



First Steps in **Mayday 2.0**

Nils Gehlenborg, December 2005

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Part 1

Introduction

General Information

- user-friendly microarray data analysis workbench
- name stands for “Microarray Data Analysis”
- developed at the Center for Bioinformatics (ZBIT) at the University of Tuebingen in Kay Nieselt’s group
 - Nils Gehlenborg, Janko Dietzsch, Matthias Zschunke, Stephan Symons, Markus Riester and Kathrin Deubel
- modular architecture
 - lean core
 - functionality delivered by plug-ins
- implemented in Java
- open source software
 - GPL (core) and LGPL (plug-ins)

- “users” (wet lab people)
 - Mayday has a straightforward graphical user interface
 - it runs on many platforms
 - new methods can be added easily
- “developers” (dry lab people)
 - newly developed methods can be added as either Java plug-ins or R scripts
 - Mayday can be adapted to the local environment (special databases, file formats, etc.)
 - it runs on many platforms

- supports cDNA and oligonucleotide arrays
- works on preprocessed, normalized expression matrices (rows = genes, columns = conditions)
- plug-in categories
 - visualization
 - clustering
 - data import and export
 - database
 - statistics
 - R
 - filters
 - machine learning (soon)

- Sun Java Runtime Environment (JRE) 1.5, also known as Java 5.0
- Windows, Linux or MacOS, others might work as well
- at least 256 MB of RAM, better more than 512 MB

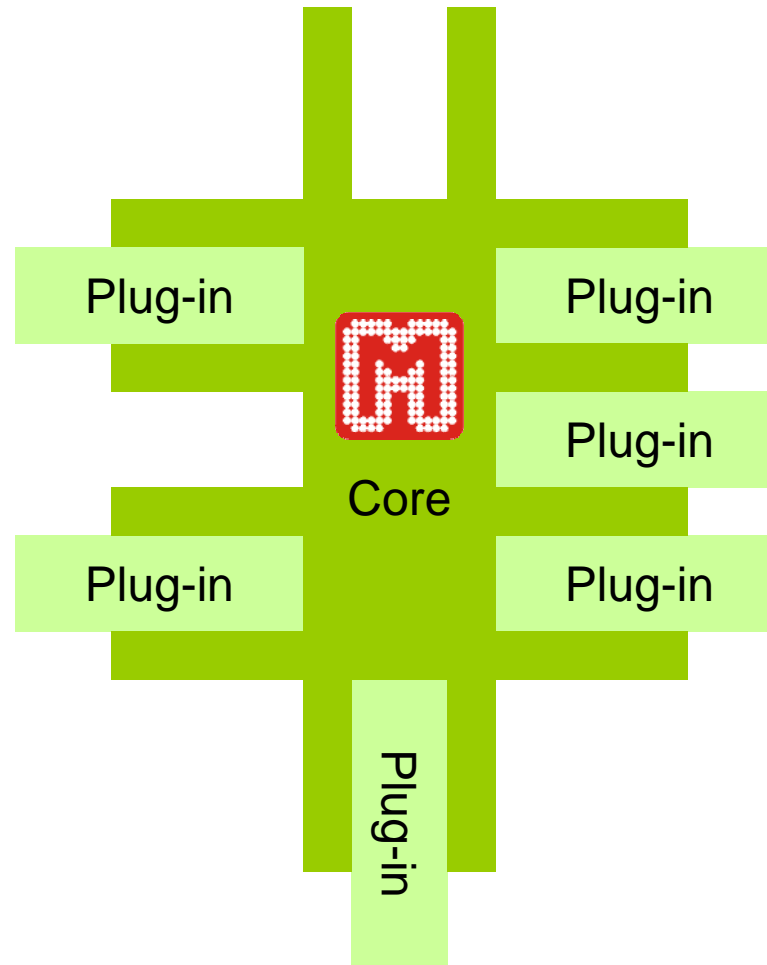
Resources

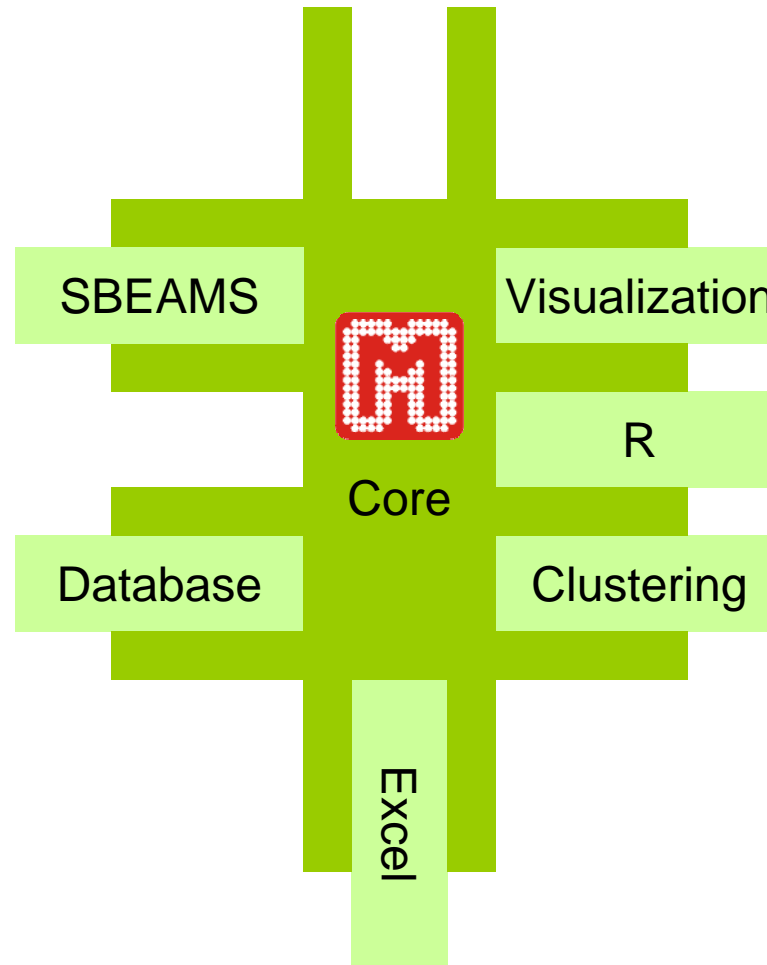
- <http://www.zbit.uni-tuebingen.de/pas/mayday>
- download
 - core software and plug-ins
 - “How-To”s (explain basic setup and installation of plug-ins)
 - posters and presentations about Mayday
 - tutorial (for Mayday 1.1)
 - technical documents explaining architecture and design of the core software and some plug-ins
- keep yourself informed about the latest updates

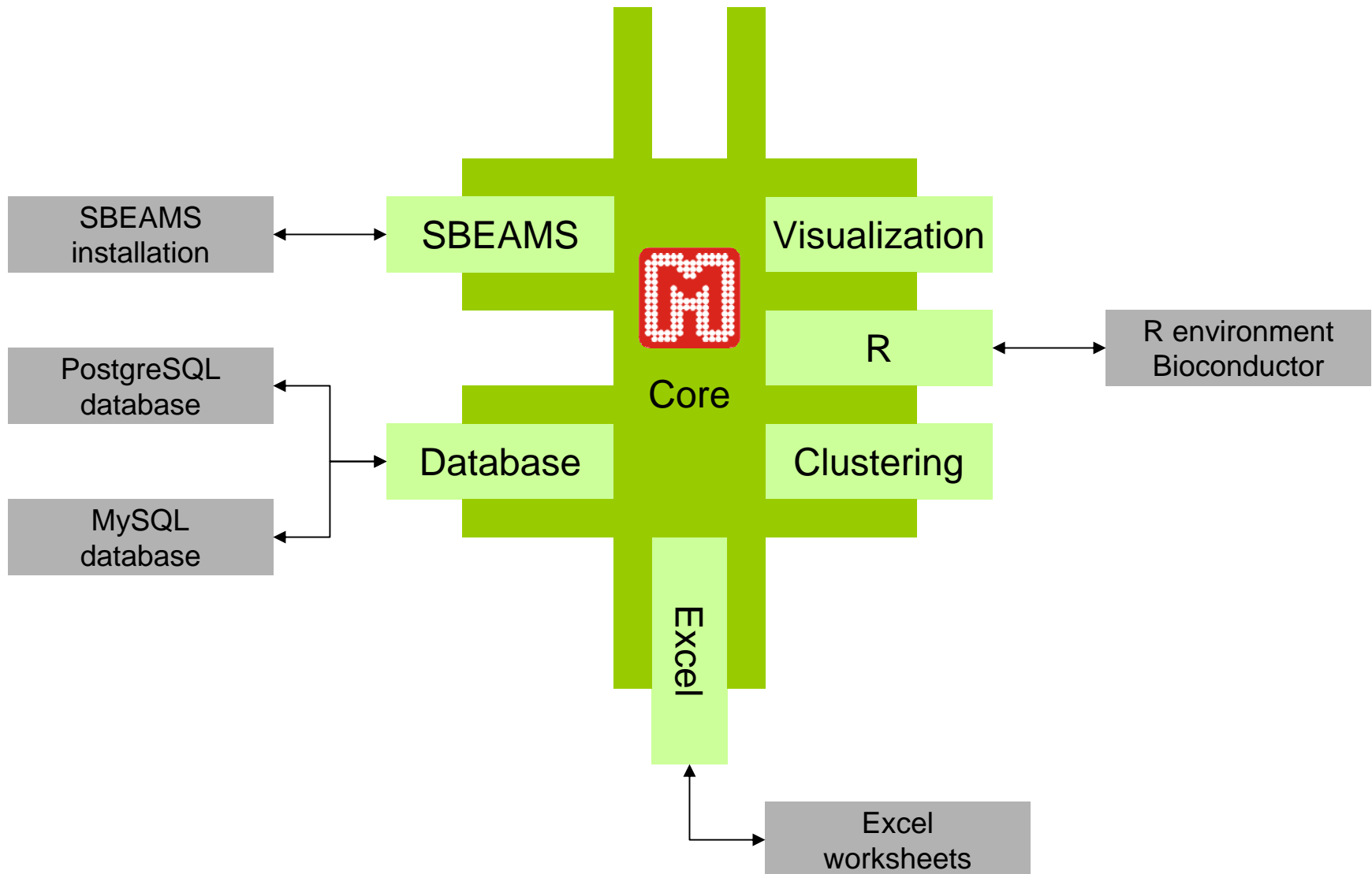
- mayday-announce@googlegroups.com
 - mailing list for announcement of new releases and major updates to the website
- mayday-discuss@googlegroups.com
 - mailing list for developers (invitation only)

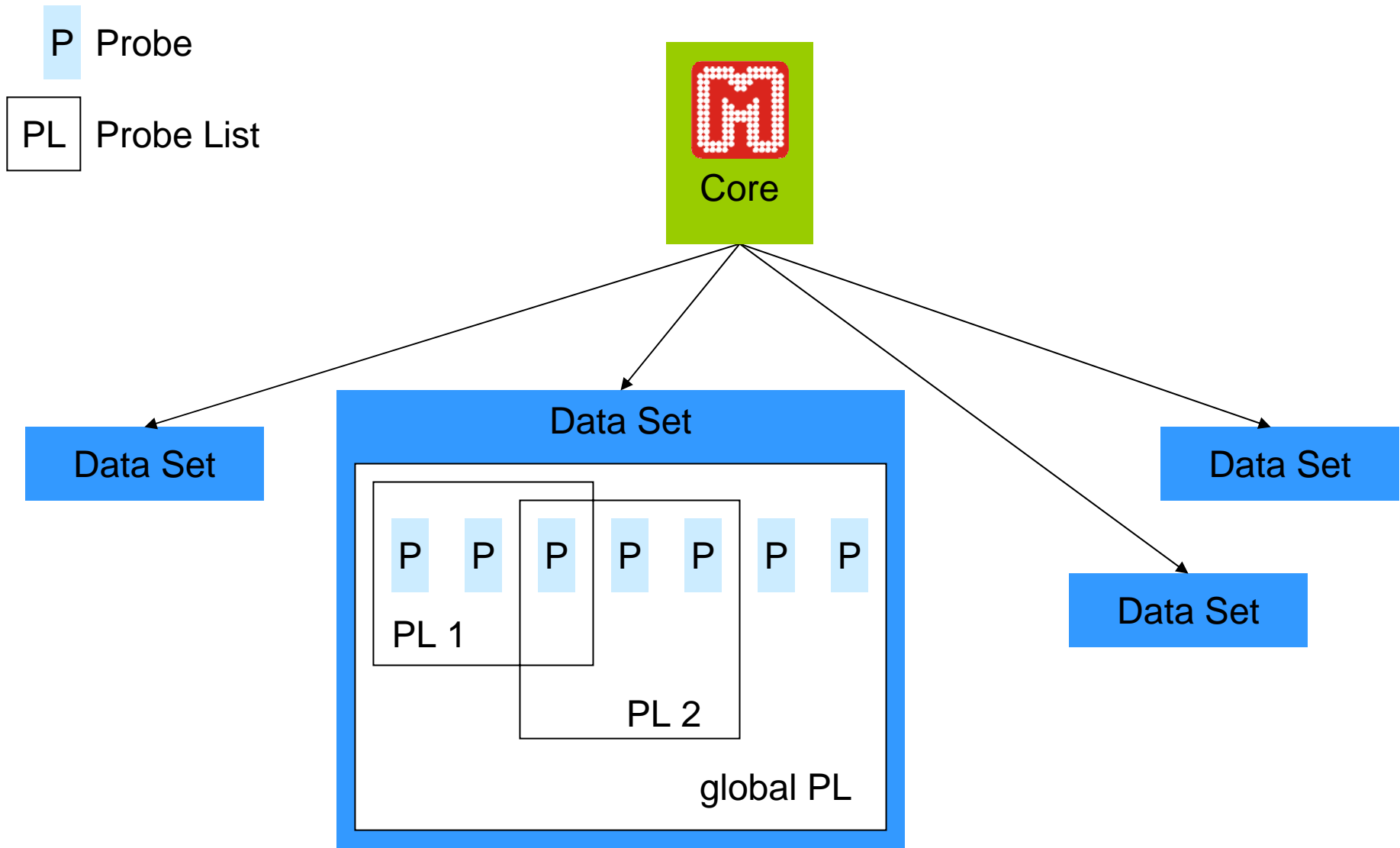
- description of the core software and some plug-ins
 - Janko Dietzsch, Nils Gehlenborg and Kay Nieselt, *Mayday – a microarray data analysis workbench*, submitted to Bioinformatics.
- description of the heatmap implementation in Mayday and its special features
 - Nils Gehlenborg, Janko Dietzsch and Kay Nieselt, *A Framework for Visualization of Microarray Data and Integrated Meta Information*, Information Visualization, Volume 4, Number 3, 2005, 164 – 175.
- preprints are available

Architecture









- core manages data sets (one or more)
- core exchanges data structures with plug-ins
 - probe lists play a very important role in this
- probe data structures represent genes, probe sets, etc. depending on the array type
- probes store expression values (usually ratios) for one or more conditions
- probe lists are not lists but sets in the mathematical sense
 - “probe set” unfortunately already has another meaning (Affymetrix)

Part 2

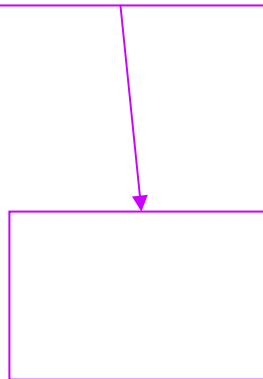
Tutorial

- Mayday configured with all available plug-ins
 - all external libraries must be installed (Batik, JDBC drivers, CLI, ...)
 - R plug-in must be configured and ready to go, i.e. R must be installed
- ZIP archive with tutorial files downloaded and extracted
- MayDB configured and accessible
 - must contain tutorial data sets (with and without meta information)

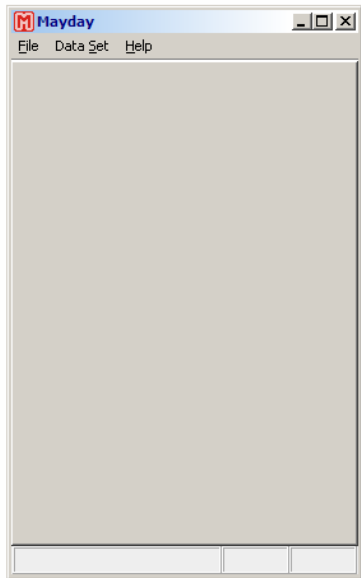
Text in this box describes what is going on.

