is marked in the Analysis.
<b>Automatically mark in visualization</b>	If this option is selected, the node that is selected in the gene ontology hierarchy will automatically be marked in the Analysis.

► **To reach the Gene Ontology: Properties dialog:**

1. Select **Tools > Gene Ontology Browser**.
2. Click the Menu  button on the Gene Ontology toolbar.
3. Select **Properties....**

### 8.3.3.8 Gene Ontology: Node Information Dialog



Option	Description
Node Information window	<p>Contains information about GOID, Term, Genes, Synonyms, References and Parents for the selected node. The dialog is automatically updated once the selected node is changed.</p> <p>The Genes displayed are the genes that are annotated by this specific term (node) in the annotation file. Genes that are retrieved to the Gene Ontology Browser are shown in green color.</p> <p>Clicking on either of the links will send a query to the external web site selected under Web Links below, to search for information about the specific GOID, term or gene.</p>
Web Links	<p>Select the desired Web Link for searches from the drop-down list. The list displays all web links currently available in the Web Links tool. You can edit the links, or add new ones through the Web Links tool.</p>

► **To reach the Gene Ontology: Node Information dialog:**

1. Select **Tools > Gene Ontology Browser**.
2. Click the Menu  button on the Gene Ontology toolbar.
3. Select **Show Node Information**.

## 8.3.4 Theory and Methods

### 8.3.4.1 P-values for Gene Ontologies

When selecting a set of genes, e.g., after a cluster analysis or similar in DecisionSite, and looking at how the genes are annotated to terms in the gene ontology, it is important to find terms that are significant in the sense that the annotations do not occur by chance. For example, if all genes in a list are associated with the term "DNA repair", this term would be significant for that list. If no genes in a list are associated with the term "lipid metabolism", this term would not be significant. The term "biological process" is not significant even though all genes in the list are annotated to it, because all annotated genes are indirectly associated with this term.

The probability value (p-value) of a statistical hypothesis test is defined as the probability of getting a value of the test statistic as extreme as, or more extreme than that observed by pure chance, if the null hypothesis (that a certain number of genes in the list are annotated to the term by pure chance) is true. The p-value is compared with the actual significance (threshold) level of the test and, if it is smaller, the result is significant. Typically,  $p < 0.05$  is used as the significance level. A small p-value suggests that the null hypothesis is unlikely to be true.

Hence, the p-values can be used to describe how well a certain gene ontology term represents the selection (the retrieved genes) of a specific list (e.g., a certain cluster) in DecisionSite.

The p-values are calculated according to the hypergeometric distribution:

$$p(N, G, n, x) = \sum_{i=x}^n \frac{\binom{G}{i} \binom{N-G}{n-i}}{\binom{N}{n}} = \sum_{i=x}^n \frac{G!(N-G)!}{(i!(G-i)!((n-i)!(N-G-n+i)!))} \cdot \frac{N!}{n!(N-n)!}$$

Term	Retrieved Genes	Annotated Genes	p-value
Gene_Ontology	92 (0)	7273 (0)	1.000e+000
molecular_function	92 (0)	7197 (0)	1.000e+000
biological_process	<b>n</b> 92 (0)	<b>N</b> 7270 (0)	1.000e+000
biological_process un...	87 (87)	2797 (2797)	5.730e-032
physiological processes	5 (0)	4432 (0)	1.000e+000
metabolism	5 (1)	3209 (6)	1.000e+000
biosynthesis	1 (0)	1124 (0)	1.000e+000
catabolism	1 (0)	297 (0)	8.955e-001
energy pathways	1 (0)	180 (0)	6.696e-001
lipid metabolism	<b>x</b> 1 (0)	<b>G</b> 190 (11)	6.985e-001
lipid biosynt...	1 (0)	111 (2)	4.117e-001
membra...	1 (0)	62 (0)	1.848e-001
phos...	1 (1)	48 (13)	1.231e-001
phosph...	1 (1)	48 (13)	1.231e-001

Where:

N = Ontology node (molecular\_function, biological\_process or cellular\_component) number of Annotated Genes (the total number of genes with GO annotations).

G = Number of Annotated Genes for a particular term (the number of unique genes annotated to a particular term (directly or indirectly)).

n = Ontology node (molecular\_function, biological\_process or cellular\_component) number of Retrieved Genes (number of genes in the investigated list).

x = Number of Retrieved Genes for a particular term (number of unique genes in the list annotated to a particular term (directly or indirectly)).

The following conditions must apply for each sum in the equation:

$x \leq G$

$n-x \leq N-G$

$x > 0$   
 $N > 0$   
 $G > 0$   
 $n \geq 0$

If either of the conditions fail,  $p = 0$  for this sum. The root node Gene\_Ontology is a special case where the p-value is set to 1.0.

### Example

7272 genes in a data set have one or more GO annotations. Out of these 7272 genes, 190 unique genes are directly or indirectly associated with the term "lipid metabolism", i.e., 190 genes are annotated to "lipid metabolism" or at least one of the terms in its subtree. In this case,  $N = 7272$  and  $G_{\text{lipid metabolism}} = 190$ .

You may create a list of genes by marking 50 records. Suppose that 4 of these genes (G1, G2, G3 and G4) are directly or indirectly associated with the term "lipid metabolism", as shown below.

GO term	Genes
... – lipid metabolism	G3
... – lipid metabolism – membrane lipid metabolism	G1
... – lipid metabolism – membrane lipid metabolism – phospholipid metabolism	G2
... – lipid metabolism – steroid metabolism	G3, G4
... – lipid metabolism – lipid biosynthesis – steroid biosynthesis	G1, G2, G4

The Genes column shows genes that are directly associated with each term. In this case,  $n = 50$ ,  $x_{\text{lipid metabolism}} = 4$ , since 4 unique genes are associated with the term "lipid metabolism" or at least one of the terms in its subtree. Similarly,  $x_{\text{membrane lipid metabolism}} = 2$ , since 2 unique genes (G1 and G2) are associated with the term "membrane lipid metabolism" or at least one of the terms in its subtree.  $N$  and  $n$  are independent of the terms in the ontology, while  $G$  and  $x$  vary from one term to another.

Using the definitions listed above, the probability of a randomly selected gene being annotated to a particular GO term is  $p = G / N$ .

In order to calculate the probability that  $x$  out of  $n$  genes are directly or indirectly associated with a certain term in the ontology by pure chance, the hypergeometric distribution is used.

### Reference

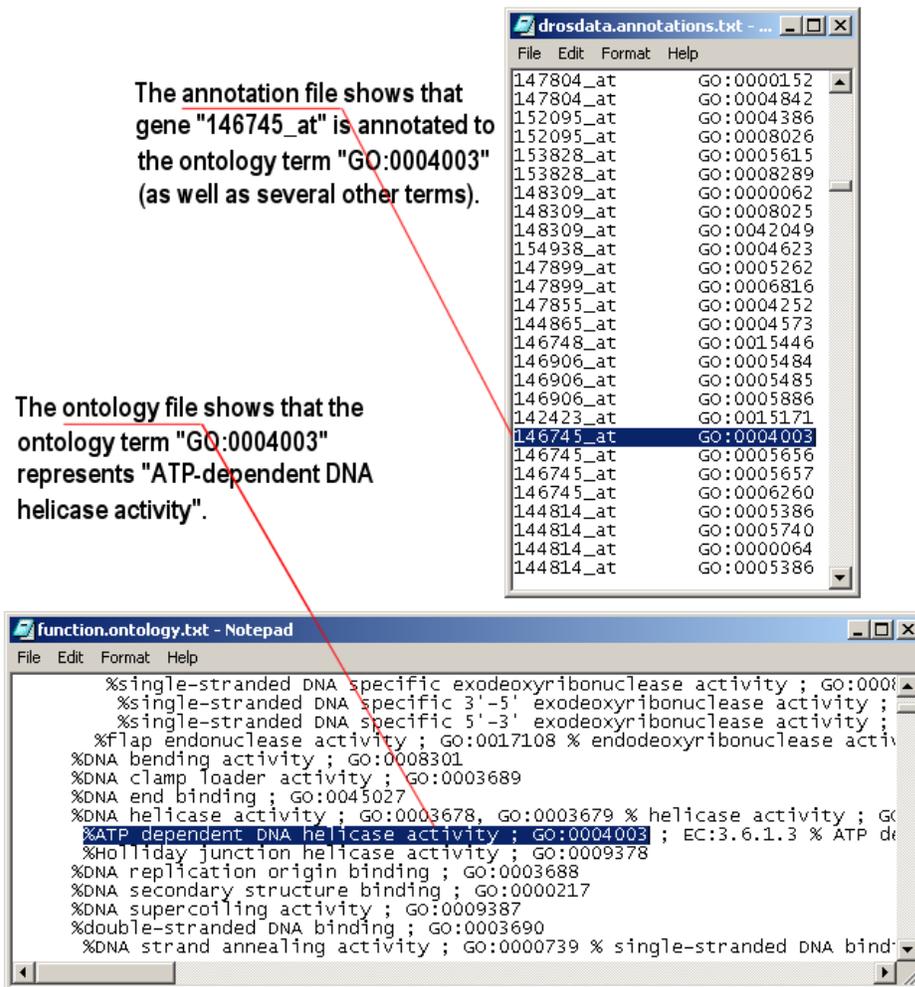
Tavazoie, S., Hughes, J.D., Campbell, M.J., Cho, R.J., Church, G.M., Systematic determination of genetic network architecture, *Nature Genetics*, 22 (3), 1999, pp 281-285

## 8.3.4.2 Required Input for Gene Ontology Browser

You need three different files to use the Gene Ontology Browser:

- A data set in DecisionSite
- One or more ontology files containing the various ontology terms (see Gene Ontology File Formats).
- An annotation file to link the data set to the ontology file (see Gene Annotation File Formats).

**Note:** You have to make sure that you are using an annotation file that includes the same IDs as the ones in your data set in order to obtain any hits using this tool.



## 8.4 Portfolio

### 8.4.1 Portfolio Overview

The Portfolio tool allows records to be arranged into lists. You can also add annotations to both lists and records.

You work with the same portfolio all the time. It is automatically saved when you make changes to it. You can import and export contents to and from the Portfolio.

Records are identified using any column in your data set. The record identifier is selected in the Portfolio: Options dialog.

### 8.4.2 Using Portfolio

#### 8.4.2.1 Working with Lists

##### 8.4.2.1.1 Working with Lists in Portfolio

This chapter shows you how to add, edit, compare and remove lists in the Portfolio.

### 8.4.2.1.2 Adding an Empty List to the Portfolio

#### ► To add an empty list:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Click on the list (or the Portfolio root) beneath which you want to add the new list.  
Comment: A new list is always added to the end of a current collection of lists or records.
3. Select **New > Empty List...** from the **Portfolio** menu.  
Response: The Portfolio: New List dialog is displayed.
4. Type a **List name** of the new list and click **OK**.  
Response: The new list is added to the Portfolio below the selected list.  
Comment: You can use cut & paste or drag & drop to paste records and annotations into the new list.

**Tip:** You can also select **Add New Empty List...** from the pop-up menu or click on the **Add new empty list** button, , to add an empty list to the Portfolio.

### 8.4.2.1.3 Adding a New List of Records to the Portfolio

#### ► To add a new list from marked records:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Mark the records you want to include in the new list.
3. Select **New > Add New List from Marked Records** from the Portfolio menu.  
Response: The Portfolio: New List dialog is displayed.
4. Type a **List name** of the new list and click **OK**.  
Response: The new list is added to the Portfolio as the last item on the root level.

**Tip:** You can also click on the **Add new list from marked** button, , to add a list of records to the Portfolio.

#### ► To add a new list from search result:

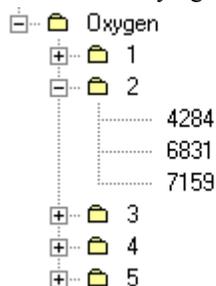
1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Select **Search** from the Portfolio menu and enter your search string.  
Response: The hits from your search are shown beneath the Search pane.
3. Select **New > Add New List from Search Result** from the Portfolio menu.  
Response: The Portfolio: New List dialog is displayed.
4. Type a **List name** of the new list and click **OK**.  
Response: The new list is added to the Portfolio as the last item on the root level.  
**Note:** The new list only contains one copy of each record, even if the search found the record in many different portfolio lists. If one of the search results is a list name, all of the records included in that list will be added to the new list.

#### ► To add marked records to the current list:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Mark the records you want included in your current list.
3. Select **New > Add Marked Records to List** from the Portfolio menu.  
Response: The records are added to the end of the current Portfolio list.

### 8.4.2.1.4 Adding a Grouped List to the Portfolio

Categorical data can be added as a grouped list to the Portfolio. An example of such a grouped list would be one based on a column with the number of Oxygen atoms. The grouped list would include underlying lists with records for each number of oxygen atoms.



#### ► To add a grouped list:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Mark the records you wish to include in the new list.
3. Select **New > Grouped List...** from the **Portfolio** menu.  
Response: The Portfolio: New Grouped List dialog is displayed.
4. From the **Group new list by** field, select the column you wish to base the underlying lists on.
5. Type a **List name** of the new list and click **OK**.  
Response: The new grouped list is added to the Portfolio as the last item on the root level.

### 8.4.2.1.5 Changing the Name of a List in the Portfolio

#### ► To change the name of a list:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Click to select the list whose name you want to change.
3. Select **Rename...** from the Portfolio menu.  
Response: The Portfolio: Rename List dialog is displayed.
4. Edit the **List name**.
5. Click **OK**.  
Response: The name of the list is updated in the Portfolio.

**Tip:** You can also right-click and select **Rename...** from the pop-up menu or press **F2** to bring up the Portfolio: Rename List dialog for a selected list.

### 8.4.2.1.6 Removing a List or Record from the Portfolio

#### ► To remove a list or a record:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Click on the list or record you want to remove.  
Comment: Removing a list also removes all underlying lists, records and annotations.
3. Select **Delete** from the **Portfolio** menu.  
Response: The list or record is removed from the Portfolio.

**Tip:** You can also right-click on a list or record and select **Delete** from the pop-up menu or press **Delete** on the keyboard to remove it from the *Portfolio*.

### 8.4.2.1.7 Adding a New Column from the Portfolio

This function can be used to express the location of records in the Portfolio. You can find out in which marked lists your records are present. The information is added to your data set as a new column showing the Portfolio Role for all records.

For each record, the names of the marked lists where the record appears are put together as strings separated by a semicolon (;). Lists are referred to by the name you have given to them, and not by the full path through the Portfolio. Records that are not present in any of the marked lists get the value "Not included" in the new column.

**Note:** The records that you are studying in the Portfolio must be part of your current data set in Spotfire DecisionSite. It is only the existing records that get a value in the new column. Any other records, present either in the Portfolio or Spotfire DecisionSite, get an empty value.

#### ► To add a new column from the Portfolio:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Click on the root list if you want to base the new column on the entire Portfolio.  
Comment: You can restrict yourself to smaller sections of the Portfolio. Click to select only the list(s) you want to include. Records that are not present below the selected list(s) get the value "Not included" in the new column even if they are present in other unselected lists within the Portfolio.
3. In the Portfolio: Options dialog, select the **Overwrite old column** check box if you want to overwrite the last column added by the Portfolio tool.
4. Select **Add New Column** from the **Portfolio** menu.

Response: A new column is added to the data set.

Comment: Lists are referred to by the name you have given to them, and not by the full path through the Portfolio. If you have lists with identical names in your Portfolio, (which is allowed) you will have no way of separating these in the created column. If you want a unique identification of each list, you must edit the names of the lists to ensure that there are no duplicate names before the new column is added.

**Tip:** You can also click on the **Add new column** button, , to perform this function.

### 8.4.2.1.8 Multiple Venn Comparison

Venn diagrams are used to visualize the various overlaps between different lists of data. Traditional Venn Diagrams are convenient ways to visualize the relationship between two or three lists. In Spotfire DecisionSite you can use the Portfolio in combination with the Pie Chart visualization to generate an alternative visualization to Venn diagrams that allows you to investigate the overlaps between any number of lists.

#### ► To use the Portfolio for multiple Venn comparisons:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Create the lists that you want to compare in the Portfolio.  
**Tip:** First create a main list that will contain all of the lists that you want to compare. Then add the different lists containing the desired subsets to this list. The result could be list names like "Greater than 2-fold change", "Unknown bioprocess" and "Unknown molecular function", for example.
3. Click on the main list containing all of the subset lists (or press **Ctrl** and click on all subset lists that you want to investigate).  
Comment: Records that are not present below the selected lists get the value "Not included" in the new column even if they are present in other unselected lists within the Portfolio.
4. Select **Add New Column** from the Portfolio menu.  
Response: A new column called Portfolio Role is added to the data set.
5. Select **Visualization > New Pie Chart** from the main DecisionSite menu bar.

Response: A new pie chart is created.

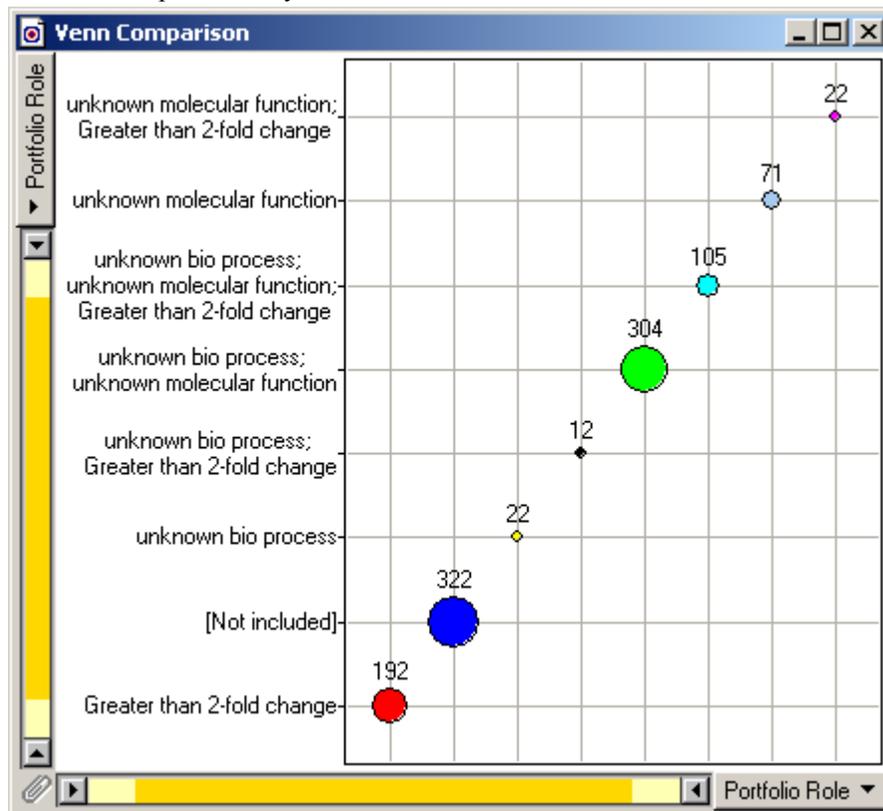
6. Select **Portfolio Role** as the column to be mapped on both axes.
7. In the **Properties** dialog of the Pie Chart, select to **Color - By Portfolio Role**.
8. Select **Size - By records count**.
9. Click the **Labels - All records** radio button.
10. Select the **Pie records count** check box.

Comment: This displays the number of records in each pie.

11. Make sure the Sector value and Sector percentage check boxes are cleared.

Response: Now you have created a pie chart with several pies where each pie represents the number of records included in each list or combination of lists.

Examining the resulting visualization can quickly give you an overview of the size of the various overlaps between your lists:



## 8.4.2.2 Working with Annotations

### 8.4.2.2.1 Working with Annotations in Portfolio

You can add annotations to lists and records, and to the Portfolio itself. Annotations can be text strings, integers, real numbers or URLs.

### 8.4.2.2.2 Adding a New Annotation in the Portfolio

#### ► To add a new annotation:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Click to select the object in the Portfolio where you want to add the annotation.
3. Select **New > Annotation...** from the Portfolio menu.

Response: The Portfolio: New Annotation dialog is opened.

4. Enter the **Annotation**.  
Comment: Press **Enter** to get a line break in the annotation text.
5. Click **Advanced** >> to show optional settings.  
Comment: The Advanced settings lets you enter both **Type** and **Name** for the annotation. This could be useful if you have a URL annotation, for example. A short description can be entered in the Name field to help remember the contents of the web link. Click << **Hide** to hide the optional settings.
6. Click **OK**.  
Response: The annotation is added to the selected object in the Portfolio.

**Tip:** You can also click on the **Add new annotation** button, , to add an annotation. You can double-click on a URL annotation in the Portfolio to open up the specified URL in a separate browser.

### 8.4.2.2.3 Editing an Annotation in the Portfolio

#### ► To edit an annotation:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Click on the annotation you want to modify.
3. Select **Edit...** from the **Portfolio** menu.  
Response: The Portfolio: Edit Annotation dialog is opened.
4. Edit the **Annotation**.  
Comment: Press **Enter** to get a line break in the annotation text.
5. Click **Advanced** >> to show optional settings  
Comment: The Advanced settings lets you edit both the **Type** and the **Name** of the annotation. Click << **Hide** to hide the optional settings.
6. Click **OK**.  
Response: The annotation is updated in the Portfolio.

**Tip:** You can also right-click and select **Edit...** from the pop-up menu or press **F2** to bring up the Portfolio: Edit Annotation dialog for a selected annotation.

### 8.4.2.2.4 Removing an Annotation from the Portfolio

#### ► To remove an annotation:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Click on the annotation you want to remove.
3. Select **Delete** from the **Portfolio** menu.  
Response: The annotation is removed from the Portfolio.

**Tip:** You can also right-click on an annotation and select **Delete** from the pop-up menu or press **Delete** on the keyboard to remove the annotation.

## 8.4.2.3 Importing and Exporting

### 8.4.2.3.1 Importing a Portfolio

You can import other portfolios into the Portfolio. An imported portfolio will appear as a list within the Portfolio in Spotfire DecisionSite for Lead Discovery.

#### ► To import a portfolio:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Select **Import...** from the Portfolio menu.  
Response: The Open File dialog is opened.

3. From the **Files of type** drop-down list box, select the format of the portfolio you want to import.

Comment: You can import files of formats SRP or LST. You can also import XML files exported from the *Portfolio*.

4. Locate the portfolio you want to import and click on it.
5. Click **Open**.

Response: The imported portfolio appears as the last list on the root level in the Portfolio.

**Note:** If you export the entire Portfolio from Spotfire DecisionSite for Lead Discovery and import it again, it will appear as a list in the Portfolio, as will all other portfolios that are imported.

### 8.4.2.3.2 Exporting the Portfolio

You can export the contents of the Portfolio in order to share your lists with other users or to save an old list configuration.

#### ► To export the Portfolio:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Click on the root list if you want to export the entire Portfolio.  
Comment: You can also export parts of the Portfolio. Press **Ctrl** and click to select only those parts you want to export.
3. Select **Export Marked Contents...** from the **Portfolio** menu.  
Response: The Save File dialog is displayed.
4. Select a location from the **Save in** drop-down list box.
5. Select a format from the **Save as type** drop-down list box.
6. Enter a **File name** and click **Save**.

**Note:** If you export the entire Portfolio from Spotfire DecisionSite for Lead Discovery and import it again, it will appear as a list in the Portfolio, as will all other portfolios that are imported.

### 8.4.2.4 Cutting, Copying and Pasting in the Portfolio

#### ► To cut, copy or paste objects in the Portfolio:

1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. Click on the object you want to cut or copy.  
Comment: Press **Ctrl** and click to select multiple objects in the Portfolio.
3. Click the **Portfolio** menu button, , to display the Portfolio menu.
4. Select **Cut**.  
Response: The selected object is removed from the Portfolio and placed on the clipboard.  
Comment: Select **Copy** to place a copy of the selected object on the clipboard.
5. Click on the list or record in the Portfolio where you want to paste the contents of the clipboard.  
Comment: Lists or records can only be pasted to lists. Annotations can be pasted to lists or to records.
6. Select **Paste** from the **Portfolio** menu.  
Response: The list, record or annotation that was placed on the clipboard is pasted into the Portfolio.  
Comment: Lists can also be pasted into tools outside of Portfolio, such as a text editor.

**Tip:** You can use drag and drop to move objects in the Portfolio. The commands **Cut**, **Copy** and **Paste** are also available from the pop-up menu.

## 8.4.2.5 Searching the Portfolio

You can do a free text search of the Portfolio including lists, records and annotations. The search is case insensitive and uses the wildcards ? and \*.

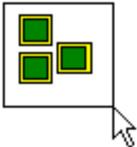
### ► To search the Portfolio:

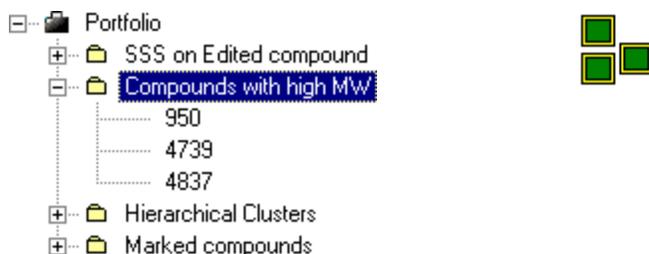
1. If the Portfolio tool is not already open, select **Tools > Portfolio**.
2. If the Search pane in the Portfolio is hidden, click on the **Search** button, , in the toolbar to display it.  
Response: The Search pane is displayed.
3. Enter your search string in the provided field.  
Comment: Enter the full element name or add a wildcard symbol to the truncated name to retrieve the search results.
4. Click **Search**.  
Response: The total number of hits is shown below the Search pane. The first appearance of the search string is highlighted in the Portfolio.
5. Use the **Previous** (<<) and **Next** (>>) buttons to step through all matches to the search string in the Portfolio.  
Response: Each found appearance of the search string is highlighted in the Portfolio, one at a time, as you step through the result of the search.

**Tip:** If you want all records found during the search to be automatically marked in the visualizations, select the **Mark on search** check box in the Portfolio: Options dialog.

## 8.4.2.6 Data Interaction in Portfolio

### 8.4.2.6.1 Marking in Portfolio

Do this in a visualization...	...and this happens in Portfolio
Mark some records in a visualization.	Nothing happens in the Portfolio.
	
Do this in Portfolio...	...and this happens in all visualizations
Click to select a list (or record) in the Portfolio. You can press <b>Ctrl</b> and click to select multiple objects in the Portfolio.	The corresponding records are marked in the visualizations.



**Note:** To achieve this interaction, the records in the Portfolio must be part of the current data set in Spotfire DecisionSite. Also, the **Mark on browse** check box must be selected in the Portfolio: Options dialog. All records with the same record identifier will be marked, regardless of whether the specific record was a part of the records used to create the list or not.

**Tip:** If you only want to mark the records from a selected list and still want to be able to browse the other lists in the Portfolio, select the list and then choose **Mark in Visualization** from the Portfolio menu. Make sure that the **Mark on browse** check box in the Portfolio: Options dialog is cleared.

#### 8.4.2.6.2 Activating in Portfolio

##### Do this in a visualization...

Activate a record in a visualization.

##### ...and this happens in Portfolio

The ID of the active record is shown in the Search pane in the Portfolio.

If the Search pane is hidden, click on the Search button in the toolbar to display it.



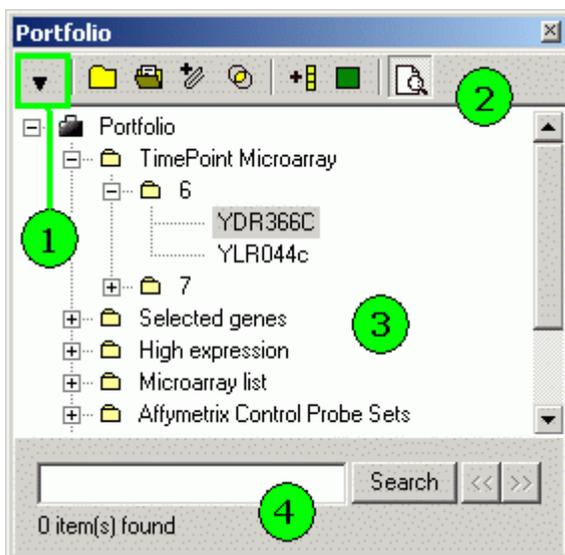
You can now click on the **Search** button to search for the active record within the Portfolio.

**Note:** You cannot activate lists or records in the Portfolio. When you click an object, it gets marked.

### 8.4.3 User Interface

#### 8.4.3.1 Portfolio User Interface Overview

This is the Portfolio user interface:



### 1. Portfolio menu



The Portfolio menu contains all menu commands required to work with the Portfolio.

### 2. Portfolio toolbar



Includes shortcuts for some of the most common commands in the Portfolio menu. Click [here](#) for a description of the buttons.

### 3. Portfolio

This displays the contents of the Portfolio. You can toggle the display of subtrees in the Portfolio by clicking the plus (+) or minus (-) sign beside a list. The left and right arrow keys on the keyboard can also be used to collapse or expand a node. All subnodes can be expanded/collapsed simultaneously by standing on the top node, e.g., Portfolio, and pressing the multiplication sign (\* or x) or the minus sign (-) on the numeric keypad.

### 4. Search



Via this pane, you can perform a full text search of the contents of the Portfolio. Enter a string in the search field and click on **Search**. You can use the Back (<<) and Forward (>>) buttons to browse the result from the search. The number of hits from the search are displayed right below the field. You can use the wildcards ? and \* in the search string.

## 8.4.3.2 Portfolio Menu

The Portfolio menu is displayed by clicking  and contains all commands necessary for working with the Portfolio.

Option	Description
<b>Undo</b>	Undoes the last delete, edit, move, cut, copy, paste or import operation in the Portfolio. You can only undo the last operation and not a series of operations.
<b>Cut</b>	Removes the selected objects from the Portfolio and places them on the clipboard.
<b>Copy</b>	Places a copy of the selected objects from the Portfolio on the clipboard.
<b>Paste</b>	Pastes the contents of the clipboard below the selected list in the Portfolio.
<b>Delete</b>	Deletes the selected objects from the Portfolio.
<b>New &gt;</b>	
> <b>Empty List...</b>	Adds a new empty list to the Portfolio below the selected list.
> <b>List from Marked...</b>	Adds a new list with the marked records to the Portfolio. The list is placed as the last item on root level.
> <b>Grouped List...</b>	Adds a new grouped list with the marked records to the Portfolio. This function first opens the Portfolio: New Grouped List dialog where the new list is defined. The list is placed as the last item on root level.
> <b>Annotation...</b>	Adds a new annotation to the active object in the Portfolio. This function first opens the Portfolio: New Annotation dialog where the annotation is defined.
> <b>Add New List from Search Result</b>	Adds a new list containing the results from your free-text search using the Search pane to the Portfolio. The list is placed as the last item on root level. <b>Note:</b> The new list only contains one copy of each record, even if the search found the record in many different portfolio lists. If one of the search results is a list name, all of the records included in that list will be added to the new list.
> <b>Add Marked Records to List</b>	Adds the marked records from your current visualization into the Portfolio list. <b>Note:</b> You can also right-click in the visualization and add your marked records into your currently active Portfolio list.
<b>List Logic...</b>	Brings up the List Logic dialog where you can compare the marked lists using Boolean operators (OR, AND or ONLY).
<b>Add New Column</b>	Adds a new column to the data set, with information about the location of the records within the marked list(s) in the Portfolio.
<b>Rename...</b>	Lets you edit an annotation or the name of a list. This function brings up either the Portfolio: Edit Annotation dialog or the Portfolio: Rename List dialog depending on which object you have selected in the Portfolio.
<b>Import...</b>	Imports a portfolio from a file. The imported portfolio is displayed as a list and is placed as the last item on root level in the Portfolio.
<b>Export Marked Contents...</b>	Exports the selected parts of the Portfolio as an SRP, XML or LST file.

<b>Mark in Visualization</b>	Marks the records that belong to the selected Portfolio list in the DecisionSite data set and visualizations.
<b>Search</b>	Displays or hides the Search pane, where you can perform a free text search of the contents of the Portfolio including lists, records and annotations.
<b>Sort Alphabetic</b>	Lets you sort the contents of your lists alphabetically.
<b>Sort Numeric</b>	Lets you sort the contents of your lists numerically. <b>Note:</b> This sorting only applies to the leading digits.
<b>Options...</b>	Displays the Portfolio: Options dialog.
<b>Help</b>	Opens this help file to the Portfolio overview page.

### 8.4.3.3 Portfolio Pop-up Menu

To bring up the pop-up menu, right-click in the part of the Portfolio that shows its contents.

Option	Description
<b>Add New Empty List...</b>	Adds a new empty list to the Portfolio beneath the selected list.
<b>Add New Annotation...</b>	Adds a new annotation to the active object in the Portfolio. This function first opens the Portfolio: New Annotation dialog where the annotation is defined.
<b>Add New List from Search Result</b>	Adds a new list containing the results from your free-text search using the Search pane to the Portfolio. The list is placed as the last item on root level.
<b>Add New List from Marked Records</b>	Adds a new list with the marked records to the Portfolio. The list is placed as the last item on root level.
<b>Add Marked Records to List</b>	Adds the marked records from your current visualization into the Portfolio list. <b>Note:</b> You can also right-click in the visualization and add your marked records into your currently active Portfolio list.
<b>Edit...</b>	Lets you edit an annotation or the name of a list. This function brings up either the Portfolio: Edit Annotation dialog or the Portfolio: Rename List dialog depending on which object you have selected in the Portfolio.
<b>Cut</b>	Removes the selected objects from the Portfolio and places them on the clipboard.
<b>Copy</b>	Places a copy of the selected objects from the Portfolio on the clipboard.
<b>Paste</b>	Pastes the contents of the clipboard below the selected list in the Portfolio.
<b>Delete</b>	Deletes the selected objects from the Portfolio.
<b>Undo</b>	Undoes the last delete, edit, move, cut, copy, paste or import operation. Only the very last operation can be undone.
<b>Sort Alphabetic</b>	Lets you sort the contents of your lists alphabetically.

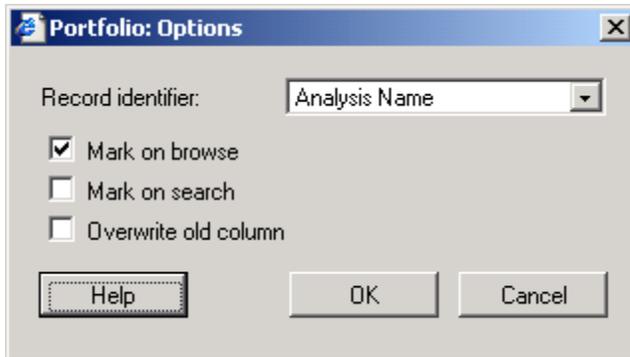
**Sort Numeric** Lets you sort the contents of your lists numerically.  
**Note:** This sorting only applies to the leading digits.

### 8.4.3.4 Portfolio Toolbar

The Portfolio toolbar includes shortcuts for some of the most common commands in the Portfolio menu. Click on the buttons on the toolbar to activate the corresponding functions.

-  This is the Portfolio menu selector. When you click on it, a menu is displayed. Click here for a description of the available menu options.
-  Adds a new empty list to the Portfolio below the selected list.
-  Adds a new list with the marked records to the Portfolio. The list is placed as the last item on root level.
-  Adds a new annotation to the selected object in the Portfolio. First, the Portfolio: New Annotation dialog is opened. This is where the annotation is defined.
-  Brings up the List Logic dialog where you can compare the marked lists using Boolean operators (OR, AND or ONLY).
-  Adds a new column to the data set with information about the location of the records within the selected list(s) in the Portfolio.
-  Marks the records that belong to a selected list in the visualizations.
-  Displays or hides the Search pane, where you can perform a free text search of the contents of the Portfolio including lists, records and annotations.

### 8.4.3.5 Portfolio: Options Dialog



Option	Description
<b>Record identifier</b>	Defines which column in the data set should be used as the identifier. You can choose the identifier from any column that contains strings or integers.
<b>Mark on browse</b>	Automatically marks records in the visualizations when browsing a list using the mouse or arrow keys.
<b>Mark on search</b>	Automatically marks records in the visualizations when they are found in a Search.
<b>Overwrite old column</b>	Select this check box if you want to overwrite a previously added column (from the Portfolio tool) when you add a new portfolio role column. Clear if you do not wish to overwrite.

► **To reach the Portfolio: Options dialog:**

Select **Options...** from the **Portfolio** menu.

### 8.4.3.6 Portfolio: New Annotation Dialog

Option	Description
<b>Annotation</b>	The contents of your annotation are entered here. Press <b>Enter</b> to force a line break in the annotation text.
<b>Type</b>	The type of annotation; can be String, Long, Real or URL. The type is set to String as default.
<b>Name</b>	An alias for the annotation can be entered here. If filled in, the alias is displayed before the contents of the Annotation field in the Portfolio.
<b>Advanced &gt;&gt;</b>	Shows the advanced settings.
<b>&lt;&lt; Hide</b>	Hides the advanced settings.

► **To reach the Portfolio: New Annotation dialog:**

- Select **New > Annotation...** from the **Portfolio** menu or
- select **Add New Annotation...** from the pop-up menu or
- click on the **Add new annotation** button, 

### 8.4.3.7 Portfolio: New Grouped List Dialog

Option	Description
<b>Group new list by</b>	Displays all available columns that you can choose to base your new grouped list on. The grouped list will contain an underlying list for each unique value in this column. Click on a column to select it.
<b>List name</b>	A name for the new list is entered here.

► **To reach the Portfolio: New Grouped List dialog:**

Select **New > Grouped List...** from the **Portfolio** menu.

## 8.5 List Logic

### 8.5.1 Comparing Lists Using List Logic

You can compare lists using Boolean operators. This lets you determine which records are present or not in a certain combination of lists. The result is added as a new list, and you can select where you want to put it.

**Note:** The List Logic function only compares records in the list and its sublists. Annotations and names of sublists are not considered.