Text in this box describes what you are supposed to do.

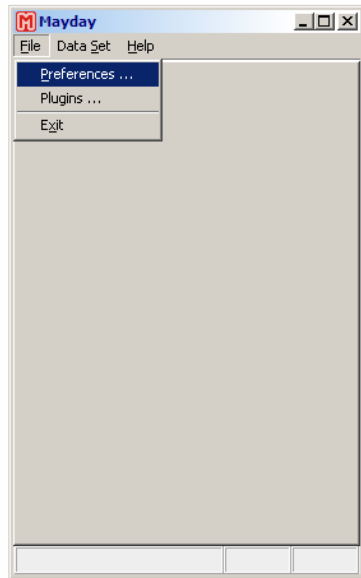
Text in this box describes specific parts of the user interface.



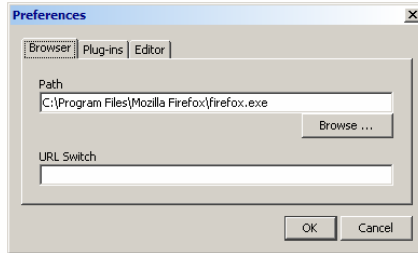
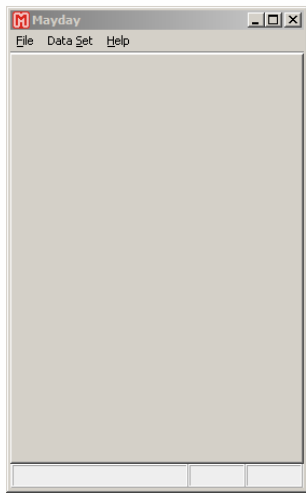
Preferences and the Plug-In Manager



Start Mayday and wait until all plug-ins have been loaded.
Then open the “File” menu.

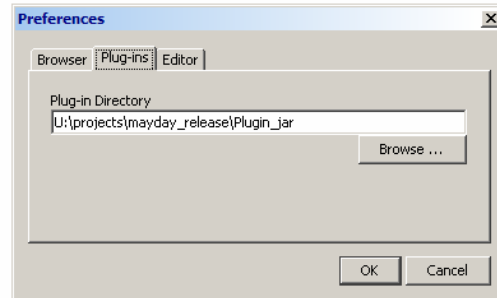
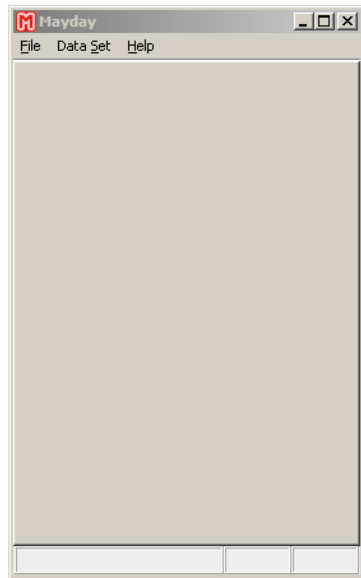


Click “Preferences ...”



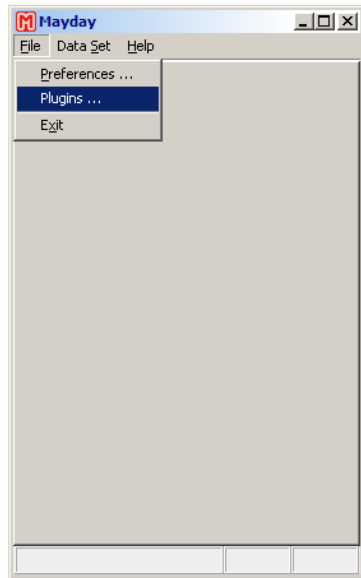
In this dialog you can set the global preferences for Mayday, i.e. preferences that are used by all plug-ins.

Review the information, then select tab “Plug-ins”.

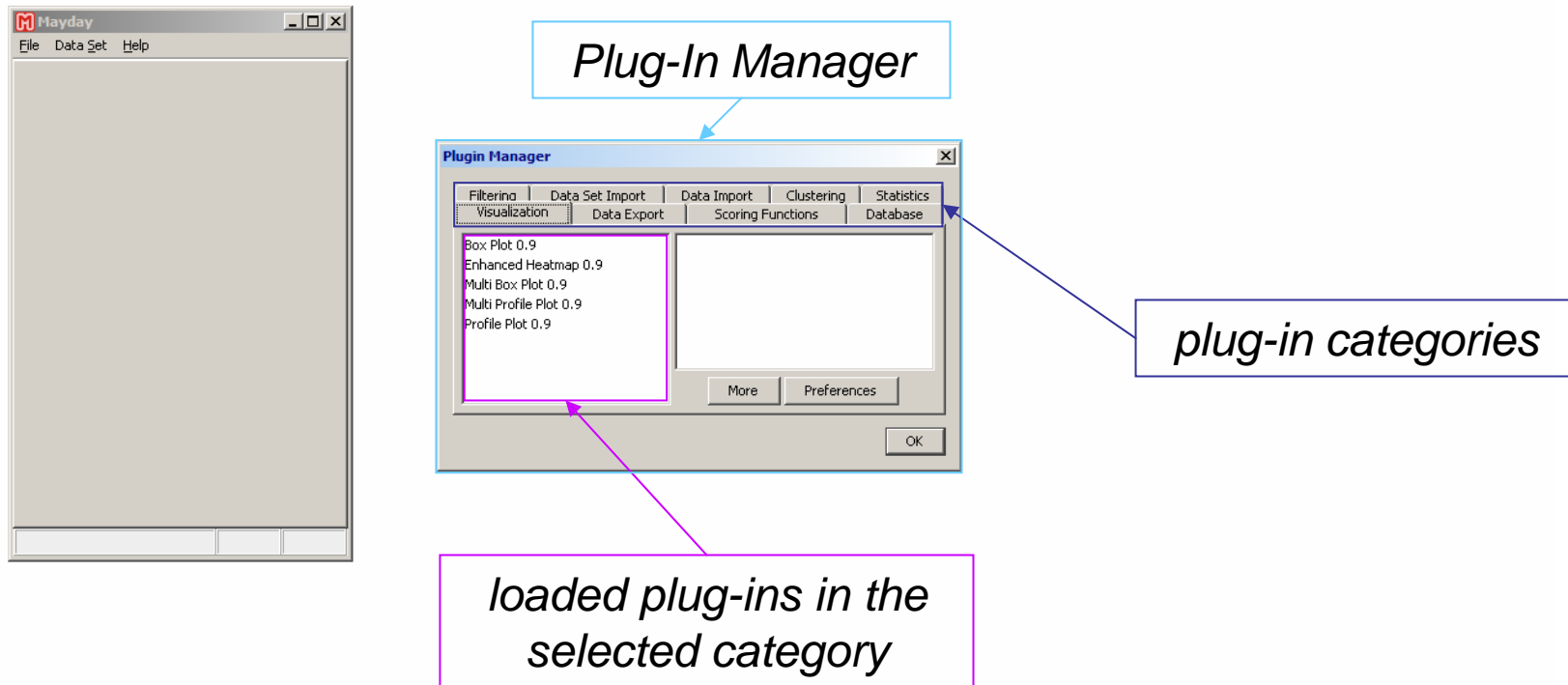


This is the directory that will be searched for plug-ins. Make sure you update this if you ever move your Mayday installation.

Review the information. Then click “Cancel” to close the dialog without confirming changes.

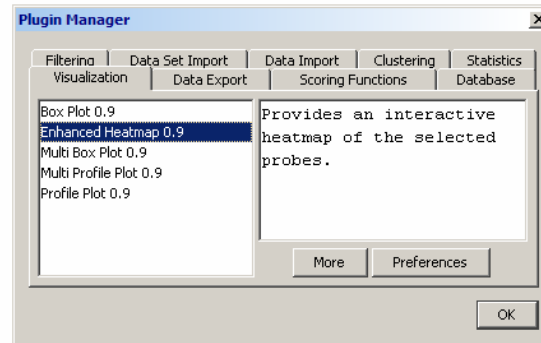
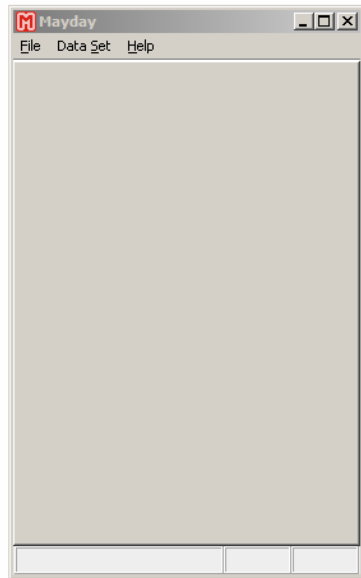


Open the file menu
and select “Plugins ...”.

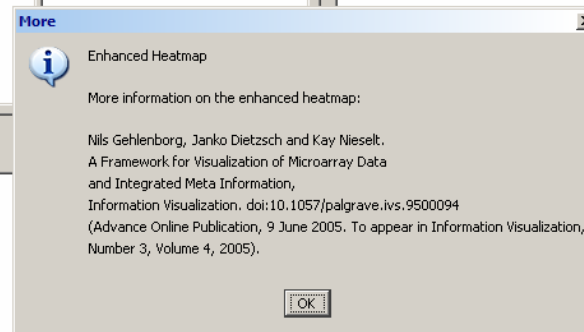
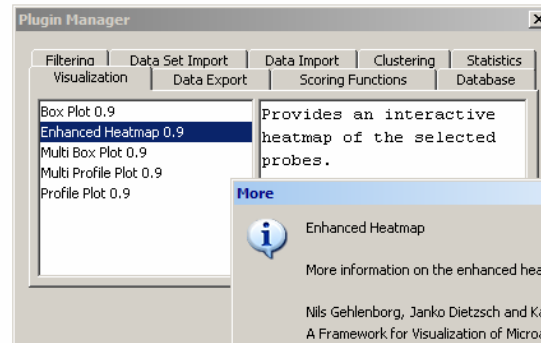
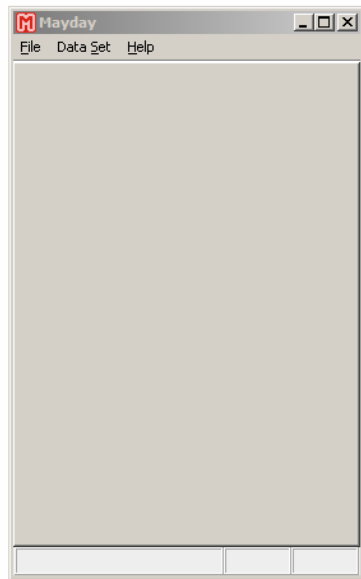


The plug-in manager displays a list of all loaded plug-ins and the categories they are assigned to. You can also obtain additional information about plug-ins here and set special preferences.

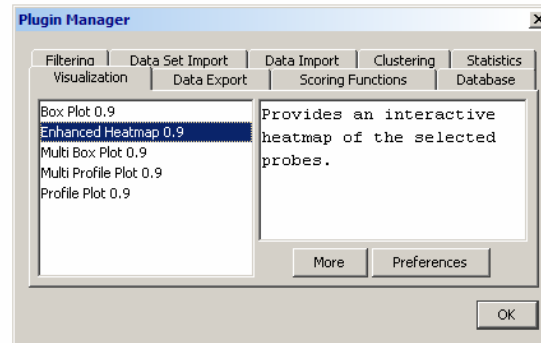
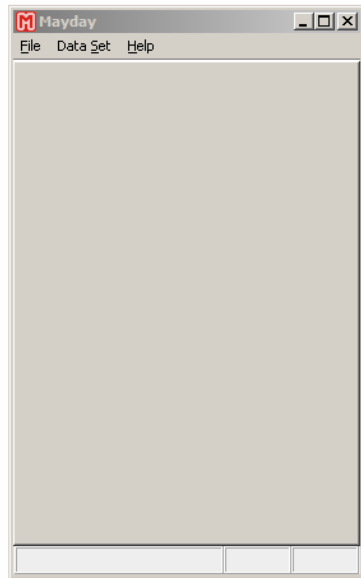
Select “Enhanced Heatmap”.



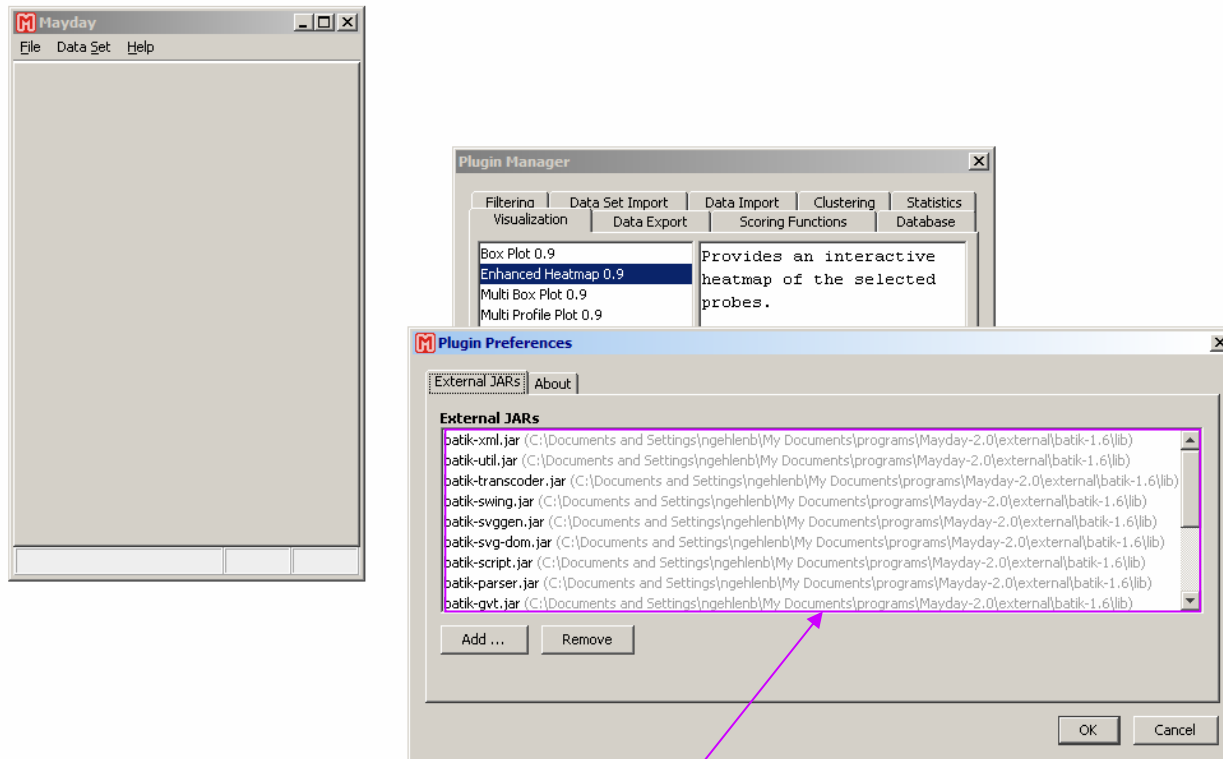
Click on "More".



Click “OK” to close the dialog.

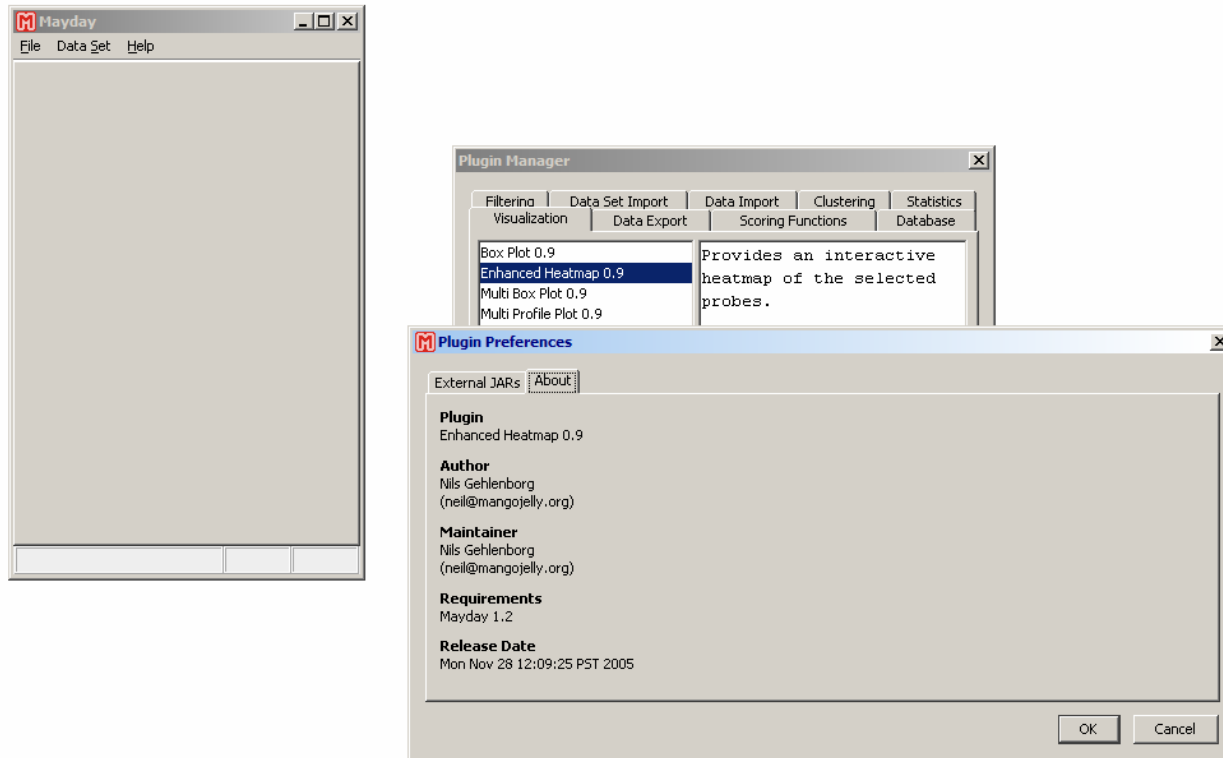


Click on "Preferences".



Select the tab “About”.

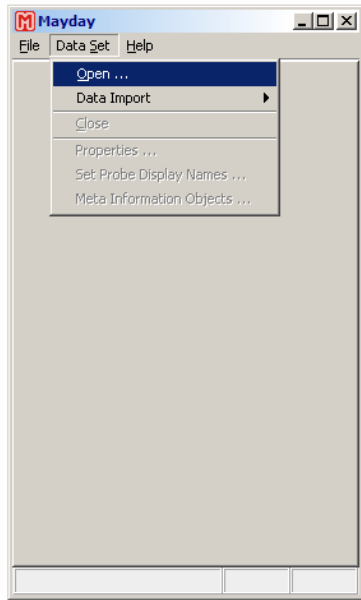
list of external JAR files (libraries) required by the plug-in to run properly; JARs will be loaded automatically when the plug-in is called; you have to add the plug-ins manually during the initial setup of Mayday (not described here)



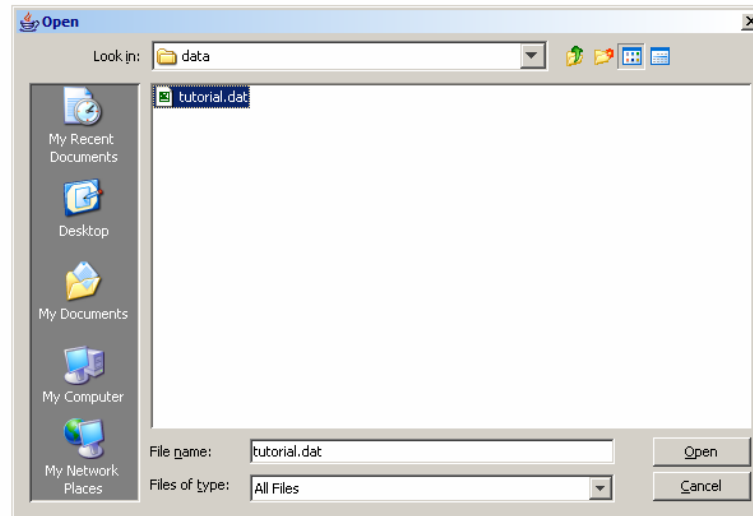
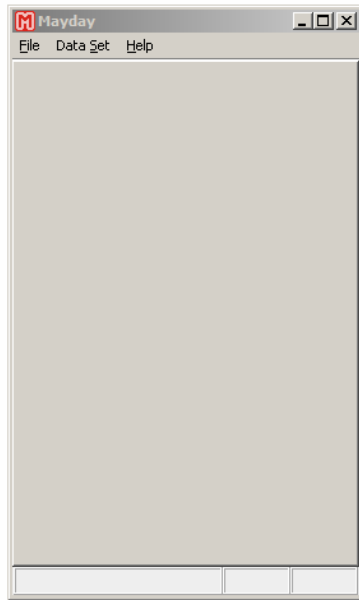
Click “Cancel” to close the dialog without confirming changes.

Loading Expression Data

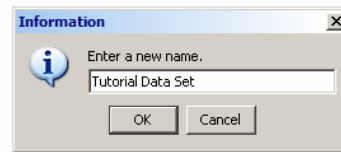
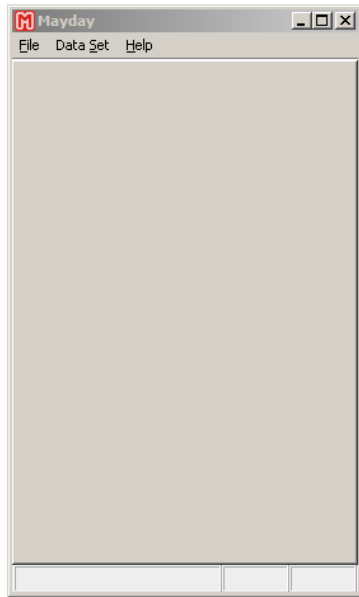
- Mayday has “native” support for a simple text file format
 - each row represents a gene/probe set/...
 - each column represents a condition/array/...
 - first row and column contain names for respective entities
 - all others contain expression values (can be missing)
 - columns are tab-delimited



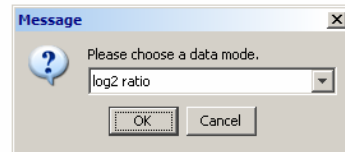
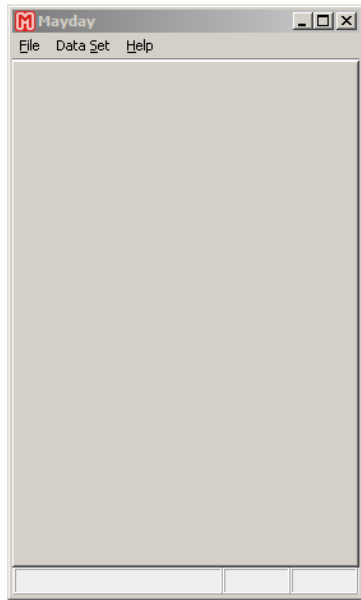
Click on the “Data Set” menu item and select “Open ...”.



Select a file that contains expression data formatted as described before.
Click "Open".



Enter a name for the data set.
The name has to be unique. It
may contains spaces.



Indicate the data mode, i.e. whether the expression data are absolute values or ratios, etc.

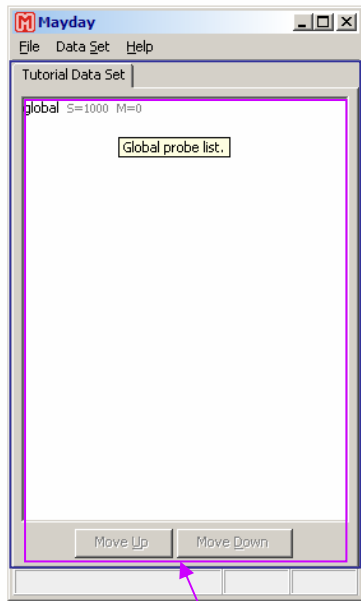


You have now loaded a data set. Mayday automatically generated a global probe list for you. “global” is the name of this probe list. Probe list names have to be unique within a data set. The size of the probe list, i.e. the number of probes it contains, is printed after the name (“S=1000”).

How to Work with Probe Lists

Getting information about probe lists

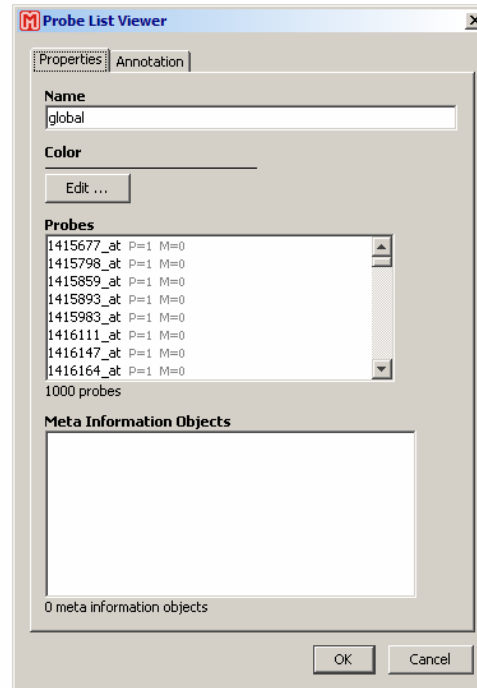
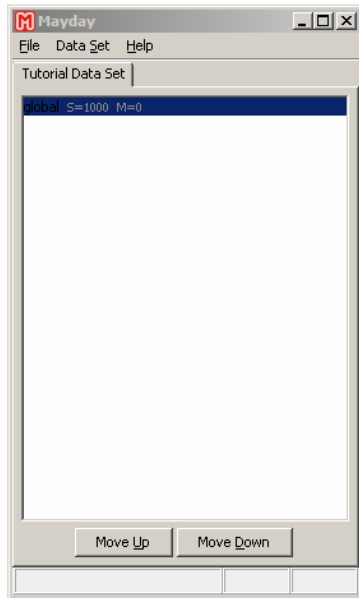
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Data Set Manager

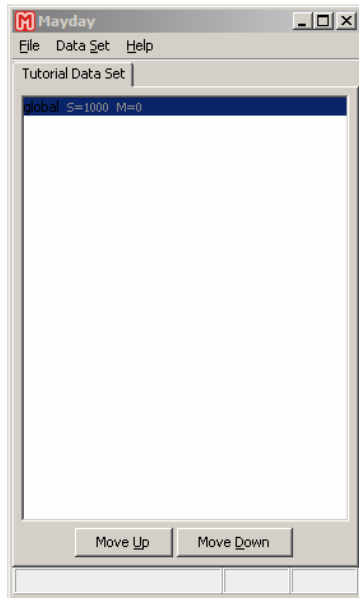
Probe List Manager

Double-click the name of the probe list to get more information about it.



This dialog shows the probes contained in this probe list and meta information associated with it (more on that later). You can edit the name, assigned color and additional annotation.