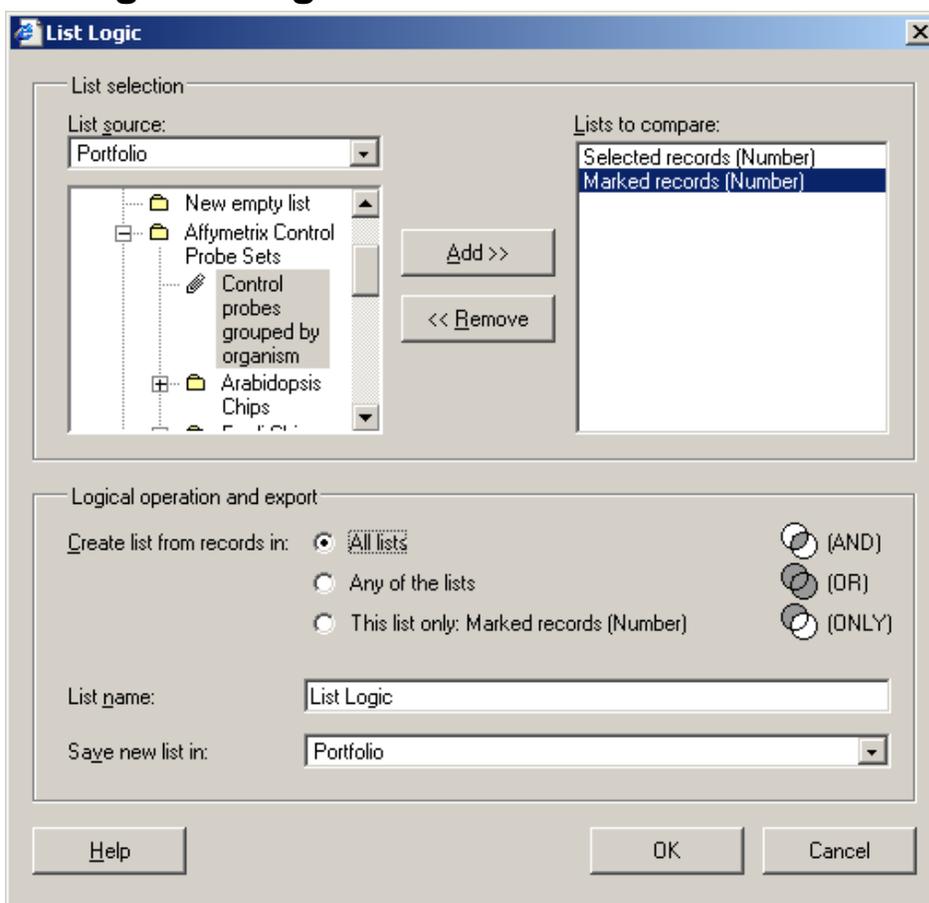
► **To compare lists:**

1. If the List Logic tool is not already open, select **Tools > List Logic...**  
Response: The List Logic dialog is displayed.
2. Select the desired **List source**.  
Comment: You can choose a list from Portfolio, Structure Viewer, from the current Data set, from an External file, or Create a new list.
3. Click to select the lists you want to compare and click **Add >>** to move them to the Lists to compare pane.  
Comment: You can only compare separate lists. In other words, you cannot compare an underlying list with its parent list. When you select a list, all underlying lists are automatically included in the selection.
4. Select one of the three methods of logical operation: **OR** (All lists), **AND** (Any of the lists), or **ONLY** (This list only).
5. Enter a new **List name**.
6. Select where you want to save the result of the list comparison.
7. Click **OK**.

Response: In the case of Portfolio and Structure Viewer, the new list is added to the selected source as the last item on the root level. An annotation with information about how the list was created is automatically added to the new list. If External file is selected, a save dialog will appear in which you can specify where you want the file to be saved.

**Tip:** You can also click on the **List Logic** button  in the Portfolio or Structure Viewer to start the tool.

## 8.5.2 List Logic Dialog



Option	Description
<b>List source</b>	Displays the sources from which you can select lists to be added. Select a source from the List Source pane. Click a list name in the pane to select it. To select more than one list, press <b>Ctrl</b> and click the list names in the pane.
<b>Lists to compare</b>	Displays the lists that are to be compared.
<b>Add &gt;&gt;</b>	Adds the lists that have been selected in the List source pane to the Lists to compare pane.
<b>&lt;&lt; Remove</b>	Removes a list from the Lists to compare pane.
<b>All lists</b>	Creates a new list containing only those records that are present in all of the lists.
<b>Any of the lists</b>	Creates a new list containing all records that are present in any of the lists. Each record will appear only once in the new list, even if that record is present in several of the selected lists.
<b>This list only</b>	Creates a new list containing only those records that are present in the selected list and not in any of the other lists.
<b>List name</b>	The name of the new list that is created.
<b>Save new list in</b>	Selects the location where the result of the list comparison will be

saved.

► **To reach the List Logic dialog:**

Select **Tools > List Logic...**, or click on the **List Logic** button  in Portfolio or Structure Viewer.

## 8.6 Web Links

### 8.6.1 Web Links Overview

The Web Links tool enables you to send a query to an external web site to search for information about marked records. The search results are displayed in a separate web browser.

The Web Links tool is shipped with a number of predefined web sites that are ready to use. You can also set up new links to web sites of your choice.

### 8.6.2 Using Web Links

#### 8.6.2.1 Sending a Query Using Web Links

**Note:** You need to have data in Spotfire DecisionSite to be able to send a query. The query is sent for the marked records in the visualizations. If more than one record is marked, the records are separated by the web link delimiter in the query.

► **To send a query using Web Links:**

1. In a visualization, mark those records you want to search for information about.
2. Select **Tools > Web Links...**  
Response: The Web Links dialog is displayed.
3. Click to select the link to the web site where you want the query to be sent.  
Comment: Some web sites only allow you to search for one item at a time. If you do not get any hits from a search, mark one record at a time in the visualizations and try again.
4. Select the **Identifier column** that you want to use as input to the query.  
Comment: You can choose from any column in your data set.
5. Click **OK**.  
Response: The query is sent to the web site and the results are displayed in a new web browser.

#### 8.6.2.2 Setting Up a New Web Link

► **To set up a new web link:**

1. Select **Tools > Web Links...**  
Response: The Web Links dialog is displayed.
2. Click **Options...**  
Response: The Web Links Options dialog is displayed.
3. Click **New**.  
Response: A New web link is created and selected in the list of Available web links.  
Comment: The Preview helps you see what the finished query will look like when it is sent.
4. Edit the name of the new link in the **Web link name** text box.
5. Edit the **URL** to the web link.

---

Comment: A dollar sign within curly brackets {\$} should be used as placeholder for the ID. Anything you enter between the left bracket and the dollar sign will be placed before each ID in the query. In the same way, anything placed between the dollar sign and the right bracket will be placed after each ID in the query.

6. Enter the **Delimiter** to use to separate the IDs in a query.

Comment: The identifiers in a query with more than one record are put together in one search string separated by the selected Delimiter. You can use AND, OR or ONLY as delimiters.

7. Click **OK**.

Response: The new web link is saved and is displayed together with the other available web links in the user interface.

### 8.6.2.3 Editing a Web Link

#### ► To edit a web link:

1. Select **Tools > Web Links...**

Response: The Web Links dialog is displayed.

2. Click **Options...**

Response: The Web Links Options dialog is displayed.

3. Click on the web link you want to edit in the list of **Available web links**.

Response: The Web link name, URL and Delimiter for the selected web link are displayed and can be edited directly in the corresponding fields.

Comment: All changes that are made are reflected in the Preview which helps you see what the finished query will look like.

4. Make desired changes to the web link and click **OK**.

Response: The web link is updated according to your changes and the Web Links Options dialog is closed.

### 8.6.2.4 Removing a Web Link

#### ► To remove a web link:

1. Select **Tools > Web Links...**

Response: The Web Links dialog is displayed.

2. Click **Options...**

Response: The Web Links Options dialog is displayed.

3. Click on the web link you want to remove in the list of **Available web links**.

Response: The Web link name, URL and Delimiter for the selected web link are displayed in the corresponding fields.

4. Click **Delete**.

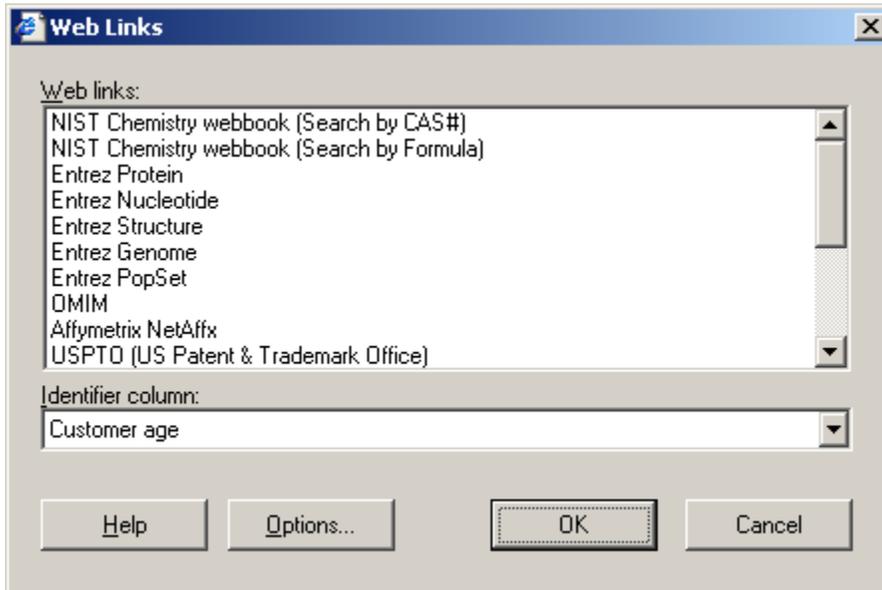
Response: All the fields are cleared.

Comment: You can delete many web links at a time if you select several web links in the list of **Available web links** and click **Delete**. Press **Ctrl** and click on the web links in the list to select more than one.

**Tip:** If you have deleted some of the default web links by mistake, you may retrieve them again by clicking the **Add defaults** button. This adds all of the default links to the Available web links list, regardless of whether or not the links already exist.

## 8.6.3 User Interface

### 8.6.3.1 Web Links Dialog

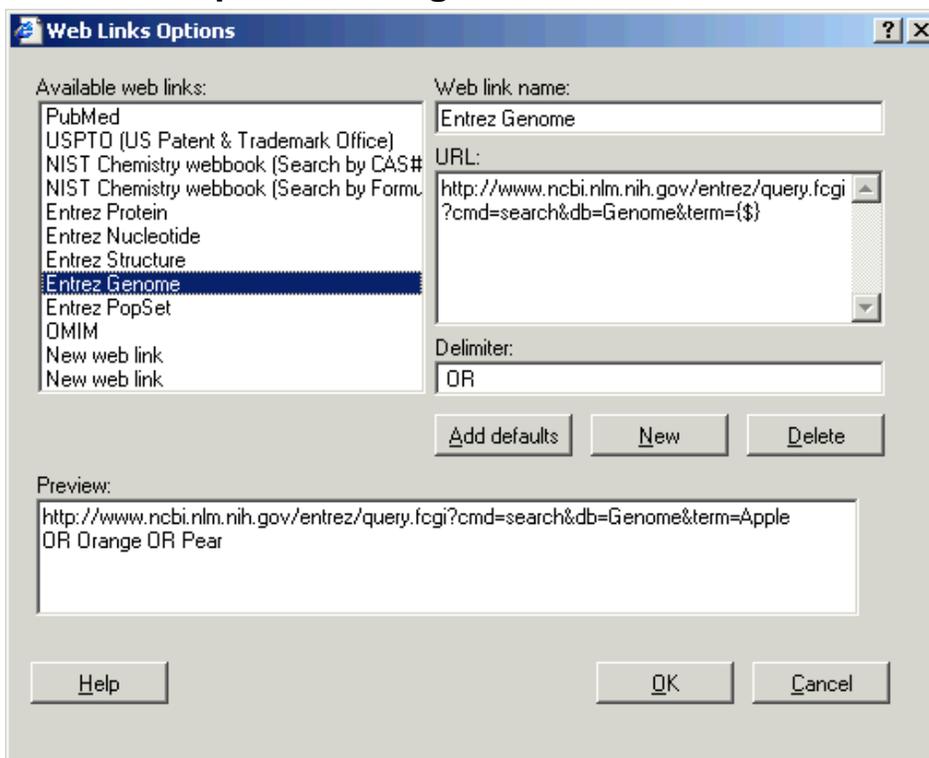


Option	Description
<b>Web links</b>	The available web links. The web links tool is shipped with a number of default links, but you can edit or add new web links to the list via the Web Links Options dialog. Click to select the link to which you want to send a query for the marked records.
<b>Identifier column</b>	This is where you specify which identifier to use when you send a query for marked records to a web site.
<b>Options...</b>	Opens the Web Links Options dialog.

► **To reach the Web Links dialog:**

Select **Tools > Web Links...**

### 8.6.3.2 Web Links Options Dialog



Option	Description
<b>Available web links</b>	The available web links that are listed in the Web Links user interface.
<b>Web link name</b>	The name of the web link. Click on a web link in the list of Available web links to edit the name in this field.
<b>URL</b>	The URL to the web link. Click on a web link in the list of Available web links to edit the URL in this field. A dollar sign within curly brackets is used as a placeholder for the ID in the query. Anything you enter between the left bracket and the dollar sign will be placed before each ID in the query. Likewise, anything placed between the dollar sign and the right bracket will be placed after each ID in the query. The preview shows you what the query will look like.
<b>Delimiter</b>	The separator that should be used between the IDs in a query with more than one record. Click on a web link in the list of Available web links to edit the delimiter in this field.
<b>Add defaults</b>	Adds the default web links (that Spotfire DecisionSite Statistics is shipped with) to the list of Available web links. The current links are not updated, instead copies of the links are added. This allows you to have two different versions of the default links. For example, one version could contain your own personal settings.
<b>New</b>	Adds a New web link to the list of available web links and lets you edit its name, URL and Delimiter in the fields to the right.
<b>Delete</b>	Deletes the selected web link(s) in the list of Available web links.

<b>Preview</b>	Shows you a preview of the URL with three IDs (Apple, Orange and Pear) instead of the placeholder {\$} (dollar sign within curly brackets).
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► **To reach the Web Links Options dialog:**

Select **Tools > Web Links...** to display the Web Links dialog. Then click on the **Options...** button to the lower left in the **Web Links** dialog.

## 8.7 Pathway Viewer

### 8.7.1 Adding Pathway Information

The Pathway Viewer is a tool which allows you to integrate Pathway Map information with your data set. You can merge multiple pathways and select identifiers to join your data.

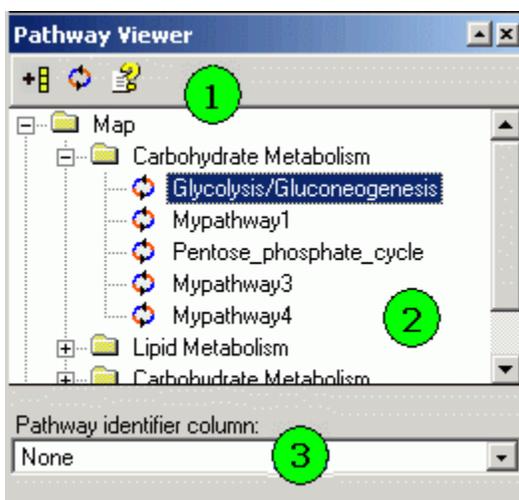
**Note:** The setting up of available maps is an administrative function that is done on the server. Please contact your Spotfire Administrator if you do not have access to all your required pathway maps.

► **Adding pathway information to the data set:**

1. If the Pathway Viewer is not already open, select **Tools > Pathway Viewer...** to display it.  
Response: The Pathway Viewer window is displayed. It is possible to use other tools while the Pathway Viewer is open.
2. If you already have a data set with a Pathway identifier column, select the column containing pathway ID information from the drop-down list.  
Comment: If your data set does not contain pathway IDs, the Pathway Viewer can add this column in a later step.
3. Click on the **Add new column with Pathway Hits** button, .
4. If you did not select a Pathway ID column, the Pathway Viewer dialog is displayed. Select the internal identifier column on which to join the Pathway ID identifiers.
5. Click **OK**.  
Response: A new column, called PathwayID, is added to the data set containing all Pathway identifiers.

### 8.7.2 Pathway Viewer User Interface

This is the Pathway Viewer user interface:



### 1. Pathway Viewer toolbar

The toolbar contains three buttons which perform the following actions:

	<b>Add new column with Pathway Hits</b>	Adds a new column with pathway hits to the data set.
	<b>Show Pathway Map</b>	Displays a map of the selected pathway in a separate window.
	<b>Help on Pathway Viewer</b>	Opens this help file to a page with links related to this tool.

### 2. Pathways

Displays the available pathways. You can toggle the display of subtrees by clicking the plus (+) and minus (-) signs to the left of any list icon. Click to select the pathway of interest.

**Note:** The setting up of available maps is an administrative function that is done on the server. Please contact your Spotfire Administrator if you do not have access to all your required pathway maps.

### 3. Pathway identifier column

This is where you select which column contains the pathway identifier.

#### ► To reach the Pathway Viewer:

Select **Tools > Pathway Viewer**....

## 8.8 Computation Services

### 8.8.1 Computation Services Overview

The Computation Services is built to allow you to add any specific type of computation or "tool" to your analysis. Different types of statistical calculations can be added to the data set or included in Guides for easy distribution to others.

The out-of-the-box version of Computation Services supports connection to R, S-PLUS and SAS servers, but other types of connectors can also be added. For more information, see Spotfire Developer Network.

**Note:** This help file does not contain any information regarding how to write your scripts. For specific information on how to write scripts, see literature for the respective scripting language.

## 8.8.2 Using Computation Services

### 8.8.2.1 Computation Services Quick Reference

Action	Instruction
<b>Start Computation Services</b>	From the main menu bar of DecisionSite, select <b>Tools &gt; Computation Services &gt; SAS or R or S-PLUS</b> or whatever type of server you want to connect to.
<b>Create a new configuration</b>	In Computation Services, click <b>File &gt; New</b> . Write or paste a script in the Script field, add input and output parameters and result handlers. Test the configuration. See Suggested Workflow or Example Configuration for more information.
<b>Open an earlier saved configuration</b>	In Computation Services, click <b>File &gt; Open...</b> . Browse to locate the configuration of interest and click <b>Open</b> .
<b>Add an input parameter</b>	Select the parameter in the script and click on the Add as Input Parameter button,  . Select the <b>Data type</b> of the parameter from the drop-down list. <b>Tip:</b> You can also start by clicking Add on the Input Parameters tab, edit the default parameter name and then write the script that includes the parameter.
<b>Add prompts</b>	Add at least one input parameter. Select the <b>Data type</b> of the parameter from the drop-down list. In the Input Parameters tab, select Prompt: [prompt type] from the <b>Value</b> drop-down list. Configure the prompt in the <b>Prompt Settings dialog</b> by adding a label and other information.
<b>Add an output parameter</b>	Select the parameter in the script and click on the Add as Output Parameter button,  . Select the <b>Data type</b> of the parameter from the drop-down list. <b>Tip:</b> You can also start by clicking Add on the Output Parameters tab, edit the default parameter name and then write the script that includes the parameter.
<b>Define what to do with the results</b>	Make sure that you have defined the output parameter that you want to use as result. On the <b>Result Handling tab</b> , click <b>Add</b> . From the menu, select the type of result handler that you want to use. If applicable, configure the selected result handler to work on the desired output parameter.

<b>Add resulting columns to the data set</b>	<p>Make sure that you have defined at least one output parameter as the data type Dataset.</p> <p>On the <b>Result Handling tab</b>, click <b>Add</b>.</p> <p>From the menu, select one of the following alternatives: Add to Current Data Set (Automatic Key Matching), Add to Current Data Set (Row by Row), Replace Current Data Set, or Open in Other DecisionSite Instance.</p> <p><b>Note:</b> The result handlers for adding columns will only be visible in the Add menu if you have defined at least one output parameter of the type Dataset.</p>
<b>Add resulting output as a file</b>	<p>Make sure that you have defined at least one output parameter as the data type File.</p> <p>On the <b>Result Handling tab</b>, click <b>Add</b>.</p> <p>From the menu, select the <b>Launch File</b> option.</p> <p><b>Note:</b> The Launch File result handler will only be visible in the Add menu if you have defined at least one output parameter of the type File.</p>
<b>Test a configuration</b>	In Computation Services, select <b>Execute &gt; Run</b> .
<b>Save a configuration</b>	In Computation Services, select <b>File &gt; Save</b> .
<b>Incorporate a configuration in a Guide</b>	<p>Test your configuration to make sure it is fully functional.</p> <p>In Computation Services, select <b>File &gt; Send to Analysis Builder</b>.</p> <p>In Analysis Builder, select the action <b>Start Data computation - SAS</b> (or R, S-PLUS, etc.).</p> <p>Click <b>&lt; Add Link</b>.</p> <p>Complete the Guide in Analysis Builder and <b>Save</b> it.</p> <p><b>Tip:</b> For more information about how to create Guides, see Analysis Builder Overview.</p>
<b>Minimize Computation Services</b>	Click on the top right x-button. This will hide Computation Services, but the current configuration will be remembered when you reopen the tool.
<b>Close Computation Services</b>	In Computation Services, select <b>File&gt; Exit</b> .

## 8.8.2.2 Suggested Workflow

### ► To create a new script configuration using Computation Services:

1. If Computation Services is not already open, select **Tools > Computation Services > SAS or R or S-PLUS**, or whatever the type of computation server you are running against.
2. Select **File > Connector Settings...** and specify the address to your **Server**.
3. Select whether to **Keep session open until manually closed** or not. See Connector Settings dialog for more information about this option.
4. Create the script by either typing or pasting existing script code in the Script field of Computation Services.
5. Add the desired input parameters to the **Input Parameters** tab and specify whether they should be prompted or not.

6. Add the desired output parameters to the **Output Parameters** tab.
7. Specify how you want to present your results on the **Result Handling** tab.
8. Test the configuration by selecting **Execute > Run**.
9. View the **Execution Log** to see if there were any errors during execution.
10. If there were any problems, go back to fix them.
11. Select **File > Send to Analysis Builder** and add the **Start Data computation - R** action (or whatever the type of computation you have created) to a suitable Guide.

### 8.8.2.3 Example Configuration

Below is the creation of a very simple configuration shown in detail to exemplify how you can work with Computation Services. The workflow would be exactly the same for S-PLUS and SAS servers.

**Note:** For information on how to write scripts, please refer to any literature for the respective scripting language.

#### ► Creating an R configuration which adds a user specified integer to selected columns in the data set:

1. In DecisionSite, open the data set in which you want to modify columns.  
Comment: It is not necessary to have data loaded in DecisionSite when defining or running a configuration, but in this example the data is used for testing purposes further down in this step instruction.
2. Select **Tools > Computation Services > R**.  
Response: Spotfire Computation Services for R is displayed.
3. In Computation Services, select **File > Connector Settings...**  
Response: The Connector Settings dialog is displayed.
4. Specify the address to your R **Server** by either typing in the text field (e.g., http://myRserver:9080) or selecting a predefined server from the list shown by clicking on .
5. On the Input Parameters tab, type a suitable **Prompt dialog title** in the specified field. In this example we use the text "Add Integer to Columns".  
Comment: According to Spotfire UI Guidelines the title should be short and concise and written using book title capitalization, without any closing punctuation.
6. On the Input Parameters tab, type a suitable **Prompt dialog description** in the specified field. In this example we use the text "This is an example R-script calculation which adds the integer provided below to all specified columns in the data set."  
Comment: The description is not necessary in all configurations, but it can be useful to further explain what the configuration does, or to add more guidance to the end users during execution.
7. In the **Script** field, type **dataout <- x + datain**.

```
Script:
dataout <- x + datain
```

Comment: This is the actual script which will be computed on the R server. In this example we want a user-specified integer, x, to be added to the values of the input columns in the datain parameter, and finally the resulting columns in the dataout parameter to be returned to the current data set as new columns.

8. Select the input parameter **x** in the script:

```
Script:
dataout <-  + datain
```

9. Click on the Add as Input Parameter button, .

Response: The parameter x is added to the Input Parameters tab.

10. On the Input Parameters tab, from the **Data type** drop-down list, select **Integer**.

11. From the **Value** drop-down list, select **Prompt: Integer**.

Response: The Prompt Settings: Integer dialog is displayed.

12. In the dialog, specify the **Label** that you want the end user of the configuration to see upon execution. In this example we use the text "**Integer to add to the selected columns:**".

Comment: Try to make the label as clear as possible to ensure that the end users of the script understand what the input parameter should be. According to Spotfire UI Guidelines, the label for a text field should use sentence-style capitalization and end with a colon.

13. If desired, add a default value and/or min and max values to limit the allowed input values.

14. Click **OK**.

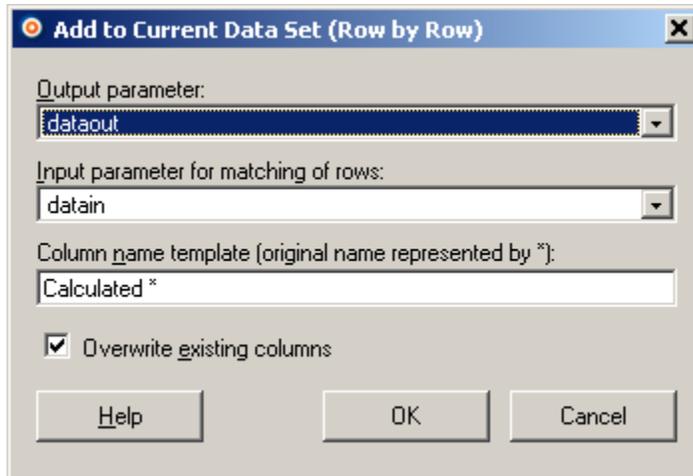
15. In the **Script** field, select the input parameter **datain** and click on the Add as Input Parameter button, .

16. On the Input Parameters tab, from the **Data type** drop-down list, select **Dataset**.

17. From the **Value** drop-down list, select **Prompt: Data set**.

18. Response: The Prompt Settings: Data Set dialog is displayed.

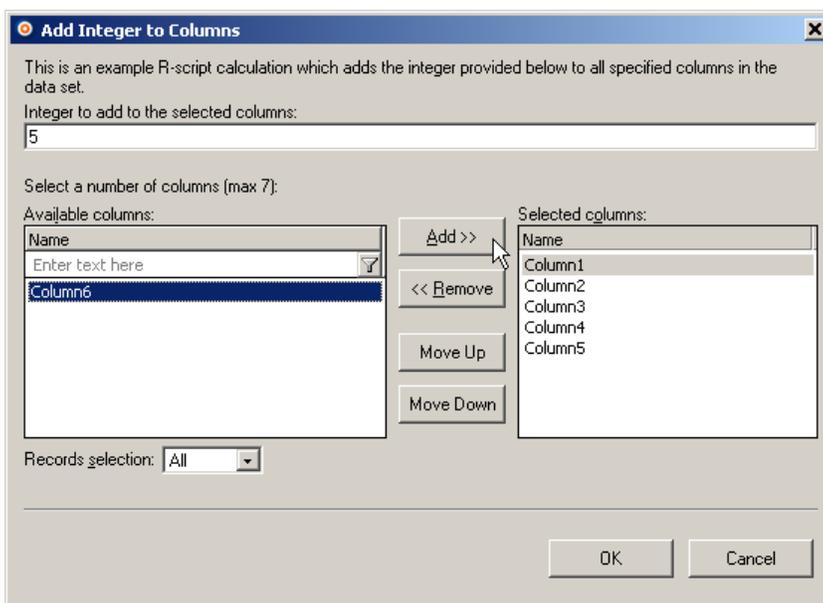
19. In the dialog, specify the **Label** that you want the end user of the configuration to see upon execution. In this example we use the text "**Select a number of columns (max 7):**".
20. Select the **Data types** of the columns that will be available for selection. In this example we will add an integer to the values of the specified columns, so Integer and Real are suitable data types.
21. If desired, add a Minimum number of columns (in this example we use 1) and a Maximum number of columns (in this example we use 7).
22. Click **OK**.
23. In the **Script** field, select the output parameter **dataout** and click on the Add as Output Parameter button, .
24. On the Output Parameters tab, from the **Data type** drop-down list, select **Dataset**.
25. On the **Result Handling tab** click on **Add**.
26. From the Add menu select **Add to current data set (row by row)**.  
Response: The Add to Current Data Set (Row by Row) dialog is displayed.



Comment: This is just one of many result handlers available. See Result Handling tab for more information about the other options.

27. In the dialog, make sure that dataout is selected as Output parameter and datain is selected as Input parameter for matching of rows.
28. If desired, modify the **Column name template** to add a custom prefix and/or suffix to the calculated columns.
29. Test the script by selecting **Execute > Run**.

Response: The prompt dialog is displayed with the title you provided in step 3.



Comment: What columns you see in the Available columns list depends on which data set you have opened and which data types you specified in step 18. You can also right-click on the Name header and select the Show search field option, if you want to further limit the number of shown columns in this list.

30. In the dialog, type the desired integer and select the desired columns.
31. Click **OK**.

Response: The computation is performed and the resulting columns are added to the data set.

32. **Save** the configuration or send it to Analysis Builder (**File > Send to Analysis Builder**) to incorporate the action **Start Data computation - R** in a Guide. In the latter case you should also remember to save the Guide.

### 8.8.2.4 General Concepts

The handling of forbidden characters in column names differs for different computation servers. To avoid possible problems with forbidden characters in column names, Computation Services temporarily translates the column names that are sent to a server in the following manner:

- Allowed characters are a-z, A-Z, 0-9. Any other characters will be temporarily removed from the column names when the configuration is executed on the server.
- The column name cannot start with a number. If the available column name starts with a number, the number will be removed.
- The column name may be a maximum of 32 characters long. If the available column names are longer, they will be shortened and, if necessary, supplied with a suffix number to be distinguished from other columns with the same name.
- All column names will be converted to lower case, since some computation servers do not make any difference between upper and lower case characters.

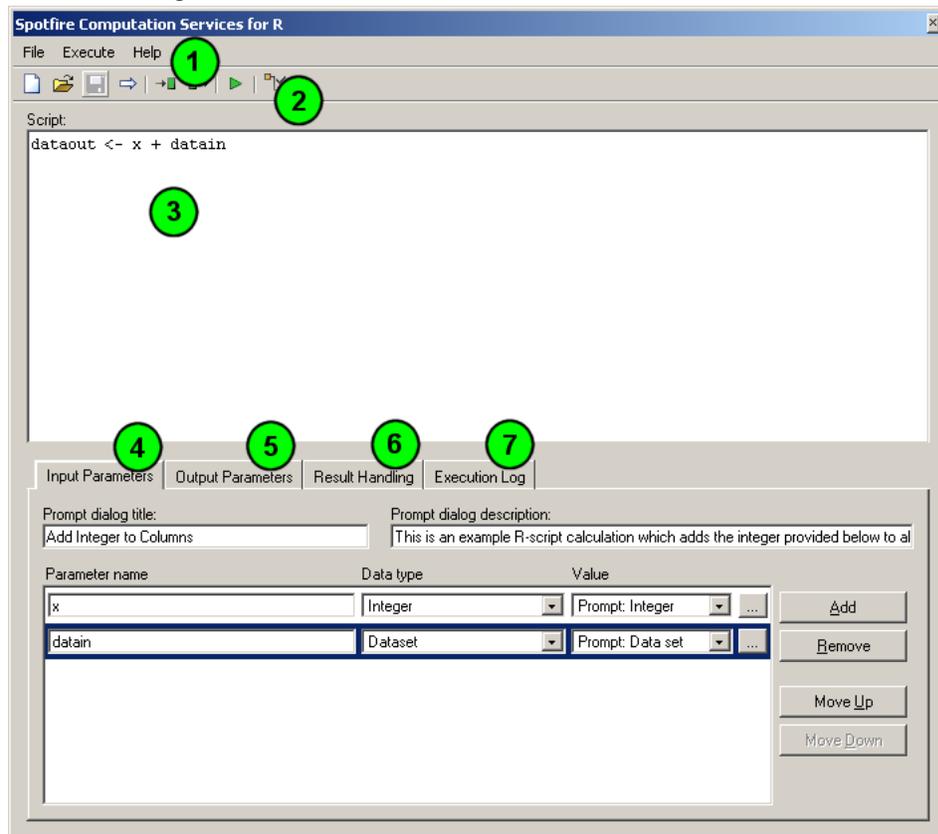
The translation is initiated by each connector separately. Any columns that are sent to a server as input parameters will be translated, provided they contain any of the forbidden characters. When the columns are returned from the server as output parameters, they will receive their original names again, if applicable. The translated column names will be used during the whole computation server session.

**Tip:** If you are interested in seeing what the actual column name used in the computation looked like, you can retrieve this information from the Execution Log.

## 8.8.3 User Interface

### 8.8.3.1 Computation Services User Interface Overview

This is the Computation Services user interface:



#### 1. Computation Services menus

The File, Execute and Help menus contain menu commands used to work with Computation Services.

#### 2. Toolbar



Includes shortcuts for some of the most common commands in Computation Services. See Computation Services toolbar for a description of the different buttons.

#### 3. Script

This pane displays the contents of your current script. This is where you create a new script or modify an existing script. Depending on what type of computation server you have selected, the scripting language should be R, SAS, S-PLUS or some other type of script. This help file does not contain any information regarding how to write your scripts.

#### 4. Input Parameters

The Input Parameters tab contains the selected input parameters and handles any type of prompt settings for these parameters.

The prompt settings determine what the end user of the configuration will see upon execution. All defined prompts will be shown in a single prompt dialog. The title of the prompt dialog is defined on the Input Parameters tab, along with a field with room for a more thorough description of what the configuration does.

## 5. Output Parameters

The Output Parameters tab contains the selected output parameters.

## 6. Result Handling

The Result Handling tab is where you specify what kind of result you want to receive when running the configuration.

## 7. Execution Log

The Execution Log tab contains a read-only text field displaying the progress of execution of a configuration along with any errors.

### ► To reach Computation Services:

Select **Tools > Computation Services > R** or **SAS** or **S-PLUS** or whatever the type of your current computation server.

## 8.8.3.2 Computation Services Menus

### File menu:

Option	Description
<b>New</b>	Empties Computation Services, so that you can start a new configuration. Any information you have currently open in the Script pane, or in any of the tabs, will be cleared.
<b>Open...</b>	Opens an earlier saved configuration. This configuration contains the actual script along with any defined input and output parameters, as well as the specified result handlers and prompt settings.
<b>Save</b>	Saves the current configuration including the script, all input and output parameters, as well as the specified result handlers and prompt settings to an earlier specified file.
<b>Save As...</b>	Saves the current configuration including the script, all input and output parameters, as well as the specified result handlers and prompt settings, after you have provided a file name in the Save dialog.
<b>Send to Analysis Builder</b>	Sends the current configuration to Analysis Builder as an available action, so that the calculation can be incorporated in a Guide.
<b>Connector Settings...</b>	Displays the Connector Settings dialog, which handles the connection to the computation server.
<b>Close All Sessions</b>	Closes all sessions currently open on the computation server. This option may be necessary to use if you have selected the option to <b>Keep session open until manually closed</b> in the Connector Settings dialog and you encounter any problems due to data left on the server from earlier computations.
<b>Exit</b>	Closes Computation Services.

**Execute menu:**

Option	Description
<b>Run</b>	Runs the current configuration.
<b>Log Level &gt;</b>	Defines the level of details to be shown in the Execution Log tab when a configuration is run. The log level is saved in the registry per user and connector.
> <b>Inform</b>	Use this log level if you just want to view warnings and errors.
> <b>Debug</b>	Use this log level if you want to display all log information available.

**Help menu:**

Option	Description
<b>Computation Services Help</b>	Launches the online help system.

**8.8.3.3 Computation Services Toolbar**

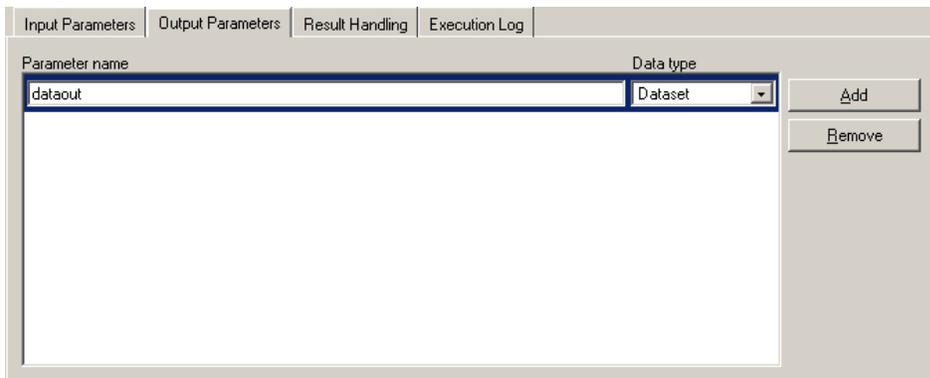
The Computation Services toolbar includes shortcuts for some of the most common commands in the menus. Click on the buttons on the toolbar to activate the corresponding functions.

	Empties Computation Services, so that you can start a new configuration. Any information you have currently open in the Script pane, or in any of the tabs, will be cleared.
	Opens a configuration earlier saved using Computation Services. This configuration contains the actual script along with any defined input and output parameters, as well as the specified result handlers and prompt settings.
	Saves the current configuration including the script, all input and output parameters, as well as the specified result handlers and prompt settings to an earlier specified file.
	Sends the current configuration to Analysis Builder as an available action, so that the calculation can be incorporated in a Guide.
	Adds the selected text in the script text area as an input parameter. Same functionality as the Add button on the Input Parameters tab.
	Adds the selected text in the script text area as an output parameter. Same functionality as Add button on the Output Parameters tab.
	Runs the current script configuration.
	Displays the Connector Settings dialog, which handles the connection to the computation server.

### 8.8.3.4 Input Parameters Tab

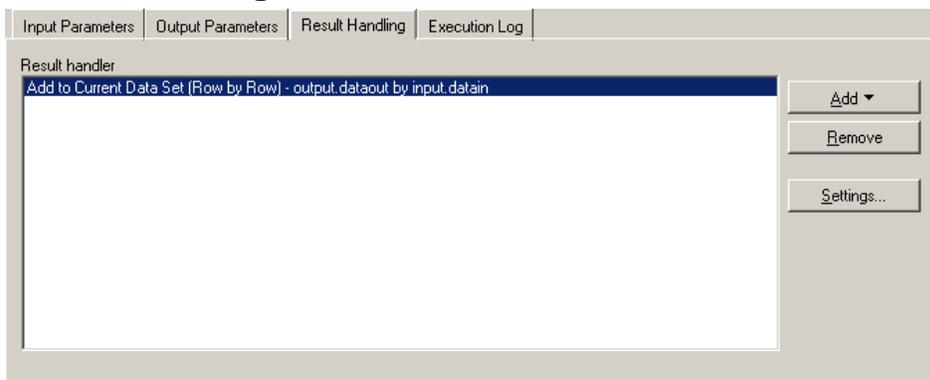
Option	Description
<b>Prompt dialog title</b>	The text in this field is displayed as the title of the prompt dialog when the configuration is executed. Maximum length is 80 characters.
<b>Prompt dialog description</b>	The text entered here is also displayed in the prompt dialog. Typically, this would be a description of what the configuration does or a more thorough description of the parameters that the end user of the tool should provide. Maximum length is 1000 characters.
<b>Parameter name</b>	A string matching a parameter in the script. If you have selected a parameter in the Script field and then clicked on the Add as input parameter button,  , the parameter name is already set to the selected text. If no parameter was selected before you clicked Add, a default parameter is added and you can edit the parameter name in the text box. <b>Note:</b> Make sure you type a correct parameter name. The allowed parameter names differ for the various scripting languages.
<b>Data type</b>	Select the data type of the parameter from the drop-down list. Not all data types described in this help file is available for all types of connectors.
<b>Value</b>	A drop-down list with the possibility to select either a constant or one of the prompt types available for the selected data type.
	Opens a dialog with the possibility to enter a constant when the constant value is selected, and a prompt setting when a prompt value is selected.
<b>Add</b>	Adds the text selected in the Script field as an input parameter. Same functionality as the Add as Input Parameter button on the toolbar.
<b>Remove</b>	Removes the selected input parameter.
<b>Move Up</b>	Moves the selected input parameter up one step. The position defines the order in the prompt dialog.
<b>Move Down</b>	Moves the selected input parameter down one step. The position defines the order in the prompt dialog.

### 8.8.3.5 Output Parameters Tab



Option	Description
<b>Parameter name</b>	A string matching a parameter in the script. If you have selected a parameter in the Script field and then clicked on the Add as Output Parameter button,  , the parameter name is already set to the selected text. If no parameter was selected before you clicked Add, a default parameter is added and you can edit the parameter name in the text box. <b>Note:</b> Make sure you type a correct parameter name. The allowed parameter names differ for the various scripting languages.
<b>Data type</b>	Select the data type of the parameter from the drop-down list.
<b>Add</b>	Adds the text selected in the Script field as an output parameter. Same functionality as the Add as Output Parameter button on the toolbar.
<b>Remove</b>	Removes the selected output parameter.

### 8.8.3.6 Result Handling Tab

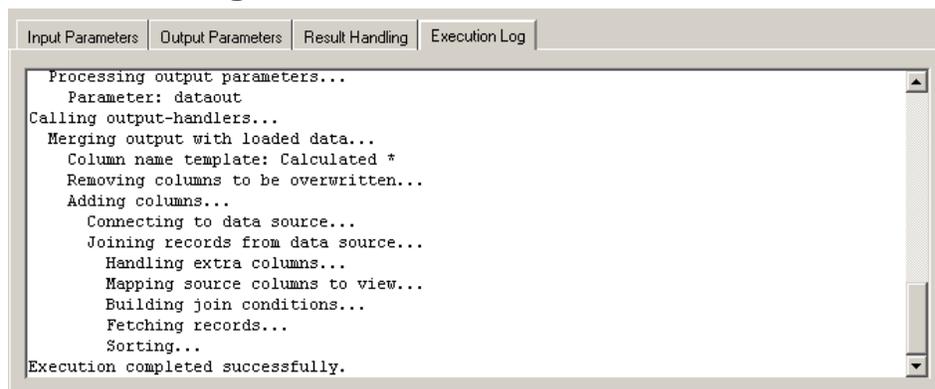


Option	Description
<b>Result Handler</b>	Displays all result handlers currently in use.
<b>Add</b>	Displays a list of the available result handlers. What result handlers are available depends on the data types of your current output parameters. The current version of Computation Services allows you to present your

	<ul style="list-style-type: none"> <li>results in the following manners:</li> <li>View in Result Dialog</li> <li>Add to Current Data Set (Automatic Key Matching)</li> <li>Add to Current Data Set (Row by Row)</li> <li>Replace Current Data Set</li> <li>Open in Other DecisionSite Instance</li> <li>Launch File</li> </ul>
<b>Remove</b>	Removes the selected result handler.
<b>Settings...</b>	Displays the settings for the selected result handler.

If you remove an output parameter that has been used to define a result handler, the result handler will turn red in the list. Either delete the incorrect result handler, or open the Settings... for the result handler and change it to work on another output parameter. You can also add the missing parameter again to fix the problems.

### 8.8.3.7 Execution Log Tab

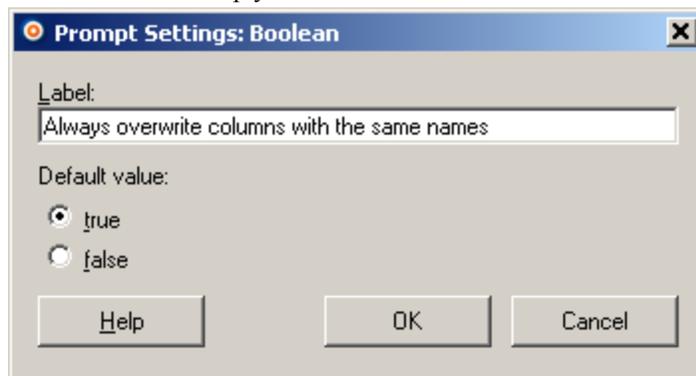


The Execution Log shows detailed information about a configuration when it is run. The level of details is set under the menu option **Execute > Log Level**. If desired, the resulting log can be copied using the right-click menu and saved for future reference.

### 8.8.3.8 Prompt Dialogs

#### 8.8.3.8.1 Prompt Settings: Boolean Dialog

Use this type of prompt for user input of the type yes/no. The resulting prompt will be a check box which can be empty or selected.



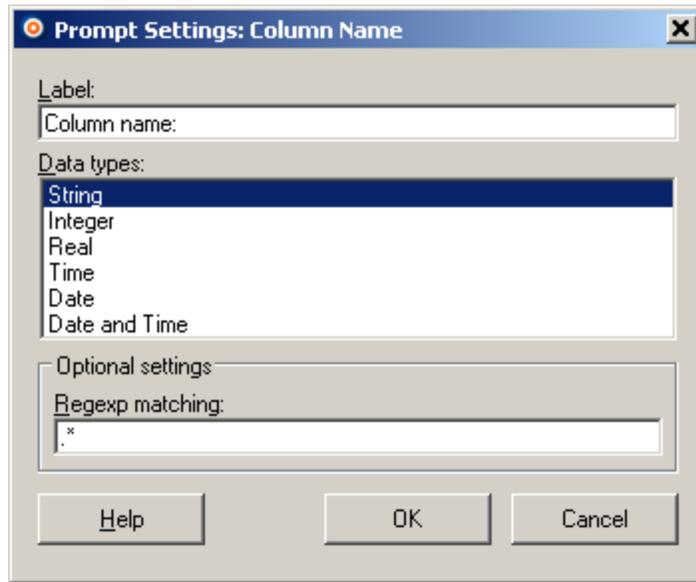
According to Spotfire UI Guidelines the label for a check box should use sentence-style capitalization and end without a full stop.

Resulting prompt for the example above:



### 8.8.3.8.2 Prompt Settings: Column Name Dialog

Use this type of prompt when you want user input in the form of a column name string.



Option	Description
<b>Label</b>	The text that will be displayed above the column name selection in the prompt dialog when the configuration is executed. Try to make the label as clear as possible to ensure that the end users understand what the input parameter should be. According to Spotfire UI Guidelines the label for a drop-down list should use sentence-style capitalization and end with a colon.
<b>Data types</b>	Select the data types of the columns you want the end user to see upon prompting for the specific parameter.
<b>Regex matching</b>	Type any kind of regular expression to limit the available columns in the prompt. Example: If you type Exp in the Regex matching field, only columns containing 'Exp' somewhere in the column name will be visible, e.g., Experiment1, Experimental results, Expression, MyExperiments, etc. See Introduction to Regular Expressions in the Query Devices chapter for more information.

Resulting prompt for the example above:



### 8.8.3.8.3 Prompt Settings: Data Set Dialog

Use this type of prompt when you want user input in the form of one or more columns from the current data set.

Option	Description
<b>Label</b>	The text that will be displayed above the column selection in the prompt dialog when the configuration is executed. Try to make the label as clear as possible to ensure that the end users of the script understand what the input parameter should be.
<b>Data types</b>	Select the data types of the columns you want the end user to see upon prompting for the specific parameter.
<b>Minimum number of columns</b>	The minimum number of columns that you want to use as input for the selected parameter.
<b>Maximum number of columns</b>	The maximum number of columns that you want to use as input for the selected parameter.

Resulting prompt for the example above:

The end user of the configuration will be presented with a column selector with all columns of the specified data type in the Available columns field. The end user will also have the

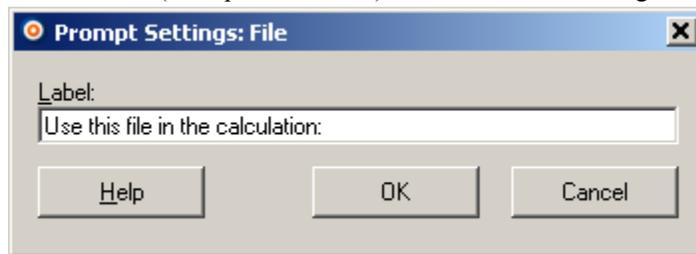
possibility to choose whether to work on All records, Marked records or Selected records by choosing the appropriate option from the Records selection drop-down list.

**Tip:** If there are too many columns to choose from in the Available columns list, it is possible to right-click on the Name header and select Show search field from the pop-up menu. Then, any search string can be used to limit the number of available columns.

### 8.8.3.8.4 Prompt Settings: File Dialog

Use this type of prompt when you want user input in the form of a file.

**Note:** If the resulting file is to be processed via one of the predefined Open, Edit or Print options in the Launch File Dialog, the output parameter name used must end with the desired file extension (example: outfile.txt). See Launch File Dialog for more information.



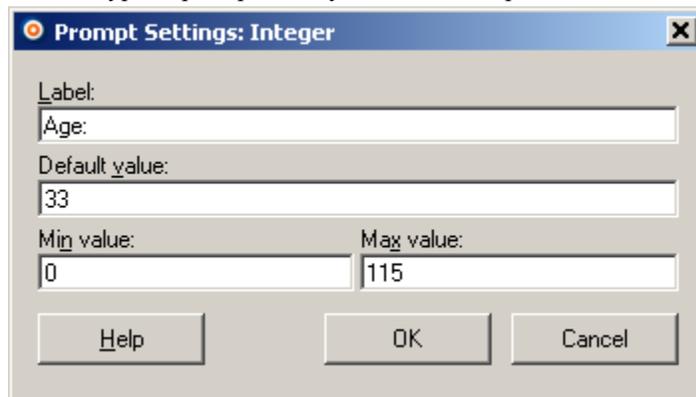
According to Spotfire UI Guidelines, the label for a text field should use sentence-style capitalization and end with a colon.

Resulting prompt for the example above:



### 8.8.3.8.5 Prompt Settings: Integer Dialog

Use this type of prompt when you want user input in the form of an integer.



Option	Description
<b>Label</b>	The text that will be displayed above the input field in the prompt dialog when the configuration is executed. Try to make the label as clear as possible to ensure that the end users of the configuration understand what the input parameter should be. According to Spotfire UI Guidelines, the label for a text field should use sentence-style capitalization and end with a colon.
<b>Default value</b>	If desired, type a value for default display in the prompt dialog.

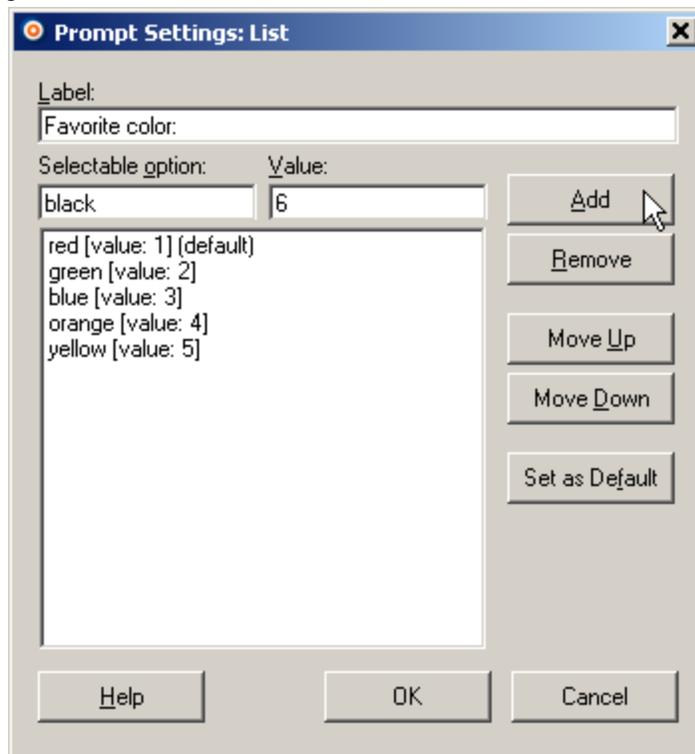
<b>Min value</b>	If desired, type the lowest acceptable value that can be used as input. If an end user tries to provide a lower value, an error message will be displayed upon execution.
<b>Max value</b>	If desired, type the highest acceptable value that can be used as input. If an end user tries to provide a lower value, an error message will be displayed upon execution.

Resulting prompt for the example above:

Age:

### 8.8.3.8.6 Prompt Settings: List Dialog

Use this type of prompt when you want user input in the form of a string selected from a predefined list.



Option	Description
<b>Label</b>	The text that will be displayed above the list selection in the prompt dialog when the configuration is executed. Try to make the label as clear as possible to ensure that the end users of the configuration understand what the input parameter should be. According to Spotfire UI Guidelines the label for a drop-down list should use sentence-style capitalization and end with a colon.
<b>Selectable option</b>	The list item text as you want it to be displayed for the end users. Each selectable option should be connected to a value to be used in the actual calculations.
<b>Value</b>	The list item value used in the calculations, which is what lies behind

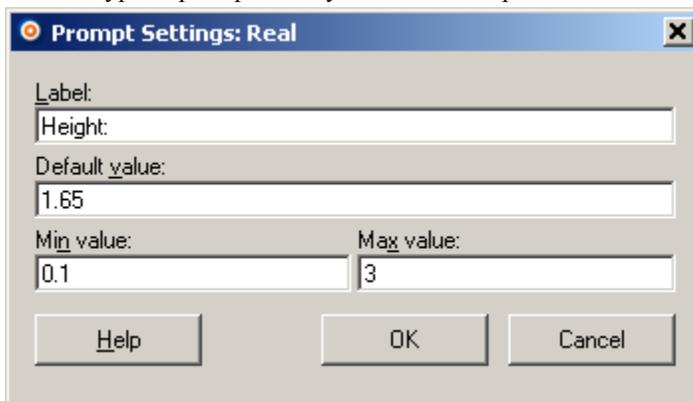
	the selectable options shown in the drop-down list.
<b>Add</b>	Adds the current pair of selectable option/value to the list.
<b>Remove</b>	Removes the selected option from the list.
<b>Move Up</b>	Moves the selected option up in the list.
<b>Move Down</b>	Moves the selected option down in the list.
<b>Set as Default</b>	Sets the selected option as the default value shown to the end user upon execution.

Resulting prompt for the example above:



### 8.8.3.8.7 Prompt Settings: Real Dialog

Use this type of prompt when you want user input in the form of a decimal number.



Option	Description
<b>Label</b>	The text that will be displayed above the input field in the prompt dialog when the configuration is executed. Try to make the label as clear as possible to ensure that the end users of the configuration understand what the input parameter should be. According to Spotfire UI Guidelines, the label for a text field should use sentence-style capitalization and end with a colon.
<b>Default value</b>	If desired, type a value for default display in the prompt dialog.
<b>Min value</b>	If desired, type the lowest acceptable value that can be used as input. If an end user tries to provide a lower value, an error message will be displayed upon execution.
<b>Max value</b>	If desired, type the highest acceptable value that can be used as input. If an end user tries to provide a lower value, an error message will be displayed upon execution.

Resulting prompt for the example above:

Height:  
1.65

### 8.8.3.8.8 Prompt Settings: String Dialog

Use this type of prompt when you want user input in the form of a string.

Option	Description
<b>Label</b>	The text that will be displayed above the text field in the prompt dialog when the configuration is executed. Try to make the label as clear as possible to ensure that the end users of the configuration understand what the input parameter should be. According to Spotfire UI Guidelines, the label for a text field should use sentence-style capitalization and end with a colon.
<b>Default value</b>	If desired, type a text for default display in the prompt dialog.
<b>Maximum string length (1-999)</b>	If desired, type the maximum length of the string to be used as input. If an end user tries to provide a longer string, an error message will be displayed upon execution.

Resulting prompt for the example above:

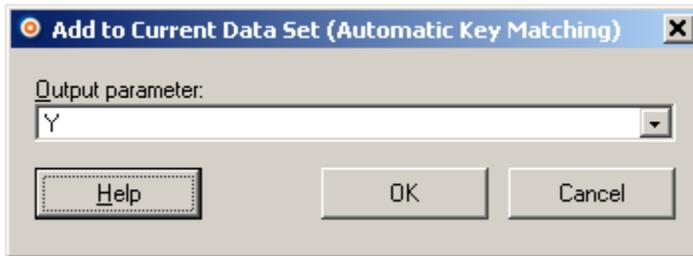
Favorite color:  
green

### 8.8.3.9 Result Handling Dialogs

#### 8.8.3.9.1 Add to Current Data Set (Automatic Key Matching)

Use this result handler when you want the resulting columns to be added to your current data set using an automatic primary key matching.

**Note:** This method requires that you actually have good primary keys available, that is, that there is a column on the server with exactly the same name as one in your DecisionSite data set, and that some of the values are matching. If not, you should probably use the Add to Current Data Set (Row by Row) result handler instead.



Select the output parameter that you want to add to your DecisionSite data set from the drop-down list. Only output parameters defined as the data type Dataset are available in the list.

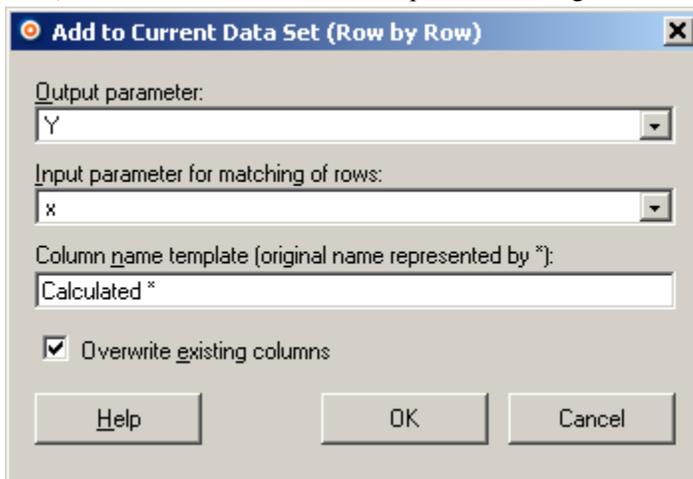
**How it works:**

For all column names that are identical in DecisionSite and on the server, the contents of the columns will be compared. If the values are identical, new values are added to the rows where there was a match. If the same value occurs in more than one place in the key column, the first value will be used.

**Tip:** If your key columns have names that do not match, it is easy to change the names in DecisionSite.

**8.8.3.9.2 Add to Current Data Set (Row by Row)**

Use this result handler when you want the resulting columns to be added to your current data set using a row by row matching. This will make sure that the results are added to the correct rows, even if the calculation has been performed using marked or selected records only.

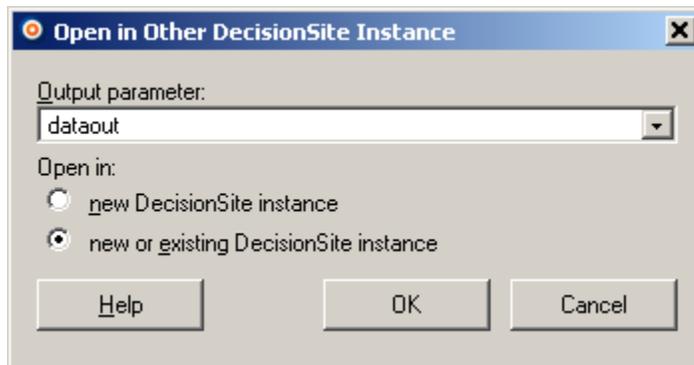


Option	Description
<b>Output parameter</b>	Select the output parameter that you want to add to your DecisionSite data set from the drop-down list. Only output parameters defined as the data type Dataset are available in the list.
<b>Input parameter for matching of rows</b>	Select the input parameter whose settings will be used in the matching of rows to the existing data set. Example: If several input parameters are available, but the x prompt uses marked records only, it might be suitable to use the x input parameter for matching of rows and, hence, not add anything to those rows where the x input parameter was empty upon calculation.
<b>Column name</b>	Used for adding prefix and/or suffix to all calculated columns. Type

<b>template</b>	[prefix]*[suffix] in the text field, where * is the original input column names. Example: If 'Calculated * Result' is typed in the Column name template field, and columns with the names 'Height' and 'Weight' are used in the calculation, the resulting names added to DecisionSite will be 'Calculated Height Result' and 'Calculated Weight Result'.
<b>Overwrite existing columns</b>	Select the check box if you want any columns with the same names as specified in the Column name templates field to be overwritten upon execution.

### 8.8.3.9.3 Open in Other DecisionSite Instance

Use this result handler when you want the result of the calculation to be a new data set in either a new DecisionSite instance or another, currently running DecisionSite instance. Any previous data set in the selected DecisionSite instance will be closed when the new data set is opened.



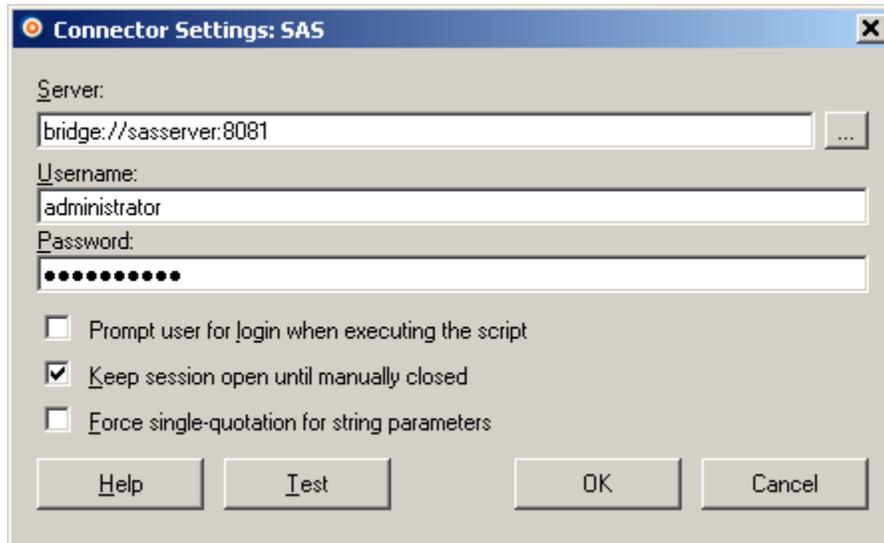
Option	Description
<b>Output parameter</b>	Select the output parameter that you want to send as a new data set to another DecisionSite instance from the drop-down list. Only output parameters defined as the data type Dataset are available in the drop-down list.
<b>Open in: new DecisionSite instance</b>	Use this option to open the resulting data set in a new DecisionSite instance.
<b>Open in: new or existing DecisionSite instance</b>	Use this option to allow the end user of the configuration to select whether to open the resulting data set in a new or in an existing DecisionSite instance. If this option is selected, the Open Resulting Data Set in DecisionSite dialog will be displayed upon execution.

## 8.8.3.10 Other Dialogs

### 8.8.3.10.1 Connector Settings Dialog

This dialog may look different depending on the type of computation server you are connecting to. It is used to define what server to use and possibly also which other settings to use upon script execution.

**Note:** No connection is made until you actually run the script. If you want to test the connection when you set up the configuration, use the Test button (see below).



Option	Description
<b>Server</b>	Enter the address to the calculation server that you want to use. Type "(local)" in this field if you want to run against a local SAS Base client on your own computer.
	Opens the Servers dialog where you can select from a list of predefined calculation servers.
<b>Username</b>	Type the user name required to work against the calculation server. In some cases this field may be missing.
<b>Password</b>	Type the password required to work against the calculation server. In some cases this field may be missing.
<b>Request timeout (minutes)</b>	If your computation takes a long time, you can increase the Request timeout to prevent that the execution is interrupted before the calculation is finished.
<b>Prompt user for login when executing the script</b>	This option is available in the design phase of a configuration only. Select this check box if you want the end users of the configuration to log into the server upon execution. If this option is cleared, the configuration will always use the connector settings provided during the design phase.
<b>Keep session open until manually closed</b>	This option is available in the design phase of a configuration only. Select this check box to use a single session on the server for all Computation Services calculations run during a DecisionSite session. This means that the data is built up and changed on the server as the various configurations are run. <b>Note:</b> When you use this option the different steps of a Guide with many calculations will not be independent of one another. This may increase the risk of errors upon execution if links in a Guide are clicked in the wrong order or if requests times out.
<b>Force single-quotation for string parameters</b>	Use this option to be able to run SAS configurations created with DecisionSite 8.1.1. This option should normally be cleared.

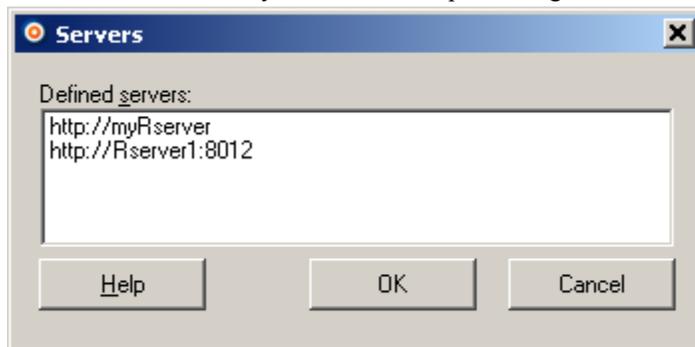
<b>Test</b>	Validates the connection without closing the dialog.
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► **To reach the Connector Settings dialog:**

1. If Computation Services is not already started, select **Tools > Computation Services > SAS, R or S-PLUS** or whatever the name of the computation server you want to connect to.
2. Select **File > Connector Settings...**

### 8.8.3.10.2 Servers Dialog

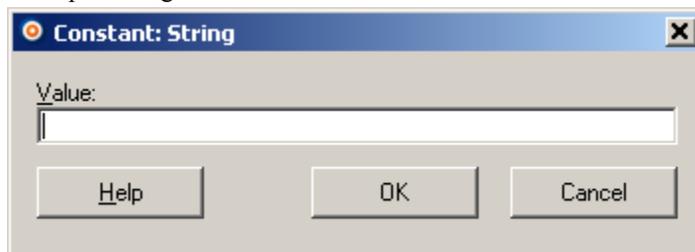
This dialog lists all servers currently defined as calculation servers for a specific connector. Click on the server that you want to use upon configuration execution, then click OK.



### 8.8.3.10.3 Constant Definition Dialog

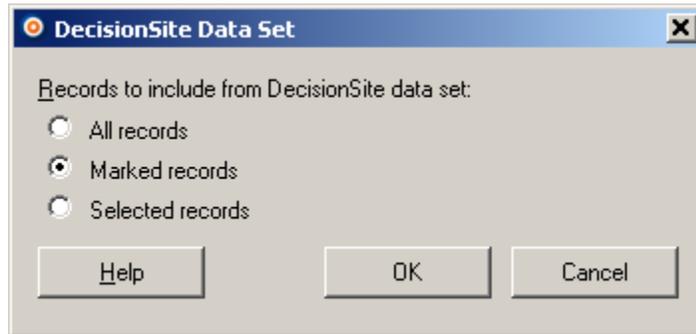
The constant definition dialog's appearance varies depending on what data type you are defining a constant for. Just enter the value that you want to use in the calculation and click OK.

Example dialogs:



### 8.8.3.10.4 DecisionSite Data Set Definition Dialog

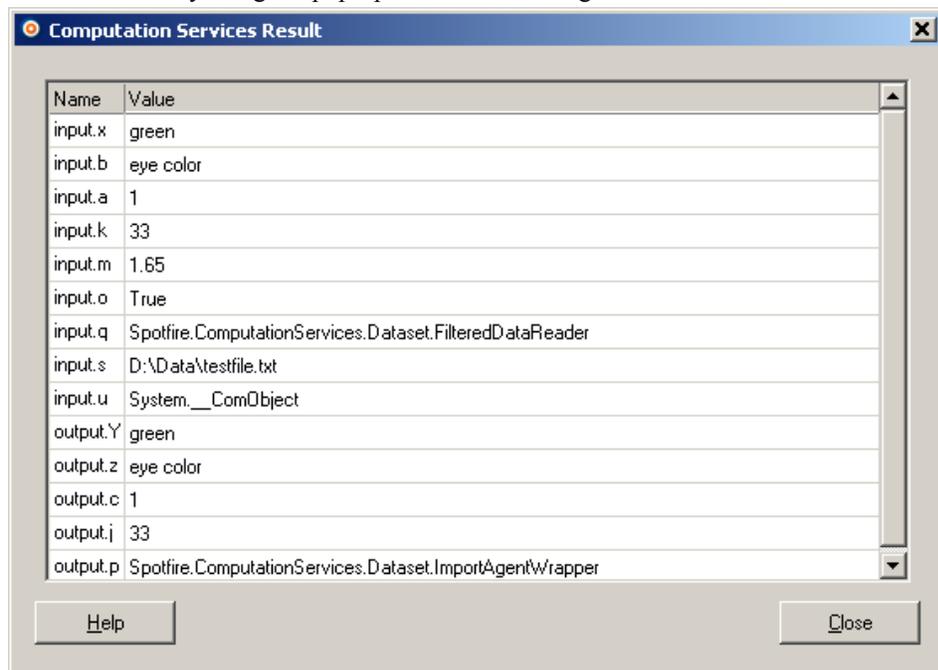
This dialog defines what data to use in the calculation when the Input: Data set option has been chosen for an input parameter.



Click the appropriate radio button to select whether the calculation shall be performed on all records, marked records or on records selected using the query devices or zooming only.

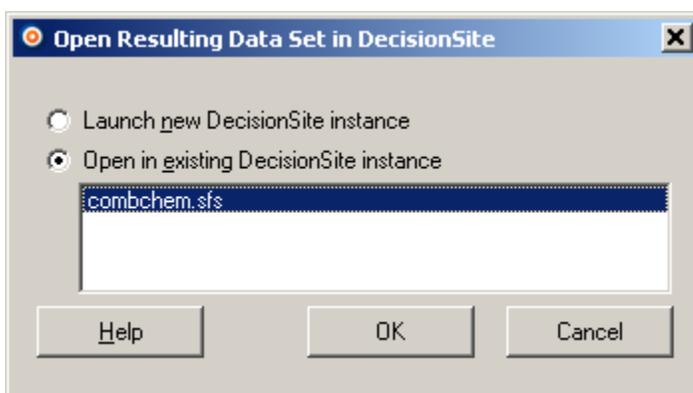
### 8.8.3.10.5 Computation Services Result Dialog

This is a dialog containing the results from a Computation Services calculation. It displays the input parameters and the output parameters of the executed configuration. You can copy selected results by using the pop-up menu in the dialog.



### 8.8.3.10.6 Open Resulting Data Set in DecisionSite Dialog

This dialog is presented when the creator of a Computation Services configuration has chosen to open the result of a calculation in a DecisionSite instance other than the one running the configuration.



Option	Description
<b>Launch new DecisionSite instance</b>	Select this option to launch a completely new DecisionSite instance with the result of the calculation as a new data set.
<b>Open in existing DecisionSite instance</b>	Select this option to choose from a list of existing DecisionSite instances. The data set currently open in the instance of your choice will be replaced by the new data set.

## 8.9 Distance Calculator

You can calculate the distance between two markers in a 2D or 3D scatter plot by using the Distance Calculator.

Click on the marker you want to use as the origin. Then move the mouse pointer over other markers and the distance to the origin will be displayed in the Distance Calculator window. The Distance Calculator also displays the distance from one marker to another along the different axes.

More specifically the distances calculated are:

$$distance = \sqrt{(\Delta x)^2 + (\Delta y)^2 + (\Delta z)^2}$$

$$\Delta x = |x(active) - x(highlighted)|$$

$$\Delta y = |y(active) - y(highlighted)|$$

$$\Delta z = |z(active) - z(highlighted)|$$

**Note:** The Distance Calculator only handles Real, Float and Integer types. If a column contains other types, no values will be displayed in the Distance Calculator window.

### ► To reach the Distance Calculator:

Select **Tools > Distance Calculator**.

## 8.10 Administration Tools

### 8.10.1 Administration Tools Overview

The Administration section contains the tools needed to organize the DecisionSite environment. These tools are only available for users with Administrator privileges. The Library provides

publishing of all analysis material for sharing with colleagues. Using the Library, you can collaborate with colleagues in a distributed environment and organize your analysis material. See the Library Help for more information.

<b>DecisionSite Administrator</b>	The DecisionSite Administrator can be reached by selecting <b>Tools &gt; Administration &gt; DecisionSite Administrator</b> . This will open a Microsoft® Internet Explorer window where Administrators can manage user privileges. Refer to the DecisionSite Administrator Help for more information.
<b>DecisionSite Library</b>	The Library can be accessed for various purposes. By selecting <b>Tools &gt; Administration &gt; DecisionSite Library</b> , the main view of the Library is opened. This will open a Microsoft® Internet Explorer window with the Library. Use this view to open Library items and to administrate it. Refer to the Library Help for more information.
<b>DecisionSite Library Administrator</b>	The DecisionSite Library Administrator can be reached by selecting <b>Tools &gt; Administration &gt; DecisionSite Library Administrator</b> . This will open a Microsoft® Internet Explorer window where Administrators can edit who is allowed to create new Library Sections, configure DecisionSite Library and Poster settings. See DecisionSite Analytic Server - Installation and Upgrade manual for more information.
<b>Server Usage</b>	Server usage statistics can be reached by selecting <b>Tools &gt; Administration &gt; Server Usage</b> . This will open the log file dssaccess.sfs in DecisionSite, for an easy analysis and overview. This file contains information about all logins and logouts from all DecisionSite Clients to the DecisionSite Analytics Server. It shows which user logged in/out and when. The log is always enabled, and it is unaffected by Log Configuration File settings.

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## 9 Guides

### 9.1 What is the Guides Pane?

The Guides pane is a web browser, fully integrated into the Spotfire DecisionSite environment. It is used to connect to the Spotfire DecisionSite Analytics Server, providing access to Guides as well as a location for a customized start page.

The Guides Pane is closed by default when you launch Spotfire DecisionSite. You can close and open it by clicking the Guides Pane button to the far left of the Guides Toolbar. The button on the right directs the page to the current start page.

#### The Guides Toolbar

The Guides Toolbar is used to open the Guides pane or to launch your own custom start page. This start page is configurable by right-clicking in the Guides Pane.



The toolbar can be made visible or hidden by selecting **View > Guides Toolbar**.

#### Guides

The Guides pane is primarily used to run Guides. It contains preconfigured Guides which can be run with a single click, but it can also show any custom made Guides for yourself or for others. See Guides below for more information.

### 9.2 Guides Pane Options

If you right-click in the Guides pane a pop-up menu appears. Select **Options...** to display the Guides Pane Options dialog.

#### Page viewed when starting DecisionSite

By default, the Guides pane displays a list of your available guides. You can also select to show another web page as your start page.

To do this, type in the URL of the custom start page in the **Address** field (or click **Browse...**). This does not change which DecisionSite Analytic Server you are connected to, but merely provides a way to access other pages from DecisionSite.

The Custom Start Page will be displayed each time you start Spotfire DecisionSite. Finally, click **OK** to make the changes take effect.

If the new **Custom Start Page** is not on your local intranet or among the **Trusted Spotfire sites** (see below), a pop-up dialog will appear in which you are asked if you would like to add the URL to the list of trusted sites.

#### Trusted Spotfire Sites

Only sites on your local intranet, or present in the list of Trusted Spotfire sites, are allowed to access Spotfire DecisionSite using scripts or active content. Each time you enter a new **Custom Start Page** you will be prompted whether or not you want to add that site to the list of Trusted Spotfire sites.

If you want to remove a site from the list, select it and then click on the **Remove** button. Some sites in the list may be grayed out and cannot be removed. These are sites that are predefined for your installation and needed by Spotfire DecisionSite.

## 9.3 Run from Library...

### 9.3.1 Open Guide from Library

The Library introduces convenient sharing of analysis material. The **Open Guide from Library...** link in the **Guides pane** allows you to access Guides located in the Library with a single click. Using this link, Guides located in the Library can be run in the Guides pane as any other Guide.



#### ► To open Guides from Library

1. Click **Open Guide from Library...** in the **Guides pane** or select **Guides > Run from Library...**

Response: The Open Guide from Library Dialog is shown.

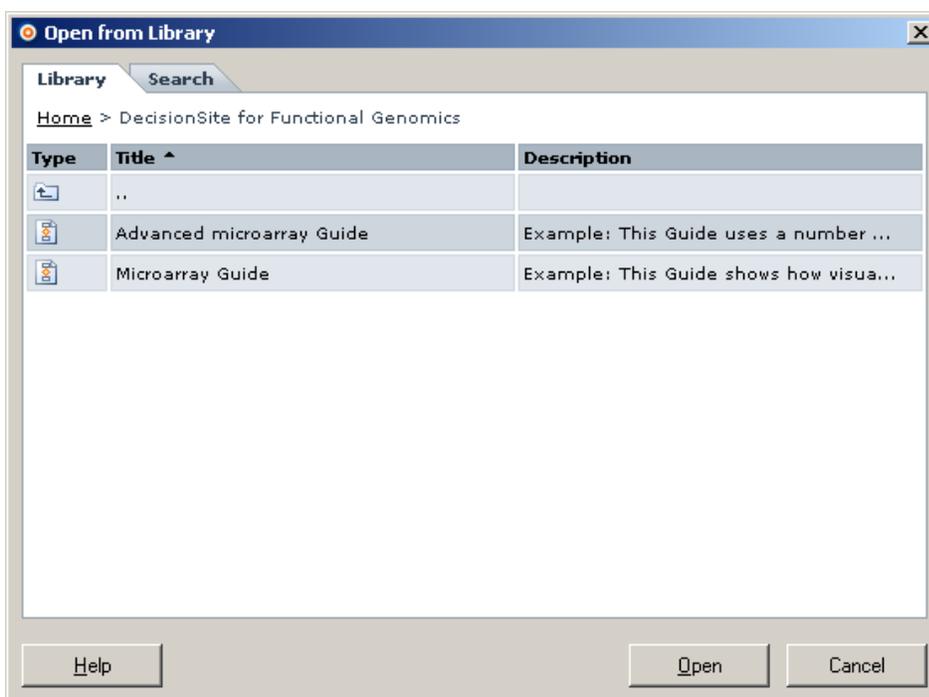
2. In the Open Guide from Library Dialog, locate the Guide you want to open and click **Open**.

Response: The Guide is opened in the Guides pane.

### 9.3.2 Open Guide from Library Dialog

This dialog lets you select and open a Guide that is located in the Library. To find a Guide, either look through a Library Section's content, or search for the Guide.

**Note:** Only Guides created with Analysis Builder are available to be opened and edited in Analysis Builder.



### Library tab options

### Description

#### Library

All Guides, folders and Library Sections are listed on this tab.  
**Note:** Only Library Sections that you have access to are listed.

#### Open

Select the Guide you want and click **Open** to open it in the Guides pane (or in Analysis Builder if you have reached this dialog from there). You can also double-click the Guide to open it.

### Search tab options

### Description

#### Search tab

Use **Search** to search for the item you want to open.

#### Search for:

Enter the search string in the **Search for:** field and click **Search**. See Searching in the Library for information about search strings.  
 If you click a folder in the **Search** result, you will be redirected to the Library View under the **Library** tab.

#### Look in:

Select which Library Section you want to perform your search in. Either one or all Library Sections can be searched. Only Library Sections you have access to are listed.

### ► To reach the Open Guide from Library dialog:

- Click **Open Guide from Library** in the **Guides** pane, or
- select **Guides > Run from Library...** from the menu, or
- in Analysis Builder, click **Guide > Open from Library...**

**Note:** Opening a Guide in Analysis Builder will open the Guide for editing in Analysis Builder and not to the Guides pane as in the previous cases.

## 9.4 Create and Edit Guide

### 9.4.1 Analysis Builder Overview

With the Analysis Builder you can capture your commonly performed analysis processes into Guides. Creating your own Guides does not require your having to write a single line of code.

### 9.4.2 Using Analysis Builder

#### 9.4.2.1 Guides Created with Analysis Builder

Guides created with the Analysis Builder can contain text and links. However, the Guides can also be extended with any number of complex tasks if you have programming experience or access to a person with these types of skills. An example of a Guide created with Analysis Builder is presented below:



#### 1. Contents and Title

This is the flight view which is automatically added at the top of every Guide page. It includes the *Contents* link followed by the Guide title. The *Contents* link closes the Guide and goes back to the main page of the Guides pane. The title of your Guide can be configured via **Guide > Properties** in Analysis Builder.

#### 2. Text and Links

This is the main part of the Guide, which you can design via Analysis Builder. You can add text and links to the Guide.

#### 3. Back and Next

These are navigation links which are automatically added at the end of every Guide page. The first page of the Guide gets a *Next* link, following pages get a *Back* and a *Next*, and the last page of the Guide gets a *Back* and a *Back to Contents* link (same function as the *Contents* link in the flight view).