Select “Annotation” to view and edit additional information about this probe list

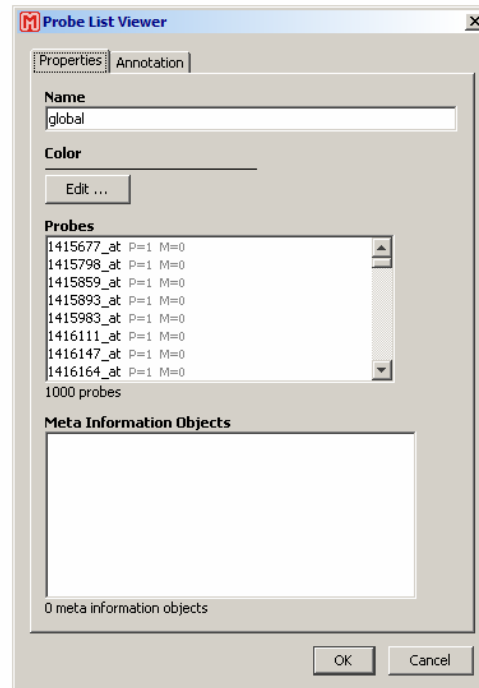
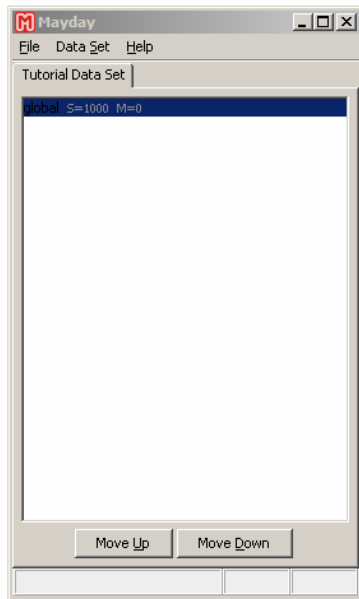


Add information about the selected probe list here. This is useful for notes (quick info) and for in-depth information (info, which can be HTML-formatted).

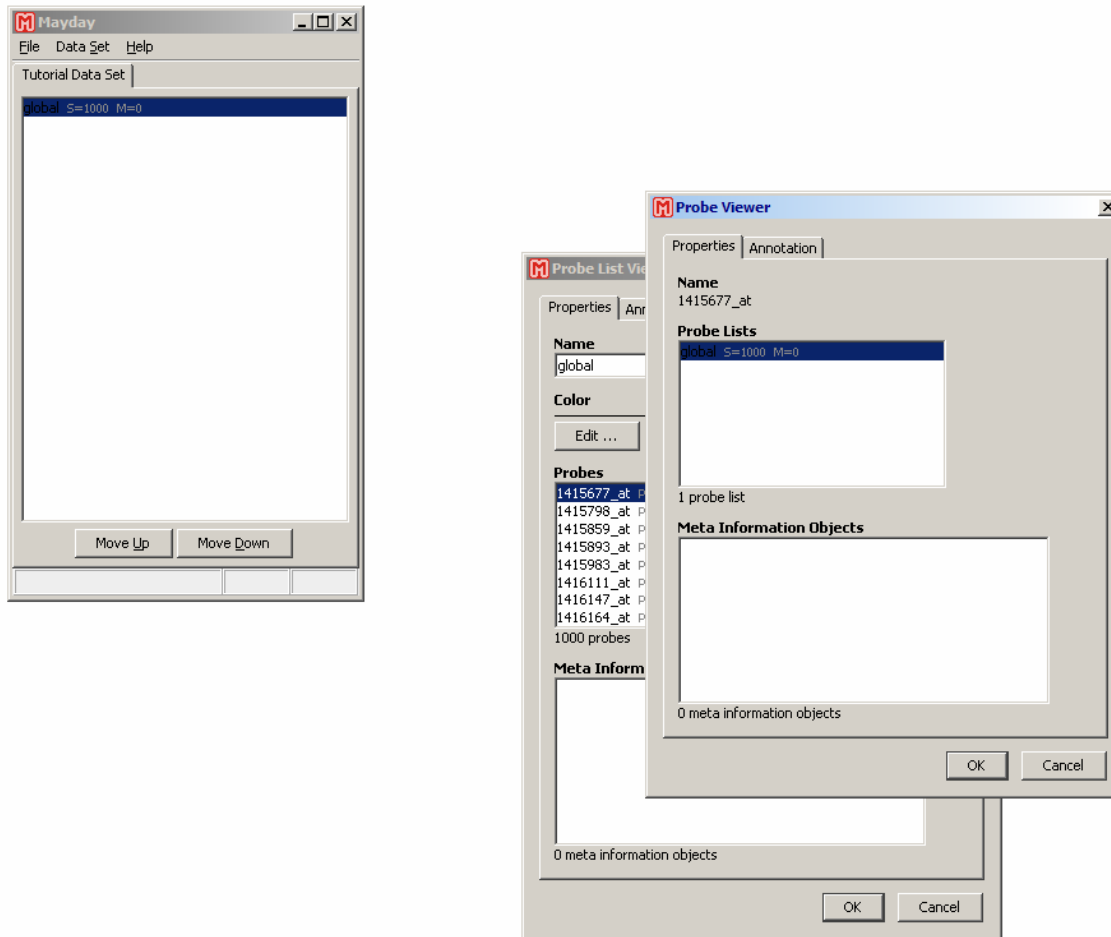
Select "Properties" to go back to the previous view.

Getting information about probes

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Double-click the first probe in the list to get more information about it.

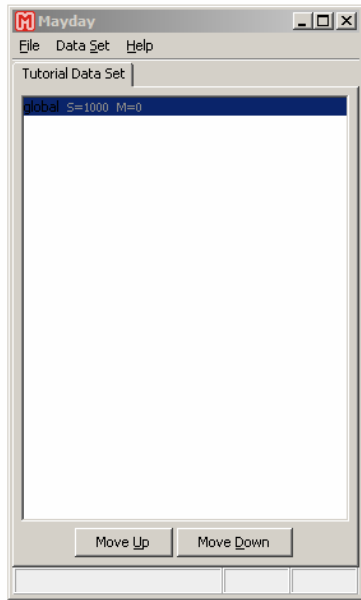


This dialog shows all probe lists that the probe is contained in as well as meta information assigned to it. The tab “Annotation” is the same as for probe lists and can be used to store information about the probe.

Hit “OK” in both dialogs to confirm any changes before closing.

Creating a probe list from scratch

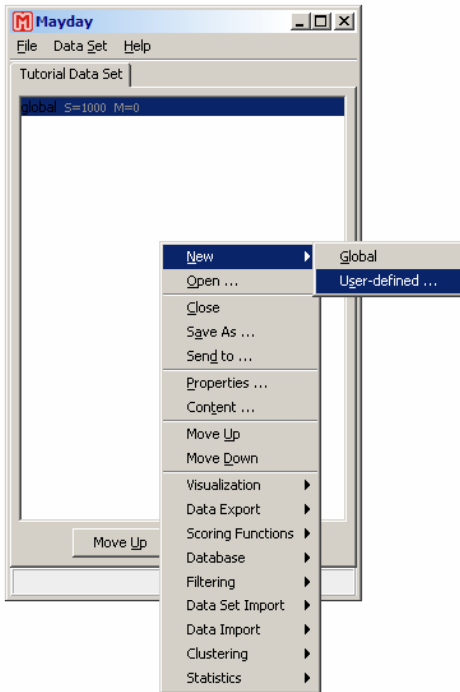
47



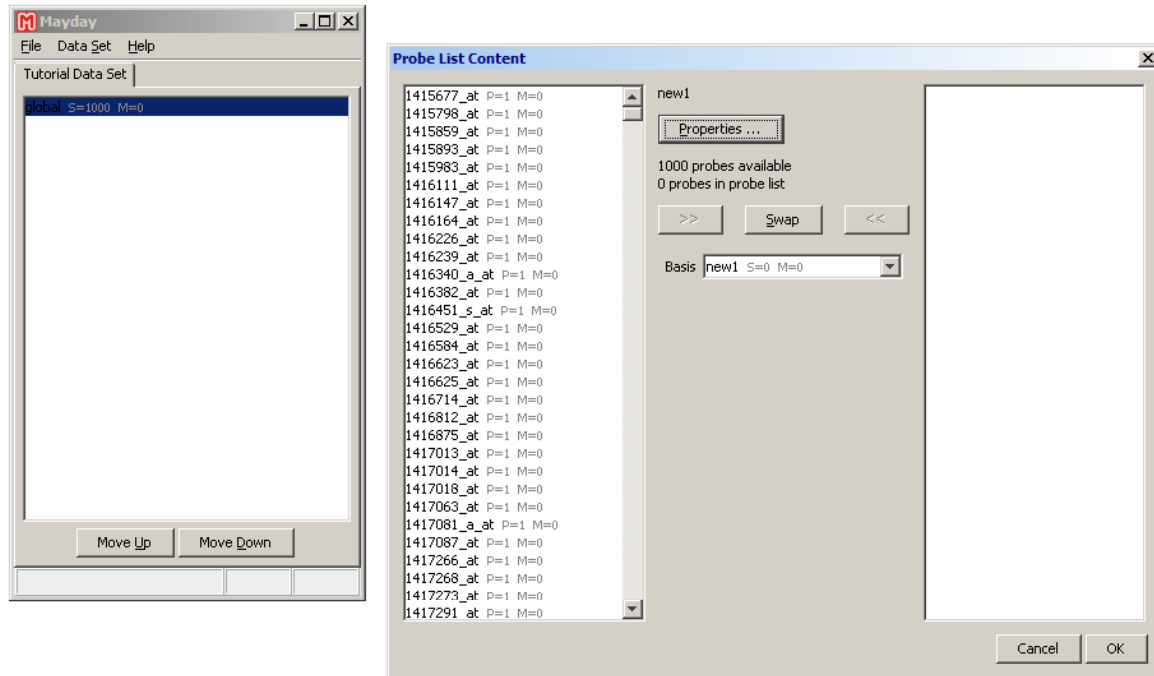
Right-click somewhere in the list of probe lists to get the probe list manager context-menu.

Creating a probe list from scratch

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Select sub-menu “New” and click “User-defined ...”.

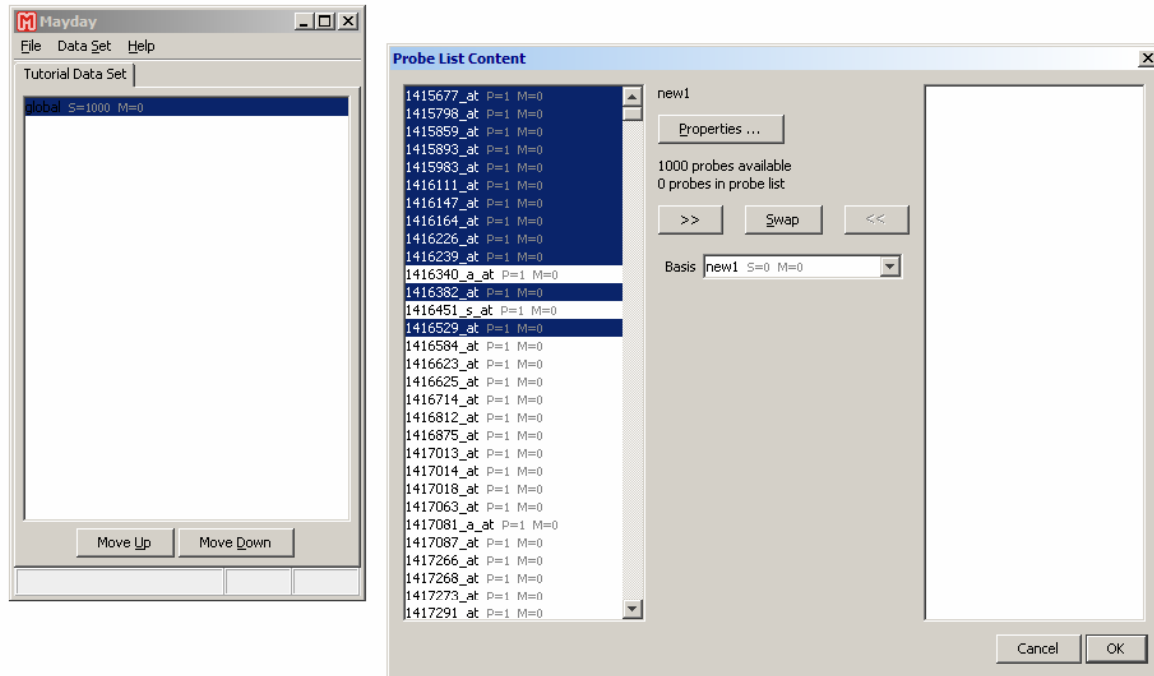


The left list contains all probes of the data set. The right list contains all probes that are contained in the probe list you are about to create. Select a probe list a basis if you want to create a new probe list similar to an existing one.

Select one or more probes. You need to keep the CTRL key or the SHIFT key pressed to select multiple probes.

Creating a probe list from scratch

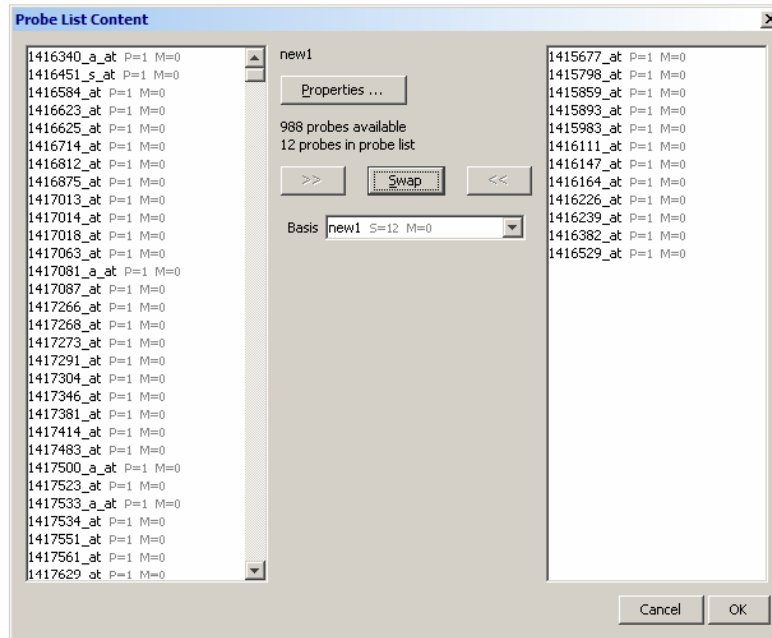
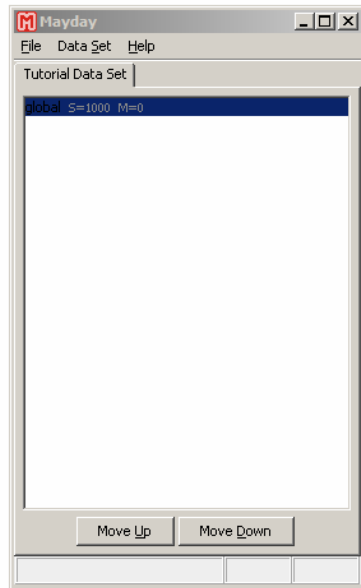
50



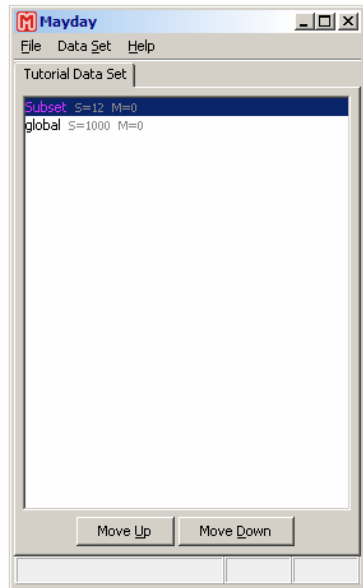
Hit the “>>” button to add the selected probes to the new probe list.