#### 9.4.2.2 Suggested Workflow

##### ► To create a new Guide using Analysis Builder:

1. Open a data set in Spotfire DecisionSite and start to perform your analysis the way that you want it to be done in the Guide.
2. If the Analysis Builder tool is not already open, click **Guides > Create and Edit Guide**.

3. Create the Guide in Analysis Builder by adding links and text to the Guide contents list. By adding actions (links) to your Guide simultaneously when you perform the analysis, you can make sure that you capture the settings used this very moment. This way you can also add links that update the same visualization to several places in the Guide
4. Test the Guide by selecting **Guide > Run**. The Guide will be displayed in the Guides pane. Note that if you are testing Guide steps that include opening a data set, you will clear the current Actions in DecisionSite list. Make sure that you have added all steps of your current analysis to the Guide before testing the parts of the Guide that involve switching data sets.
5. When you are finished with the Guide, select **Guide > Save As...** or publish it to the Library with **Guide > Publish to Library...**
6. You can now send the Guide to a colleague or to your IT department for extended functionality or deployment.

### 9.4.2.3 Analysis Builder Quick Reference

Action	Instruction
<b>Start Analysis Builder</b>	From the main menu bar of DecisionSite, select <b>Guides &gt; Create and Edit Guide</b> .
<b>Create a new Guide</b>	In Analysis Builder, click <b>Guide &gt; New</b> . Edit the Guide by adding text and links.
<b>Open a Guide from the Library</b>	In Analysis Builder, click <b>Guide &gt; Open from Library...</b> Browse the Library to locate the Guide that you want to edit. Edit the Guide by adding or removing text and links. See Open from Library for more information.
<b>Edit an existing Guide</b>	In Analysis Builder, click <b>Guide &gt; Open...</b> Browse to locate the Guide that you want to edit. Edit the Guide by adding or removing text and links. <b>Tip:</b> Run the Guide prior to editing to populate the Actions in DecisionSite list.
<b>Add text to a Guide</b>	In Analysis Builder, click <b>Add &gt; Text</b> . Enter the text that you want to add in the Text Properties dialog. Click <b>OK</b> to close the dialog.
<b>Add new actions to the Actions in DecisionSite list</b>	Open a data set, run a tool or create a visualization in Spotfire DecisionSite. All actions that you have performed on your current data set are logged and included in the Actions in DecisionSite list.
<b>Add links to a Guide</b>	Make sure you have performed the action you want to add as a link in DecisionSite. Select the item or items you want to add to your Guide in the Actions in DecisionSite list. Click <b>&lt; Add Link</b> . See How the Actions in DecisionSite list works for more information.

<b>Update an existing visualization</b>	Add a link that creates a visualization. Add the action for the specific visualization to a new link.
<b>Add a hyperlink to a Guide</b>	Double-click on a text item or select <b>Add &gt; Text</b> to add a new text item. This will display the Text Properties dialog. Select the word that you want to create a hyperlink from.  Click on the Hyperlink button,  .
<b>Test a Guide</b>	In Analysis Builder, select <b>Guide &gt; Run</b> . <b>Comment:</b> The Guide will be displayed in the Guides pane as any other Guide.
<b>Save a Guide</b>	In Analysis Builder, select <b>Guide &gt; Save</b> .
<b>Publish a Guide to the Library</b>	In Analysis Builder, select <b>Guide &gt; Publish to Library</b> . See Publish to Library for more information.
<b>Add a new page to a Guide</b>	In Analysis Builder, select <b>Add &gt; New Page</b> . <b>Comment:</b> A flight view linking back to Contents as well as Next [page] and Back links are automatically added to each page in the Guide.
<b>Minimize the Analysis Builder</b>	Click on the top right x-button. This will hide the Analysis Builder, but both the <i>Guide contents</i> list and the <i>Actions in DecisionSite</i> list will be remembered when you reopen the tool.
<b>Close the Analysis Builder</b>	In Analysis Builder, select <b>Guide &gt; Exit</b> .

#### 9.4.2.4 How the Actions in DecisionSite List Works

##### Adding Links to a Guide

All actions in the right list called Actions in DecisionSite can be added as a link to the Guide. Click to select an action in the list (use Ctrl to select several actions), and then click the < **Add Link** button to create a link in the Guide.

##### Adding Actions to the List

Actions are automatically logged in the Actions in DecisionSite list as you perform them in DecisionSite. First load data and perform the analysis as you would normally do. Your data, the visualizations you create, and the tools you start will appear as actions in the list.

**Tip:** To edit a previously created Guide, start by running the Guide in DecisionSite. This will furnish the list of actions with the data, visualizations and tools used in the Guide.

##### Automatic Logging

You do not have to turn on Analysis Builder in order for your actions to be logged. It is done automatically when you load data in DecisionSite Client, even if you have not started Analysis Builder. However, if you log out from the server, no actions will be logged while you are disconnected.

##### Clearing the List of Actions

The list of actions will be emptied if you close your data via File > Close in DecisionSite.

**Note:** The Actions in DecisionSite list will be cleared if you open a new data set. Since you can only have one data set open at a time in Spotfire DecisionSite, the previous data will be closed

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when you open the new data set. If you log out from the server, the Analysis Builder will be closed and the Actions in DecisionSite list will be cleared.

### 9.4.2.5 Settings Captured in Links

All actions that you have performed on your current data set are included in the Actions in DecisionSite list. See How the Actions in DecisionSite list works for more information about the Actions in DecisionSite list.

**Note:** The Analysis Builder will log all actions that you perform in DecisionSite, even if it has not been started. The Actions in DecisionSite list will be cleared if you open a new data set.

#### Information links

If an information link is added via the Information Library or the Information Builder, the created Guide will include a reference to the information link or the actual query, respectively. If the information link is prompted, the end users of the Guide will see the prompts and be able to make their own selection. There is, however, no reference to the server that the Information Link is located on, so if you intend to distribute your Guide containing information links to users who work on a different server to your own, you must copy the Information Model to their server. For more information on copying data layers, see the chapter "Information Designer" of the Spotfire DecisionSite Analytics Server - Administrator's Guide, and contact your DecisionSite Analytics Server administrator.

If you want the end user of the Guide to be able to choose a different information link, you should instead include a link that starts the tool Information Library. To make the action **Start Information Library** appear in the Actions in DecisionSite list, start the tool once more after opening the information link that you used when creating the Guide and select Cancel in the Information Library dialog.

#### Open data (saved with Guide)

If a data set has been opened by some other means than by opening an information link, you will have the option to save the data with the Guide. This means that the data set that you are currently using will be a part of the Guide file. This can be useful for reference data that are never changed or if you want to create a prototype Guide where some IT personnel will later on modify your Guide to open data from a data source that is currently not supported by Analysis Builder.

The data set that is saved with the Guide is the currently available data. That means that if you have added or removed columns from the original data set prior to adding the link to your Guide, the embedded data will contain the modified data set.

If you want to save the data from an information link with the Guide, e.g., for testing purposes, you can first open the information link, save the data as an Analysis in DecisionSite, open the Analysis with the data and add the new action Open data (saved with Guide) to your Guide.

#### Visualizations

The visualizations appear in the Actions in DecisionSite list when they are created, but the actual settings for the visualization are retrieved when a link is added to the Guide contents list. All properties are saved with the specific visualization. For example, you can specify that a scatter plot should be created with two defined columns on the axes and with the markers colored by a third column. Query device settings (filtering), transformed columns and background images are also included in the link. It is also possible to add steps to the Guide where the end user of the Guide is prompted to specify which settings to use. See Prompting Guide users for input for more information.

#### Set query device filters

Adding this action in a link will set all query devices and also the selected properties of the Columns tab to the current state. This means that you can apply log scale, show or hide empty values, specify query device types and filter on specific columns without having to add a new

visualization. This way, you can create several links in the Guide that update your visualizations, thus creating a "bookmark" kind of function.

**Note:** If the data set that the end user of a Guide is using differs from the one that you were using while creating the Guide, there might be occasions when the query device settings will not be applicable.

## Tools

In the current version of Analysis Builder, settings are not always saved with the tools. The various tool links will, in some cases, open the tool to the end users of the Guide, but they will have to make the calculation selections and click OK in the tool dialog for themselves. If you want the end users to use some specific settings in one of those tools, you should state this information as text in the Guide.

A number of tools, e.g., the New Column from Expression tool, can be run silently (without input from the end user). When a link is added to such a tool, you can set the Tool Option to specify whether you want the link to run the tool using the settings that you specified in the current analysis, or if you want to display the dialog to the end user of the Guide.

To add a tool which you have created using Computation Services you must first open the configuration in Computation Services and select File > Send to Analysis Builder. This will create the action Start Data computation in the Actions in DecisionSite list, which can be included in your Guide as any other action.

## Multiple action links

It is possible and also often recommended to include several actions in a single link. For example, if you want the Guide to open an information link and also display one or more visualizations upon clicking the link, you can combine these actions to one link. Make sure you have performed all actions that you want to include. Then click to select all of the actions that should be included and click < **Add Link**. The actions will be performed in the order that they appear in the Actions in DecisionSite list, i.e., the order you performed them in your analysis.

### 9.4.2.6 Running Guides Locally

While you are developing a Guide, or if you create Guides that are for your own use only, you may want to run a Guide locally on your own computer, without giving other users access to it on the server.

#### ► To run a Guide locally:

1. In the main menu bar of DecisionSite, select **Guides > Run from File...**

Response: An Open dialog is displayed.

2. Browse to the Guide file that you want to run.

Comment: Spotfire Guide files (SFG) or HTML files may be opened.

3. Click **Open**.

Response: The Guide that you have selected is opened in the Guides pane. Follow the instructions in the Guide as usual.

**Tip:** If you want to test the Guide during development, select **Guide > Run** in Analysis Builder. This will immediately display the Guide inside the Guides pane. It is not necessary to save the Guide prior to testing.

### 9.4.2.7 Prompting Guide Users for Input

All properties are saved with their respective visualization when you add that visualization to the Guide. However, there may be occasions when you want the end user of the Guide to be able to specify which columns to use on different axes, which column to color the markers by, etc., upon running the Guide.

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► **To prompt for input to visualizations:**

1. In the *Actions in DecisionSite* list, click to select the visualizations that you want the new link to create.  
Comment: See How the Actions in DecisionSite list works for more information on how to populate the list.
2. Make sure that **Edit > Show Add Link Dialogs** is selected with a check mark.
3. Click **< Add Link**.  
Response: The Link Properties dialog is displayed
4. Click on the visualization action that you want to add prompting to in the **Actions performed when clicking the link** list.  
Response: The Prompts... button is activated.  
Comment: Prompting is not supported for multiple color bands in pie charts.
5. Click **Prompts...**.  
Response: The Prompt for... dialog is displayed.  
Comment: This dialog varies depending on which type of visualization that you have selected.
6. Select the check box for the things that you want the user to specify.  
Comment: Each selected object will result in the appearance of a setting selection in a dialog which is presented to the end user of the Guide.
7. If desired, change the **Title for input field in prompt dialog** to a different title.  
Comment: This is the title that the end user of the Guide will see above the selected setting.
8. Click **OK**.  
Response: In the Link Properties dialog, the visualization action is updated with the information [Settings modified].
9. Repeat steps 4-7 if you want to create a multiple action link with several prompt steps.
10. Click **OK**.  
Response: The link is added to the Guide contents list.

► **To prompt for input to tools:**

1. In the *Actions in DecisionSite* list, click to select the tool that you want the new link to start.  
Comment: See How the Actions in DecisionSite list works for more information on how to populate the list.
2. Make sure that **Edit > Show Add Link Dialogs** is selected with a check mark.
3. Click **< Add Link**.  
Response: The Link Properties dialog is displayed
4. Click on the tool action that you want to add prompting to in the **Actions performed when clicking the link** list.  
Response: The Prompts... button is activated.
5. Click **Prompts...**.  
Response: The Tool Option dialog is displayed.
6. Select the **Display the tool dialog, so the user can provide input** radio button.  
Comment: For many of the tools in DecisionSite, this is the only alternative available. The number of tools that can be run silently (without input from the end user of the Guide) will increase in coming releases of Analysis Builder.
7. Click **OK**.  
Response: The Tool Option dialog is closed.
8. Click **OK**.  
Response: The link is added to the Guide contents list.

## 9.4.2.8 Open and Publish Guides to the Library

The Library introduces convenient publishing of analysis material. Guides can be published to the Library for sharing with your colleagues. Located in the Library, the Guide can be opened by anyone with read access.

### ► To open Guides from Library in Analysis Builder:

1. In Analysis Builder, select **Guide > Open from Library...**
2. In the Open from Library Dialog, locate the Guide you want to open and click **Open**.  
Response: The Guide is opened in Analysis Builder.  
**Note:** Only Guides created with Analysis Builder can be opened.

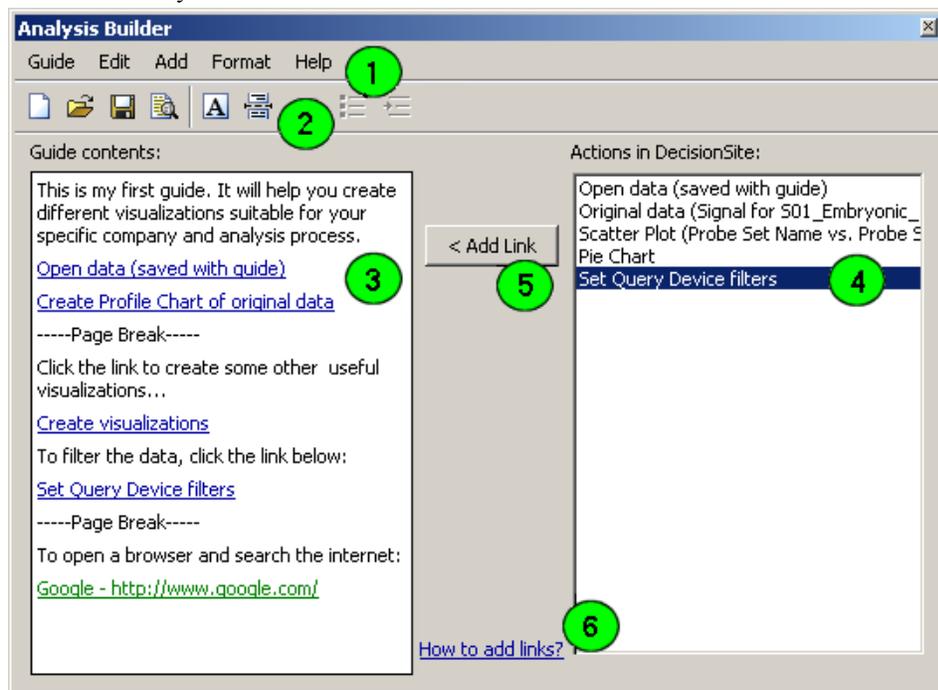
### ► To publish Guides to the Library:

1. In Analysis Builder, select **Guide > Publish to Library...**
2. In the Publish to Library Wizard Step 1(2), browse to the location where you want to publish the Guide.
3. In the **Guide Title** text box, enter the name of the Guide and click **Next >**.
4. Please enter properties of your Guide in Publish to Library Wizard Step 2(2).
5. Click **Finish**.  
Response: Your Guide is published to the Library.
6. In the Publish to Library Guide Published step, decide if you want to email your colleagues about your new Library Guide. Click **Close** when done.

## 9.4.3 User Interface

### 9.4.3.1 Analysis Builder User Interface Overview

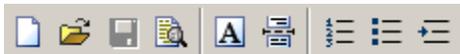
This is the Analysis Builder user interface:



#### 1. Analysis Builder menus

The Guide, Edit, Add, Format and Help menus contain menu commands required to work with the Analysis Builder.

## 2. Toolbar



Includes shortcuts for some of the most common commands in the Analysis Builder. See Analysis Builder toolbar for a description of the different buttons.

## 3. Guide contents

This window contains the contents of your current Guide. This is where you create a new Guide or modify an existing Guide. Text is added by double-clicking where it says **Double-click to edit text** or by selecting **Add > Text** from the menu. Links to actions are added from the *Actions in DecisionSite* list, see below.

You can move text items, comments, links and page breaks in the Guide contents list to the desired position using a simple drag-and-drop operation.

## 4. Actions in DecisionSite

This list contains all actions that you have performed in DecisionSite during the latest session. A session is defined as the time from when you have opened your current data set until you close it. The Analysis Builder does not have to be started to log the events. Closing the data set will clear the action list.

Select one or more actions from this list and click **< Add Link** to include the action (or combined action) in the Guide. If you want to add an action that is currently not available in the action list, first perform the action in DecisionSite and it will immediately show up in the list.

## 5. < Add Link

Select one or more actions from the *Actions in DecisionSite* list and click this button to include the action (or combined action) in the Guide. The link will by default include the settings used in DecisionSite at the very moment you add the link.

## 6. How to add links?

This link opens this help file to a page with tips on how to add links to a Guide.

### ► To reach the Analysis Builder:

Select **Guides > Create and Edit Guide**.

## 9.4.3.2 Analysis Builder Toolbar

The Analysis Builder toolbar includes shortcuts for some of the most common commands in the menus. Click on the buttons on the toolbar to activate the corresponding functions.



Creates a new, empty Guide. This resets the *Guide contents* window but not the *Actions in DecisionSite* list.



Opens a dialog where you can select a previously saved Guide file (SFG) that you can continue to work on or modify and save as a new Guide.



Saves the current Guide as an SFG file.



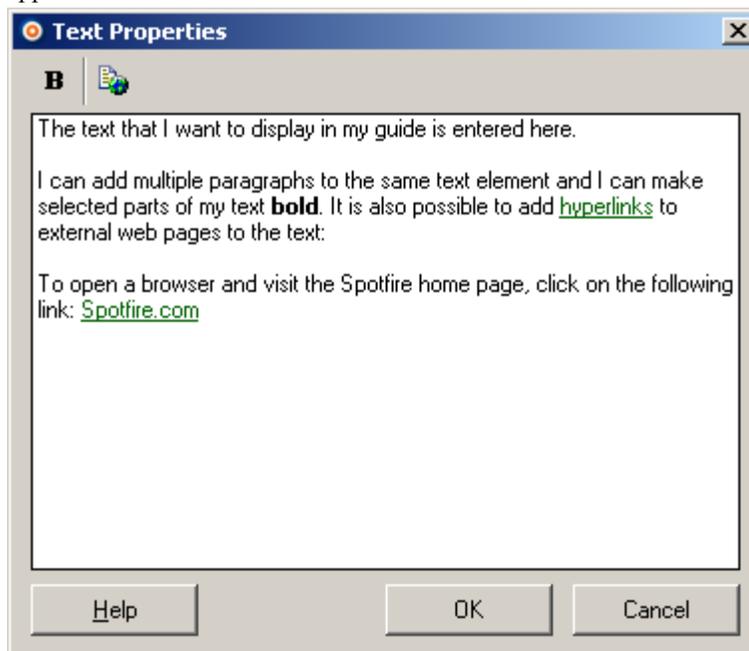
Launches the current Guide in the Guides pane. It is not necessary to save the Guide prior to using this command in Analysis Builder. Therefore, it is useful for iterative testing of the design of the Guide.

**Note:** If you are testing Guide steps that include opening a data set, you will clear the current *Actions in DecisionSite* list! Make sure that you have added all steps of your current analysis to the Guide before you test the parts of the Guide that involve switching data sets.

	Adds a new text element below the currently selected item, or, if no item is selected, at the bottom of the Guide contents list. The Text Properties dialog is displayed with the default text "Enter text here".
	Creates a new page in the Guide. The beginning of the new page is labeled -----Page Break----- in the Guide contents list.
	Adds a number before the selected text, link or comment item. Subsequently following text, link or comment items on the same Guide page get the next number (2, 3...), if this button is selected.
	Adds a bullet before the selected text, link or comment item.
	Indents the selected text, link or comment item.

### 9.4.3.3 Text Properties Dialog

The Text Properties dialog is used to enter and edit the text of a text element. Multiple paragraphs can be written within the same text element, bold formatting and hyperlinks can be applied to selected text.



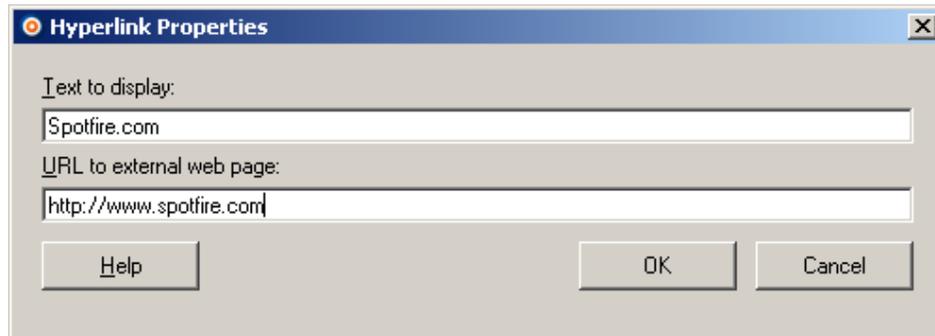
	Applies bold formatting to the selected text. Also available using the short command <b>Ctrl+B</b> .
	Opens the Hyperlink Properties dialog, where you can create a hyperlink to an external web page from the selected text. Also available using the short command <b>Ctrl+K</b> .

#### ► To reach the Text Properties dialog:

The Text Properties dialog is displayed when a new text element is added to the Guide in Analysis Builder, e.g., via **Add > Text**. It can also be displayed by double-clicking on a previously entered text element.

### 9.4.3.4 Hyperlink Properties Dialog

The Hyperlink Properties dialog is used to insert hyperlinks to external web pages in the Guide. To add links that perform actions in DecisionSite (opens data, creates visualizations, etc.), see How the Actions in DecisionSite list works.



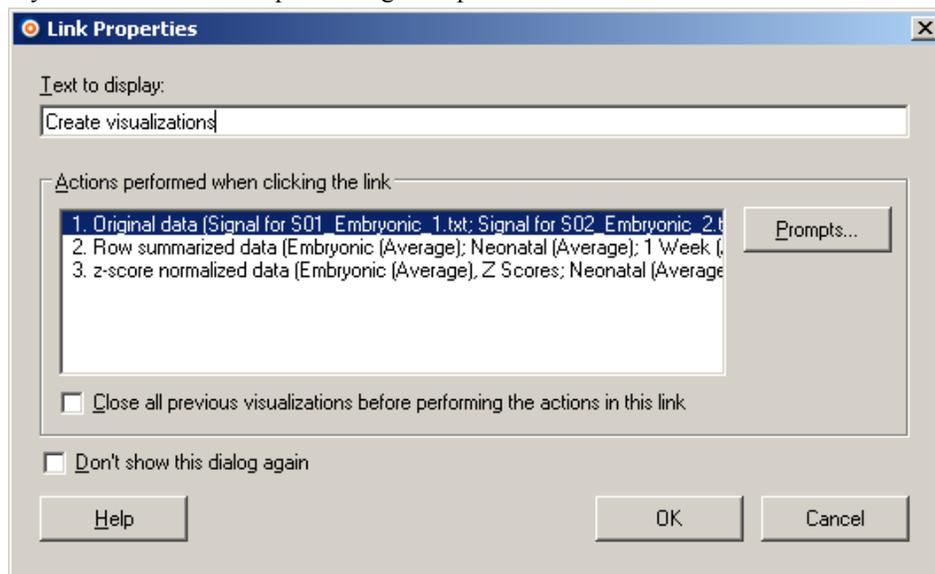
Option	Description
<b>Text to display</b>	The text that will be displayed as a hyperlink (green and underlined).
<b>URL to external web page</b>	The address to the external web page where you want to go when clicking on the hyperlink. The address must begin with either http:// or file://.

#### ► To reach the Hyperlink Properties dialog:

1. In the Text Properties dialog, select the word that you want to create a hyperlink from.
2. Click on the Hyperlink button, .

### 9.4.3.5 Link Properties Dialog

The Link Properties dialog is specific to each link in your Guide. Here, you can edit the link text and view which actions will be performed upon clicking the link. This is especially useful if you have created links performing multiple actions.



Option	Description
<b>Text to display</b>	Edit the default text to display a link text of your choice in the new Guide.
<b>Actions performed when clicking the link</b>	Displays the actions that are part of the current link. If multiple actions are included in the link, the actions are ordered in a numbered list where the action first performed is number 1.
<b>Prompts...</b>	Displays the Prompt for... dialog, if the selected action is a visualization, or the Tool Option dialog, if the selected action is a tool.
<b>Close all previous visualizations before performing the actions in this link</b>	Adds an action with the title <i>Close all visualizations</i> to the top of the list of actions in this dialog. This means that all visualizations that were open when the end user of the Guide clicked on this link will be closed. This can be used to prevent the desktop from being cluttered with visualizations.
<b>Don't show this dialog again</b>	Select this check box if you do not want to see this dialog automatically upon adding new links. To display it again, select <b>Edit &gt; Show Add Link Dialogs...</b>

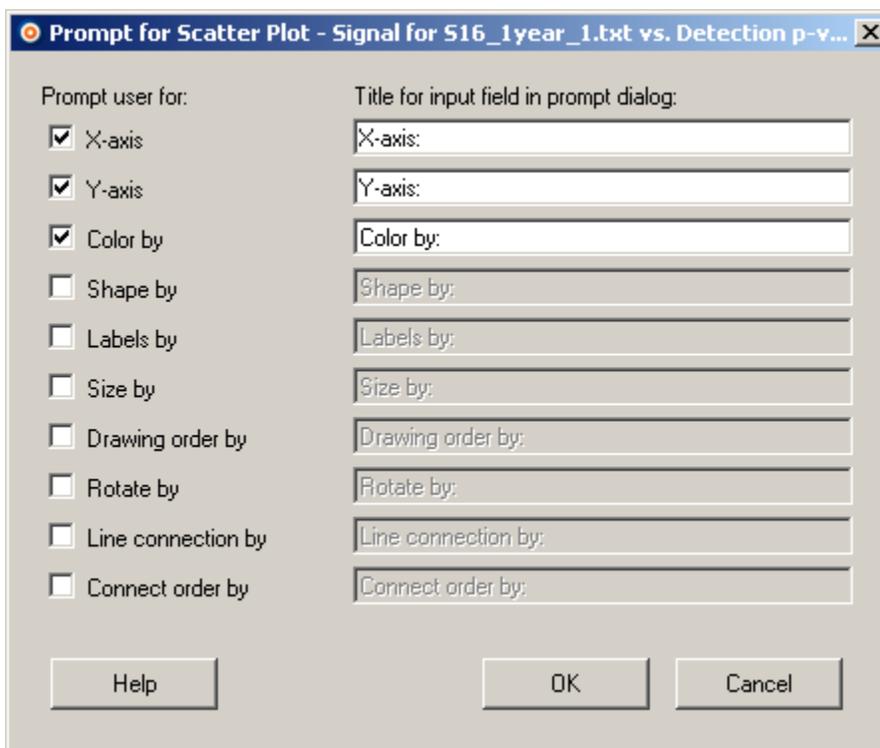
► **To reach the Link Properties dialog:**

The Link Properties dialog is automatically displayed when a new link is added to the Guide in Analysis Builder. If the check box *Don't show this dialog again* has been selected earlier, the dialog for a specific link can be displayed by double-clicking the link in the Guide contents list.

### 9.4.3.6 Prompt for... Dialog

The Prompt for... dialog is specific to each visualization in a link. If you have selected a scatter plot (as in the example below) the dialog will be called Prompt for Scatter Plot (or whatever the title of the visualization is) and the column names of the selected axes. This dialog allows you to decide for which properties the end user of the Guide should provide input.

**Note:** Only properties that you have used in your current version of the plot will be available. Hence, if you want the end user of the Guide to be able to select by which column to color by, you must make sure that you have selected some column in the Properties dialog of the visualization (in DecisionSite). Also note that prompting is not supported for multiple color bands in pie charts.



Option	Description
<b>Prompt user for</b>	Select the check box for each of the properties that you want the end user of the Guide to be able to specify upon running the Guide. <b>Note:</b> If you want the end user of the Guide to use exactly the same settings as your current visualization, you should not allow any prompting at all.
<b>Title for input field in prompt dialog</b>	Enter a descriptive title to be shown in the Settings for... dialog of the selected visualization. This is what the end user of the Guide will see above the drop-down list for each selected property.

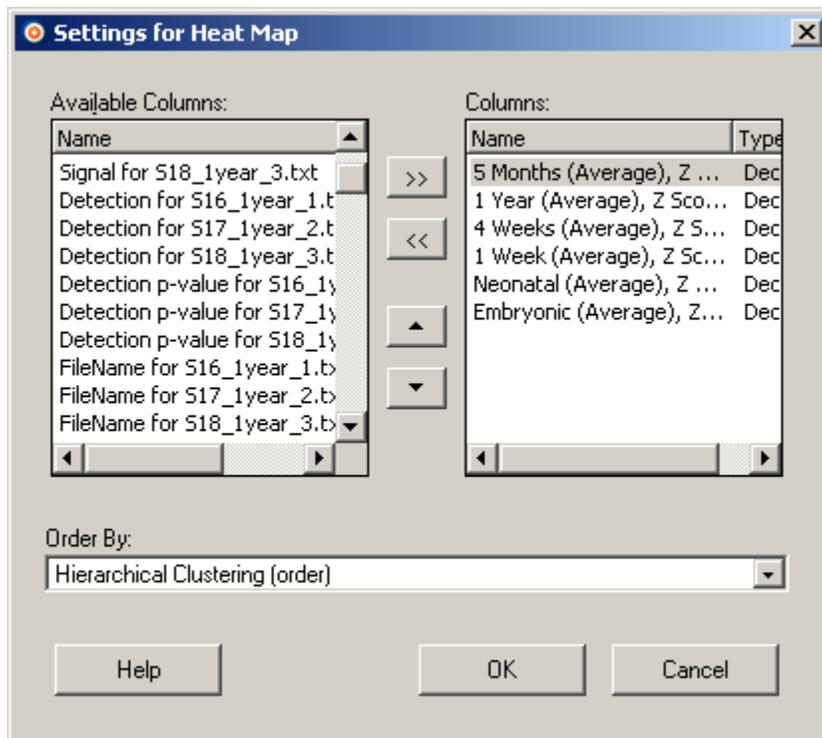
► **To reach the Prompt for... dialog:**

1. Create visualizations and edit their properties in DecisionSite (**Edit > Properties** in main application).
2. Add a link that creates one or more visualizations to the Guide.
3. In the Link Properties dialog of the desired link, click to select the visualization that you want to add prompting for.
4. Click **Prompts...**

### 9.4.3.7 Settings for... Dialog

The Settings for... dialog is displayed when running a Guide that includes prompted steps. It is specific to each visualization in a link. If you have selected a heat map, the dialog will be called Settings for Heat Map.

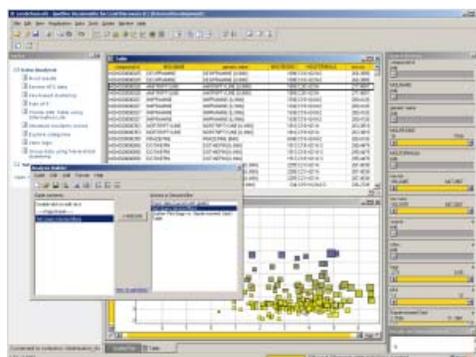
This dialog allows the end user of a Guide to select to certain properties for a specific visualization at run-time of the Guide. Only the properties specified by the creator of the Guide will be available.



This dialog varies depending on both the type of visualization and the selections that you have made in the Prompt for.. dialog.

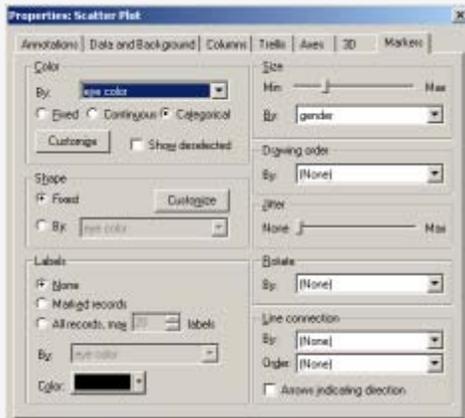
**Example:**

A data set containing height, weight and eye color of a group of men and women is opened in DecisionSite and two visualizations are created; The first visualization is a scatter plot with height on the X-axis and weight on the Y-axis, and the markers are colored by eye color and sized by gender. The second visualization is a table showing all available columns in the data set.



A Guide created using Analysis Builder can be edited to prompt its end user to specify certain visualization settings as indicated below:

Settings in **Properties dialog** for visualization (in DecisionSite):



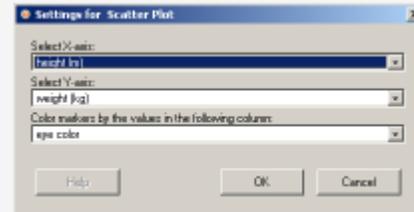
The Properties dialog of a scatter plot.

Settings and titles specified in the **Prompt for... dialog**:

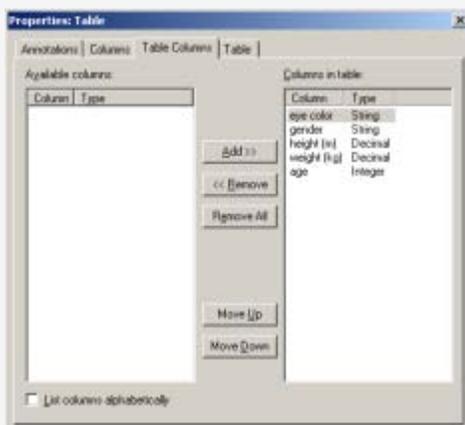


Here, the scatter plot properties that were set to something other than [None], that is, Color and Size, together with the axis-selections, are shown as possible prompts. The creator of this Guide has determined that the size should always be set by gender as she specified when she created the original scatter plot, so this check box is not selected in the Prompt for... dialog.

Resulting **Settings for...** dialog displayed upon running Guide:



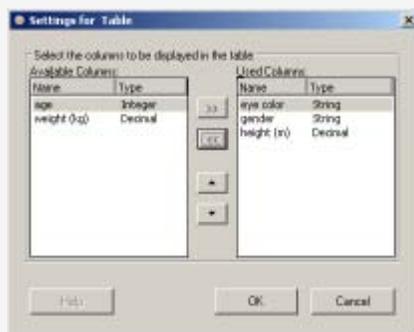
The resulting Settings for... dialog shows the three selected prompt lists upon running the Guide. The titles of the lists are the ones entered by the Guide creator in the Prompt for... dialog.



The Properties dialog of a table visualization.



In this case, the only setting that had been modified was the columns displayed in the table. Hence, this is the only item available for prompting in the Prompt for... dialog.



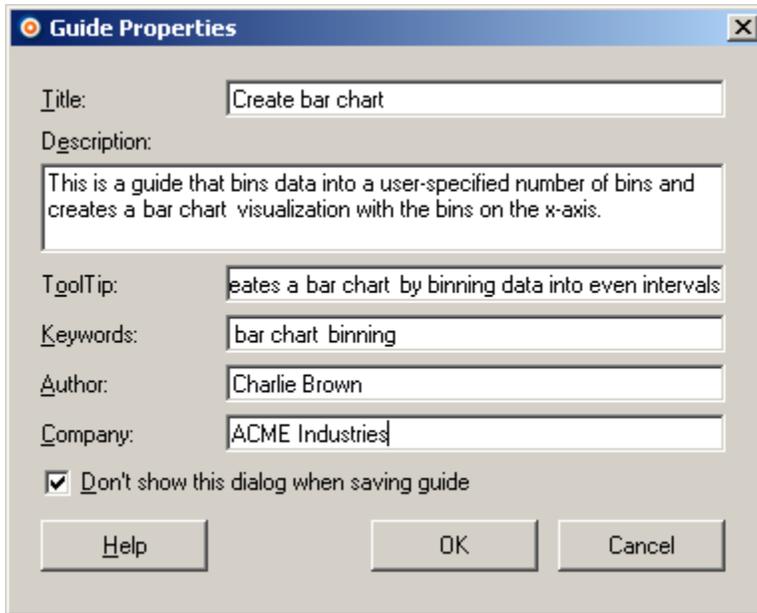
If the selected prompt item is a list of columns, the resulting Settings for... dialog will contain two list boxes where the end user of the Guide can move columns from Available Columns to Used Columns using the arrows >> and <<, and also sort the columns with the up and down arrows.

### ► To reach the Settings for... dialog during development of a Guide:

1. Add one or more prompt steps to a visualization link using the Prompt for... dialog.
2. Select **Guide > Run** from the Analysis Builder menu.
3. Step through the Guide to locate the edited visualization link and click on it.

## 9.4.3.8 Guide Properties Dialog

The Guide Properties dialog controls important properties like the title and ToolTip of the Guide after it has been deployed to a server. It is recommended that you fill in all fields of the Guide Properties to facilitate efficient administration of Guides on the server.



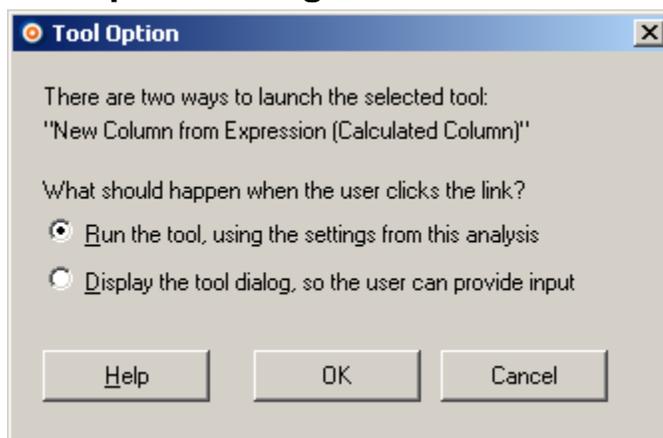
Option	Description
<b>Title</b>	<p>The title of your Guide as it will be displayed in the Guides pane when it is published to a server. The title is also displayed in the flight view when you are running the Guide. It is important that the title is informative with regards to what the Guide really does.</p> <p>If the Guide will be published to a server, no characters other than a-z, A-Z, 0-9, ! \$ ( ) , - . ; _ { } ~ and blank spaces should be used in this field due to restrictions in DecisionSite Builder.</p>
<b>Description</b>	<p>A description of the functions of the Guide. The description can make it easier for the server administrator to group similar Guides together and remove duplicates, etc.</p>
<b>ToolTip</b>	<p>A short description of the Guide to be displayed as a ToolTip when you hover with the mouse pointer over the Guide title in the Guides pane. Example: "Creates a bar chart by binning data into even intervals"</p>
<b>Keywords</b>	<p>Keywords specific to the contents of the Guide. Keywords are separated by semicolon, i.e., if you write "bar chart binning" it will be interpreted as a single keyword. To produce two keywords the words must be separated with semicolon. Hence, "bar chart ;binning" will result in the two keywords "bar chart" and "binning".</p>
<b>Author</b>	<p>The name of the Guide author. The default value is the user name that you used when logging in to DecisionSite Analytics Server. The author name can be especially important to your IT personnel if they want to perform any changes to your Guide and want to check with you that their changes are correct.</p>
<b>Company</b>	<p>The company for which you have created the Guide. This is commonly used in the package name of the Guide resource when the Guide is deployed to a server. If the Guide will be published to a server, no characters other than a-z, A-Z, 0-9, ! \$ ( ) , - . ; _ { } ~ and blank spaces should be used in this field due to restrictions in DS Builder.</p>

**Don't show this dialog when saving Guide** Select this check box if you do not want to see this dialog automatically when you are saving your Guides.

► **To reach the Guide Properties dialog:**

In Analysis Builder, click **Guide > Properties**.

### 9.4.3.9 Tool Option Dialog



Option	Description
<b>Run the tool, using the settings from this analysis</b>	The tool will be run silently (without any input from the end user of the Guide) using the same settings that you used in your calculation.
<b>Display the tool dialog, so the user can provide input</b>	The tool is started, but the end user of the Guide must provide input and click OK in the tool dialog for any calculation to be performed.

► **To reach the Tool Option dialog:**

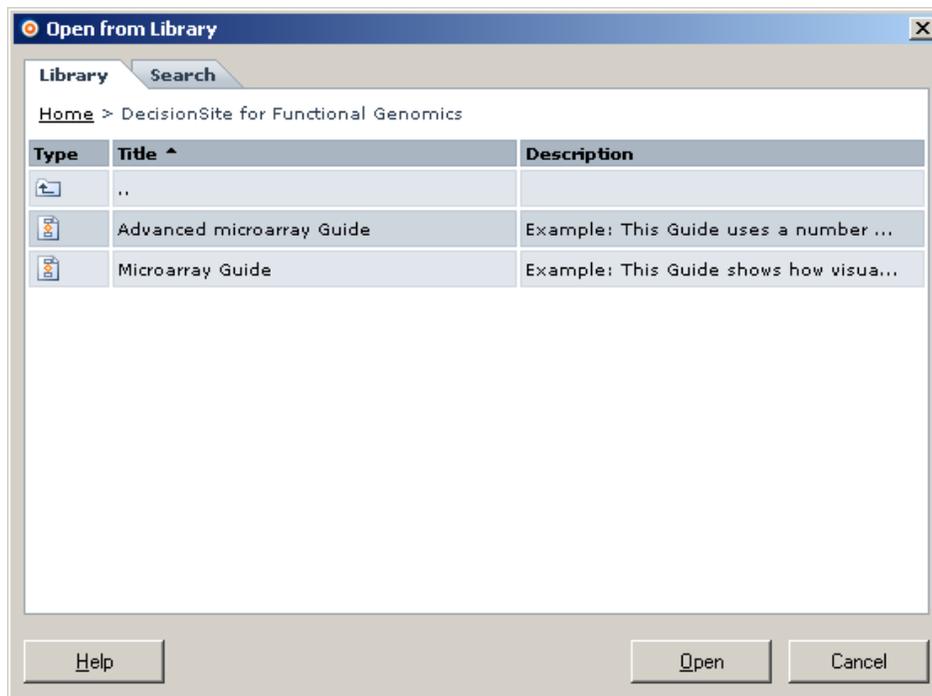
1. Run a tool in DecisionSite.
2. Add a Run-the-tool link to the Guide.
3. In the Link Properties dialog of the desired link, click to select the tool that you want to add prompting for.
4. Click **Prompts...**

**Note:** In the current version of Analysis Builder, not all tools have the possibility to be run silently.

### 9.4.3.10 Open Guide from Library Dialog

This dialog lets you select and open a Guide that is located in the Library. To find a Guide, either look through a Library Section's content, or search for the Guide.

**Note:** Only Guides created with Analysis Builder are available to be opened and edited in Analysis Builder.



### Library tab options

#### Library

### Description

All Guides, folders and Library Sections are listed on this tab.  
**Note:** Only Library Sections that you have access to are listed.

#### Open

Select the Guide you want and click **Open** to open it in the Guides pane (or in Analysis Builder if you have reached this dialog from there). You can also double-click the Guide to open it.

### Search tab options

#### Search tab

Use **Search** to search for the item you want to open.

#### Search for:

Enter the search string in the **Search for:** field and click **Search**. See Searching in the Library for information about search strings.  
 If you click a folder in the **Search** result, you will be redirected to the Library View under the **Library** tab.

#### Look in:

Select which Library Section you want to perform your search in. Either one or all Library Sections can be searched. Only Library Sections you have access to are listed.

### ► To reach the Open Guide from Library dialog:

- Click **Open Guide from Library** in the **Guides** pane, or
- select **Guides > Run from Library...** from the menu, or
- in Analysis Builder, click **Guide > Open from Library...**

**Note:** Opening a Guide in Analysis Builder will open the Guide for editing in Analysis Builder and not to the Guides pane as in the previous cases.

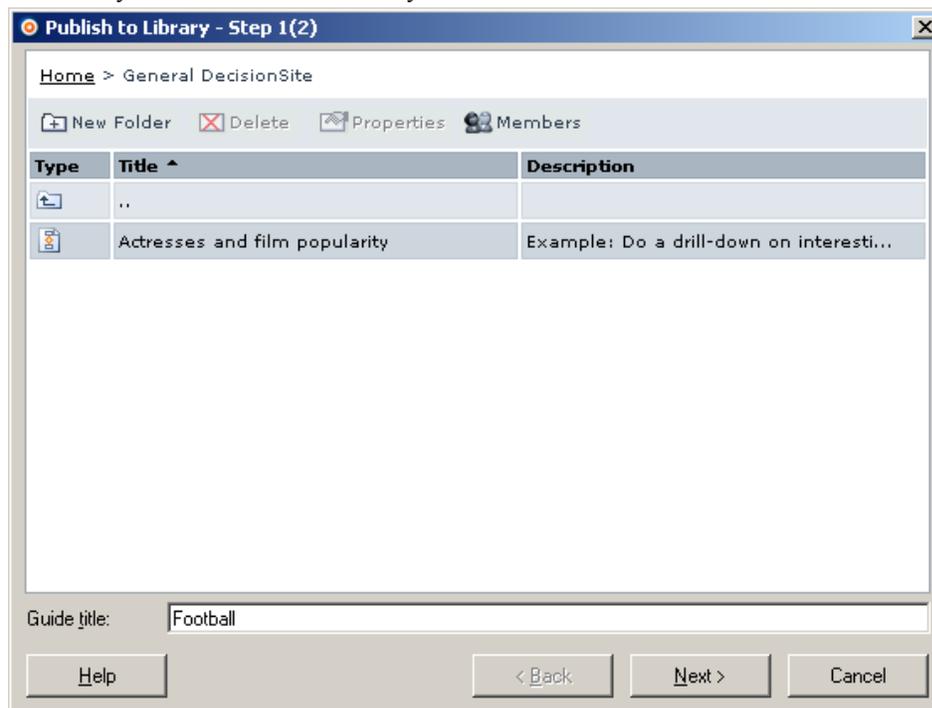
## 9.4.3.11 Publish to Library Wizard

### 9.4.3.11.1 Publish to Library Wizard: Step 1(2)

This wizard helps you to publish a Guide in the Library. Using the Library, your colleagues can use your Guide from a Library Section.

This step lets you specify where in the Library your Guide should be published. Navigate in the Library by double-clicking on Library Sections and folders.

**Note:** Only Guides created with Analysis Builder are available.



Options	Description
<b>New Folder</b>	Creates a new folder where you can publish your Guide. A dialog will prompt you for the new folder name. <b>Note:</b> The New Folder button is only displayed inside a Library Section.
<b>Members</b>	Lists all users with at least read access to the current Library Section. Each Library Section has its own set of access permissions. <b>Note:</b> The Members button is only displayed inside a Library Section.
<b>Guide title</b>	The name of the Guide as it will be displayed in the Library. This title will be displayed as a link in the Guides pane. It is important that the title is informative with regards to what the Guide actually does. <b>Note:</b> The title can be 50 characters at the most, and the following characters are not supported: \\/: * ? " < > +   \$ & + = @ # % : ; , { [ ] } ^ ' ~ `
<b>Next &gt;</b>	Proceeds to Publish to Library Wizard: Step 2(2) where properties can be edited further.

#### ► To reach the Publish to Library Wizard Step 1(2) dialog:

In Analysis Builder, click **Guide > Publish to Library...**

### 9.4.3.11.2 Publish to Library Wizard: Step 2(2)

This dialog lets you enter all properties of the Guide. By using detailed properties, the organization and search capabilities in the Library are greatly enhanced.

**Publish to Library - Step 2(2)**

Guide title:

Description:

Keywords:   
For multiple keywords use semicolon ";" as separator

Tooltip:

Author:

Company:

Buttons: Help, < Back, Finish, Cancel

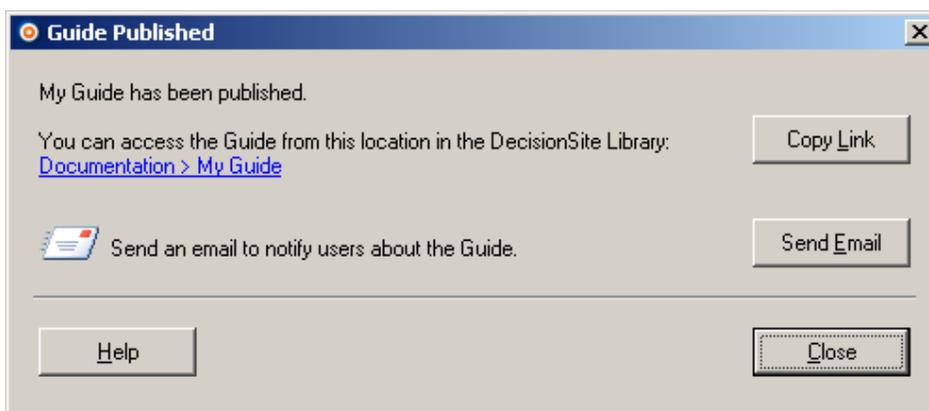
Option	Description
<b>Guide title</b>	The name of the Guide as it will be displayed in the Library. This is the title you provided in the previous step.
<b>Description</b>	A description of the functions of the Guide. The description can make it easier for the server administrator to group similar Guides together and remove duplicates, etc. <b>Note:</b> The description can be at most 650 characters. (Certain Unicode characters may take up 6 character spaces in this regard.)
<b>Keywords</b>	Keywords specific to the contents of the Guide. Keywords are separated by semicolon, i.e., if you write "bar chart binning" it will be interpreted as a single keyword. To produce two keywords the words must be separated with semicolon. Hence, "bar chart;binning" will result in the two keywords "bar chart" and "binning". Keyword are used to enhance organization and search capabilities. Use keywords for precise searches.
<b>ToolTip</b>	A short description of the Guide to be displayed as a ToolTip when you hover with the mouse pointer over the Guide title in the Guides pane. Example: "Creates a bar chart by binning data into even intervals"
<b>Author</b>	The name of the Guide author.
<b>Company</b>	Here you can specify the company that owns the Guide.
<b>Finish</b>	Click <b>Finish</b> to publish your Guide and proceed to the Publish to Library: Guide Published dialog where you can find information on notify your colleagues.

► **To reach the Publish to Library Wizard: Step 2(2) dialog:**

1. In Analysis Builder, click **Guide > Publish to Library...**
2. In the Publish to Library Wizard: Step 1(2), select Library location, enter a title, and click **Next >**.

### 9.4.3.11.3 Publish to Library: Guide Published

As soon as you have saved your Guide in the Library, a dialog window will appear with a confirmation that your Guide is published. This dialog will also include a hyperlink to the Library folder containing the Guide you just published, which you can click on to view the final result.



Example of a confirmation from DecisionSite Library about a published item.

Option	Description
Link	Click on the link to open the Library folder containing your published Guide.
Close	Closes the notification dialog

► **To reach the Publish to Library Guide Published dialog:**

1. In Analysis Builder, click **Guide > Publish to Library...**
2. In the Publish to Library Wizard: Step 1(2), select Library location, enter a title , and click **Next >**.
3. Enter properties in Publish to Library Wizard: Step 2(2) and click **Finish**.

## 9.4.3.12 Menus

### 9.4.3.12.1 Analysis Builder Add Menu

The Add menu contains the following commands:

Option	Description
Text	Opens the Text Properties dialog where you can enter a new text which will be inserted below the currently selected item, or, if no item is selected, at the bottom of the Guide contents list. The Text Properties dialog is displayed with the default text "Enter text here".
New Page	Creates a new page in the Guide. The beginning of the new page is labeled - ---Page Break----- in the Guide contents list.
Comment	Adds a new text box with text in italics below the currently selected item, or, if no item is selected, at the bottom of the Guide contents list. The new

comment item is displayed with the default text "Click to add comment". The purpose of comments is normally to indicate that something in this Guide should be changed or added by the IT department of the Guide creators company. Therefore, comments should normally be removed before the Guide is deployed to all users.

### 9.4.3.12.2 Analysis Builder Help Menu

The Help menu contains the following command:

Option	Description
<b>Analysis Builder Help</b>	Opens this help file to the Analysis Builder Overview topic.

### 9.4.3.12.3 Analysis Builder Pop-up Menu

The pop-up menu which is displayed upon right-clicking on an item in the Guide contents list contains the following commands:

Option	Description
<b>Move Up</b>	Moves the currently selected text, comment, link or Page Break in the Guide contents list up one step.
<b>Move Down</b>	Moves the currently selected text, comment, link or Page Break in the Guide contents list down one step.
<b>Delete</b>	Deletes the selected text, comment, link or Page Break from the Guide contents list. You can also press Delete on your keyboard to perform the same function.
<b>Text Properties</b>	Displays the Text Properties dialog. Comments are directly opened for editing by double-clicking on the comment.
<b>Link Properties</b>	Displays the Link Properties dialog.

## 9.5 Publish to Library

### 9.5.1 Publish to Library Overview

The Publish to Library tool allows you to publish custom Guides and Analysis Builder Guides to the Library. By publishing your Guides, colleagues can use them in a convenient way.

To publish Analyses and Posters, see Publishing Analyses to Library and Publishing Posters to Library.

#### ► To publish Guides to the Library:

1. Select **Guides > Publish to Library**.
2. In Publish to Library Wizard Step 1(3), select if you want to publish a custom made Guide or a Guide created with Analysis Builder. Click **Next >**.
3. Select the location in the Library for your Guide in Publish to Library Wizard Step 2(3). Click **Next >**. Navigate in the Library by using double-click on Library Sections and folders.
4. Enter properties of your Guide in Publish to Library Wizard Step 3(3). Click **Finish**.

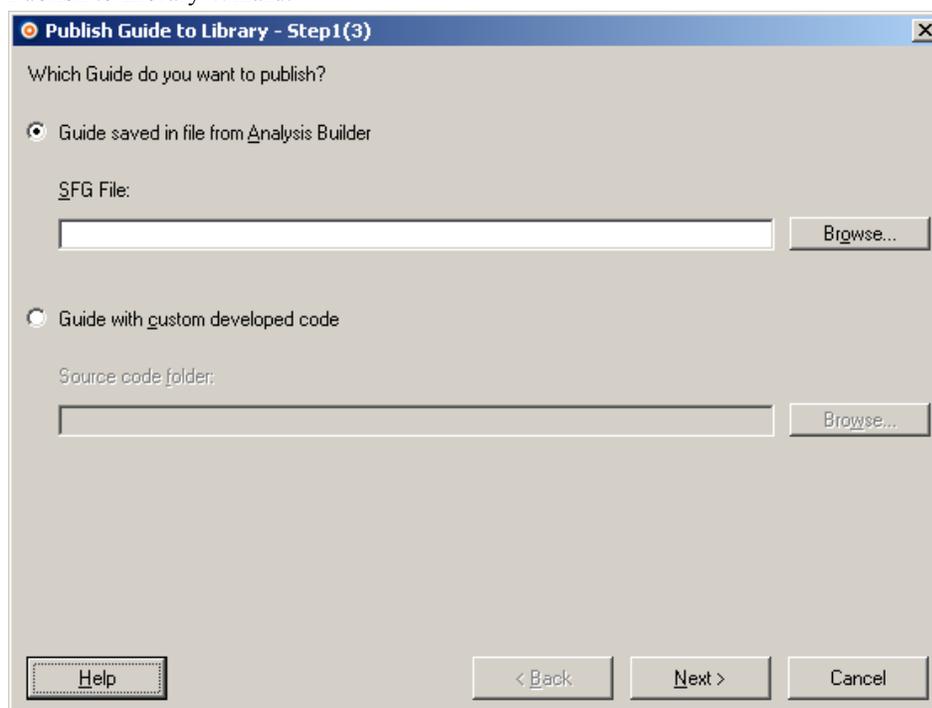
5. In the Publish to Library Wizard Guide Published dialog, select if you want to notify your colleagues. In this dialog you can send an email with a link to the Guide.  
Response: Your Guide is published to the Library in the specified location. Anyone with read access to that Library Section can now use the Guide.

## 9.5.2 Publish to Library Wizard

### 9.5.2.1 Publish Guide to Library Wizard: Step 1(3)

This wizard helps you to publish a Guide in the Library. Using the Library, your colleagues can use your Guide from a Library Section.

Both custom made Guides and Guides created with Analysis Builder can be published with the Publish to Library Wizard.

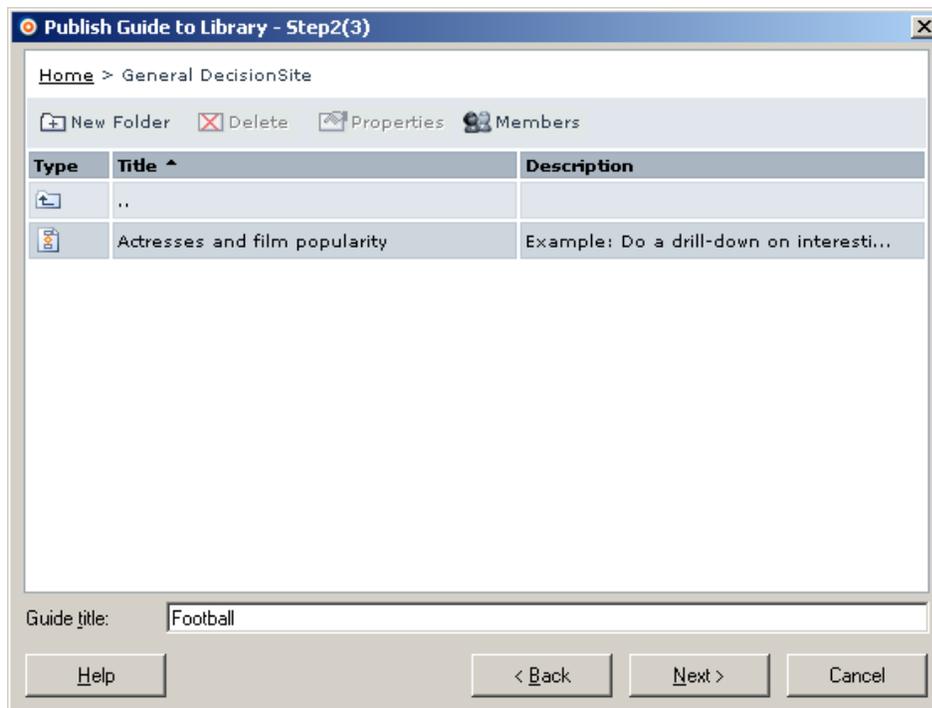


Option	Description
<b>Guide saved in file from Analysis Builder (SFG File)</b>	To publish a Guide created with Analysis Builder, click <b>Browse...</b> to locate the SFG file containing the Guide. <b>Tip:</b> You can publish Analysis Builder Guides directly in Analysis Builder.
<b>Guide with custom developed code (Source code folder)</b>	To Publish a custom made Guide, click <b>Browse...</b> to locate the folder in which it is stored. Custom made Guides are Guides not created with Analysis Builder.
<b>Next &gt;</b>	Proceeds to Publish Guide to Library Wizard: Step 2(3).

- **To reach the Publish Guide to Library Wizard: Step 1(3) dialog:**  
Select **Guides > Publish to Library...** from the menu.

### 9.5.2.2 Publish Guide to Library Wizard: Step 2(3)

This step lets you specify where in the Library your Guide should be published. Navigate in the Library by using double-click on Library Sections and folders.



Options	Description
<b>New Folder</b>	Creates a new folder where you can publish your Guide. A dialog will prompt you for the new folder name. <b>Note:</b> The New Folder button is only displayed inside a Library Section.
<b>Members</b>	Lists all users with at least read access to the current Library Section. Each Library Section has its own set of access permissions. <b>Note:</b> The Members button is only displayed inside a Library Section.
<b>Guide title</b>	The name of the Guide as it will be displayed in the Library. This title will be displayed as a link in the Guides pane. It is important that the title is informative with regards to what the Guide actually does. <b>Note:</b> The title can be 50 characters at the most, and the following characters are not supported: \\ : * ? " < > +   \$ & + = @ # % : ; , { [ ] } ^ ' ~ `
<b>Next</b>	When you have selected a location where you want to publish your Guide, click Next to continue to Publish to Library Wizard: Step 3(3).

► **To reach the Publish Guide to Library Wizard: Step 2(3) dialog:**

1. Select **Guides > Publish to Library...** from the menu.
2. Select which type of Guide you want to publish in Publish Guide to Library Wizard: Step 1(3) and click **Next >**.

### 9.5.2.3 Publish Guide to Library Wizard: Step 3(3)

This dialog lets you to enter all properties of the Guide. By using detailed properties, the organization and search capabilities in the Library are greatly enhanced.

**Publish Guide to Library - Step3(3)**

Guide title:

Description:

Keywords:   
For multiple keywords use semicolon ";" as separator

Tooltip:

Author:

Company:

Buttons: Help, < Back, Finish, Cancel

Option	Description
<b>Guide title</b>	The name of the Guide as it will be displayed in the Library. This is the title you provided in the previous step.
<b>Description</b>	A description of the functions of the Guide. The description can make it easier for the server administrator to group similar Guides together and remove duplicates, etc. <b>Note:</b> The description can be at most 650 characters. (Certain Unicode characters may take up 6 character spaces in this regard.)
<b>Keywords</b>	Keywords specific to the contents of the Guide. Keywords are separated by semicolon, i.e., if you write "bar chart binning" it will be interpreted as a single keyword. To produce two keywords the words must be separated with semicolon. Hence, "bar chart;binning" will result in the two keywords "bar chart" and "binning". Keyword are used to enhance organization and search capabilities. Use keywords for precise searches.
<b>ToolTip</b>	A short description of the Guide to be displayed as a ToolTip when you hover with the mouse pointer over the Guide title in the Guides pane. Example: "Creates a bar chart by binning data into even intervals"
<b>Author</b>	The name of the Guide author.
<b>Company</b>	Here you can specify the company that owns the Guide.
<b>Start page</b>	If you are publishing a custom made Guide you need to specify which file that is the start page of the Guide. <b>Note:</b> Only visible if you selected to publish a custom Guide in Publish to Library Wizard: Step 1(3).
<b>Finish</b>	Click <b>Finish</b> to publish your Guide and proceed to the Publish to Library: Guide Published dialog where you can find information on

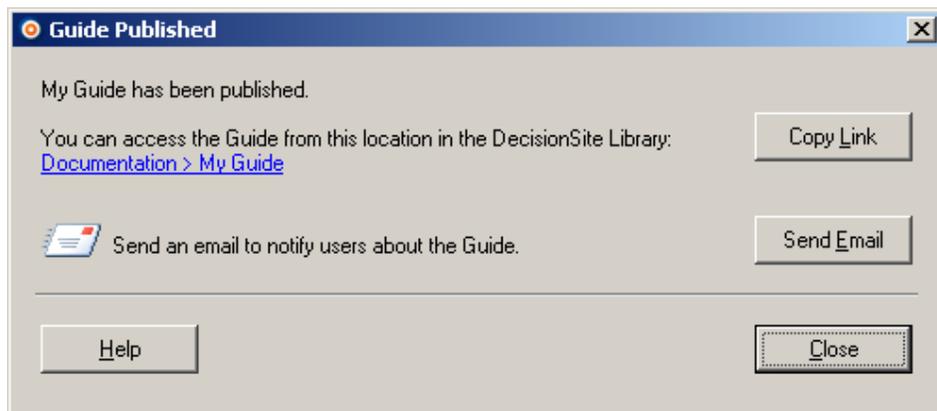
notify your colleagues.

► **To reach the Publish Guide to Library Wizard: Step 3(3) dialog:**

1. Select **Guides > Publish to Library...** from the menu.
2. Select which type of Guide you want to publish in Publish Guide to Library Wizard: Step 1(3) and click **Next >**.
3. Specify the location in the Library in Publish Guide to Library Wizard: Step 2(3) and click **Next >**.

## 9.5.2.4 Publish Guide to Library: Guide Published

As soon as you have saved your Guide in the Library, a dialog window will appear with a confirmation that your Guide is published. This dialog will also include a hyperlink to the Library folder containing the Guide you just published, which you can click on to view the final result.



Example of a confirmation from DecisionSite Library about a published item.

Option	Description
<b>Link</b>	Click on the link to open the Library folder containing your published Guide.
<b>Copy Link</b>	Copies the link to the clipboard for later use. Using the link, the Guide can easily be referenced in email discussions or from web pages or portals. Using the links retrieved with <b>Copy Link</b> , Guides can be accessed from any web environment using the URL and name supplied.
<b>Send Email</b>	Launches a new email with your default email client.
<b>Close</b>	Closes the notification dialog

If you want to send an email notification, click on the **Send Email** button. This opens an email dialog where you may enter:

- **To:** The email address of one or more recipients, separated by comma or semicolon.
- **From:** Your own email address, mandatory.
- **Subject:** The subject of the email.
- **Comment:** Any additional text you wish to appear in the email.

► **To reach the Publish Guide to Library Wizard: Guide Published dialog:**

1. Select **Guides > Publish to Library...** from the menu.

2. Select which type of Guide you want to publish in Publish Guide to Library Wizard: Step 1(3) and click **Next >**.
3. Specify the location in the Library in Publish Guide to Library Wizard: Step 2(3) and click **Next >**.
4. Edit the Guide properties in Publish Guide to Library Wizard: Step 3(3) and click **Finish**.

# 10 Saving and Exporting Data

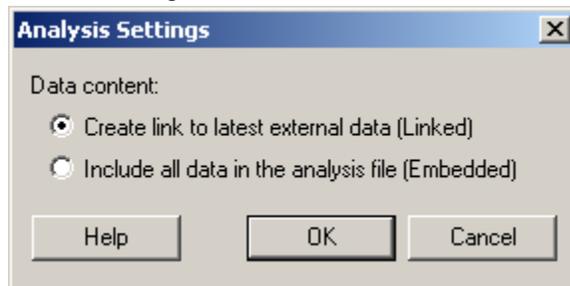
## 10.1 Saving SFS files

Save your Analysis by selecting **Save As...** in the **File** menu. Make sure that **Spotfire Analysis File (\*.sfs)** is selected in the **Save as type** list box.

### How the data is stored

If the data was loaded from a source other than the clipboard, you will get an option on how to save the actual data used in the Spotfire DecisionSite session. There are two options available:

- Saving a link to the data in a *dynamic* report file (Linked) – no actual data is stored in the SFS file, merely a reference describing how to retrieve, and how to view the data.
- Saving the data in a *static* report file (Embedded) – the actual data used in the session is saved in the SFS file. This is the only option available if the data was loaded from the clipboard.



For a number of reasons, saving the data as an SFS file with Linked data should be the preferred method, since it:

- Ensures data integrity – avoids inconsistencies.
- Reduces the file size – essential if you want to distribute the data.
- Ensures that the data is up-to-date.

However, since a link only references its data source, the dynamic SFS file is not good if the actual data is removed or damaged.

Files with column names that contain characters that could be interpreted as column separators, e.g., comma, semicolon, tab, etc., should always be saved with linked data to prevent Spotfire DecisionSite from finding the wrong column separators when reopening the file. If you must save the data embedded within the file, you can prevent the problem by saving the data as a TXT, SKV, or CSV file and opening it with the import agent. Column names should never contain characters that can be interpreted as column separators.

The saved link includes the file name if the data was imported from a text file, or the ODBC data source name and the SQL query used if the data was retrieved from a database using ODBC.

The way the data was saved has some implications on how the Analysis can be used and how it will behave:

- If the data itself is saved in the Analysis, the session becomes static. In other words, if the source for the data is updated, the Analysis will still show the old data. If only a link to the data was saved, the Analysis reflects all changes made to the data source each time the file is opened.
- If the Analysis is to be distributed, the recipients must have access to the data source to be able to link to the data. Static report files containing the actual data create no distribution problems.
- A static SFS file is considerably larger than a dynamic SFS file, since the latter only contains a link to the data.

## 10.2 Spotfire Files

### 10.2.1 SFS Files

All information and settings in a Spotfire DecisionSite session can be saved as a Spotfire Analysis File. This file has the file extension *.sfs*, and contains information such as:

- Current settings of the query devices, both selected values and the query device types
- Visualizations
- Coloring schemes
- Information on how to regenerate derived columns, i.e., those created by calculation and binning
- Attached background image files
- Data (either as a reference to a data source, or embedded in the Spotfire Analysis File)

By saving your current session as an Spotfire Analysis File, you can pick up your work later exactly where you left it off.

The handling of Spotfire Analysis Files differs depending on whether you include the data set in the Analysis (static SFS file), or reference the data with a link (dynamic SFS file).

### 10.2.2 SFT Files

SFT (Template) files are similar to Spotfire Analysis Files but are used as templates for quickly applying a whole range of visualization settings to a new data set.

#### ► To create a template:

1. Open a data file.
2. Make the required visualization settings (query devices, coloring, multiple visualizations, etc).
3. Select **File > Save As...**
4. Enter a name for the template.
5. From **Save as type**, select **Spotfire Template Files**.
6. Click **OK**.

For a template file to work properly, it should only be applied to data with the same column names as the data set used to create the template. If applied to a data set with different column names, only those settings that are independent of column name will be used (e.g., visualization types, fixed color, fixed shape, size and jittering, but not query device settings, Color by, etc.).

**Note:** Columns created from marked records cannot be saved in templates (SFT files).

#### ► To apply a template:

1. Open a data file.
2. Select **File > Apply Template**.
3. Select an SFT file.
4. Click **OK**.

You can use any SFS file in the same way as a template file, applying the settings in the Spotfire Analysis File to your loaded data set. Use the procedure described above, but select an Spotfire Analysis File instead of SFT.

**Note:** The Spotfire Interactive Report Settings dialog allows you to save your visualization settings only in Spotfire DecisionSite version 7.x. In newer versions, all settings are always included in a template.

## 10.2.3 SFA Files

In their most simple form, SFA (Spotfire Application) files are identical to Spotfire Analysis Files. You can save your Analysis as an SFA file and open that file again just like an Spotfire Analysis File. The only difference is that when you open an SFA file, the resulting Analysis is not automatically associated with that same file. You can only save it by using **Save As** and enter a name. This helps you avoid accidentally over-writing the application file.

However, SFA files can also incorporate an application that is launched when opening the file. This application, implemented using scripts and possibly involving a visible user interface, could for instance establish database connections and perform preprocessing. The benefit is that you can fetch the data, preprocess it, and get exactly the initial visualization that you want—all by just double-clicking a file icon.

Please contact the Spotfire Central for more information on how to integrate code in SFA files.

## 10.2.4 Version 8.0 and Prior

For legacy reasons you can also save your Analysis as Spotfire DecisionSite 8.0 and version 7 files. There are two kinds of files used in older versions of Spotfire DecisionSite, SFS and XSF files.

### Spotfire File, version 8.0 (\*.sfs)

The 8.0 file is actually an 8.1 file with the possibility to be opened in a DecisionSite 8.0 environment. Data will always be embedded if you select this option (linked data is not supported).

### Spotfire File, version 7 (\*.sfs)

This format saves a binary SFS file in the same format as version 7.3 and is only recommended for files that must be backward compatible with Spotfire DecisionSite version 7. Linked data is not supported.

### XSF Files, version 7 (\*.xsf)

XSF files store exactly the same information as SFS files, but in an XML based format. Since the files are in text format rather than binary, they can be searched from a file system. XML also makes the structure of the content more clear.

## 10.2.5 Spotfire DecisionSite Mapping Files (SFM Files)

The Spotfire DecisionSite mapping file (\*.sfm) format first establishes a coordinate system, which relates the data set's coordinate system to that of the polygon set being defined. After that, a number of polygons are defined. A polygon is defined by a fill color, an origin point, a border color, the number of points and the X, Y, and Z coordinates of the points.

The Z coordinates are ignored, but they must be included. The format of the file as follows (with variables in italics):

```
COORDSYS xmin xmax ymin ymax zmin zmax
ADD
POLY fillcolor xorigin yorigin zorigin
!yes
numberofpoints
x1 y1 z1
x2 y2 z2
...
```

A sample file could look as follows:

```

COORDSYS 0.0 1.0 0.0 1.0 0.0 1.0
ADD
POLY LimeGreen 0.0 0.0 -0.02 0.0
!yes
5
0.677419 0.976261 0.0
0.680645 0.977745 0.0
0.680645 0.983680 0.0
0.677419 0.985163 0.0
0.677419 0.988131 0.0

```

The *env.sfm* file in the Spotfire DecisionSite distribution serves as an example of this background map format.

To map a data file to a Spotfire mapping file:

In your visualization, select the two axes from the data that serve as coordinates.

In the **Data and Background** tab in the **Properties** dialog, select an SFM file which has a coordinate system matching the coordinates in the axes file.

## 10.3 Publish Analysis to Library

### 10.3.1 Publishing Analyses to the Library

Using the Library, you and your colleagues can collaborate on the same Analysis, keeping everyone up to date. When publishing your Analysis, everything you save in a DecisionSite file (SFS) is stored in the Library.

**Note:** The Open from Library functionality is not available if you are working offline (without a connection to a server).

#### ► How to publish an Analysis to the DecisionSite Library:

1. Start DecisionSite and open a data set.
2. Select **File > Publish Analysis to Library...**  
Response: The first step of the wizard is displayed.  
Comment: This step lets you specify where in the Library your Analysis should be published. Navigate in the Library by using double-click on Library Sections and folders to the location you want publish your Analysis to. Only Analyses, folders, and Library Sections are visible in this view.
3. Enter the name of your Analysis in **Analysis title** as it will be displayed in the Library.  
Comment: It is important that the title is informative with regards to what the Analysis actually does. The title can be 50 characters at the most, and following characters are not supported:  
`\/ : * ? " < > + | $ & + = @ # % : ; , { [ ] } ^ ' ~ '`
4. Click **Next >**.  
Response: The second step of the wizard is displayed.  
Comment: This dialog lets you enter properties of the Analysis. By designating detailed properties, the organization and search capabilities in the Library are greatly enhanced.
5. Enter a **Description** of the functions of the Analysis.
6. Enter **Keywords** specific to the content of the Analysis.  
Comment: Keywords are separated by a semicolon, i.e., if you write "primary screening; quality" this will be two keywords, "primary screening" and "quality".
7. Use the **Data content** radio buttons to specify how you want to include your Analysis data. The options are:

"Linked (Load data from the data source)" Use this option when your data resides in a data source always accessible to all users with read access of your published Analysis.

"Embedded (Save the current data set in the Analysis)" Use this option when your data cannot be accessed by all users.

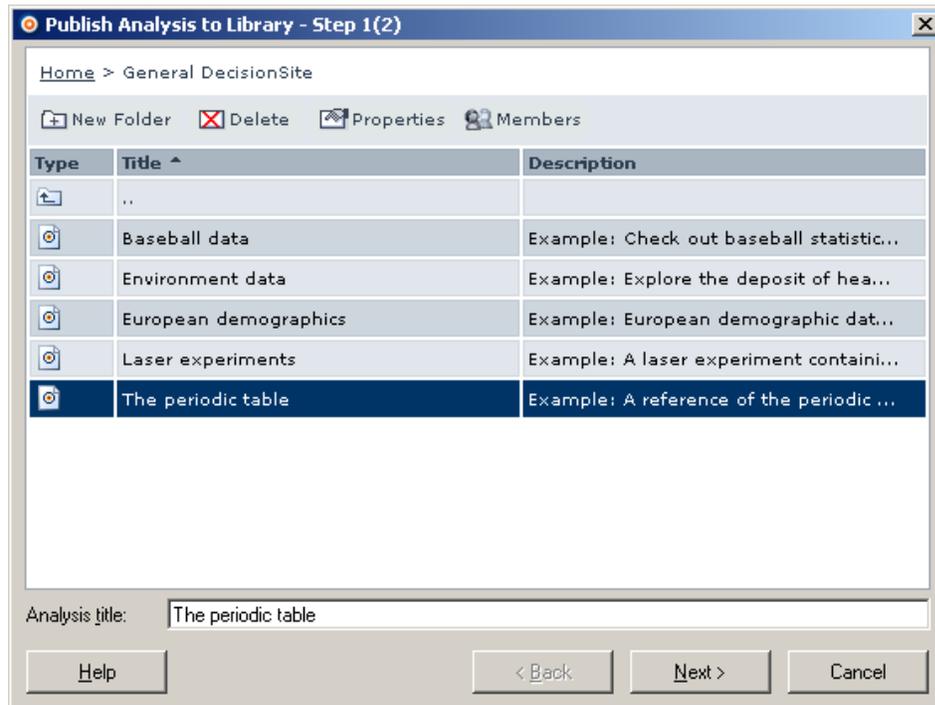
8. Click **Finish**.

Response: The Analysis is published and the confirmation dialog for the wizard is displayed. This dialog also includes a hyperlink to the Library folder containing the Analysis you just published, which you can click on to view the final result.

### 10.3.2 Publish Analysis to Library Wizard: Step 1(2)

This wizard helps you to publish your Analysis to the Library. Using the Library, you and your colleagues can collaborate on the same Analysis, keeping everyone up to date. Everything you save in your DecisionSite file (SFS) is stored in the Library.

This step lets you specify where in the Library your Analysis should be published. Navigate in the Library by using double-click on Library Sections and folders.



Library tab options	Description
<b>New folder</b>	Creates a new folder where you can publish your Analysis. A dialog will prompt you for the new folder name.
<b>Delete</b>	Deletes a selected item permanently from the Library.
<b>Properties</b>	Use Properties to edit the properties of selected Library items such as folders.
<b>Members</b>	Displays a list of all users with at least read access to the current Library Section. Each Library Section has its own set of access permissions.
<b>Analysis title</b>	The name of the Analysis as it will be displayed in the Library. It is important that the title is informative with regards to what the Analysis actually does. <b>Note:</b> The title can be 50 characters at the most, and the following characters are not supported:

\ / : \* ? " < > + | \$ & = @ # % ; , { [ ] } ^ ' ~ `

**Next**

Select the folder in which you want to publish your Analysis, and click **Next** to proceed to Publish Analysis to Library: Step 2(2). You can also select an existing Analysis if you want to overwrite it.

► **To reach the Publish Analysis to Library: Step 1(2) dialog:**

Click **File > Publish Analysis to Library...**

### 10.3.3 Publish Analysis to Library Wizard: Step 2(2)

This dialog lets you enter all properties of the Analysis. By using detailed properties, the organization and search capabilities in the Library are greatly enhanced.

Option	Description
<b>Analysis title</b>	The name of the Analysis as it will be displayed in the Library. This is the title you provided in the previous step.
<b>Description</b>	A description of the functions of the Analysis. The description could contain detailed information about the Analysis enabling quick overviews.
<b>Keywords</b>	Keywords specific to the content of the Analysis. Keywords are separated by a semicolon, i.e., if you write "primary screening; quality" this will be two keywords, "primary screening" and "quality". Keywords are used to enhance organization and search capabilities.
<b>Data content</b>	Use the Data content radio buttons to specify how you want to include your Analysis data. The options are: "Linked (Load data from the data source)" Use this option when your data resides in a data source always accessible to all users with read access of your published Analysis.

"Embedded (Save the current data set in the Analysis)" Use this option when your data cannot be accessed by all users. The "Linked (Load data from the data source)" option might be disabled. This happens when it is impossible to maintain a link.