Creating a probe list from scratch

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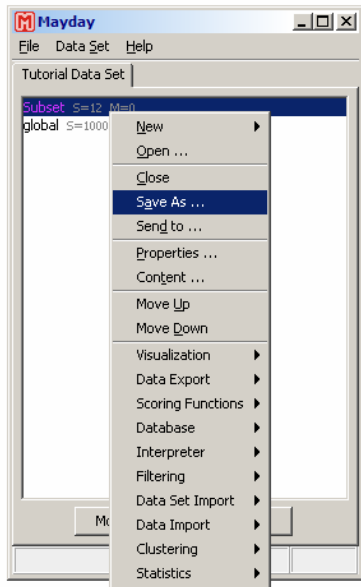


Hit the “Properties” button to change the name of the new probe list and to assign another color. Then confirm your changes and close the Probe List Content Dialog by clicking “OK”.

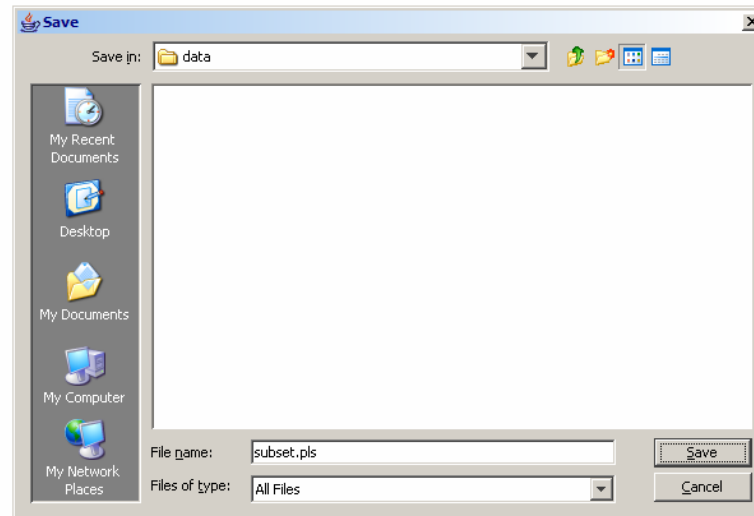
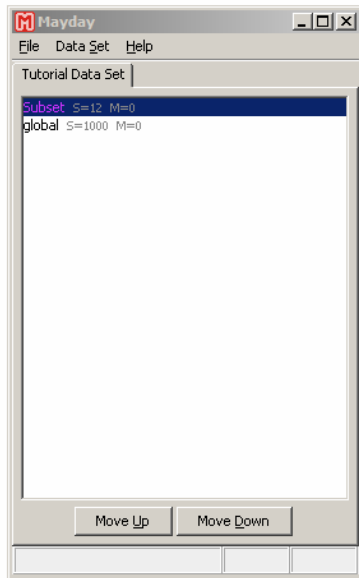


You can see the new probe list (called “Subset”). It has been assigned a specific color, which will come in handy when we visualize the probes of this probe list later on.

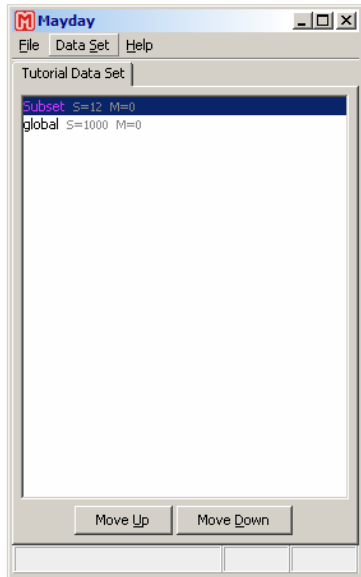
Select probe list “Subset” and open the probe list manager’s context menu.



Select “Save As ...”.



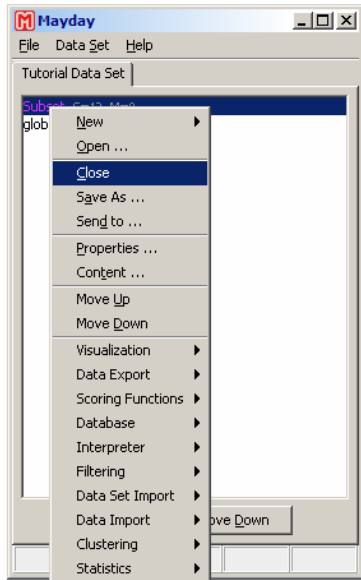
Enter a name for the probe list file and click "Save".



Select probe list “Subset”
and open the probe list
manager’s context menu.

Closing a probe list

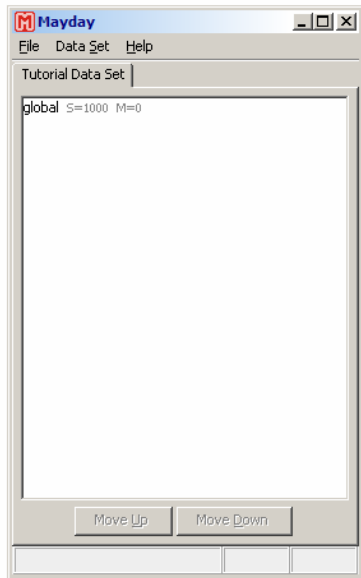
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Select “Close”.

Opening a probe list

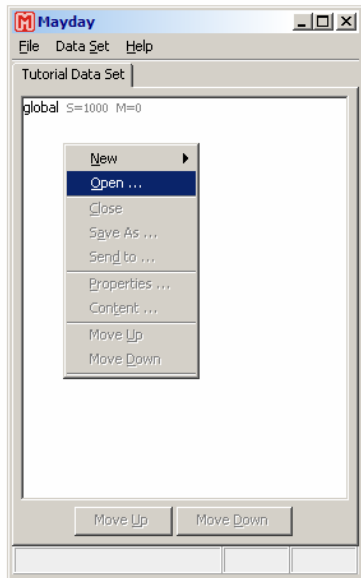
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Open the probe list manager's context menu.

Opening a probe list

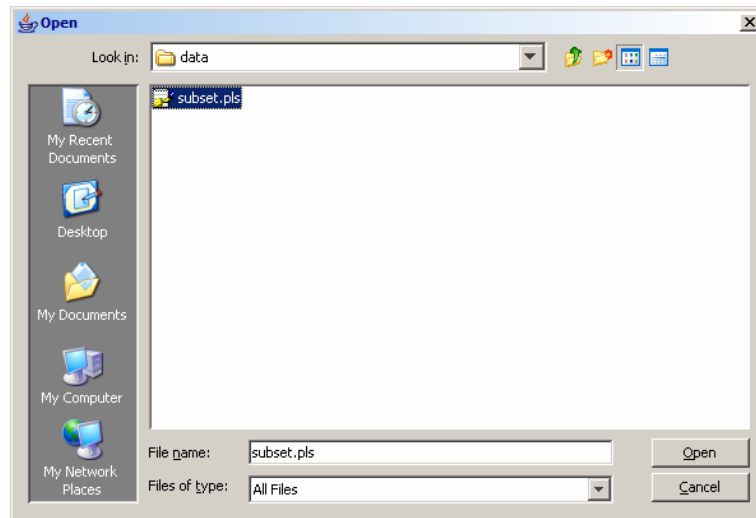
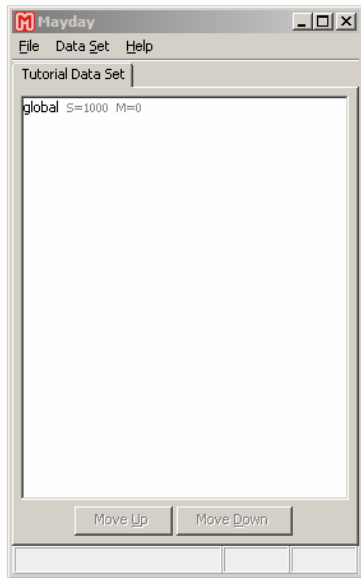
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Select “Open ...”.

Opening a probe list

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Go to the directory where you just saved probe list "Subset". Select it and click "Open".



Now you know how to save your probe lists for use in later sessions. The probe lists are stored as a list of probe identifiers in an XML file format. You can edit those files with a text editor of your choice. Besides the probe identifiers the name, color and annotation is stored.

Clustering Expression Data

Calling a plug-in on a probe list

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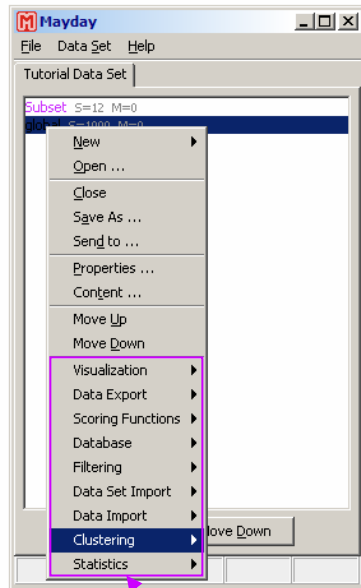
Select the global probe list.



Right-click somewhere in the list of probe lists to get the probe list manager context-menu for the selected probe list.

Calling a plug-in on a probe list

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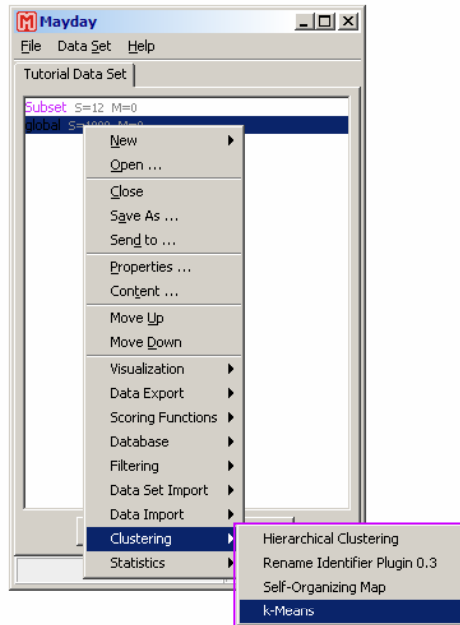


Select sub-menu "Clustering".

*plug-in categories,
depends on
installed plug-ins*

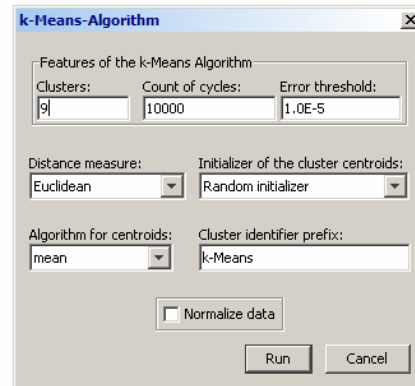
Calling a plug-in on a probe list

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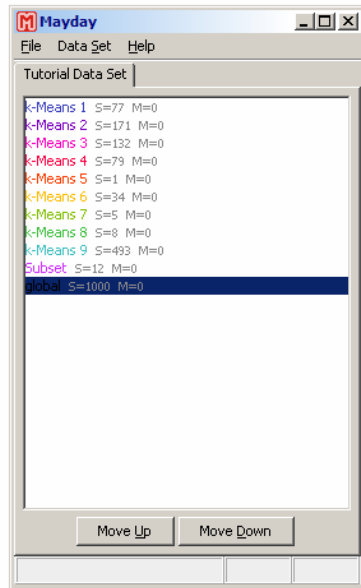
Click “k-Means”.

*plug-ins in category
“Clustering”, depends
on installed plug-ins*



Here you see the k-Means clustering setup dialog. It is provided by the k-Means clustering plug-in and not part of the core software.

Leave all settings as they are and click on "Run".



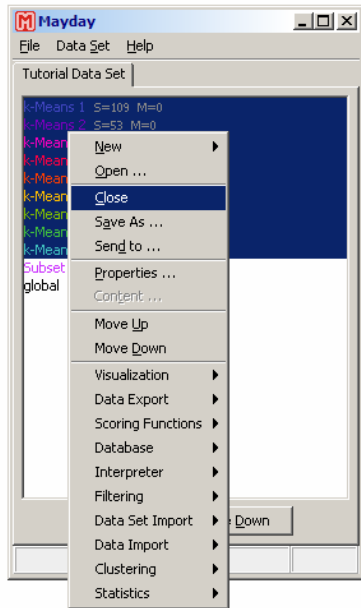
The result of the clustering algorithm is a new set of probe lists. Each probe list represents a cluster. The size of the clusters is indicated behind the cluster names.

Select the newly created probe lists.



You will now close remove your clusters and load a probe lists for nine clusters. This is to make sure your clusters are the same that were used to create this tutorial.

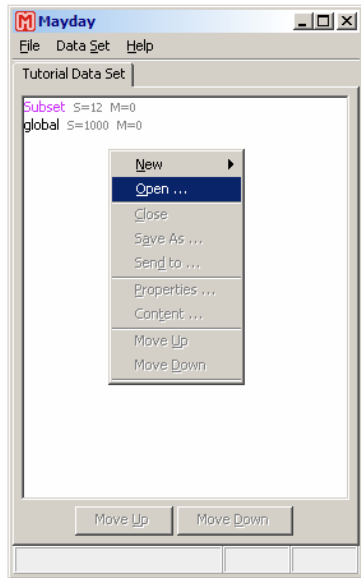
Open the probe list manager's context menu.