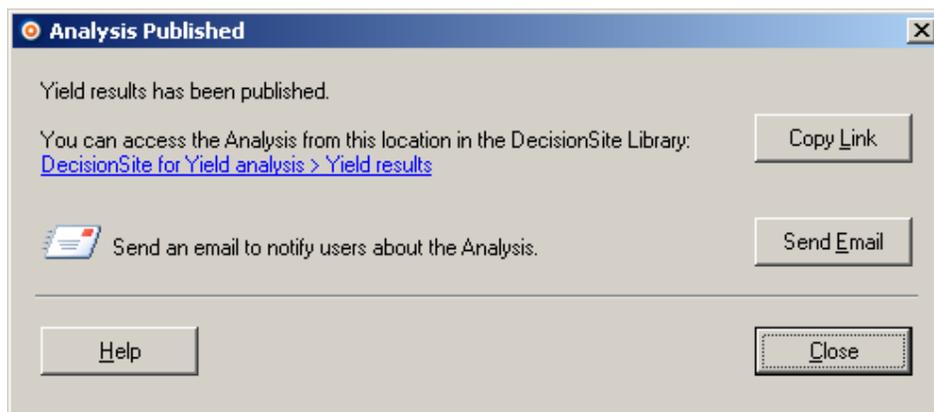
**Finish** Click **Finish** to publish your Analysis. When your Analysis is published, the Publish Analysis to Library: Analysis Published dialog is shown.

► **To reach the Publish Analysis to Library: Step 2(2) dialog:**

1. Click **File > Publish Analysis to Library...**
2. In the Publish Analysis to Library: Step 1(2), select Library location, enter a title, and click **Next >**.

### 10.3.4 Publish Analysis to Library: Analysis Published

As soon as you have saved your Analysis in the Library, a dialog window will appear with a confirmation that your Analysis is published. This dialog will also have a hyperlink to the Library folder containing the Analysis you just published, which you can click on to view the final result.



Option	Description
<b>Link</b>	Click on the link to open the Library folder containing your published Analysis.
<b>Copy Link</b>	Copies the link to the clipboard for later use. Using the link, the Analysis can easily be referenced in email discussions or from web pages or portals. Using the links retrieved with <b>Copy Link</b> , Analyses can be accessed from any web environment using the URL and name supplied.
<b>Send Email</b>	Launches a new email with your default email client.
<b>Close</b>	Closes the notification dialog

If you want to send an email notification, click on the **Send Email** button. This opens an email dialog where you may enter:

- **To:** The email address of one or more recipients, separated by comma or semicolon.
- **From:** Your own email address, mandatory.
- **Subject:** The subject of the email.
- **Comment:** Any additional text you wish to appear in the email.

► **To reach the Publish to Library Wizard: Analysis Published dialog:**

3. Click **File > Publish Analysis to Library...**
4. In the Publish Analysis to Library: Step 1(2), select Library location, enter a title and click **Next >**.
5. Edit the Analysis properties in Publish Analysis to Library: Step 2(2) and click **Finish**.

## 10.4 Publish Poster to Library

### 10.4.1 Publishing Posters to the Library

Publishing a DecisionSite Poster of your Analysis enables your colleagues to participate in your decision process from a Microsoft® Internet Explorer window.

**Note:** The Library functionality is not available if you are working offline (without a connection to a server).

**Note:** To open this tool and publish DecisionSite Posters, a license is required. Please contact your DecisionSite Administrator for more information.

► **How to publish a Poster to the DecisionSite Library:**

1. Start DecisionSite Client and open a data set.
2. Create the visualizations you want, and adjust the query devices to filter out data the way you want it in your Poster.
3. Select **File > Publish Poster to Library...**  
 Comment: You need a DecisionSite Poster license to see this option.  
 Response: The first step of the wizard is displayed. A dialog about unsupported features may appear. Please see below for more information.
4. Use the dialog to specify which parts of the Analysis you want to include in the Poster. Select the **Visualizations** you want to include.  
 Comment: See Poster Visualizations for more information. The visualizations in the Poster can be displayed either as a vertical list of large plots, or tiled smaller plots next to each other.
5. Select whether or not you wish to **Use list layout as default view mode**.  
 Comment: If the visualizations in DecisionSite Client are tiled, the Publish Poster to Library tool will try to emulate the layout by default. The person looking at the published Poster can switch between Tiled and List layout.
6. Select the **Query Devices** you want to enable data filtering with.  
 Comment: See the Poster Query Devices for more information.
7. Select which type of **Details-on-Demand** you want to present; either Table or Web search.  
 Comment: See Poster Details-on-Demand for more information.
8. When your Poster is designed, click **Next >**.  
 Response: The second step of the wizard is displayed.
9. Select the **Library Section** and folder you want the Poster to be published in.
10. Enter a **Poster title** as it will be displayed in the Library.  
 Comment: It is important that the title is informative with regards to what the Analysis actually does. The title can be 50 characters at the most, and the following characters are not supported:  
 \ / \* ? " < > + | \$ & = @ # % : ; , { [ ] } ^ ' ~ ` `
11. Click **Next >**.  
 Response: The third step of the wizard is displayed.

Comment: This dialog lets you enter properties of the Poster. By designating detailed properties, the organization and search capabilities in the Library are greatly enhanced.

12. Enter a **Description** of the purpose of the Poster.
13. Enter **Keywords** specific to the content of the Poster.

Comment: Keywords are separated by a semicolon, i.e., if you write "primary screening; quality" this will be two keywords, "primary screening" and "quality".

14. Use the **Data content** radio buttons to specify how you want to include your Poster data. The options are:

"Linked (Load data from the Information Link)" Use this option when your data resides in an Information Link accessible to all users with read access to your published Poster.

"Embedded (Save the current data set in the Poster)" Use this option when your data cannot be accessed by all users.

15. Click **Finish**.

Response: The Poster is published and the confirmation dialog for the wizard will appear, asking if you want to send an email notification to your colleagues. This dialog also includes a hyperlink to the Library folder containing the Poster you just published, which you can click on to view the final result.

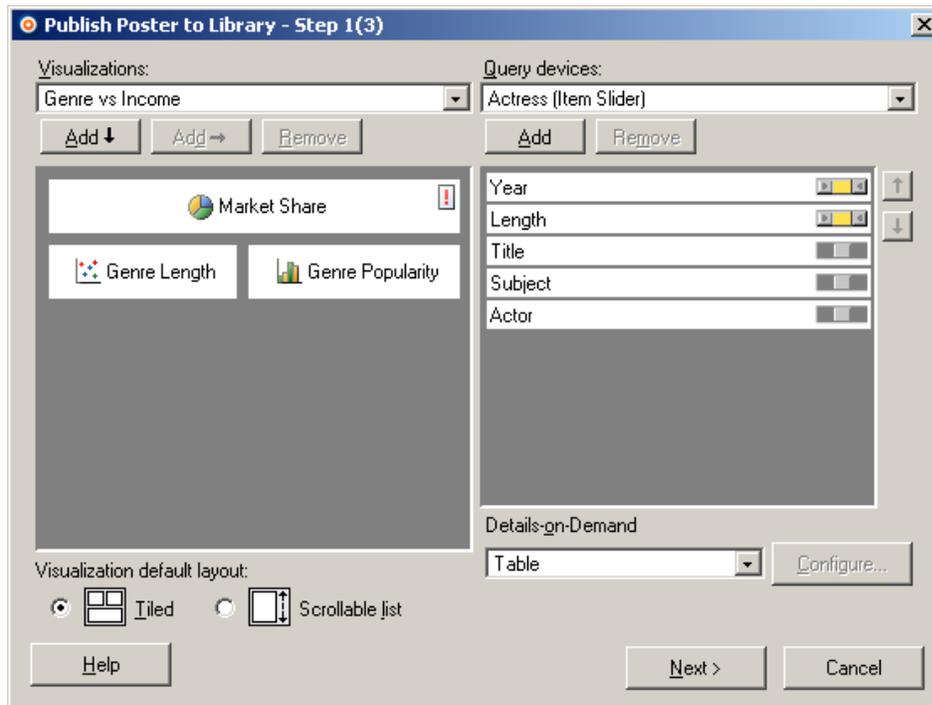
## 10.4.2 Publish Poster to Library Wizard: Step 1(3)

Using this wizard you can publish a DecisionSite Poster of your Analysis, enabling your colleagues to participate in the decision process from a Microsoft® Internet Explorer window.

Use Spotfire DecisionSite Client to create the visualizations you want, and adjust the query devices to filter out the data you want in your Poster. Launch the Publish Poster wizard by selecting **File > Publish Poster to Library...**

**Note:** You need a license for DecisionSite Posters to use this feature.

Use the dialog to specify which parts of the Analysis you want to include in the Poster.



Option	Description
<b>Visualizations</b>	Select the visualizations of your Analysis you want to include in

<b>Visualization default layout</b>	<p>your Poster. See Poster Visualizations for more information.</p> <p>The visualizations in the Poster can be displayed either as a scrollable list of large plots, or tiled smaller plots next to each other. Select which default layout you want.</p> <p>A exclamation mark icon means that some aspect of that visualization is not supported in DecisionSite Posters. Move the mouse cursor over the icon to display more information.</p>
<b>Query devices</b>	Select the Query Devices you want to enable data filtering with. See Poster Query Devices for more information.
<b>Details-on-Demand</b>	Select which type of Details-on-Demand that you want to present; either Table or Web search. See Poster Details-on-Demand for more information.
<b>Next</b>	When your Poster is designed, click <b>Next &gt;</b> to proceed publishing.

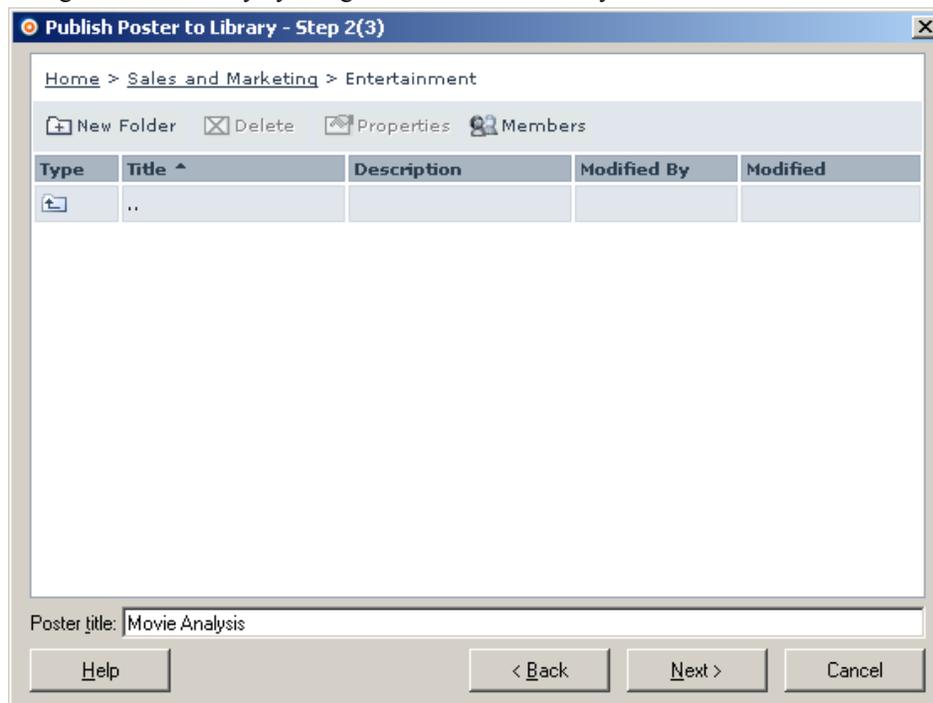
For information about which features can be included in a DecisionSite Poster, see Poster Supported Features.

► **To reach the Publish Poster to Library – Step 1(3) dialog:**

Click **File > Publish Poster to Library...**

### 10.4.3 Publish Poster to Library Wizard: Step 2(3)

In this step you specify where in the Library your DecisionSite Poster should be published. Navigate in the Library by using double-click on Library Sections and folders.



Options	Description
<b>New Folder</b>	Creates a new folder where you can publish your Poster. A dialog will prompt you about the new folder name.
<b>Delete</b>	Deletes a selected item permanently from the Library.

<b>Properties</b>	Use Properties to edit the properties of selected Library items such as folders.
<b>Members</b>	Lists all users who have at least read access to the current Library Section. Each Library Section has its own set of access permissions.
<b>Poster title</b>	The name of the Poster as it will be displayed in the Library. It is important that the title is informative with regards to what the Poster actually does. Note: The title can be 50 characters at the most, and the following characters are not supported: \\ / : * ? " < > +   \$ & = @ # % ; , { [ ] } ^ ' ~ `
<b>Next</b>	Select the folder in which you want to publish your Poster and click Next to proceed to Publish Poster to Library – Step 3(3). You can also select an existing Poster if you want to overwrite it.

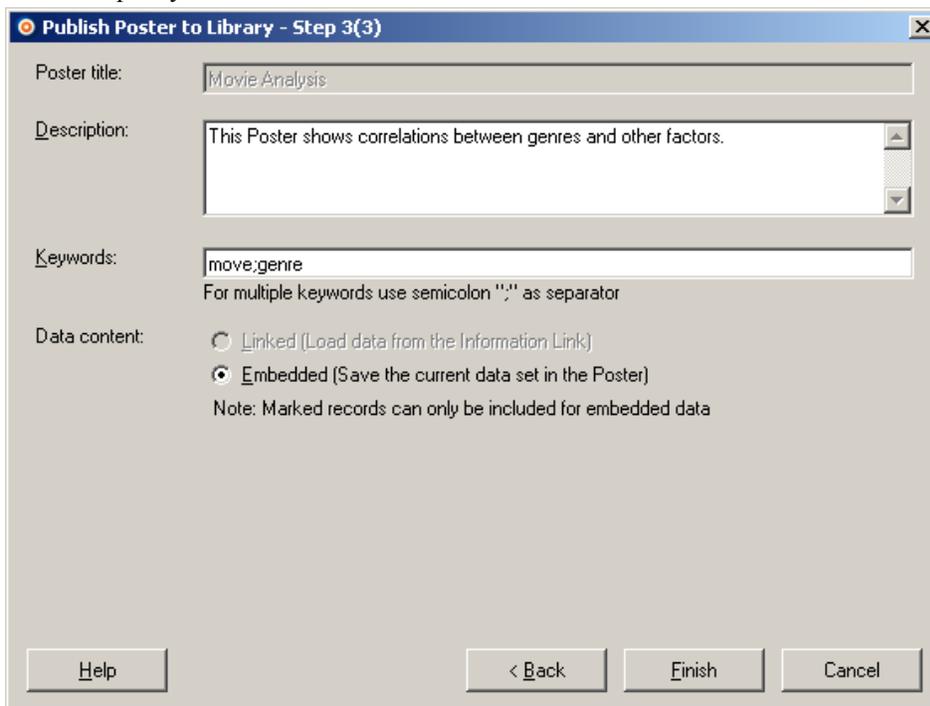
► **To reach the Publish Poster to Library – Step 2(3) dialog:**

1. Click **File > Publish Poster to Library...**
2. Design your DecisionSite Poster in Publish Poster to Library – Step 1(3) and click **Next >**.

## 10.4.4 Publish Poster to Library Wizard: Step 3(3)

This dialog lets you enter properties of the Poster. By using detailed properties, the organization and search capabilities in the Library are greatly enhanced.

You also specify how the data should be handled here. See Poster data for more information.



Option	Description
<b>Poster title</b>	The name of the Poster as it will be displayed in the Library. This is the title you provided in the previous step.
<b>Description</b>	A description of the functions of the Poster. The description could

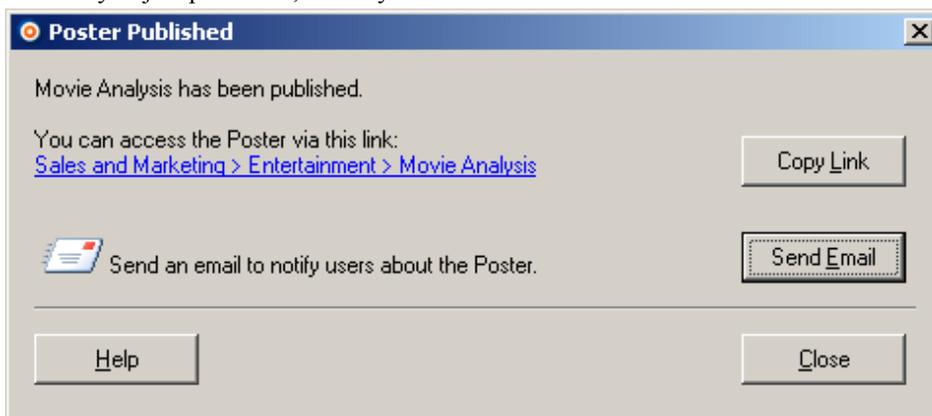
	contain detailed information about the Poster enabling a quick overview.
<b>Keywords</b>	Keywords specific to the content of the Poster. Keywords are separated by a semicolon, i.e., if you write "primary screening; quality" this will be two keywords, "primary screening" and "quality". Keywords are used to enhance organization and search capabilities.
<b>Data content</b>	Use the Data content radio buttons to specify how you want to include your Poster data. The options are: "Linked (Load data from the Information Link)" Use this option when your data resides in an Information Link accessible to all users with read access to your published Poster. "Embedded (Save the current data set in the Poster)" Use this option when your data cannot be accessed by all users. The "Linked (Load data from the Information Link)" option will be disabled unless an Information Link was used to open the data. See Poster Data for more information.
<b>Finish</b>	Click Finish to publish your Poster. When your Poster has been published, Publish Poster to Library Wizard: Poster Published is shown, in which you can send emails inviting colleagues to join your analysis.

► **To reach the Publish Poster to Library – Step 2(2) dialog:**

1. Click **File > Publish Poster to Library...**
2. Design your DecisionSite Poster in Publish Poster to Library Wizard: Step 1(3) and click **Next >**.
3. Edit the Poster properties in Publish Poster to Library Wizard: Step 2(3) and click **Next >**.

## 10.4.5 Publish Poster to Library: Poster Published

As soon as you have published your Poster in the Library, a dialog will appear asking if you want to send an email notification to your colleagues. This dialog will also have a hyperlink to the item you just published, which you can click on to view the final result.



Option	Description
<b>Link</b>	Click the link to open your Poster and view the result.
<b>Copy Link</b>	Copies the link to the clipboard for later use. Using the link, the Poster can easily be referenced in email discussions or from web

	pages or portals. Using the links retrieved with Copy Link, Posters can be accessed from any web environment using the URL and name supplied.
<b>Send Email</b>	Opens a dialog from which you can send an email with a link to the Poster.
<b>Close</b>	Closes the notification dialog

If you want to send an email notification, click on the **Send Email** button. This opens an email dialog where you may enter:

- **To:** The email address of one or more recipients, separated by comma or semicolon.
- **From:** Your own email address, mandatory.
- **Subject:** The subject of the email.
- **Comment:** Any additional text you wish to appear in the email.

A new DecisionSite Poster, *Movie Analysis*, has been published to the DecisionSite Library. Take a look and tell me what you think.

(Click [here](#) to login to the full Spotfire DecisionSite Poster)

[Login information](#)

Spotfire DecisionSite Poster

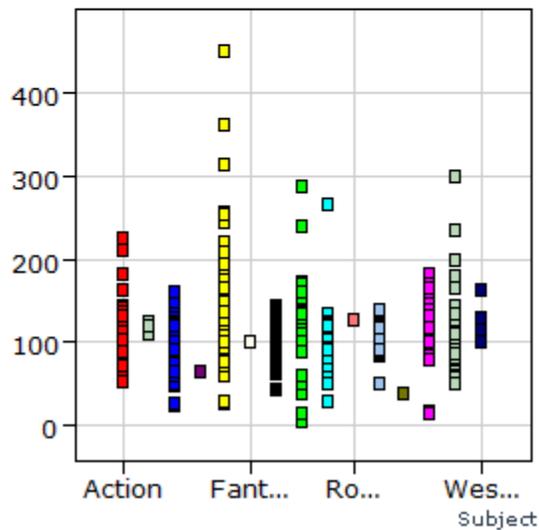
## Movie Analysis

*blade*, 2004-12-06

This Poster shows correlations between genres and other factors.

Clippings

**Genre Length**  
Length



Example of Poster notification email.

► **To reach the Publish Poster to Library Wizard: Poster Published dialog:**

1. Click **File > Publish Poster to Library...**
2. Design your DecisionSite Poster in Publish Poster to Library Wizard: Step 1(3) and click **Next >**.
3. In the Publish Poster to Library Wizard: Step 2(3), select Library location, enter a title, and click **Next >**.

4. Edit the Poster properties in Publish Poster to Library Wizard: Step 3(3) and click **Finish**.

## 10.4.6 Poster Content

### 10.4.6.1 Poster Visualizations

You can include one or several visualizations in your Poster. The visualizations in the Poster can be displayed either as a vertical list of large plots, or tiled smaller plots next to each other. Select whether or not you wish to **Use list layout as default view mode**.

If you choose to include several visualizations and not use the list layout as default, you can create a layout for how they should be displayed: horizontally, vertically, or a combination of the two. The default layout will try to mimic the layout as seen in DecisionSite.

Note: Not all visualizations available in Spotfire DecisionSite can be used in a Poster. Please see Poster Supported Features for more information.

#### ► How to include visualizations:

1. Select a visualization from the Visualizations drop-down list.
2. Mark a cell in the layout section (below the drop-down list) by clicking on it.
3. Click on the  button to add the new visualization below the marked cell, or click on the  button to add the new visualization adjacent to the marked cell.

#### ► How to remove visualizations:

1. Mark a cell in the layout section (below the drop-down list) by clicking on it.
2. Click on the  button to remove the visualization from the layout section. The visualization will be placed in the Visualizations drop-down list, from where you can add it again later if you wish.

### 10.4.6.2 Poster Query Devices

You can include one or several query devices in your Poster. If you choose to include several query devices, you can sort them in any order you like. It is recommended that you include only those query devices that are needed, so as to keep the Poster simple and straightforward.

A query device that has been set to specific values in DecisionSite will keep these settings when the Poster is opened. Note that the entire data set will still be transferred to the Poster, so no data will be lost.

#### ► How to include query devices:

1. Select the query device you want to add from the Query devices drop-down list.
2. Click on the query device in the layout section, beneath which you want the new query device to be inserted.
3. Click on the Add button to include the new query device.
4. Repeat steps 1 to 3 for each query device you want to include.
5. If you want to remove a query device, select it from the list by clicking on it, and then click on the Remove button (or press the Delete key). Tip: Press Ctrl+A to select all query devices, or use Ctrl+Click or Shift+Click to select several query devices at once.
6. If you want to change the order of the included query devices, select one by clicking on it, and move it up or down by clicking on the  or  button.

### 10.4.6.3 Poster Details-on-Demand

There are two kinds of Details-on-Demand windows that can be included in the Poster: Table or Web Search. Select the one you want from the drop-down list.

#### Table

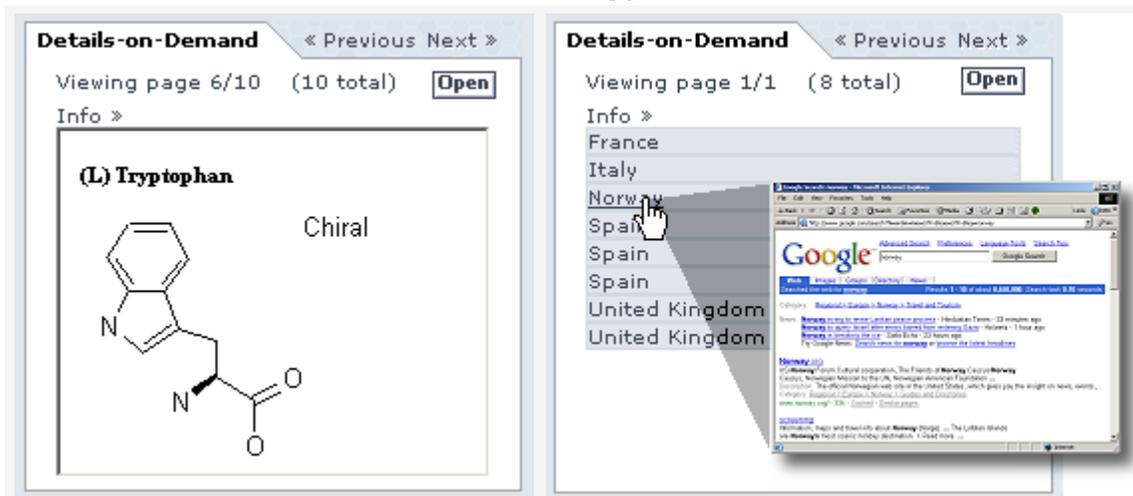
This option includes a standard Details-on-Demand window in which the information about marked records in the visualization is displayed in a table.

#### Web Search

The Web Search Details-on-Demand can be configured to send a query to an external web site to search for information about marked records. For example, you can link to a search engine such as Google, or an MDL ISIS database in order to view molecular structures.

You can create several customized Details-on-Demand web searches, which will appear in the drop-down list. Either you select a pre-configured one from the drop-down list, or you select the **Add new...** option which lets you configure a new Web Search Details-on-Demand.

**Note:** The DecisionSite administrator can setup preconfigured ISIS Direct Details-on-Demand options from the Library Administrator tool. Such options will appear in the drop-down menu automatically for all Poster authors, and can easily be selected when publishing a new Poster. Please see the *DecisionSite Installation and Upgrade manual* for information on how to do this.



A Web Search Details-on-Demand can be set to show the search results directly in the Poster. This is useful for molecular structures among other things.

A Web Search Details-on-Demand can also be set to show links for the selected records, which launches a separate browser search window when clicked.

Whether the search results should be displayed directly in the details-on-demand window of the Poster, or displayed in a new browser window, can be switched from within the Poster. You cannot configure this aspect from the **Publish Poster...** wizard.

#### ► To create a new custom Web Search:

1. Select **Add new...** from the drop-down list. A dialog appears.
2. Edit the **URL** to the web link.  
Comment: For example, open [www.google.com](http://www.google.com) and make a search for "replaceme". Then copy the entire URL "<http://www.google.com/search?hl=en&ie=UTF-8&oe=UTF-8&q=replaceme>" and paste it into the Web Search field.
3. Enter a dollar sign within curly brackets {\$} as a placeholder for the ID variable that will be inserted from the Poster.  
Comment: For example, replace the "replaceme" variable above with {\$} so that the URL reads "[http://www.google.com/search?hl=en&ie=UTF-8&oe=UTF-8&q={\\$}](http://www.google.com/search?hl=en&ie=UTF-8&oe=UTF-8&q={$})".

Comment: Anything you enter between the left bracket and the dollar sign will be placed before each ID in the query. Similarly, anything placed between the dollar sign and the right bracket will be placed after each ID in the query.

4. Select the **ID column** which contains the information you want to use as input to the web search.  
**Note:** If you intend to link to an ISIS database, use the column with the Compound ID.
5. Enter a Name for the custom Details-on-Demand you have just configured. This is the name which will appear in the drop-down list.
6. Click **OK**.

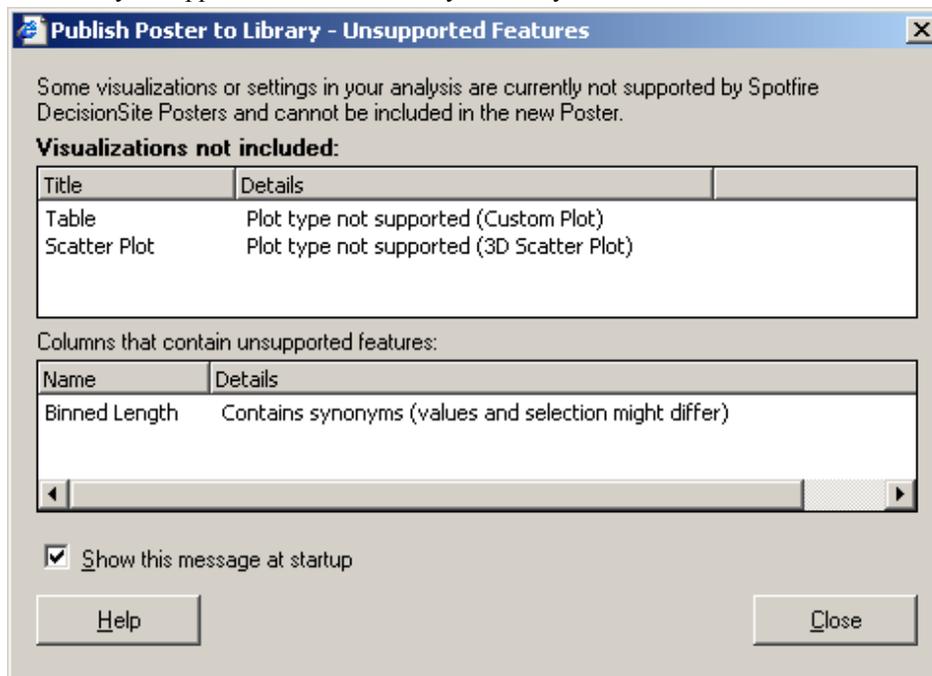
► **To configure a previously created Web Search:**

1. Select the Web Search you want from the drop-down list.
2. Click on the **Configure...** button.
3. The dialog opens and you can configure the web search.
4. Click **OK** when you are done.

#### 10.4.6.4 Poster Supported Features

Not all functionality available in Spotfire DecisionSite Client can be used in a Poster. When you create a Poster and your Analysis contains unsupported features, a notification dialog will be displayed with information about unsupported features.

**Note:** Only unsupported features used in your Analysis are shown.



Option	Description
<b>Visualizations not included</b>	All unsupported visualizations in your Analysis are listed here with the details of the reason. You will not be able to use these visualizations in your Poster.
<b>Columns that contain unsupported features</b>	Each column with a formatting not supported is listed here. The columns can be used in the Poster. However, no formatting will be applied. Also, some binned columns from older versions are not supported.

The table below explains which features and settings can be transferred to a Poster.

**Note:** Since version 8.0, DecisionSite Client includes a new type of Bar Chart, which replaces Bar Charts and Histograms version 7.x. Bar Charts and Histograms of version 7.x must be converted to 8.x bar charts in DecisionSite Client before being published as a Poster.

**Note:** All Spotfire DecisionSite users can launch Spotfire DecisionSite Client from within a Poster. This will provide full DecisionSite functionality.

**Tip:** Move the mouse pointer over the visualization template in the Create Poster dialog to display a ToolTip text which states any unsupported properties of the visualization.

Aspect	Supported	Comment
<b>Visualizations</b>		
2D Scatter Plot	Yes	<b>Note:</b> All available coloring options are not supported. See 2D Scatter Plot Markers below for more information.
3D Scatter Plot	No	
Bar Chart	Yes	
Bar Chart version 7.x	No	Needs to be converted to Bar Chart 8.x in DecisionSite Client.
Histogram version 7.x	No	Needs to be converted to Bar Chart 8.x in DecisionSite Client.
Line Chart	No	
Profile Chart	Yes	
Pie Chart	Yes	
Heat Map	Yes	Heat maps using a mixture of color ranges and categorical values, which became possible with DecisionSite Client 9.0, are not supported by DecisionSite Posters. Change the coloring to a traditional continuous range prior to publishing the Poster, if needed.
Table	No	
<b>General Visualization Properties</b>		
X and Y-axis labels	Yes	Labels will always appear in the Poster. Horizontal or Vertical labels can be set, but no other label settings will be transferred.
X and Y-axis grid	Yes	
Visualization Annotations	Yes	
Marked Records	Yes	Only if the data set is embedded in the Poster.
Data Range	Yes	
Margins	No	Margins will not be transferred to the Poster, but ToolTips are available on labels that are abbreviated.
HTML Details-on-Demand	No	You can create a custom Web Search when publishing the Poster.

Statistical Measures	No	
Show Deselected	No	
Trellis	Yes	
Zoom	Yes	
<b>Query Devices</b>		
Range Sliders	Yes	
Check Boxes	Yes	
Radio Buttons	Yes	
Item Slider	Yes	
Full Text Search	Yes	Simple Search will be interpreted as Regular Expression.
<b>Column</b>		
Column Annotations	Yes	Shown as a tooltip icon in the Poster query devices.
<b>Column Transformation</b>		
Original Scale	Yes	
Log Scale	Yes	Also note that Categorical Coloring on a transformed column is not supported. In such a case the coloring will be changed to Fixed color.
Other Scale...	No	Will be transformed to Original Scale, and the selection is set to All.
<b>2D Scatter Plot Properties</b>		
X and Y-axis Column	Yes	
Background Image	Yes	Must be a BMP, PNG or JPG image.
Background Image Position	Yes	
<b>2D Scatter Plot Markers</b>		
Fixed Color	Yes	
Continuous Color	Yes/No	<b>Note:</b> Only continuous color schemes with two gradients, ranging from "min" to "max" are supported by Posters. Three color gradients or advanced coloring is not supported. See Advanced Color below for more information.
Categorical Color	Yes	Categorical Coloring on a transformed column is

Advanced Coloring	No	not supported. In such a case the coloring will be changed to Fixed color.  The scatter plot in Posters only supports purely categorical color schemes, or continuous color schemes with one range (from "min" to "max"). If there is a mixture of ranges and categorical values in the scatter plot, or if it uses more than one color range, or if the scatter plot uses one color range with starting/ending points that are not "min" and "max" respectively, then the coloring is not supported. This will give a warning when trying to publish the scatter plot. The scatter plot can still be published as a Poster, but the colors will most likely be wrong.
Shape	Yes	Squares, Circles and Triangles are supported. All other markers will be transformed to filled squares.
Size	Yes	
Size By	Yes	
Drawing Order	No	
Jitter	Yes	
Rotate	No	
Line Connection	Yes	
<b>Bar Chart Properties</b>		
X-Axis Column	Yes	
Background Image	Yes	Must be a BMP, PNG or JPG image.
<b>Bar Chart Bars</b>		
Fixed Color	Yes	
Categorical Color	Yes	Categorical Coloring on a transformed column is not supported. In such a case the coloring will be changed to Fixed color.
Show deselected	No	
Width	Yes	
Outline Bars	Yes	
Labels	No	No text labels above the bars, however, bar chart tool tips displays the information found in DecisionSite Client bar labels.
Stacked bars	Yes	
Side-by-side bars	Yes	
100% stacked bars	No	
100% side-by-side bars	No	
Drop empty bars	Yes	

Binning	Yes	The number of bins in DecisionSite Client will be the same in DecisionSite Posters.
Sort bars	Yes	
<b>Profile Chart Properties</b>		
Numeric Columns	Yes	Supported although not together with Date, DateTime, Time.
Date, DateTime, Time Columns	Yes	Supported although not together with Numeric.
Same Scale for All	Yes	Only supported when all columns are of the same type of scale, that is, either Original scale or Log scale.
String Columns	Yes	
Background Image	Yes	Must be a BMP, PNG or JPG image.
<b>Profile Chart Profiles</b>		
Fixed Color	Yes	
Continuous Color	Yes	
Categorical Color	Yes	Categorical Coloring on a transformed column is not supported. In such a case the coloring will be changed to Fixed color.
Individual Scale	Yes	
Same Scale	Yes	
Labels	No	
Line Width	No	
Line Width By	No	
Break on Empty	Yes	
<b>Pie Chart Properties</b>		
X-Axis Column	Yes	
Y-Axis Column	Yes	
Background Image	Yes	
<b>Pie Chart Pies</b>		
Fixed Color	Yes	
Categorical Color	Yes	
Show deselected	No	
Average Color	Yes	Not on String Columns
Number of Color Bands	No	
Size	Yes	

Fixed Size	Yes	
Size by Records Count	Yes	
Size by Average	Yes	Only for Numeric columns.
Size by Sum	Yes	Only for Numeric columns.
Labels	No	DecisionSite Posters uses ToolTips to display this information instead.
Jitter	No	
<b>Heat Map Properties</b>		
Column colors	Yes	
Color range	Yes	
Advanced colors	No	If the heat map uses a mixture of continuous color ranges and categorical values it cannot be published by the Poster Designer.
Show deselected	Yes	
Row labels	Yes	
Dendrogram	Yes	

Differences between DecisionSite Client and DecisionSite Posters:

**Bar Charts:**

- In DecisionSite Client labels are used to display information about bars. In DecisionSite Posters this information is displayed using ToolTips when hovering over a bar.

**Pie Charts:**

- In DecisionSite Client labels are used to display information about sectors. In DecisionSite Posters this information is displayed using ToolTips when hovering over a sector.
- In DecisionSite Client, marking is displayed as a continuous line around the edge of a pie. In DecisionSite Posters, marking is indicated as separate lines beside each sector that has records included in the marking.

**Heat Maps:**

- Cluster node similarity ToolTip is not supported.
- The dendrogram menu is not supported.
- Cannot zoom in column dendrogram.

**Number Formatting:**

- Combining scientific notation and parentheses negative format will force negative format to default.
- Combining the parentheses negative format and default number of decimals will force two decimals. To avoid this, set the number of decimals explicitly in DecisionSite Client.
- Combining the thousands separator and default number of decimals will force two decimals. To avoid this, set the number of decimals explicitly in DecisionSite Client.

**Shared Ranges:**

- Some plots that use Shared Ranges look different in Posters compared to DecisionSite Client. In DecisionSite Client 9.0 and forward, shared ranges are only shared between

columns of compatible types. In Posters, as well as in earlier versions of DecisionSite Client, shared ranges could be applied to a mixture of column types.

- Compatible types are:
  - A) Numeric columns: integer, real
  - B) String columns
  - C) Date columns: date, timestamp
  - D) Time columns

In other words, if two incompatible columns use the same color scheme, their color ranges will be calculated individually in DecisionSite Client 9.0, but DecisionSite Posters will still use shared ranges.

### 10.4.6.5 Poster Data

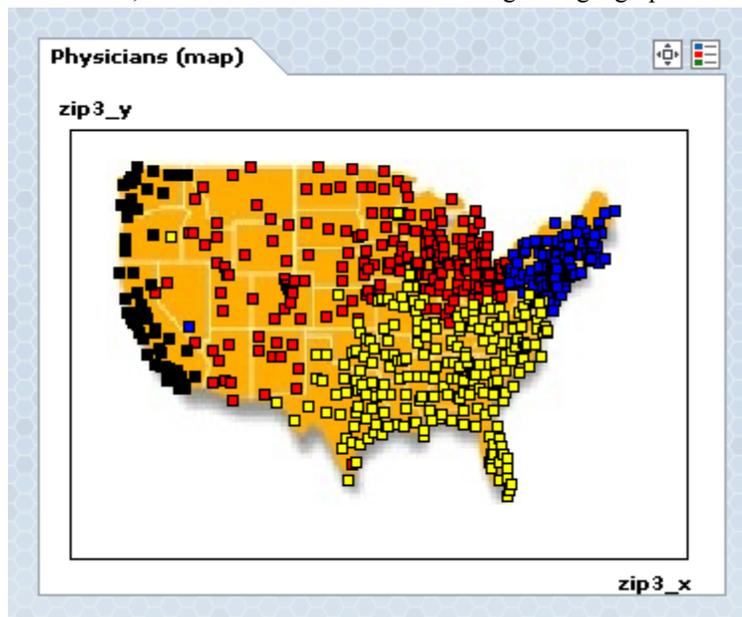
You can choose from two kinds of data links. One choice is to embed the data into the Poster. That way, the data is stored within the Poster, and will not be altered if you later change the original data set.

The other alternative is only available if you have imported data into Spotfire DecisionSite by use of Information Links. If created in this way, you can choose to save the Poster with an active data link to the original data so that the Poster will always be based on the latest data, and will be (automatically) updated every time a user opens the Poster. If the range of the data should become larger after the publishing date, the entire data set will still be opened in the Poster regardless of the initial query device settings, etc.