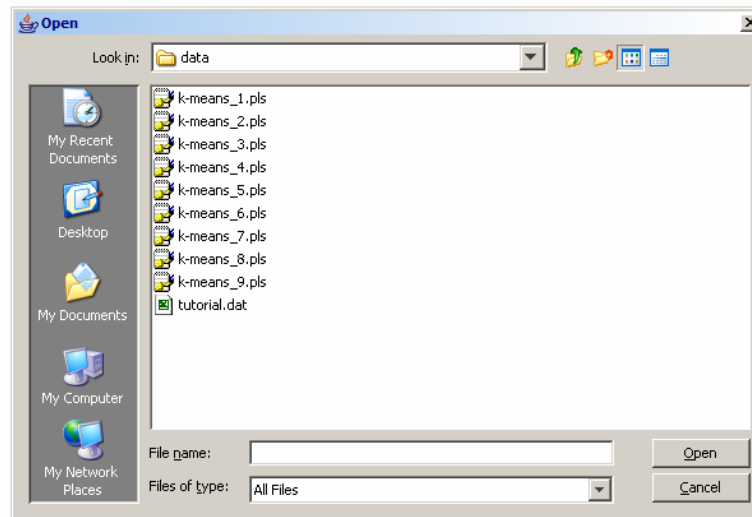
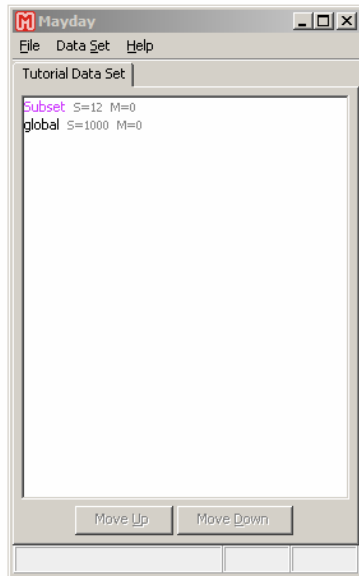
Select "Close".



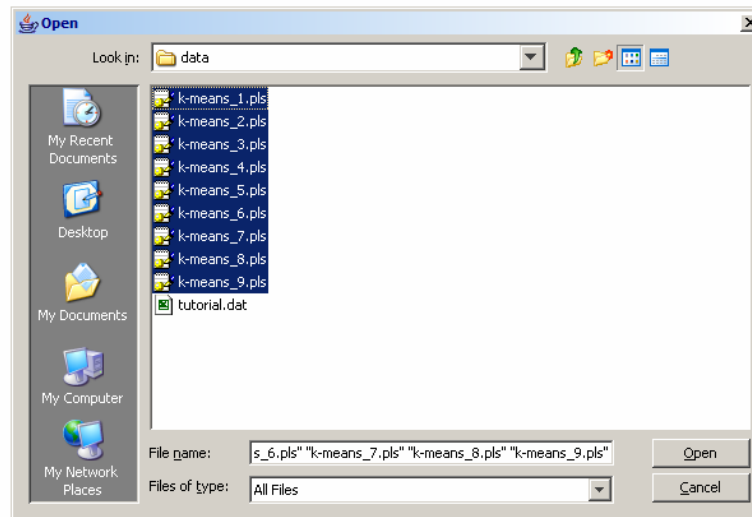
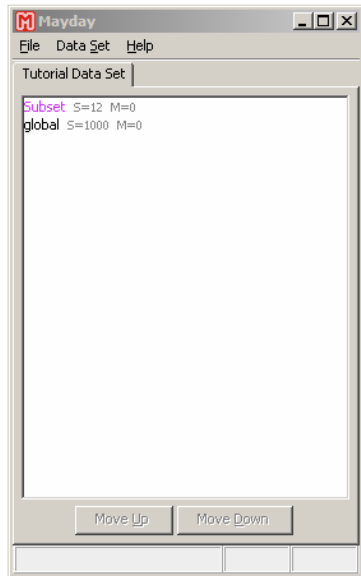
Open the probe list manager's context menu.



Select "Open ...".



Select the probe lists that came with the tutorial data set file. Begin probe list “k-means_9.pls”, then select “k-means_8.pls” and so on.



In particular for loading clusters it is very useful to select multiple probe lists at the same time. Note that the probe lists will be loaded in the inverse order in which you selected them.

Click “Open” to load the selected probe lists.

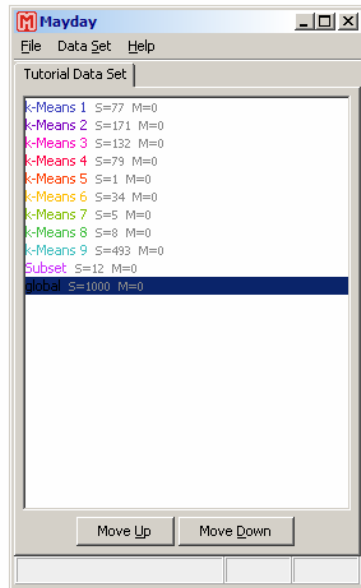


You have now loaded the clusters that were used when the tutorial was created. Colors and cluster shapes are going to be the same in your Mayday session and the tutorial slides.

Visualization for Data Exploration

Visualizing a single probe list

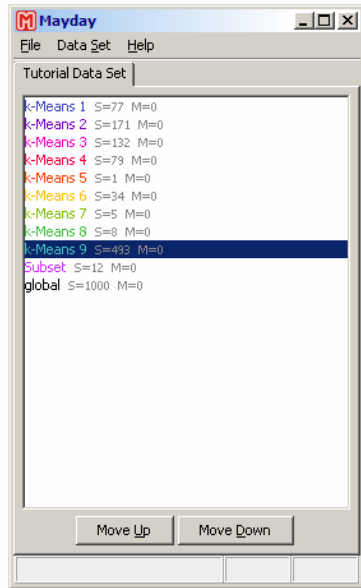
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Select the probe list named “k-Means 9” from the probe list manager.

Visualizing a single probe list

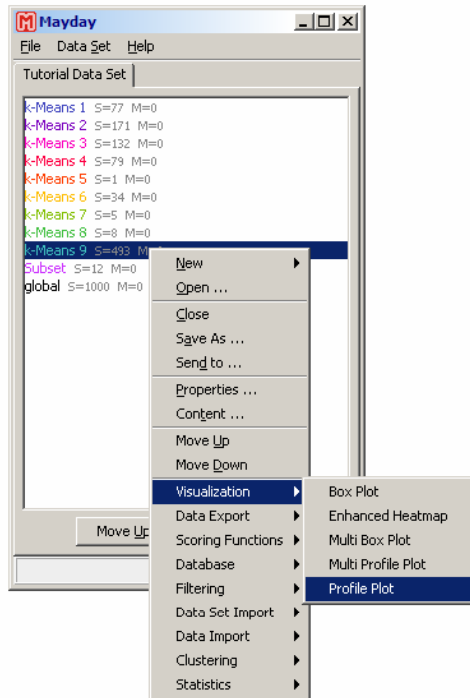
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Right-click the probe list.

Visualizing a single probe list

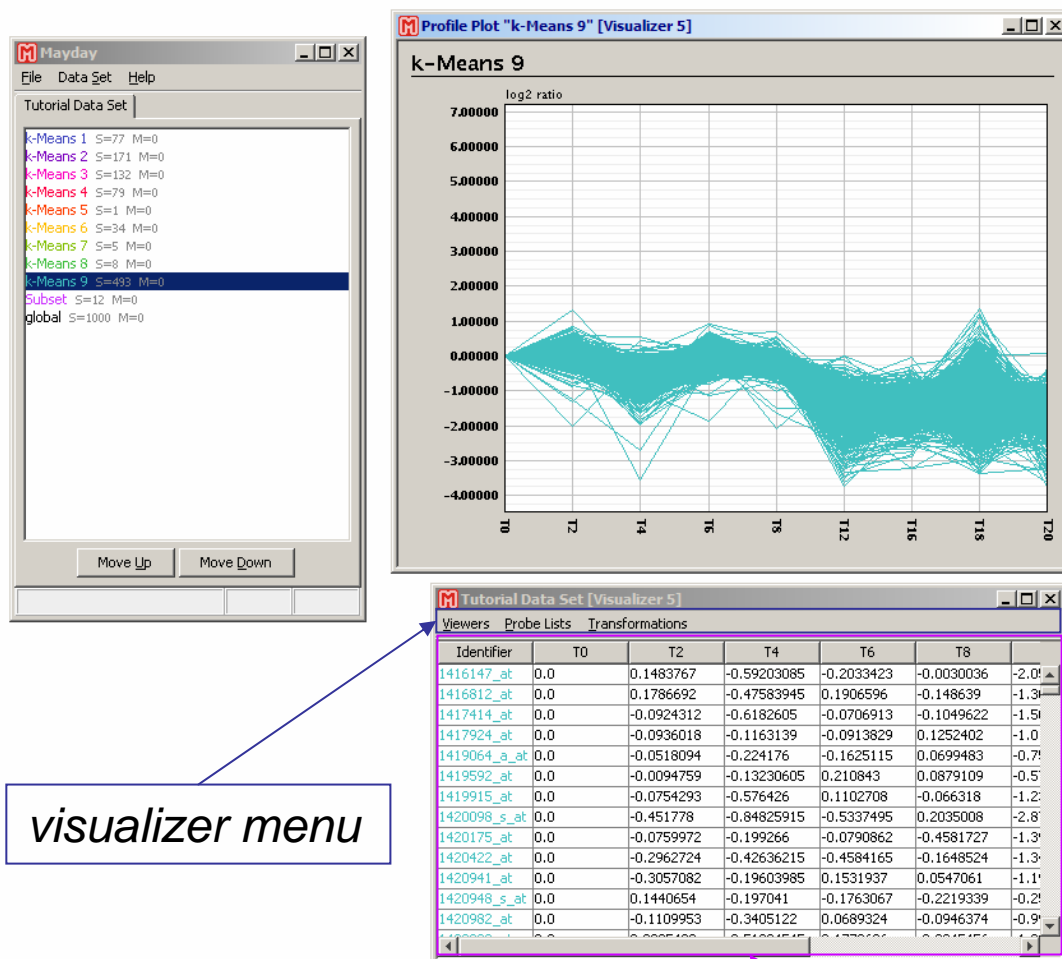
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Select “Profile Plot” from the “Visualization” submenu.

Visualizing a single probe list

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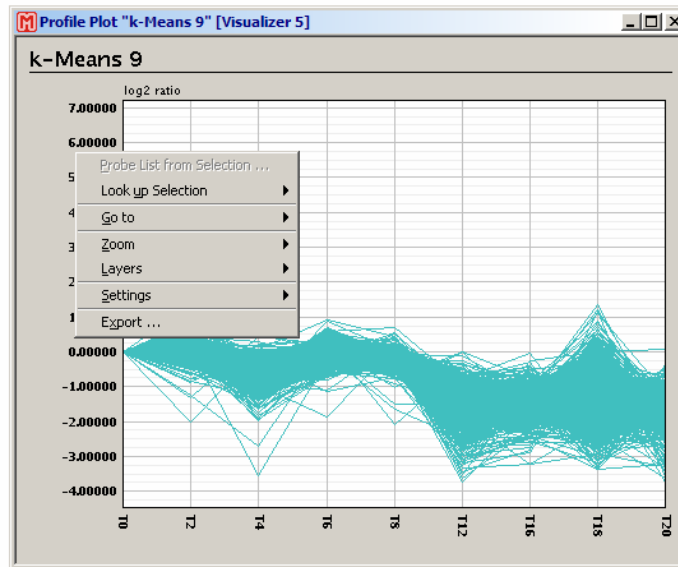
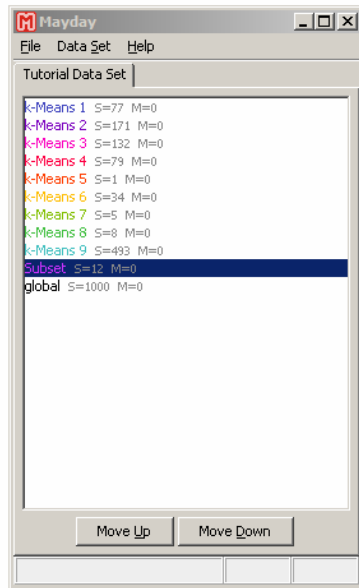


The profile plot plug-in also opened a so-called “visualizer” that contains an integrated tabular viewer. The visualizer manages the viewers, i.e. you can add further viewers using the visualizer. All viewers managed by a visualizer share a common list of probes lists and a selection. You will learn more about this later.

Right-click somewhere in the profile plot window to open the plots context menu.

Zooming into a graphical viewer

80



Open the "Zoom" submenu.