**Note:** It is not possible to use the linked data option if you have added a column (binned, add columns, calculation, etc.) to a data set imported via Information Links. Also, information about which records are currently marked cannot be stored in a Poster with linked data, this is only possible using embedded data.

### 10.4.6.6 Poster Background Images

Scatter Plots, Bar Charts, Profile Charts and Pie Charts can display a background image behind the markers, which can be useful when working with geographical maps, etc.



BMP, PNG and JPG images that are used as background images in DecisionSite Client can be published in a Poster; other formats are invalid. Position properties set in DecisionSite Client are carried over to the Poster to align the image properly.

Background Images are particularly useful when running Spotfire Map Interaction Services. This product gives users an easy way of linking data that includes both longitudinal and

latitudinal information to geographic images and data. It also provides a means to dynamically interact with geographic data within Spotfire DecisionSite.

## 10.5 Microsoft PowerPoint Presentation

### 10.5.1 Exporting Visualizations to PowerPoint

The Microsoft® PowerPoint® Presentation tool exports the selected visualizations to PowerPoint®. Each visualization is added as a new slide along with the annotation, legend and title.

**Tip:** Also note, other Export options can be found under the File menu.

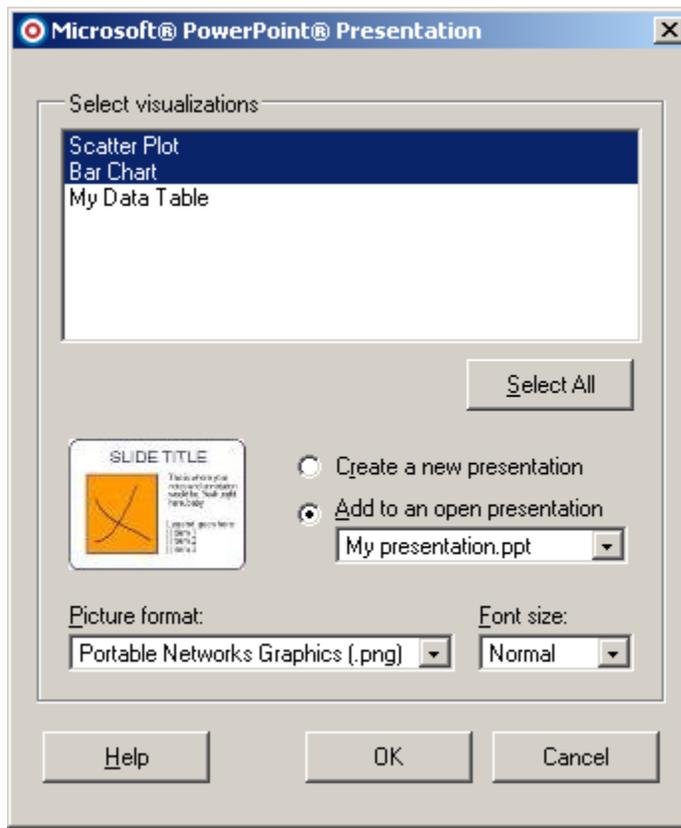
#### ► To export visualizations to PowerPoint®:

1. Create visualizations in Spotfire DecisionSite.
2. If necessary, edit the titles and annotations of the visualizations.
3. Select **File > Export > Microsoft® PowerPoint® Presentation...**  
Response: The Microsoft® PowerPoint® Presentation dialog is displayed.
4. Click to select the visualizations you want to export.  
Comment: To select all visualizations click **Select All**. For multiple selection, press **Ctrl** and click on the desired visualizations or click one visualization and drag to select the subsequent ones.
5. Select if you want to **Create a new presentation** or **Add to an open presentation**.
6. If desired, select a different type of **Picture format**.  
Comment: The visualization can be exported in a EMF, JPG or PNG format.
7. If desired, change the **Font size** of the exported labels.
8. Click **OK**.

Response: If Create a new presentation is chosen, PowerPoint® is started and the selected visualizations are shown in a new presentation. If Add to an open presentation is chosen, the selected visualizations are appended to the end of an open presentation.

**Note:** Microsoft® PowerPoint® must be installed on the machine for this tool to be used.

## 10.5.2 Microsoft PowerPoint Presentation Dialog



Option	Description
<b>Select visualizations</b>	The list box shows the titles of all visualizations available for PowerPoint® export. Click a visualization name to include the visualization in the PowerPoint® presentation. For multiple selection, press <b>Ctrl</b> and click the desired visualizations.
<b>Select All</b>	Click this button to select all available visualizations.
<b>Create a new presentation</b>	This exports the Spotfire DecisionSite visualizations to a new PowerPoint® presentation.
<b>Add to an open presentation</b>	This appends pictures of the selected visualizations as new slides at the end of an open presentation. If several presentations are open, select one from the drop-down list box.
<b>Picture format</b>	Select a visualization output format from the drop-down list. Choose from PNG, JPG, or EMF formats.
<b>Font size</b>	Select whether to use a Small, Normal, Large or Extra Large font size when exporting to PowerPoint®. The selection made here affects all labels in the visualization, including the axis labels and the legend.

The image in the dialog shows what the PowerPoint® presentation might look like.

► **To reach the Microsoft® PowerPoint® Presentation dialog:**

Select **File > Export > Microsoft® PowerPoint® Presentation...**

## 10.6 Microsoft Word Presentation

### 10.6.1 Exporting Visualizations to Word

The Microsoft® Word Presentation tool exports the selected visualizations to Microsoft® Word. Each visualization is added to a new page in a Word document, along with the annotation, legend and title.

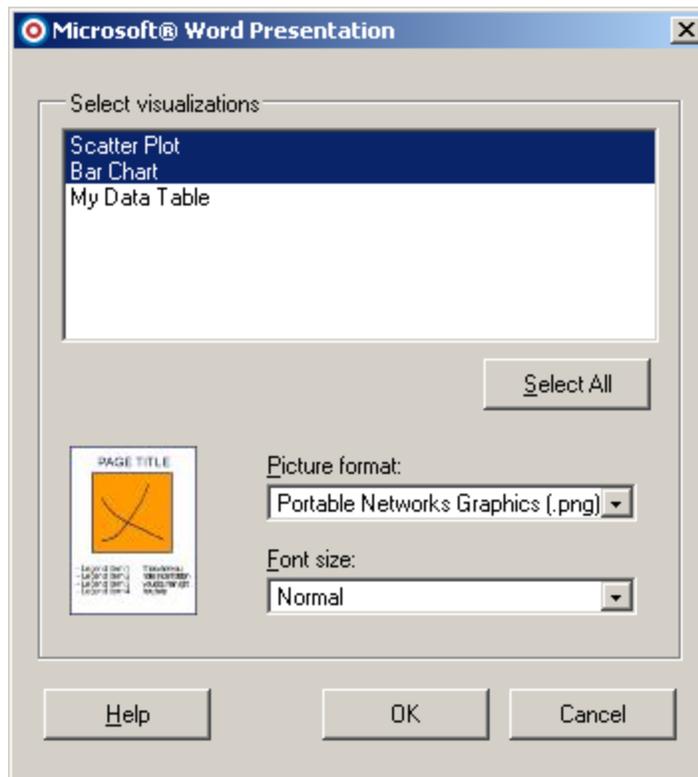
**Tip:** Also note, other Export options can be found under the File menu.

► **To export visualizations to Word:**

1. Create visualizations in Spotfire DecisionSite.
2. If necessary, edit the titles and annotations of the visualizations.
3. Select **File > Export > Microsoft® Word Presentation...**  
Response: The Microsoft® Word Presentation dialog is displayed.
4. Click to select the visualizations you want to export.  
Comment: To select all visualizations click **Select All**. For multiple selection, press **Ctrl** and click on the desired visualizations or click one visualization and drag to select the following.
5. If desired, select a different type of **Picture format**.  
Comment: The visualization can be exported in a EMF, JPG or PNG format.
6. If desired, change the **Font size** of the exported labels.
7. Click **OK**.  
Response: Word is started and a new document including the selected visualizations is displayed.

**Note:** Microsoft® Word must be installed on the machine for this tool to be used.

### 10.6.2 Microsoft Word Presentation Dialog



Option	Description
<b>Select visualizations</b>	The list box shows the titles of all visualizations available for Word export. Click a visualization name to include the visualization in the Word report. For multiple selection, press <b>Ctrl</b> and click the desired visualizations.
<b>Select All</b>	Click this button to select all available visualizations.
<b>Picture format</b>	Select a visualization output format from the drop-down list. Choose from PNG, JPG, or EMF formats.
<b>Font size</b>	Select whether to use a Small, Normal, Large or Extra Large font size when exporting to Word. The selection made here affects all labels in the visualization, including the axis labels and the legend.

The image in the dialog shows what the Word report might look like.

► **To reach the Microsoft® Word Presentation dialog:**

Select **File > Export > Microsoft® Word Presentation...**

## 10.7 Export as Web Page

### 10.7.1 Exporting Visualizations as a Web Page

The Export as Web Page tool exports the current visualizations as an HTML file and a set of images. You can also include the legend, annotations, the SQL query involved and information on the currently marked records.

**Tip:** Also note, other Export options can be found under the File menu.

► **To export visualizations as a web page:**

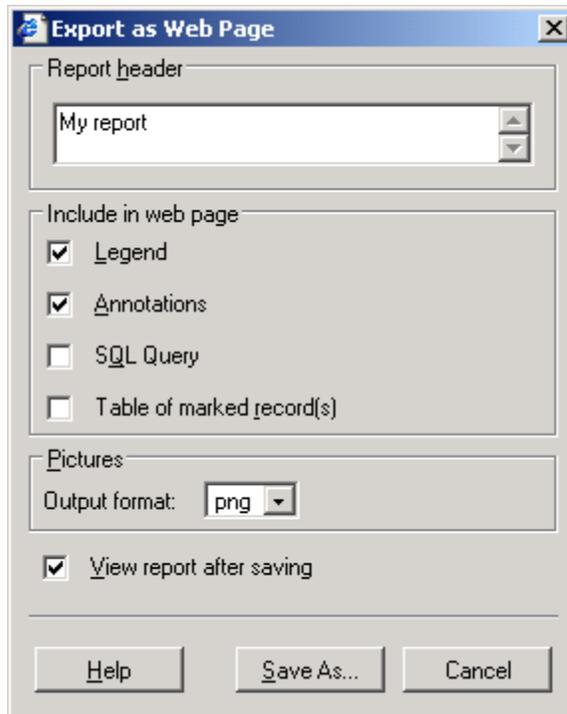
1. Create the desired visualizations and set the query devices. If you want to mark any records, do so now.
2. If you use multiple visualizations, then organize these so that they are all visible and of the right proportions.

Comment: The visualizations will be included in the report just the way you see them in the visualization area. If the visualizations are tiled, then they will appear tiled in the report. Use **Window > Auto Tile** to automatically organize your visualizations.

3. Select **File > Export > Web Page...**  
Response: The Export as Web Page dialog is displayed.
4. Enter a report header. This text will appear at the top of the report.
5. Check the options you wish to include in the report.
6. Select a graphic file format for the exported images.
7. Click **Save As...**

Response: You will be prompted to select a file name and folder for the report. The report is now saved as an HTML file in the directory you specified. A subdirectory with the same name as the HTML file is created in which all the pictures are stored. To send the report to someone, you need to copy both the HTML file and its corresponding subdirectory. If you selected to **View report after saving option**, your report will be displayed in a browser.

## 10.7.2 Export as Web Page Dialog



Option	Description
<b>Report header</b>	This text will appear at the top of the report.
<b>Legend</b>	Select this box to include the legend in the report.
<b>Annotations</b>	Select this box to include visualization annotations in the report. Note that column annotations are not included.
<b>SQL Query</b>	Select this box to include the SQL query (corresponding to the current query device settings) in the report.
<b>Table of marked record(s)</b>	Select this box to include a table with the currently marked records.
<b>Output format</b>	Select a graphics file format for the images included in the report.
<b>View report after saving</b>	Select this box if you want to launch the report in your default browser after it has been saved.
<b>Save As...</b>	Click here when you have made the desired settings. You will be asked to specify a name and folder for the generated HTML file.

► **To reach the Export as Web Page dialog:**

Select **File > Export > Web Page...**

## 10.8 Exporting Details-on-Demand

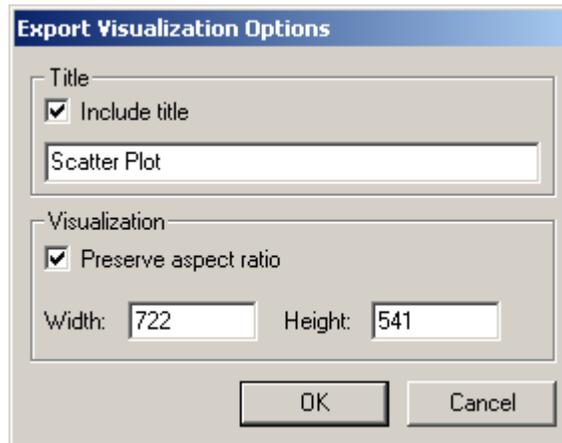
Spotfire DecisionSite provides the possibility to export the information about the active or the marked markers. If the **Details-on-Demand (HTML)** option is selected under the **View** menu, the **File > Export > Details-on-Demand** option is available. Selecting it will launch an external browser, Netscape or Internet Explorer, in which the details of the records will be presented.

**Tip:** Also note, other Export options can be found under the File menu.

## 10.9 Export Current Visualization

► **To save an image of the current visualization to a file:**

1. Select **File > Export > Current Visualization**.



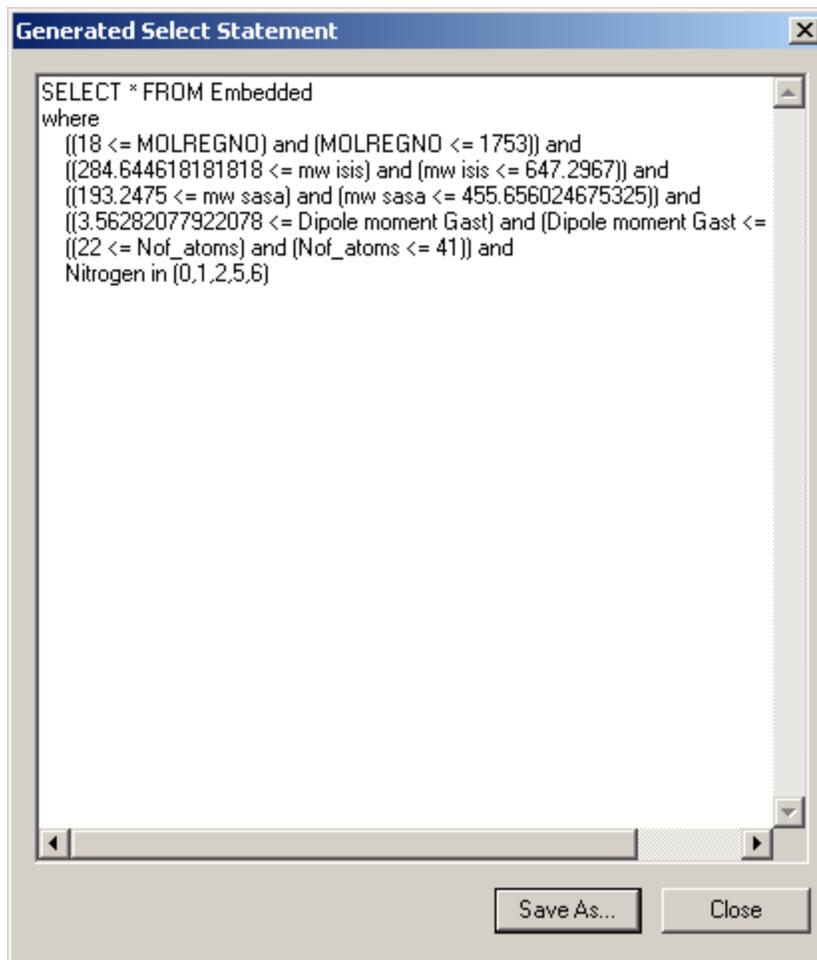
2. Enter the title to be included at the top of the image.
3. Enter the size of the exported image. If you check **Preserve aspect ratio**, the height-width ratio of the exported image will be the same as that of the visualization on screen.
4. Click **OK**.
5. Select a location, name and format for the file. The formats available are Windows BMP, JPEG and PNG.

**Tip:** The current visualization can be copied to the Windows Clipboard as a vector graphic (Windows Metafile) to be pasted into another application. This is accomplished through the **Copy Special > Visualization** option under the **Edit** menu. In the Metafile format each block of text, marker, line, etc. is an independent object that can be manipulated.

## 10.10 Export Database Queries

The current query device settings can be exported as a SQL database query. This is done by selecting the **Export > SQL Query...** option from the **File** menu. When you do this, a dialog containing the query appears. The query can be edited at this stage by clicking in the edit box and entering or erasing text. By clicking **Save As...** the query can be saved to the file system.

**Tip:** Also note, other Export options can be found under the File menu.

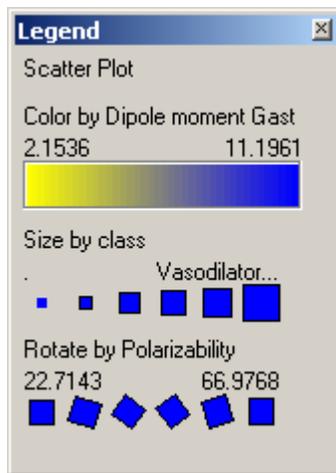


## 10.11 Export Legend Image

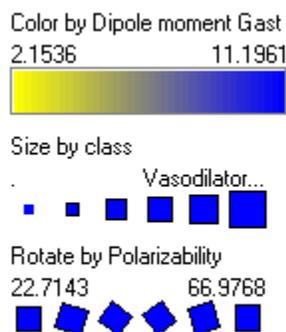
This option will place an image of the legend describing the columns that are used for size, color, rotation, etc. on the Windows Clipboard.

To make this option available you must first display the Legend in Spotfire DecisionSite. There are three ways to do this:

- Select Legend command from the View menu
- Use the keyboard shortcut [Ctrl + L]
- Click the  button on the toolbar



The legend in Spotfire DecisionSite (above) and the bitmap exported (below)



When you select the **File > Export > Legend** option, a **Save As...** dialog opens and you can browse to where you want to save the legend image; you are able to choose BMP or JPG format.

## 10.12 Export Data

All the data loaded into memory and used by Spotfire DecisionSite can be exported using this option. Records that have been removed by deleting marked markers will of course not be among the exported data. All other records—even those not currently portrayed in visualizations or those deselected by query devices—will be exported. The format of the data is as comma separated values (.csv).

When you select the **File > Export > Data** option, a **Save As...** dialog opens and you can browse to the location where you want to save the file, and save it under any viable name you wish. Available formats are TXT (tab separated columns), CSV (default list separator), SKV (semicolon), Spotfire Text Data Format and two versions of Microsoft ADO Persisted Record set (XML and ADTG binary format).

To export as Persisted Record set you need MDAC 2.5 or later installed on your computer. You can also open Persisted Record sets in DecisionSite Client via **File > Open...** and selecting **All Files (\*.\*)**.

**Note:** Data are per default exported exactly the way they are currently displayed. This means that the export of a formatted Date, Time or DateTime column may result in data loss. For example, if a Date column is formatted to be displayed as "Day of week, Monday first (day name)", the exported data will not contain the information about year and month which was originally in the data, but only the string showing day of week. Optionally, you can turn off this setting and always export the original data from the Advanced tab of the Tools > Options dialog.

**Tip:** You can export data directly from the Table visualization by right-clicking and selecting **Export Data...**

Also note, other Export options can be found under the File menu.

## 10.13 Printing

### ► To print the document with the current Print Layout settings:

1. Select **File > Print...**
2. Select a printer from the drop-down list.
3. Optionally, click **Properties** and adjust your printer settings.
4. Click **OK**.

Use the **Print Preview** option on the **File** menu to see how your printout will appear with the current Print Layout settings.

### Print Layout

Spotfire DecisionSite printouts may contain any of the information available in the visualizations.

To control which information to include select **Print Layout Options...** from the **File** menu.

Option	Explanation
<b>Header</b>	The printed document will have a header stating Date, File name, Time.
<b>Include title</b>	Select this check box to include a title, and enter a title in the text field.
<b>Include visualization</b>	Deselect this check box if you do not want to print the visualization.
<b>Keep aspect ratio</b>	Select this option if you want to keep the aspect ratio of the visualization when printed on paper.
<b>Auto fit to page</b>	Select this option if you want the printed visualization to automatically resize to cover as much of the page as possible.
<b>Footer</b>	The printed document will have a footer stating the text you enter in this field.
<b>Include query</b>	Selecting this option provides information on the filtering you have done using the query devices.
<b>Include Details-on-Demand</b>	Selecting this option includes the Details-on-demand information in the printed document.
<b>Include legend</b>	Selecting this option includes the legend in the printed document.
<b>Force single page layout</b>	Selecting this option causes as much information as possible to fit onto one page, and only prints that.
<b>Frame around areas</b>	Selecting this option displays frames around the various includes sections.
<b>Annotation</b>	This tab provides an option to include the visualization annotation.

# 11 Quick Reference

## 11.1 Menus

### 11.1.1 File Menu

Option	Hotkey	Description
Open	Ctrl+O	Opens an existing document. A browse dialog opens where you can search for files in various formats to open in Spotfire DecisionSite. You can also enter a URL in the File name field, and access data from a web server.
Apply Template...		Applies settings from an SFT or SFS file. HTML templates for presenting Details-on-Demand will be imported from the external SFS file.
Save	Ctrl+S	Saves the active document. If the document has never been saved before, this will open the same dialog as <b>Save As...</b>
Save As...	F12	Saves the document with another name, in another format, or in another location.
Close		Closes the active document. You will be prompted for saving changes.
Open from Library...		Opens an item from the DecisionSite Library. A Library dialog opens where you can browse the Library for an Analysis, Guide, or Poster you want to open. See Open From Library for more information.
Publish Analysis to Library...		Publishes the current Analysis to the Library. A dialog opens in which you specify details on how to publish. See Publishing Analyses to Library for more information.
Publish Poster to Library...		Publishes a DecisionSite Poster to the Library. A dialog opens that allows you to design your Poster. See Publishing Posters to Library for more information.
Import >		
> Import Data...	Ctrl+D	This allows you to import data in any supported format (ODBC, text files, clipboard, etc), and to apply data conditioning. See Importing Data for more information.
> Open Information Link		Launches the Information Library where you can open information links and retrieve the data. To access the online help for this application, you must first start the application by selecting it from the menu.
> Affymetrix Data from Database (Local)...		Allows you to retrieve information from local Affymetrix databases. See Retrieve Affymetrix

<b>&gt; Affymetrix Data from Database (Remote)...</b>	Data from Database for more information.
<b>&gt; Affymetrix Data from Files...</b>	Allows you to retrieve information from remote Affymetrix databases. See Retrieve Affymetrix Data from Database for more information.
<b>&gt; GenePix Data...</b>	Allows you to open text files that have been exported from the Metrics tab of Affymetrix Microarray Suite or from GeneChip. See Importing Affymetrix Data Files for more information.
<b>Export &gt;</b>	
<b>&gt; Details-on-Demand HTML</b>	Exports information about marked or active objects as text.
<b>&gt; Current Visualization...</b>	Exports the current visualization. An image of the currently active visualization is exported as a JPG or BMP image file. A Save As dialog is opened and you can navigate to where you want to save your image.
<b>&gt; SQL Query...</b>	Exports the settings of the query devices as an SQL query.
<b>&gt; Legend...</b>	Exports the legend. An image of the legend, the description of which columns are used for size, color, etc. is exported as a JPG or BMP image file. A Save As dialog is opened and you can navigate to where you want to save your image.
<b>&gt; Data...</b>	Exports data as Tab Separated Values. A Save As... dialog opens and you can save all the records in the data set as tab separated text.
<b>&gt; Microsoft® PowerPoint® Presentation...</b>	Exports the selected visualizations to PowerPoint®. See Exporting Visualizations to PowerPoint.
<b>&gt; Microsoft® Word Presentation...</b>	Exports the selected visualizations to Microsoft® Word. See Exporting Visualizations to Word.
<b>&gt; Web Page...</b>	Exports the visualization as a Web Page.
<b>Print Layout Options...</b>	Changes the report layout.
<b>Print Preview</b>	Displays full pages. Shows a preview of the visualization as it will be printed with the settings that will apply.
<b>Print...</b>	<b>Ctrl+P</b>
Prints the active visualization. A Print dialog is opened where you can choose printer and printer settings.	
<b>Switch DecisionSite &gt;</b>	Switch to another DecisionSite.
<b>Login to DecisionSite &gt;</b>	
<b>&gt; Log Out</b>	Log out of the current DecisionSite Analytics Server.
<b>&gt; Log into Server...</b>	Log into a DecisionSite Analytics Server.

> <b>Change Password...</b>	Change your current password to a new one.
> <b>Unlock New License...</b>	Opens the Add Software tool, where Spotfire Administrators can enter a product key to unlock more features to Spotfire DecisionSite.
<b># Most recent files</b>	The four most recently opened documents can be opened from the list.
<b>Exit</b>	Quit the application. You are prompted to save open documents.

## 11.1.2 Edit Menu

Option	Hotkey	Description
<b>Copy</b>	<b>Ctrl+C</b>	Copies the records corresponding to the markers, bars and pies marked with the lasso or rectangle marking tool to the Windows clipboard in text format. It also copies an image of the visualization to the clipboard, which can be pasted into other applications by using a Paste Special option.
<b>Copy Special &gt;</b>		
> <b>Marked Records</b>		Copies the set of marked records to the Clipboard. Data in all the records that have been marked is copied to the Clipboard in text format.
> <b>Selected Records</b>		Copies the selected records to the Clipboard. Data in the records that fulfill all query device constraints is copied to the Clipboard in text format.
> <b>All Records</b>		Copies all records to the Clipboard.
> <b>Visualization</b>		Copies the current visualization to the Clipboard. An image in vector graphics format of the active visualization is copied to the Clipboard. This image can be pasted into another application as a Windows Metafile.
<b>Paste</b>	<b>Ctrl+V</b>	Inserts Clipboard contents. The contents of the clipboard are pasted into a new Spotfire DecisionSite visualization. The Clipboard should contain data as text in one of the formats recognized by Spotfire DecisionSite.
<b>Reset to All</b>	<b>Ctrl+R</b>	Resets all query devices and zoom bars to show all records. Color, size, marking and other properties are unaffected.
<b>Mark Selected</b>	<b>Ctrl+A</b>	Marks all visible (selected) records. Records not selected by the current query device settings are not marked.
<b>Marked Record(s)</b>		
> <b>Unmark</b>	<b>Ctrl+E</b>	Resets the set of marked records. Unmarks all marked records.
> <b>Invert</b>	<b>Ctrl+I</b>	Inverts the set of marked records. Marks all

> <b>Select</b>	<b>Ctrl+M</b>	unmarked records and unmarks the set of marked records.
> <b>Undo Select</b>	<b>Ctrl+Shift+M</b>	Sets the selection to the marked records. Creates a temporary filter so that only the marked records are visible.
> <b>Delete</b>	<b>Del</b>	Undoes all record selections without resetting the query devices.
<b>Properties</b>	<b>Ctrl+Enter OR Alt+Enter</b>	Deletes the set of marked records. The marked records are removed from the data set in Spotfire DecisionSite's memory. This operation cannot be undone but does not affect the original data unless that file is intentionally overwritten with the diminished data.
		Set document properties. The <b>Properties dialog</b> opens in which parameters governing the appearance of the visualization can be set, annotations made, etc.

### 11.1.3 View Menu

Checkmarks in front of the options indicate that they are active; selection toggles this status.

Option	Hotkey	Description
<input type="checkbox"/> <b>Toolbars...</b>		Show or hide the toolbar.
<input type="checkbox"/> <b>Status Bar</b>		Show or hide the status bar.
<input type="checkbox"/> <b>Workbook</b>		Show visualizations with tabs.
<input type="checkbox"/> <b>Full Screen</b>	<b>F11</b>	Full screen mode, on/off.
<input type="checkbox"/> <b>Details-on-Demand (Text)</b>		Show or hide text Details-on-Demand.
<input type="checkbox"/> <b>Details-on-Demand (HTML)</b>		Show or hide HTML Details-on-Demand.
<input type="checkbox"/> <b>Details-on-Demand (External Browser)</b>		Launches an external browser displaying the Details-on-Demand.
<input type="checkbox"/> <b>Query Devices</b>		Show or hide the query devices.
<input type="checkbox"/> <b>Legend</b>	<b>Ctrl+L</b>	Show or hide the Legend.
<input type="checkbox"/> <b>Guides Toolbar</b>		Show or hide the Guides toolbar.
<input type="checkbox"/> <b>Guides</b>		Show or hide the Guides pane.
<input type="checkbox"/> <b>Getting Started</b>		Show or hide the Getting Started welcome screen.

### 11.1.4 Visualization Menu

Option	Hotkey	Description
<input type="checkbox"/> <b>New Scatter Plot</b>	<b>Ctrl+1</b>	Creates a new scatter plot visualization. A two-dimensional visualization is created. See Scatter Plots.
<input type="checkbox"/> <b>New 3D Scatter Plot</b>	<b>Ctrl+2</b>	Creates a new scatter plot visualization. A three-

		dimensional visualization is created. See Scatter Plots.
<b>New Bar Chart</b>	<b>Ctrl+4</b>	Creates a new bar chart visualization. See Bar Charts.
<b>New Pie Chart</b>	<b>Ctrl+5</b>	Creates a new pie chart visualization. See Pie Charts.
<b>New Line Chart</b>	<b>Ctrl+6</b>	Creates a new bar chart visualization. See Line Charts.
<b>New Profile Chart</b>	<b>Ctrl+7</b>	Creates a new bar chart visualization. Profile Charts.
<b>New Heat Map</b>	<b>Ctrl+8</b>	Creates a new heat map visualization. See Heat Maps.
<b>New Table</b>	<b>Ctrl+9</b>	Creates a new table visualization. See Tables.
<b>View Tip...</b>		Invokes the View Tip Dialog. Thumbnail views of visualizations are presented and can be quickly analyzed.
<b>Duplicate Visualization</b>	<b>Ctrl+U</b>	Creates a duplicate of the selected visualization.

## 11.1.5 Data Menu

Option	Description
<b>Add Columns...</b>	Allows you to incorporate new columns into your current data set. See Add Columns Overview.
<b>New Column &gt;</b>	
<b>&gt; By Binning...</b>	Allows you to sort your data into different groups or bins using different methods. See the Different Binning Methods.
<b>&gt; From Marked Records...</b>	Creates a new column from the currently marked records. See New Column from Marked Records.
<b>&gt; From Expression...</b>	Allows you to add a new column calculated from other columns in your data set. See Workflow of the New Column from Expression Tool.
<b>Normalization...</b>	Allows you to normalize your data in various ways and to do fold change calculations. See Normalization Overview.
<b>Column Normalization...</b>	Allows you to standardize the values in selected columns using a number of different normalization methods. See Column Normalization Overview.
<b>Row Summarization...</b>	Allows you to combine values from multiple samples into a single column. See Performing a Row Summarization.
<b>Pivot Data...</b>	Allows you to rotate and aggregate your data in order to use it in a better way. See Pivoting the Data Set.
<b>Depivot Data...</b>	Allows you to transform your data to a tall and skinny format. See Depivoting the Data Set.
<b>Transpose Data...</b>	Rotates your data set so that columns become records and vice versa. See Transpose Data Overview.

<b>Clustering &gt;</b>	
> <b>Hierarchical Clustering...</b>	Arranges records in a dendrogram (a tree graph) based on the similarity between them. See Hierarchical Clustering Method Overview.
> <b>Hierarchical Clustering on Keys...</b>	Groups compounds with similar sets of substructures. See Hierarchical Clustering on Keys.
> <b>Self-Organizing Maps...</b>	Groups records using an algorithm based on neural networks. See Self-Organizing Maps Overview.
> <b>K-means Clustering...</b>	A non-hierarchical clustering, which groups records into a defined number of clusters based on their similarity. See K-means Clustering Overview.
> <b>Principal Component Analysis...</b>	Reduces the dimensionality of a data set without significant loss of information. See Understanding PCA.
<b>Pattern Detection &gt;</b>	
> <b>Treatment Comparison...</b>	Provides methods for distinguishing between different treatments for an individual record. See Treatment Comparison Overview.
> <b>Profile Search...</b>	Calculates the similarity to a selected profile for all records in the data set and adds the result as a new column. See Profile Search Overview.
> <b>Coincidence Testing...</b>	Compares two columns and investigates whether or not the seeming similarity between the two distributions is a coincidence. See Coincidence Testing Overview.

## 11.1.6 Tools Menu

Option	Description
<b>Gene Ontology Browser</b>	The Gene Ontology Browser is used to see where the records in your data set are located in a gene ontology hierarchy. See Gene Ontology Browser Overview.
<b>Structure Analytics &gt;</b>	
> <b>Structure Viewer</b>	Launches the Structure Viewer tool which allows you to examine chemical structures from an ISIS database and manage lists of compound identifiers generated by this tool. See Structure Viewer Overview.
> <b>Structures in Table</b>	Launches the Structures in Table tool which allows you to incorporate structure images from an ISIS database into a table visualization. See Displaying Structures in a Table Visualization.
> <b>Structure Search...</b>	Launches the Structure Search tool which provides several search algorithms which retrieve molecules with similarities to the master structure. See Searching for Compounds Using Structure Search.
> <b>R-group Search</b>	Launches the R-group Search tool which helps you to perform searches for molecules with specified or unspecified R-groups. <b>Note:</b> You need to have ISIS/Draw installed on your computer to reach this tool. See Performing an R-group

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	Search.
> <b>List Search...</b>	Launches the List Search tool which allows you to search for structures using a list or compound identifiers. See Using List Search.
> <b>Add Structure Keys...</b>	Launches the Add ISIS Keys tool which allows you to import keys from an ISIS database; this information is added to the data set as a new column. See Adding Structure Keys.
> <b>Structure Connection...</b>	Launches the ISIS Connection tool where you can connect to a local or remote Integrated Scientific Information System (ISIS) database. See ISIS Connection Overview.
> <b>Advanced Preferences</b>	Launches a dialog where you can view and edit rules regarding which structure editor and renderer you prefer to use in your structure analytics tools. See Advanced Preferences.
<b>Portfolio</b>	Launches the Portfolio tool where you can arrange records into lists. See Portfolio Overview.
<b>List Logic...</b>	Launches the List Logic tool where you can compare lists using Boolean operators. See Comparing Lists Using List Logic.
<b>Web Links...</b>	Enables you to send a query to an external web site to search for information about marked records. See Web Links Overview.
<b>Pathway Viewer</b>	The Pathway Viewer is a tool which allows you to integrate Pathway Map information with your data set. See Viewing the Location of Records for more information.
<b>Computation Services</b>	Allows you to connect to a calculation server and add any type of statistical or mathematical calculations to your analysis. This can be a server running R, SAS, S-PLUS or custom servers.
<b>Distance Calculator</b>	Calculates the distance between two markers in a scatter plot.
<b>Decision Tree...</b>	Explaining the behavior of one column as a function of other columns in a data set. See Decision Tree Overview.
<b>Statistics &gt;</b>	
> <b>Box Plot</b>	Helps to visualize key statistical measures, such as median, mean and quartiles. See Box Plot Overview.
> <b>Summary Table</b>	Displays statistical information numerically. See Summary Table Overview.
> <b>Normal Probability Plot...</b>	Helps you to investigate to what extent a data set exhibits normal distribution. See Normal Probability Plot Overview.
> <b>Profile Anova...</b>	Provides a method for locating records where there is a significant difference between one group of columns and another group. See Profile Anova Overview.
> <b>Column Relationships...</b>	Helps you to investigate the relationships between different column pairs. See Column Relationships Overview.
<b>Create Information Link</b>	Launches the Information Builder tool where you can create and open <i>information links</i> . This tool has its own help file.

<b>Information Designer</b>	To see Information Builder help, start the tool and select <b>Help</b> . Launches the Information Designer tool where you can set up database connections. This tool has its own help file. To see Information Designer help, start the tool and select <b>Help</b> .
<b>Administration &gt;</b>	
> <b>DecisionSite Administrator</b>	Only available for users with Administrator privileges. Launches the DecisionSite Administrator tool where you can manage DecisionSite users and groups. You can organize users into groups, define profiles for the individual user and group, and assign licenses to groups and users. To see DecisionSite Administrator help, start the tool and select <b>Help</b> .
> <b>DecisionSite Library</b>	Only available for users with Administrator privileges. Starts DecisionSite Library which provides easy-to-access publishing of Analyses, Guides, and Posters. See What is DecisionSite Library.
> <b>DecisionSite Library Administrator</b>	Only available for users with Administrator privileges. Edit who is allowed to create new Library Sections, configure DecisionSite Library and Poster settings.
> <b>Server Usage</b>	Only available for users with Administrator privileges. Opens the log file dssaccess.sfs in DecisionSite, for an easy analysis and overview. This file contains information about all logins and logouts from all DecisionSite Clients to the DecisionSite Analytics Server. It shows which user logged in/out and when. The log is always enabled, and it is unaffected by Log Configuration File settings.
<b>Customize...</b>	Customize menu and toolbars. A dialog box opens with four tabs on which you can choose appearances and customize toolbars, commands and menus.
<b>Options...</b>	The Options dialog lets you specify visualization settings such as fonts, axis labels, default file location and much more. Here you can also choose to save personal settings.
<b>Select Language...</b>	The Select Language dialog lets you change the language of the main menus and the online help, if you have access to any language pack. <b>Note:</b> The dialog texts and any submenus will still be displayed in English.

## 11.1.7 Guides Menu

Option	Description
<b>Data Preparation &gt;</b>	
> <b>Transform columns to log scale</b>	Starts the Guide <b>Transform columns to log scale</b> in the Guides pane.
> <b>Filter genes</b>	Starts the Guide <b>Filter genes</b> in the Guides pane.
> <b>Average spot replicates</b>	Starts the Guide <b>Average spot replicates</b> in the Guides

	pane.
<b>Data Analysis &gt;</b>	
> <b>View gene profiles</b>	Starts the Guide <b>View gene profiles</b> in the Guides pane.
> <b>Group genes using hierarchical clustering</b>	Starts the Guide <b>Group genes using hierarchical clustering</b> in the Guides pane.
> <b>Group genes using k-means clustering</b>	Starts the Guide <b>Group genes using k-means clustering</b> in the Guides pane.
> <b>Group genes using keyword clustering</b>	Starts the Guide <b>Group genes using keyword clustering</b> in the Guides pane.
> <b>Analyze experiments using PCA</b>	Starts the Guide <b>Analyze experiments using PCA</b> in the Guides pane.
> <b>Analyze Affymetrix absence/presence calls</b>	Starts the Guide <b>Analyze Affymetrix absence/presence calls</b> in the Guides pane.
> <b>Explore categories</b>	Starts the Guide <b>Explore categories</b> in the Guides pane.
> <b>Venn logic</b>	Starts the Guide <b>Venn logic</b> in the Guides pane.
> <b>Find similar genes</b>	Starts the Guide <b>Find similar genes</b> in the Guides pane.
> <b>Find pattern</b>	Starts the Guide <b>Find pattern</b> in the Guides pane.
<b>Tutorials &gt;</b>	
> <b>Explore a film database</b>	Starts the Tutorial <b>Explore a film database</b> in the Guides pane.
> <b>Find interesting stocks</b>	Starts the Tutorial <b>Find interesting stocks</b> in the Guides pane.
<b>Run from File...</b>	Launches an Open dialog where you can Browse to the Guide file that you want to run. See Running Guides Locally.
<b>Run from Library...</b>	Opens an item from the DecisionSite Library. A Library browser opens where you can browse the Library for an Analysis, Guide, or Poster you want to open. See Open From Library.
<b>Create and Edit Guide</b>	Opens the Analysis Builder tool where you can create and edit Guides. See Analysis Builder overview.
<b>Publish to Library...</b>	Publishes the current Analysis to the Library. A dialog opens in which you specify detail on how to publish. See Publish Analysis to Library.