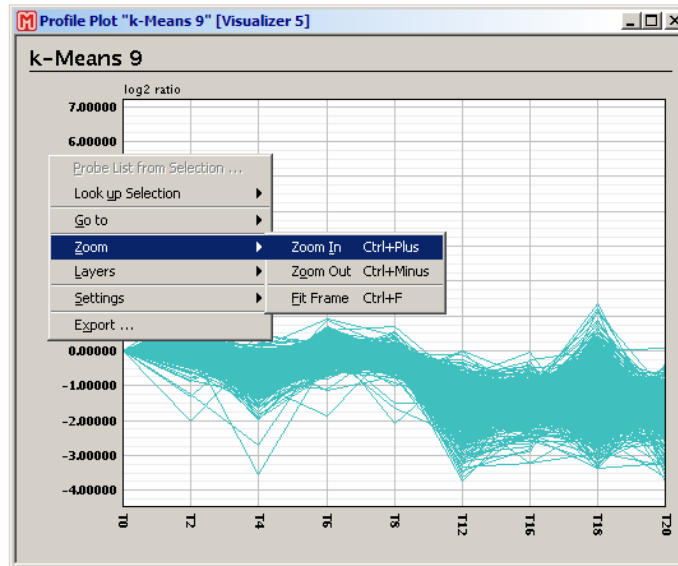
Tutorial Data Set [Visualizer 5]

Viewers Probe Lists Transformations

Identifier	T0	T2	T4	T6	T8	
1416147_at	0.0	0.1483767	-0.59203085	-0.2033423	-0.0030036	-2.0
1416812_at	0.0	0.1786692	-0.47583945	0.1906596	-0.148639	-1.3
1417414_at	0.0	-0.0924312	-0.6182605	-0.0706913	-0.1049622	-1.5
1417924_at	0.0	-0.0936018	-0.1163139	-0.0913829	0.1252402	-1.0
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.7
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9

Zooming into a graphical viewer

81

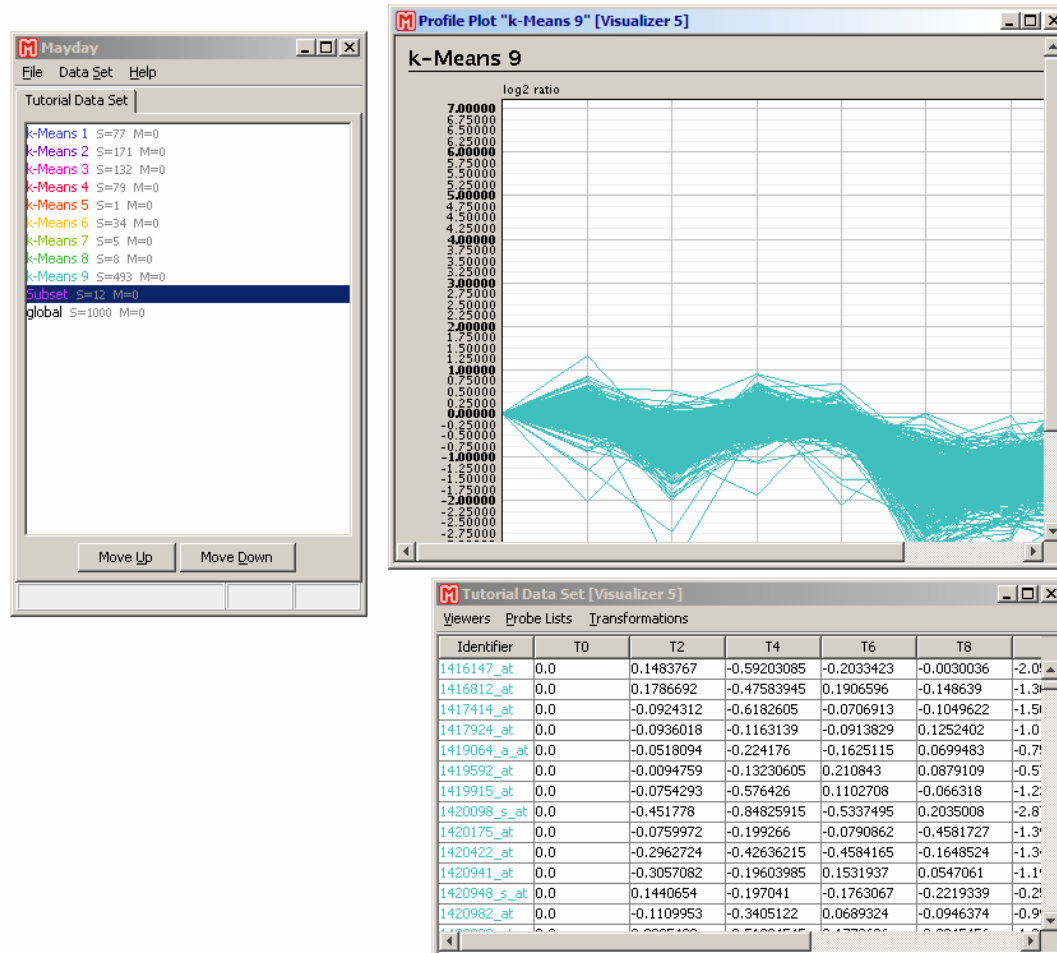


Tutorial Data Set [Visualizer 5]

Viewers Probe Lists Transformations

Identifier	T0	T2	T4	T6	T8	
1416147_at	0.0	0.1483767	-0.59203085	-0.2033423	-0.0030036	-2.0
1416812_at	0.0	0.1786692	-0.47583945	0.1906596	-0.148639	-1.3
1417414_at	0.0	-0.0924312	-0.6182605	-0.0706913	-0.1049622	-1.5
1417924_at	0.0	-0.0936018	-0.1163139	-0.0913829	0.1252402	-1.0
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.7
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9

Select "Zoom In".

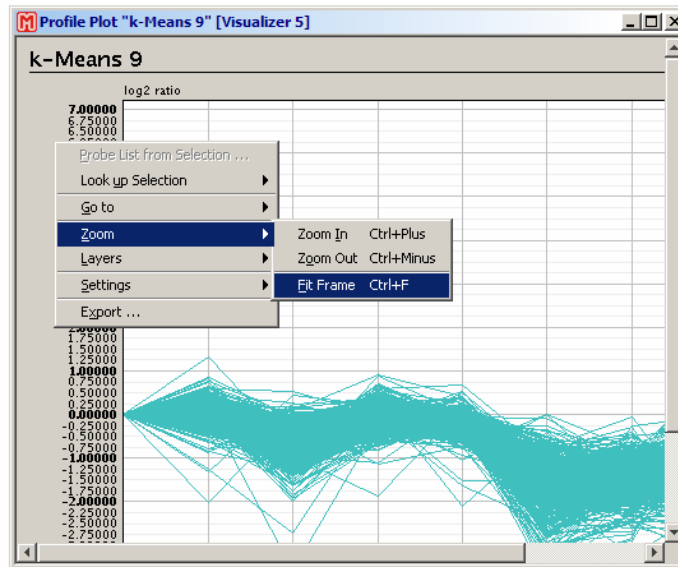


Viewers can be zoomed but only if the user explicitly demands it. Viewers don't change if the window is resized. Further, the aspect ratio of a viewer will never change because this can often causes misinterpretation of the data.

Open the profile plot's context menu again by right-clicking somewhere in the window.

Fitting a viewer's frame

83



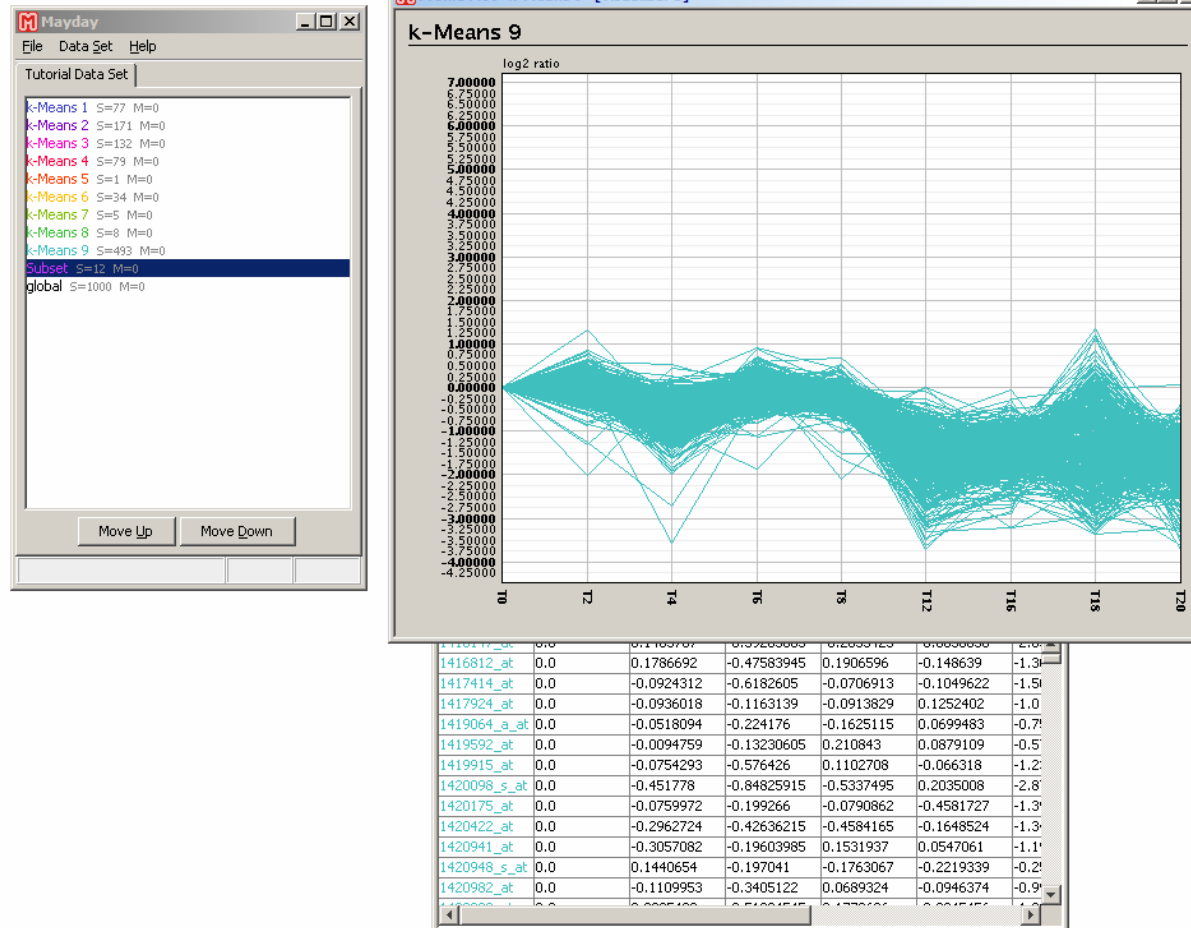
In the “Zoom” submenu select “Fit Frame”.

The 'Tutorial Data Set [Visualizer 5]' window displays a table of data. The table has columns for Identifier, T0, T2, T4, T6, T8, and a final column. The data is sorted by Identifier.

Identifier	T0	T2	T4	T6	T8	
1416147_at	0.0	0.1483767	-0.59203085	-0.2033423	-0.0030036	-2.0
1416812_at	0.0	0.1786692	-0.47583945	0.1906596	-0.148639	-1.3
1417414_at	0.0	-0.0924312	-0.6182605	-0.0706913	-0.1049622	-1.5
1417924_at	0.0	-0.0936018	-0.1163139	-0.0913829	0.1252402	-1.0
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.7
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9

Fitting a viewer's frame

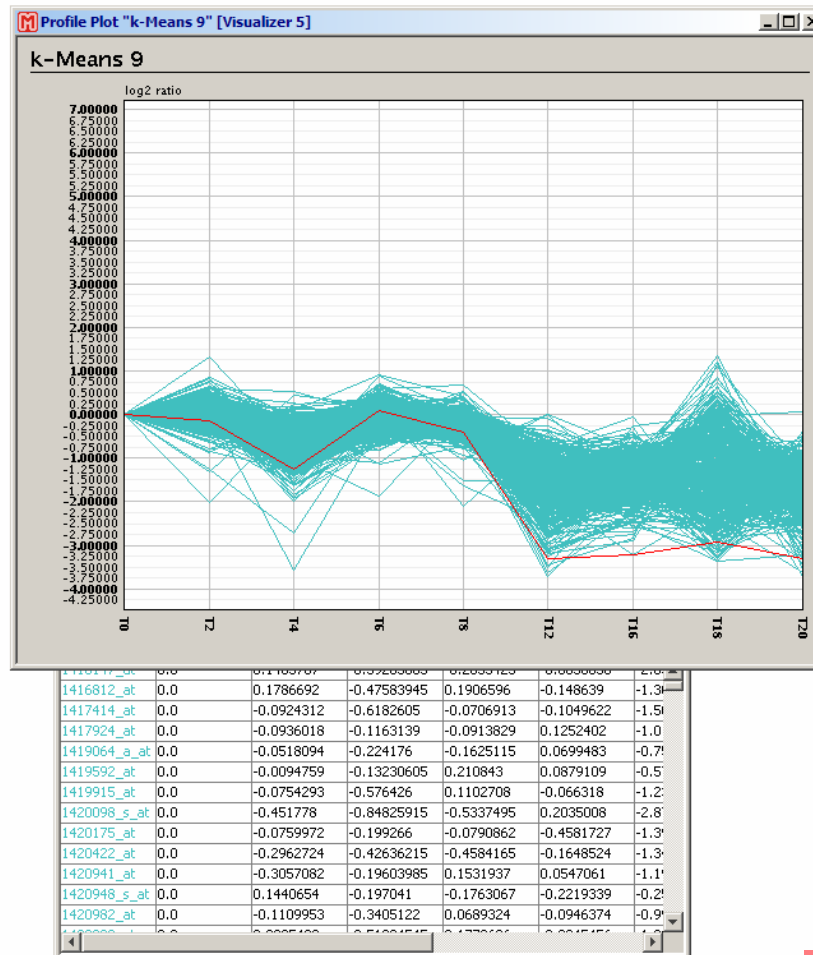
84



Click on one of the profiles displayed in the profile plot to select it.

Selecting a single probe

85

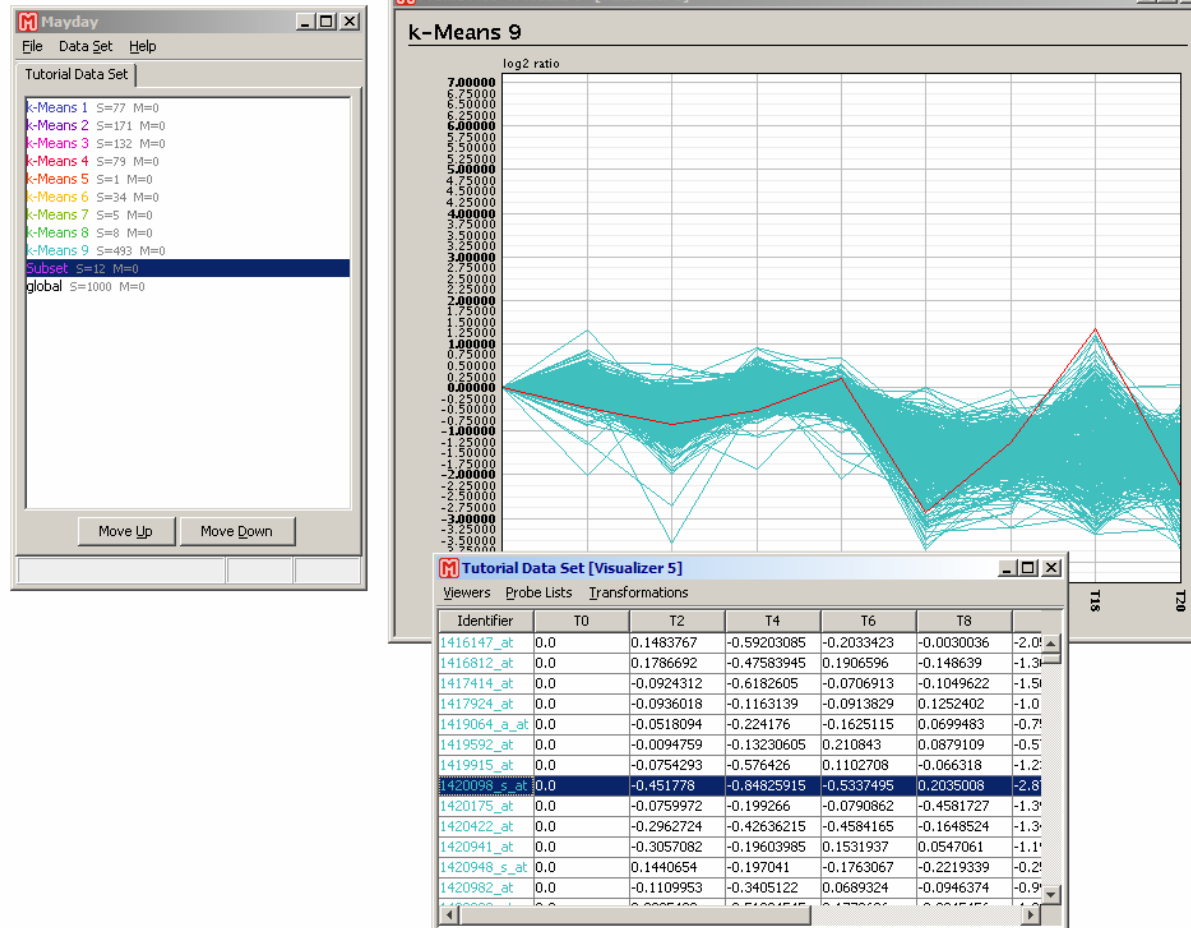


Selected profiles are highlighted in red. Be careful when choosing colors for your probe lists, you might not be able to see the selection if you choose a color to similar to the selection.