## 11.1.8 Window Menu

Option	Hotkey	Description
Close	Ctrl+F4	Closes the active visualization.
Close All		Closes all visualizations.
Auto Hide Axis Selectors		Hides axis selectors. When hidden this gives greater room for the visualizations.
Hide Window Frame		Hides window frame. With multiple

<b>Auto Tile</b>	visualizations displayed, greater room is available for the visualizations when frame and title bar are hidden.
<b>Cascade</b>	Auto tiles the visualizations. Arranges all the open visualizations to fill the visualization window.
<b>Tile Horizontal</b>	Arranges windows so they overlap. Each window is staggered so that all title bars are accessible.
<b>Tile Vertical</b>	Arranges visualizations as non overlapping horizontal tiles.
<b>(#) Visualizations</b>	Arranges visualizations as non overlapping vertical tiles.
	Pressing the key representing the number in front of the visualization title, activates that visualization.

## 11.1.9 Help Menu

### Help menu

Option	Hotkey	Description
<b>Help Topics</b>	<b>F1</b>	Launches the online Help, where you can search for specific topics or subjects.
<b>PDF Manuals</b>		Opens a web page where you can download printable manuals in PDF format.
<b>What's New</b>		Lists all the new features and latest information for Spotfire DecisionSite.
<b>Functional Genomics Companion</b>		Shows additional information on how you can use DecisionSite for Functional Genomics in genomics analysis.
<b>Ask Spotfire Support</b>		Opens the Support web page with information on how to contact Spotfire support.
<b>Support Diagnostics...</b>		Use this tool to verify that everything that is needed to run DecisionSite has been installed, and has the correct version. For example, Internet Explorer version, Operating System version, correct DLLs, etc.
<b>About Spotfire DecisionSite</b>		Displays program information, version number and copyright. License information is also found here.

## 11.2 Query Device Pop-Up Menu

Right-clicking in the query device window brings up a pop-up menu to let you modify query devices, generate new columns, change the kind of query device used, alter scale transformations, etc.

Option	Description
<b>Check Boxes</b>	If the column contains less than 500 unique values you can choose to have check boxes as query device. Values deselected by other query device constraints have red labels.
<b>Radio Buttons</b>	If the column contains less than 500 unique values you can choose to have radio buttons as query device. Only one of the values may be selected at a time.
<b>Range Slider</b>	Range sliders can be used to select numeric data.
<b>Item Slider</b>	Item sliders can be used to select alphanumeric data.
<b>full-text search</b>	Full-Text Search can search a string for any combination of characters using Boolean logic.
<b>None</b>	Select none of the records with values in this column.
<b>All</b>	Select all records with values in this column.
<b>Data Range</b>	Select all records with values in this column.
<b>From Selected</b>	Changes the data range to span only the selected records. Three small dots are displayed at the end of the slider to indicate that the current data range is not the full range.
<b>Reset</b>	Resets the data range to its original full width.
<b>Show Empty Values</b>	Display records even though values are empty (null).
<b>Show Full Name</b>	The query device is given another row with the entire name of the column.
<b>Sort</b>	Sorts the order of the Query Devices.
<b>Original</b>	Resets the original order.
<b>by Annotation</b>	Sorts alphabetically by Annotation.
<b>by Name</b>	Sorts alphabetically by Name.
<b>by Type</b>	Sorts by type of Query Device.
<b>Move</b>	Moves the query device.
<b>To the Top</b>	Moves the query device to the top of the window.
<b>Up</b>	Moves the query device up one position in the window.
<b>Down</b>	Moves the query device down one position in the window.
<b>To the Bottom</b>	Moves the query device to the bottom of the window.
<b>Hide</b>	Makes the query device invisible. Selecting the Show Query Device option on the Columns tab of the Properties dialog box makes the device visible again.
<b>New Column</b>	
<b>By Binning</b>	Create a new column by binning, a dialog box allows you to choose column to be binned and then a wizard Guides you through the binning process.
<b>From Expression</b>	Create a new column from mathematical operations on data, a wizard guides through the construction of the expression.
<b>From Marked Records</b>	Create a new column. Each record is given a value indicating whether it is marked or not.

Set Property	
<b>Color</b>	The colors of the markers, pies or bars are governed by the values of the records in the column. If there are less than 20 items in the column the coloring will be set to categorical, otherwise it will be continuous.
<b>Size</b>	The sizes of the markers, pies or bars are governed by the values of the records in the column.
<b>Axis</b>	
<b>X</b>	Set the X-axis to the column represented by the current Query Device.
<b>Y</b>	Set the y-axis to the column represented by the current Query Device.
<b>Z</b>	Set the Z-axis to the column represented by the current Query Device.
<b>Original Scale</b>	All changes to the scale of the column are removed.
<b>Ln(1+x) Scale</b>	Logarithm base e scale [ $\ln(x+1)$ ].
<b>Log Scale</b>	Logarithm base 10 scale [ $\log_{10}(x)$ ].
<b>Exp Scale</b>	Exponential scale base e [ $e^x$ ].
<b>Exp10 Scale</b>	Exponential scale base 10 [ $10^x$ ].
<b>Inverse Scale</b>	Inverse scale [ $1/x$ ].
<b>Reverse Sorting</b>	Reverse scale
<b>Edit Annotation...</b>	Go to the dialog that lets you edit the annotation for this column.

## 11.3 Visualization Pop-up Menu

If you right-click in a visualization you will bring up a pop-up menu with shortcuts to some of the most used commands. The pop-up menu is slightly different in some of the visualizations. Right-clicking on an item label (marker label, bar label, etc.) will also display the Copy Special option which allows you to copy either the value of the label, or, if you are using structure marker labels, the chemical structure.

### Scatter plots

Option	Hotkey	Description
<b>Zoom &gt;</b>		
> Zoom to Selection		Zooms to the selected records.
> Reset Zooming		Resets the zoom bars to the original state (no zooming).
<b>Trellis...</b>		Opens the Properties dialog to the Trellis tab, where you can split the visualization to display different subsets of your data.
<b>Marked Record(s) &gt;</b>		
> Delete	<b>Del</b>	Deletes the set of marked records. The marked records are removed from the data set in Spotfire DecisionSite's memory. This operation cannot be

		undone but does not affect the original data unless that file is intentionally overwritten with the diminished data.
> <b>Unmark</b>	<b>Ctrl+E</b>	Resets the set of marked records. No records will be marked after you have executed this operation.
> <b>Invert</b>	<b>Ctrl+I</b>	Inverts the set of marked records. Marks all unmarked records and unmarks the set of marked records.
> <b>Select</b>	<b>Ctrl+M</b>	Sets the selection to the marked records. Creates a temporary filter so that only the marked records are visible.
> <b>New Column...</b>		Opens the New Column from Marked Records dialog, where you can add a new column showing whether records are included in the marked group or not.
> <b>Create New Portfolio List</b>		Creates a new list with the marked records to the Portfolio. The list is placed as the last item on root level.
> <b>Add to Portfolio List</b>		Adds the marked records from the visualization into your currently active Portfolio list.
<b>Annotate...</b>		Opens the Properties dialog to the Annotations tab, where you can provide the visualization with a description of your choice.
<b>Copy</b>	<b>Ctrl+C</b>	Copies the records corresponding to the markers, bars and pies marked with the lasso or rectangle marking tool to the Windows clipboard in text format. It also copies an image of the visualization to the clipboard, which can be pasted into other applications by using a Paste Special option.
<b>Duplicate Visualization</b>		Creates a duplicate of the selected visualization.
<b>Structure Marker Labels &gt;</b>		Allows you to specify a structure column to use in the labels. Once structure marker labels are used, you also have the option to right-click on a structure label and select Structure Search, R-group Search or Export to File directly from the pop-up menu. You can also use Copy Special > Copy Structure to copy that specific structure as an image or as a structure element (depending on the application where you paste your structure.
> <b>Connection</b>		Allows you to change the connection used to display the structures into a different structure database.
> <b>Renderer</b>		Allows you to specify which renderer to use for drawing the structures in the labels. Here, you also have the option to change the settings for the selected renderer, or to turn off smooth drawing of structures.
> <b>Remove</b>		Reverts to use the column specified on the Scatter Plot Properties Markers tab in the labels instead of the structures.

<b>Reset Navigation</b>		Available for 3d scatter plots only. Resets the visualization to the original view.
<b>Properties</b>	<b>Alt+Enter</b>	Opens the <b>Properties dialog</b> in which parameters governing the appearance of the visualization can be set, annotations made, etc.

## Bar charts

Option	Hotkey	Description
<b>Zoom &gt;</b>		
> <b>Zoom to Selection</b>		Zooms to the selected records.
> <b>Reset Zooming</b>		Resets the zoom bars to the original state (no zooming).
<b>Trellis...</b>		Opens the Properties dialog to the Trellis tab, where you can split the visualization to display different subsets of your data.
<b>Marked Record(s) &gt;</b>		
> <b>Delete</b>	<b>Del</b>	Deletes the set of marked records. The marked records are removed from the data set in Spotfire DecisionSite's memory. This operation cannot be undone but does not affect the original data unless that file is intentionally overwritten with the diminished data.
> <b>Unmark</b>	<b>Ctrl+E</b>	Resets the set of marked records. No records will be marked after you have executed this operation.
> <b>Invert</b>	<b>Ctrl+I</b>	Inverts the set of marked records. Marks all unmarked records and unmarks the set of marked records.
> <b>Select</b>	<b>Ctrl+M</b>	Sets the selection to the marked records. Creates a temporary filter so that only the marked records are visible.
> <b>New Column...</b>		Opens the New Column from Marked Records dialog, where you can add a new column showing whether records are included in the marked group or not.
> <b>Create New Portfolio List</b>		Creates a new list with the marked records to the Portfolio. The list is placed as the last item on root level.
> <b>Add to Portfolio List</b>		Adds the marked records from the visualization into your currently active Portfolio list.
<b>Sort</b>		
> <b>Descending</b>		Sorts the bars from the highest to the lowest bar.
> <b>Ascending</b>		Sorts the bars from the lowest to the highest bar.
> <b>Reverse</b>		Reverses the current sort order.
> <b>Reset</b>		Resets the sorting to the original order.
<b>Annotate...</b>		Opens the Properties dialog to the Annotations tab,

<b>Copy</b>	<b>Ctrl+C</b>	where you can provide the visualization with a description of your choice. Copies the records corresponding to the markers, bars and pies marked with the lasso or rectangle marking tool to the Windows clipboard in text format. It also copies an image of the visualization to the clipboard, which can be pasted into other applications by using a Paste Special option.
<b>Duplicate Visualization</b>		Creates a duplicate of the selected visualization.
<b>Properties</b>	<b>Alt+Enter</b>	Opens the <b>Properties dialog</b> in which parameters governing the appearance of the visualization can be set, annotations made, etc.

## Pie charts

Option	Hotkey	Description
<b>Zoom &gt;</b>		
> <b>Reset Zooming</b>		Resets the zoom bars to the original state (no zooming).
<b>Trellis...</b>		Opens the Properties dialog to the Trellis tab, where you can split the visualization to display different subsets of your data.
<b>Marked Record(s) &gt;</b>		
> <b>Delete</b>	<b>Del</b>	Deletes the set of marked records. The marked records are removed from the data set in Spotfire DecisionSite's memory. This operation cannot be undone but does not affect the original data unless that file is intentionally overwritten with the diminished data.
> <b>Unmark</b>	<b>Ctrl+E</b>	Resets the set of marked records. No records will be marked after you have executed this operation.
> <b>Invert</b>	<b>Ctrl+I</b>	Inverts the set of marked records. Marks all unmarked records and unmarks the set of marked records.
> <b>Select</b>	<b>Ctrl+M</b>	Sets the selection to the marked records. Creates a temporary filter so that only the marked records are visible.
> <b>New Column...</b>		Opens the New Column from Marked Records dialog, where you can add a new column showing whether records are included in the marked group or not.
> <b>Create New Portfolio List</b>		Creates a new list with the marked records to the Portfolio. The list is placed as the last item on root level.
> <b>Add to Portfolio List</b>		Adds the marked records from the visualization into your currently active Portfolio list.
<b>Annotate...</b>		Opens the Properties dialog to the Annotations tab, where you can provide the visualization with a

<b>Copy</b>	<b>Ctrl+C</b>	description of your choice. Copies the records corresponding to the markers, bars and pies marked with the lasso or rectangle marking tool to the Windows clipboard in text format. It also copies an image of the visualization to the clipboard, which can be pasted into other applications by using a Paste Special option.
<b>Duplicate Visualization</b>		Creates a duplicate of the selected visualization.
<b>Properties</b>	<b>Alt+Enter</b>	Opens the <b>Properties dialog</b> n which parameters governing the appearance of the visualization can be set, annotations made, etc.

## Line charts

Option	Hotkey	Description
<b>Zoom &gt;</b>		
> <b>Reset Zooming</b>		Resets the zoom bars to the original state (no zooming).
<b>Trellis...</b>		Opens the Properties dialog to the Trellis tab, where you can split the visualization to display different subsets of your data.
<b>Marked Record(s) &gt;</b>		
> <b>Delete</b>	<b>Del</b>	Deletes the set of marked records. The marked records are removed from the data set in Spotfire DecisionSite's memory. This operation cannot be undone but does not affect the original data unless that file is intentionally overwritten with the diminished data.
> <b>Unmark</b>	<b>Ctrl+E</b>	Resets the set of marked records. No records will be marked after you have executed this operation.
> <b>Invert</b>	<b>Ctrl+I</b>	Inverts the set of marked records. Marks all unmarked records and unmarks the set of marked records.
> <b>Select</b>	<b>Ctrl+M</b>	Sets the selection to the marked records. Creates a temporary filter so that only the marked records are visible.
> <b>New Column...</b>		Opens the New Column from Marked Records dialog, where you can add a new column showing whether records are included in the marked group or not.
> <b>Create New Portfolio List</b>		Creates a new list with the marked records to the Portfolio. The list is placed as the last item on root level.
> <b>Add to Portfolio List</b>		Adds the marked records from the visualization into your currently active Portfolio list.
<b>Same Scale for All</b>		Sets all line charts to use the same scale. (Same as the 'One for all' scale mode option in the Properties dialog.)

<b>Cascade All</b>		Sets the Scale and Position of all columns so that each of them will occupy a separate slot of the window height.
<b>Maximize All</b>		Set the Scale and Position on every column so they utilize the whole height of the window.
<b>Show Markers</b>		Displays (or hides) markers in the line chart.
<b>Annotate...</b>		Opens the Properties dialog to the Annotations tab, where you can provide the visualization with a description of your choice.
<b>Copy</b>	<b>Ctrl+C</b>	Copies the records corresponding to the markers, bars and pies marked with the lasso or rectangle marking tool to the Windows clipboard in text format. It also copies an image of the visualization to the clipboard, which can be pasted into other applications by using a Paste Special option.
<b>Duplicate Visualization</b>		Creates a duplicate of the selected visualization.
<b>Properties</b>	<b>Alt+Enter</b>	Opens the <b>Properties dialog</b> n which parameters governing the appearance of the visualization can be set, annotations made, etc.

## Profile charts

Option	Hotkey	Description
<b>Zoom &gt;</b>		
> <b>Zoom to Selection</b>		Zooms to the selected records.
> <b>Reset Zooming</b>		Resets the zoom bars to the original state (no zooming).
<b>Trellis...</b>		Opens the Properties dialog to the Trellis tab, where you can split the visualization to display different subsets of your data.
<b>Marked Record(s) &gt;</b>		
> <b>Delete</b>	<b>Del</b>	Deletes the set of marked records. The marked records are removed from the data set in Spotfire DecisionSite's memory. This operation cannot be undone but does not affect the original data unless that file is intentionally overwritten with the diminished data.
> <b>Unmark</b>	<b>Ctrl+E</b>	Resets the set of marked records. No records will be marked after you have executed this operation.
> <b>Invert</b>	<b>Ctrl+I</b>	Inverts the set of marked records. Marks all unmarked records and unmarks the set of marked records.
> <b>Select</b>	<b>Ctrl+M</b>	Sets the selection to the marked records. Creates a temporary filter so that only the marked records are visible.
> <b>New Column...</b>		Opens the New Column from Marked Records dialog, where you can add a new column showing whether records are included in the marked group

> <b>Create New Portfolio List</b>		or not. Creates a new list with the marked records to the Portfolio. The list is placed as the last item on root level.
> <b>Add to Portfolio List</b>		Adds the marked records from the visualization into your currently active Portfolio list.
<b>Same Scale for All</b>		Sets all profile charts to use the same scale. (Same as the 'All columns use same scale' scale mode option in the Properties dialog.)
<b>Annotate...</b>		Opens the Properties dialog to the Annotations tab, where you can provide the visualization with a description of your choice.
<b>Copy</b>	<b>Ctrl+C</b>	Copies the records corresponding to the markers, bars and pies marked with the lasso or rectangle marking tool to the Windows clipboard in text format. It also copies an image of the visualization to the clipboard, which can be pasted into other applications by using a Paste Special option.
<b>Duplicate Visualization</b>		Creates a duplicate of the selected visualization.
<b>Structure Marker Labels &gt;</b>		Allows you to specify a structure column to use in the labels. Once structure marker labels are used, you also have the option to right-click on a structure label and select Structure Search, R-group Search or Export to File directly from the pop-up menu. You can also use Copy Special > Copy Structure to copy that specific structure as an image or as a structure element (depending on the application where you paste your structure.
> <b>Connection</b>		Allows you to change the connection used to display the structures into a different structure database.
> <b>Renderer</b>		Allows you to specify which renderer to use for drawing the structures in the labels. Here, you also have the option to change the settings for the selected renderer, or to turn off smooth drawing of structures.
> <b>Remove</b>		Reverts to use the column specified on the Scatter Plot Properties Markers tab in the labels instead of the structures.
<b>Properties</b>	<b>Alt+Enter</b>	Opens the <b>Properties dialog</b> n which parameters governing the appearance of the visualization can be set, annotations made, etc.

## Heat maps

Option	Hotkey	Description
<b>Zoom &gt;</b>		
> <b>Reset Zooming</b>		Resets the zoom bars to the original state (no zooming).

<b>Trellis...</b>		Opens the Properties dialog to the Trellis tab, where you can split the visualization to display different subsets of your data.
<b>Marked Record(s) &gt;</b>		
<b>&gt; Delete</b>	<b>Del</b>	Deletes the set of marked records. The marked records are removed from the data set in Spotfire DecisionSite's memory. This operation cannot be undone but does not affect the original data unless that file is intentionally overwritten with the diminished data.
<b>&gt; Unmark</b>	<b>Ctrl+E</b>	Resets the set of marked records. No records will be marked after you have executed this operation.
<b>&gt; Invert</b>	<b>Ctrl+I</b>	Inverts the set of marked records. Marks all unmarked records and unmarks the set of marked records.
<b>&gt; Select</b>	<b>Ctrl+M</b>	Sets the selection to the marked records. Creates a temporary filter so that only the marked records are visible.
<b>&gt; New Column...</b>		Opens the New Column from Marked Records dialog, where you can add a new column showing whether records are included in the marked group or not.
<b>&gt; Create New Portfolio List</b>		Creates a new list with the marked records to the Portfolio. The list is placed as the last item on root level.
<b>&gt; Add to Portfolio List</b>		Adds the marked records from the visualization into your currently active Portfolio list.
<b>Show Deselected</b>		Shows (or hides) deselected records in the heat map.
<b>Annotate...</b>		Opens the Properties dialog to the Annotations tab, where you can provide the visualization with a description of your choice.
<b>Copy</b>	<b>Ctrl+C</b>	Copies the records corresponding to the markers, bars and pies marked with the lasso or rectangle marking tool to the Windows clipboard in text format. It also copies an image of the visualization to the clipboard, which can be pasted into other applications by using a Paste Special option.
<b>Duplicate Visualization</b>		Creates a duplicate of the selected visualization.
<b>Reset Navigation</b>		Available for 3d scatter plots only. Resets the visualization to the original view.
<b>Properties</b>	<b>Alt+Enter</b>	Opens the <b>Properties dialog</b> in which parameters governing the appearance of the visualization can be set, annotations made, etc.

## Table visualizations

Option	Hotkey	Description
<b>Marked Records &gt;</b>		
> <b>Delete</b>	<b>Del</b>	Deletes the set of marked records. The marked records are removed from the data set in Spotfire DecisionSite's memory. This operation cannot be undone but it does not affect the original data unless that file is intentionally overwritten with the diminished data.
> <b>Unmark</b>	<b>Ctrl+E</b>	Resets the set of marked records. No records will be marked after you have executed this operation.
> <b>Invert</b>	<b>Ctrl+I</b>	Inverts the set of marked records. Marks all previously unmarked records and unmarks the set of marked records.
> <b>Select</b>	<b>Ctrl+M</b>	Sets the selection to the marked records. Creates a temporary filter so that only the marked records are visible.
> <b>New Column...</b>		Opens the New Column from Marked Records dialog, where you can add a new column showing whether records are included in the marked group or not.
> <b>Create New Portfolio List</b>		Creates a new list with the marked records to the Portfolio. The list is placed as the last item on root level.
> <b>Add to Portfolio List</b>		Adds the marked records from the visualization into your currently active Portfolio list.
<b>Copy</b>	<b>Ctrl+C</b>	Copies the set of marked records to the Clipboard. Data in all the records that have been marked is copied to the Clipboard in text format.
<b>Copy Special &gt;</b>		
> <b>Copy Value</b>		Copies the cell value that you right-clicked upon.
> <b>Copy Visualization</b>		Copy the current visualization to the Clipboard. An image in vector graphics format of the active visualization is copied to the Clipboard. This image can be pasted into another application as a Windows Metafile.
<b>Duplicate Visualization</b>		Creates a duplicate of the selected visualization.
<b>Export Data...</b>		Opens a dialog where you can select a folder to save the exported data to, specify a file name and determine the type and encoding to use for the new file.
<b>Add Structure Column</b>		Allows you to add a structure column to the table, so that it behaves like a Structures in Table visualization.
<b>Properties</b>	<b>Alt+Enter</b>	Opens the <b>Properties dialog</b> in which parameters governing the appearance of the visualization can be set, annotations made, etc.

If you are running DecisionSite for Lead Discovery you will have access to more options on the pop-up menu. See Structures in Table pop-up menu for more information.

## 11.4 Toolbar Buttons

The following tables describe the toolbar and shortcuts that you can use to create, open, close, save, and manipulate your visualizations. Look up the action you want to take, and perform one of the alternatives shown.

Most actions can be performed with hot-keys from the keyboard (Keyboard Shortcut), from the menu (Menu Command, or Mouse), or by clicking a toolbar button (Toolbar). The menus can be reached by pressing the Alt key in combination with the underlined letter key. Subsequent underlined letter keys activate the menu items.

	Hotkey	Menu Command, or Mouse	Toolbar Button
Open an existing file or import a database.	<b>Ctrl+O</b>	<u>F</u> ile > <u>O</u> pen	
Import data from file, clipboard or database, and perform data conditioning.	<b>Ctrl+D</b>	<u>F</u> ile > I <u>m</u> port <u>D</u> ata...	
Save the present visualization in the same format as when opened .	<b>Ctrl+S</b>	<u>F</u> ile > <u>S</u> ave	
Print the active visualization.	<b>Ctrl+P</b>	<u>F</u> ile > <u>P</u> rint	
Copy the marked records to the clipboard as text.	<b>Ctrl+C</b>	<u>E</u> dit > <u>C</u> opy	
Paste the clipboard contents into Spotfire DecisionSite.	<b>Ctrl+V</b>	<u>E</u> dit > <u>P</u> aste	
Reset all query devices and zoom bars.	<b>Ctrl+R</b>	<u>E</u> dit > <u>R</u> eset to All	
Create a new 2D scatter plot.	<b>Ctrl+1</b>	<u>W</u> indow > New <u>S</u> catter Plot	
Create a new 3D scatter plot.	<b>Ctrl+2</b>	<u>W</u> indow > New <u>3</u> D Scatter Plot	
Create a new bar chart.	<b>Ctrl+4</b>	<u>W</u> indow > New <u>B</u> ar Chart	
Create a new pie chart.	<b>Ctrl+5</b>	<u>W</u> indow > New <u>P</u> ie Chart	
Create a new line chart.	<b>Ctrl+6</b>	<u>W</u> indow > New <u>L</u> ine Chart	
Create a new profile chart.	<b>Ctrl+7</b>	<u>W</u> indow > New <u>P</u> rofile Chart	
Create a new heat map.	<b>Ctrl+8</b>	<u>W</u> indow > New Heat Map	
Create a new table.	<b>Ctrl+9</b>	<u>W</u> indow > New Table	
Auto-tile visualizations.		<u>W</u> indow > <u>A</u> uto Tile	

Place all visualizations so they partially overlap each other.		<u>W</u> indow > Cascade	
Place all visualizations next to each other.		<u>W</u> indow > Tile Vertical	
Place all visualizations under each other.		<u>W</u> indow > Tile Horizontal	
Open the Properties dialog.	<b>Ctrl+Enter</b> <b>OR</b> <b>Alt+Enter</b>	<u>E</u> dit > <u>P</u> roperties	
Display legend in separate window.	<b>Ctrl+L</b>	<u>V</u> iew > <u>L</u> egend	
Export the active visualization as an image (BMP or JPG) to disk.		<u>F</u> ile > <u>E</u> xport > <u>C</u> urrent Visualization	
Open browser and display values for the currently marked records.		<u>F</u> ile > <u>E</u> xport > <u>D</u> etails	
Show the Guides pane.	<b>Ctrl+W</b>	<u>V</u> iew > Spotfire DecisionSite	
Go to Start page.			

## 11.5 Mouse Shortcuts

### 11.5.1 Mouse Shortcuts – Scatter Plots and Line Charts

#### Mouse over marker

A thin ring highlights the marker and all markers containing the record in other visualizations.

#### Left-click on marker

Activates a record. A persistent ring surrounds the object. Information about the record corresponding to the marker that was clicked displays in the Details-on-Demand window.

#### Left-drag

Marks the records that are inside the 'rubber band box' delineated by the pointer's diagonal movement. These markers will be given another color. A table of details will be displayed in the Details-on-Demand window. If no markers are surrounded all previously marked objects will be unmarked.

#### Shift + left-drag

Marks records using the lasso tool. Draw an arbitrary shape around the markers you want to mark. If none are surrounded all objects will be unmarked.

#### Ctrl + left-drag

Adds markers to the set of marked records using the rectangle 'rubber band box' tool.

#### Ctrl + Shift + left-drag

Adds markers to the set of marked records using a lasso function.

**Ctrl + Shift + left-drag**

Adds markers to the set of marked objects using a lasso function to the set of marked records.

**Mouse wheel**

Zooms in and out in the visualization.

**Ctrl + right-click**

Zooms in from the visualization.

**Ctrl + Shift + right-click**

Zooms out from the visualization.

**Right-click in visualization**

Brings up the visualization context pop-up menu.

## 11.5.2 Mouse Shortcuts – 3D Scatter Plots

**Mouse over marker**

Identical to 2D scatter plots

**Left-click on marker**

Identical to 2D scatter plots.

**Ctrl + drag using the right mouse button  
(or drag using the middle mouse button)**

Rotation around the visualization center.

**Shift + drag using the right mouse button  
(or Shift + drag using the middle mouse button)**

Zooms in the direction of the view.

**Ctrl + Shift + drag using the right mouse button  
(or Ctrl + Shift + drag using the middle mouse button)**

Rotation in the plane of the screen; downwards and right cursor motion rotates clockwise.

**Mouse wheel  
(or Ctrl + drag using the middle mouse button)**

Zooms in and out in the visualization.

**Right-click in visualization**

Brings up the visualization context pop-up menu.

## 11.5.3 Mouse Shortcuts – Bar Charts and Pie Charts

**Mouse over object**

An outline highlights the object and corresponding objects in similar visualizations.

### **Left-click on object**

Activates an object. A persistent outline surrounds the object. Information about the bar or pie that was clicked displays in the Details-on-Demand window.

### **Left-drag**

Marks the pies or bars that are inside the rectangle delineated by the diagonal movement of the pointer. If no bars are surrounded all objects will be unmarked.

### **Shift + left-drag**

Enables marking of bars or pies with the lasso tool. Draw an arbitrary shape around the objects you want to mark. If none are surrounded all objects will be unmarked.

### **Ctrl + left-drag**

Adds bars or pies to the set of marked objects using the rectangle 'rubber band box' tool.

### **Ctrl + Shift + left-drag**

Adds bars or pies to the set of marked objects using a lasso function to the set of marked records.

### **Mouse wheel**

Zooms in and out in the visualization.

### **Ctrl + right-click**

Zooms in from the visualization (only works for pie charts when an axis different than None has been selected).

### **Ctrl + Shift + right-click**

Zooms out from the visualization (only works for pie charts when an axis different than None has been selected).

### **Right-click in visualization**

Brings up the visualization context pop-up menu.

## **11.5.4 Mouse Shortcuts – Profile Charts**

### **Mouse over profile**

A thin contour highlights the profile (record), as well as all markers associated with the record in other visualizations.

### **Left-click on profile**

Activates A persistent contour surrounds the profile. Information about the profile appears in the Details-on-Demand window.

### **Left-drag**

Marks the profiles that are fully or partially inside the 'rubber band box' delineated by the pointer's diagonal movement. These profiles will become thicker. A table of details will be displayed in the Details-on-Demand window. If no profiles are surrounded all previously marked objects will be unmarked.

**Shift + left-drag**

Enables marking of profiles with the lasso tool. Draw an arbitrary shape around the profile you want to mark. If none are surrounded all profiles will be unmarked.

**Ctrl + left-drag**

Adds profiles to the set of marked profiles using the rectangle 'rubber band box' tool.

**Ctrl + Shift + left-drag**

Adds profiles, by using a lasso function, to the set of marked records.

**Mouse wheel**

Zooms in and out in the visualization.

**Ctrl + right-click**

Zooms in from the visualization.

**Ctrl + Shift + right-click**

Zooms out from the visualization.

**Right-click in visualization**

Brings up the visualization context pop-up menu.

## 12 Glossary

The glossary only contains brief definitions of the terminology used in Spotfire DecisionSite. Links to more information are available when applicable.

### **API**

The term API stands for **A**pplication **P**rogrammer's **I**nterface, and is a set of functions available to programmers. These functions cover a wide range of tasks, such as graphics, multimedia, fonts, disk access, memory management, etc.

This functionality allows strong integration with legacy systems and novel applications.

### **Bar Charts**

A visualization displaying the data as bars. The value from each record is added to the bar's total value/ Y-axis height.

### **Binning**

The process of grouping *values* with similar properties together in a way that each Bin contains values that, in some important respect, are similar. Not to be confused with clustering, which means grouping similar *records*.

### **Bitmap**

A file format for graphics. The format is used in Spotfire DecisionSite when copying the graphical presentation of a decision tree to the clipboard.

### **Browser**

A program able to display pages encoded in HTML.

### **Categorical Coloring**

Markers, bars or pie charts are assigned distinct colors depending on their values.

### **Centroids**

The centroids are the center points of clusters. How initial centroids are chosen is determined in the K-means Clustering dialog.

### **Check Boxes**

A Query Device enabling toggling of each data value, to control which will be shown in the visualization and which will not.

### **Clustering**

A technique for grouping objects on the basis of their similarity for a specified set of characteristics. The main objective of a cluster analysis is that objects within a cluster should be more similar to each other than they are to objects in other clusters. Spotfire DecisionSite Statistics offers three different kinds of clustering: Hierarchical Clustering, K-means Clustering and Self-Organizing Maps.

### **Column**

Corresponding fields in a set of records constitute a column. (Records go by the name 'rows', in spreadsheet programs).

## Continuous Coloring

Coloring whereby the values in the column determine the shade displayed. The (dissimilar) Begin and End colors selected in the Customize dialog represent the minimum and maximum values in a column. The markers representing records having intermediate values are colored with a blend of the two; depending on their value.

## Control

A control is a graphical object (for example an icon, a button or a window) in the user interface that represents the properties or operations of other objects.

## CSV

Comma-Separated Values. This is a standardized way to save data sets. Each data record is stored as text, using the default list separator as column separator, and a line feed and return character to mark the end of each record. The default list separator is a property of the Regional Settings of your Windows system.

## Data Column

A property in a data set. Each column in your data set is represented by a query device in Spotfire DecisionSite.

## Data Conditioning

Any kind of processing performed prior to visualizing or analyzing the data, such as normalization, pivoting, de-pivoting, etc. These features can be accessed upon data import through the Import Data option. It is also possible to use either of the data conditioning tools from the Data menu after retrieving your data.

## Data Source

A database, a file, or the clipboard.

## DecisionSite Navigator

The precursor to the Guides pane. A browser window integrated into the Spotfire DecisionSite environment, able to communicate with the Spotfire DecisionSite visualization engine.

## Delimiter

This is a separator between data values, for example between columns in a data table or between IDs in a search string.

## Dendrogram

A dendrogram is a branching diagram which represents a hierarchy of categories based on the degree of similarity or number of shared characteristics.

## Deselected Records

The records that do not fulfill the constraints of the query devices.

## Details-on-Demand

A window that shows the data in a marked record. The information can be displayed as plain text, HTML styled text in a window or as styled text in an external HTML browser.

## Docked Window

By default, the Query Device window, the Details-on-Demand window, and the Legend window are docked; they stick to one of the outer borders of the Spotfire DecisionSite main window but can be moved.

### **De-pivoted Data**

Another word for Tall/Skinny data.

### **Distance Measures**

A type of similarity measures.

### **Empty Values**

Empty values are values that are missing in your data set (has a null value). If you intend to use any type of clustering tool, all empty values need to be replaced or else the clustering will not work. There are several replacement methods but all empty values in a column must be replaced using the same method.

### **Full-text Search Query Device**

A query device with which any string of characters can be located in the column under investigation. Boolean logic can be used to refine the search.

### **Glyph**

One of the shapes representing a data record in a 3D scatter plot.

### **Graphical User Interface - GUI**

This is the graphical presentation of the application that you see on the screen.

### **HTML**

**H**yper **T**ext **M**arkup **L**anguage. At its simplest, a language for formatting text. One of the primary reasons for the success of HTML and the World Wide Web is the ability to use links within or between documents.

### **Identifier Column**

The identifier column is the column that contains IDs for the records that are used in a certain calculation. The IDs should be unique for all records in the data set (see also Short/Wide).

### **ISIS**

Integrated Scientific Information System from MDL.

### **ISIS/Draw**

A desktop application from MDL, used for creating and editing models of chemical structures.

### **Item Slider**

A query device with which to select a specific value in a range.

### **Jitter**

An option that displaces the visualization objects randomly in the display window, to make overlapping records visible.

### **Lasso Function**

Enclosing a set of markers with the mouse pointer while pressing **Shift** on the keyboard. This marks the records. The resulting encircling can have any shape.

### **List**

A node in a portfolio where you can add records, annotations and other lists.

**Marker**

One of the shapes representing a data record in a scatter plot. The 3D shapes are also called glyphs.

**Marked Record**

A marker in a scatter plot becomes marked when captured using the lasso or rectangle method (left mouse button pressed while moving pointer). Marked records are given a definable color to distinguish them from the rest of the data.

**Menu Bar**

The row of commands visible at the upper border of a Windows program. Clicking any of the menu titles will display sub menus with additional choices.

**Menu Item**

One of the options available in the menu presented by one of the commands in the menu bar.

**MOL File**

This is a file format used for chemical structures. Each file contains only one structure.

**Navigate Menu**

The Navigate menu used to be located in the top left corner of the DecisionSite Navigator. From here you could reach various tools and resources, or log into and log out of the network. In DecisionSite 8.1 the corresponding functions can be reached via the main menus in DecisionSite.

**Node**

A node is a circle in a decision tree that represents either a record or a cluster of records.

**Null Value**

Empty value. Cell with no value.

**ODBC**

Open **D**ata**B**ase **C**onnectivity, a common method of accessing databases.

**Pie Chart**

A visualization showing data in aggregated "pie segments", which can be split, drilled down into and taken apart.

**Pivoted Data**

Another word for Short/Wide data.

**Pop-up Menu**

Menus that are available if you right-click directly in the graphical user interface. The content of the menu depends on where you click.

**Portfolio**

A portfolio is a data file in XML-format that can be viewed in the Portfolio tool and which makes it possible to work with genes or experimental results in a structured way.

**Profile**

Synonymous to a record (data point) in Spotfire DecisionSite.

## Profile Chart

A visualization type where column names are plotted along the X-axis, and the value in each column on the Y-axis. This means that each record is presented as a line.

## Properties

The dialog box enabling changes to query devices, visualization objects—markers, pies, bars, backgrounds and HTML code. Located in the Edit menu. Accessible with [Alt+Enter] **Edit > Properties** and a toolbar button.

## Query Device

A tool that selects data having certain values for visualization. There are five kinds of query devices: range sliders, item sliders, full-text searches, check boxes and radio buttons.

## Query Device Window

The window where the query devices are located. By default, this window is placed in the upper right corner.

## Range Slider

A Query Device used to select a range of data. The default device for numerical data. A range slider enables narrowing, broadening and moving the interval of the selected data of the designated column.

## Record

One entry or line in a database or data set. Sometimes called a row.

## Sampling

In previous versions of DecisionSite, subsets of data could be extracted using a sampling tool. This is no longer supported.

## SAR Table

*Structure-Activity Relationship* table. The SAR table combines structural and other data about compounds into a single spreadsheet.

## Scatter Plot

A visualization type showing the records as markers in a two-dimensional or three-dimensional diagram.

## SDFFile

This is a file format used for exporting ISIS data. Structure-data files contain structures and data for any number of molecules. SDFfiles can be imported into ISIS for Excel.

## Selected Records

The records explicitly chosen for display by manipulating the query devices and zoom bars. Do not confuse with the *Marked Records*. The option "Work on: Selected records" in the calculation dialogs means that only the records selected via the query devices are included in the calculations.

## Selecting Data

Using the query devices to control which data is visualized.

**SFS**

The file extension that Spotfire DecisionSite applies when saving data set in its proprietary format.

**Short/Wide**

A data table format with relatively few rows and many columns, suitable for analysis. The identifier column in a short & wide data table has a unique value for each row, in other words, all data associated with a specific ID is available on one row in the table.

**Similarity Measure**

Methods for calculating the similarity between data.

**SQL**

Structured Query Language, a common language used for formulating queries when investigating databases.

**Tall/Skinny**

A data table format with many rows and relatively few columns, commonly used for automatically generated data, but often not suitable for analysis. The identifier column in a tall & skinny data table contains multiple values, which means that the same ID and information associated with it appear on many rows. .

**Toolbar**

The bar at the top of the application or tool window that contains buttons that are shortcuts to frequent commands on the menus.

**Tools**

The tools provide the special functions of your DecisionSite, such as clustering or structure analytics. You reach the tools via the **Data** and **Tools** menus.

**Trellis plot**

A way of splitting a visualization into panes and organizing these in a grid layout.

**Visualization**

A graphical presentation of data in Spotfire DecisionSite, e.g., scatter plot, pie chart, etc. The query devices control which data is displayed.

**Web link**

A link to an external web site that lets you send a query about marked records.

**Zoom Bar**

The bars along the edges of the visualization window. By manipulating them it is possible to zoom in on details of the visualization.

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