Bring the tabular viewer to the front and select one of the probes.

Selecting a single probe

86

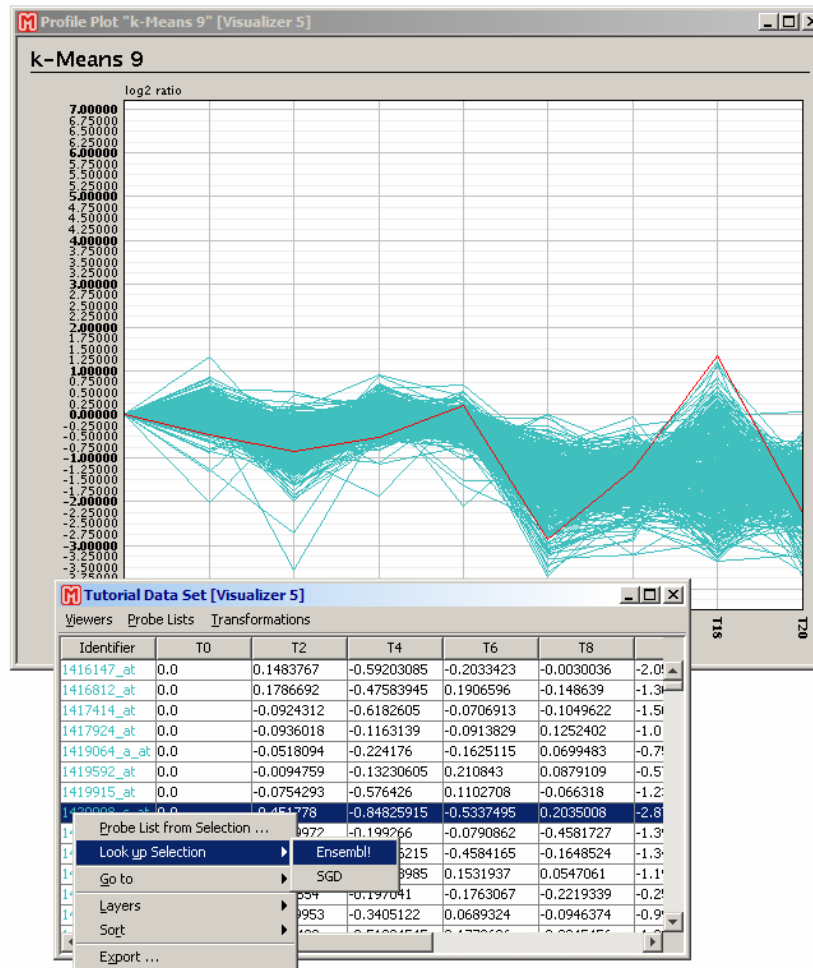


If you select a probe in one viewer of a visualizer, it will be also become highlighted in all other viewers of that visualizer. This is because the selection is managed by the visualizer, not the viewers themselves.

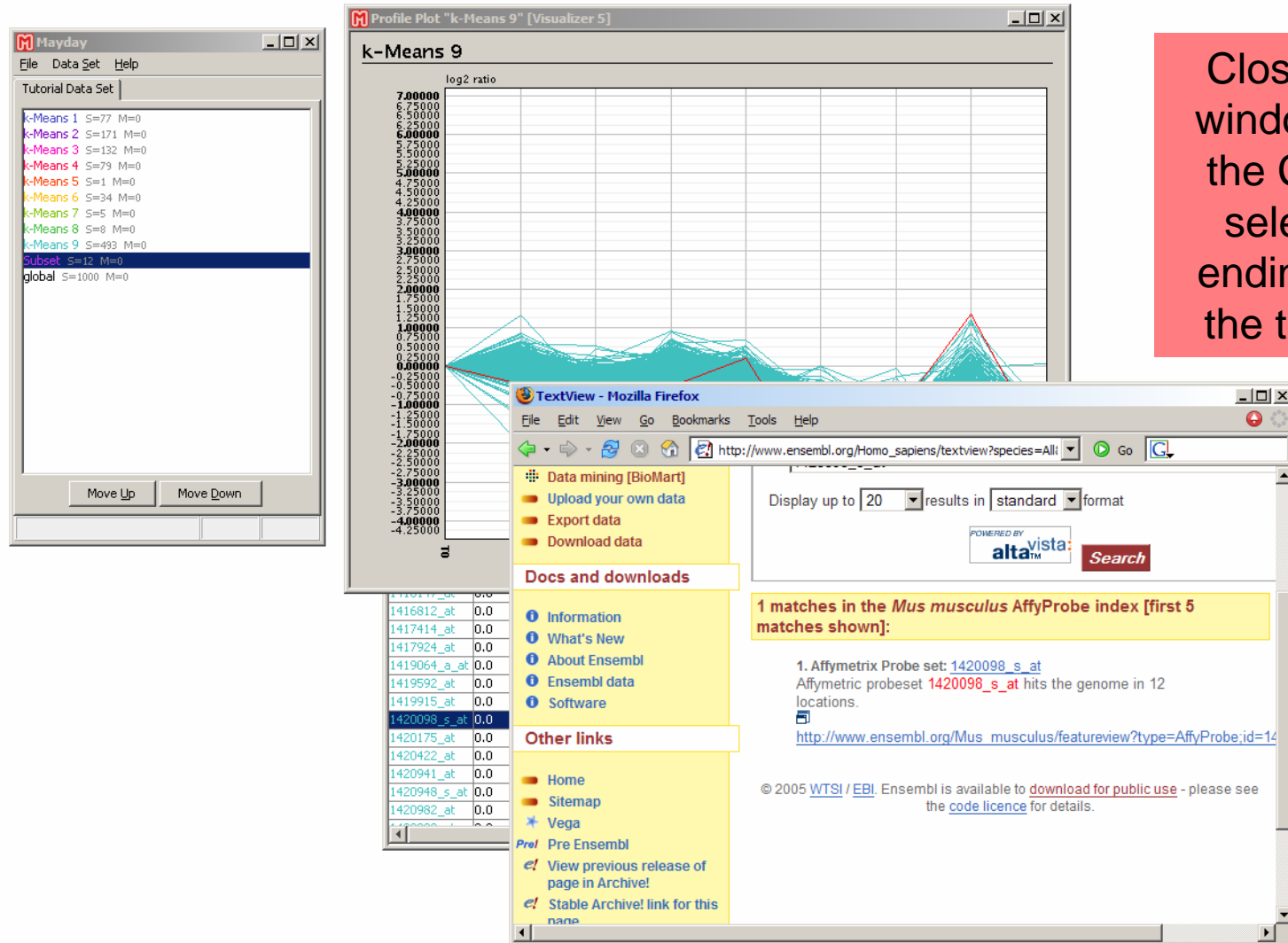
Right-click the selected probe to open the tabular viewer's context menu. Open the "Look up selection" submenu.

Looking up probe identifiers

87



Click "Ensembl!".

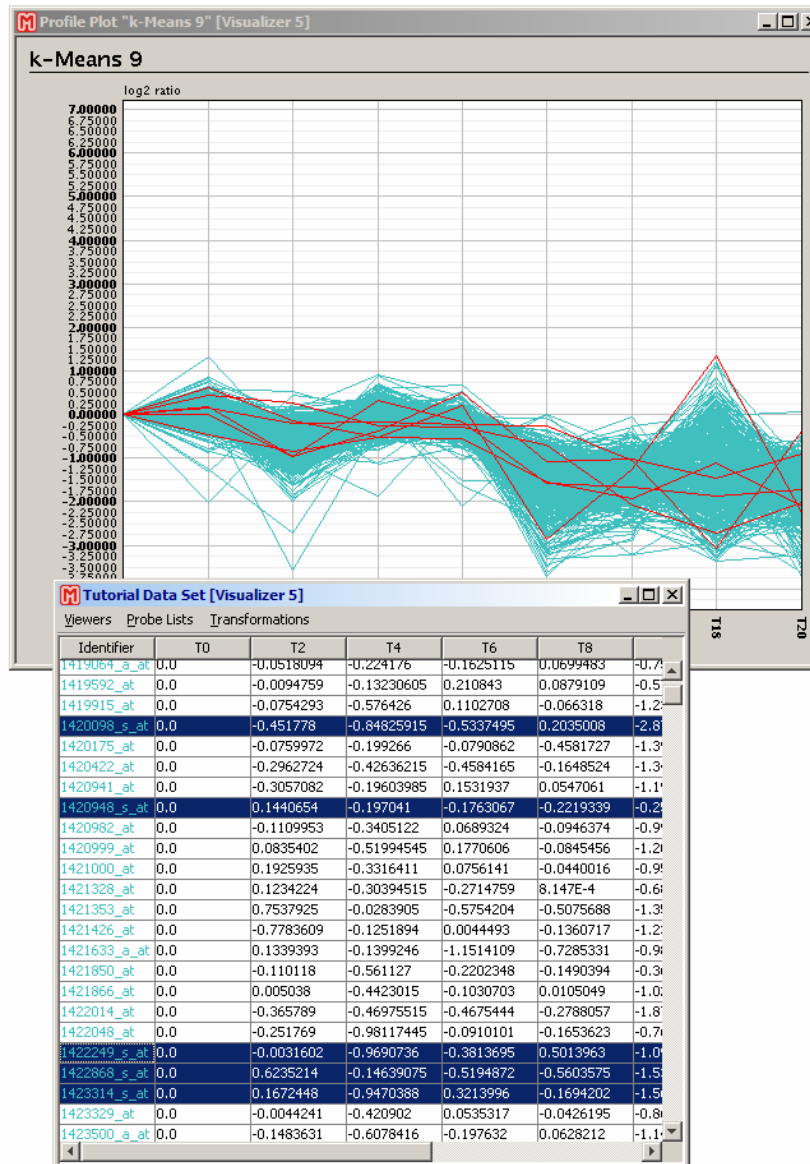


Close the browser window. Hold down the CTRL key and select all probes ending in “_s_at” in the tabular viewer.

Probes are looked up based on their identifier. If the corresponding database cannot be searched using the assigned identifiers, you won't get any results.

Selecting multiple probes

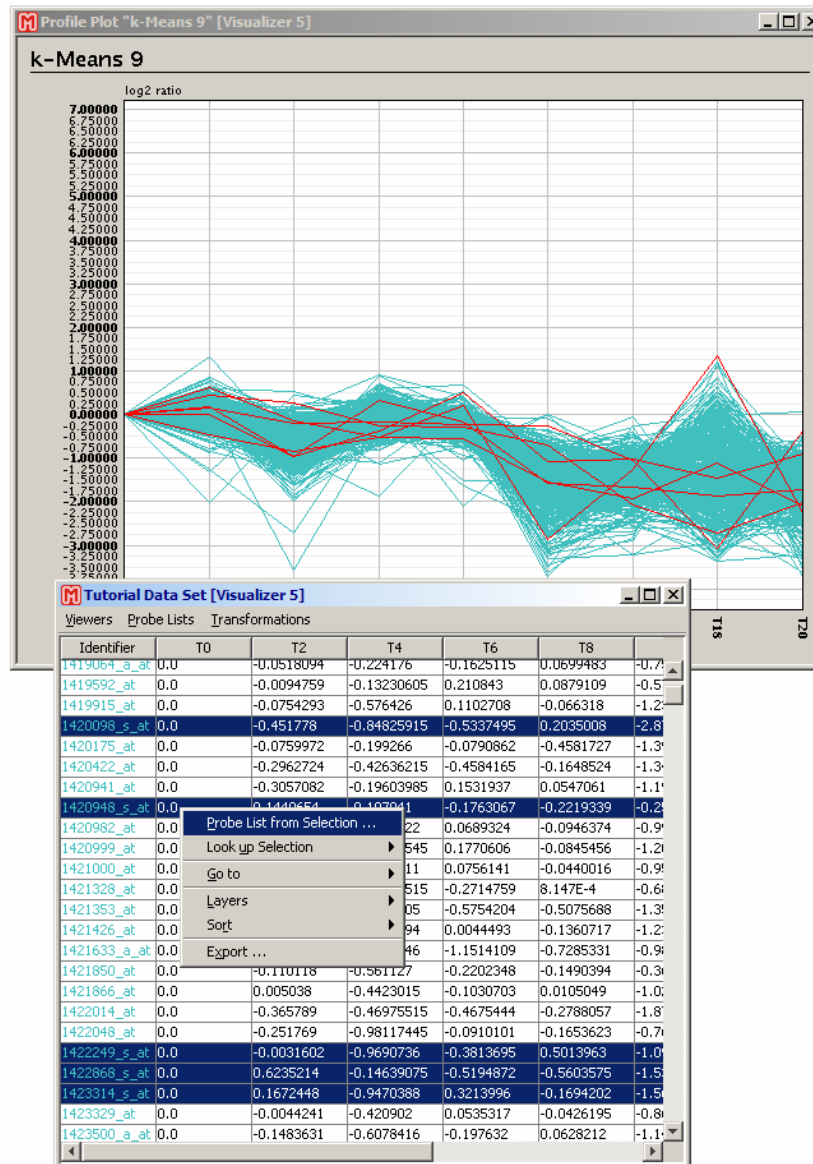
89



Continue holding the CTRL key and right-click to open the tabular viewers context menu.

Creating a probe list from selection

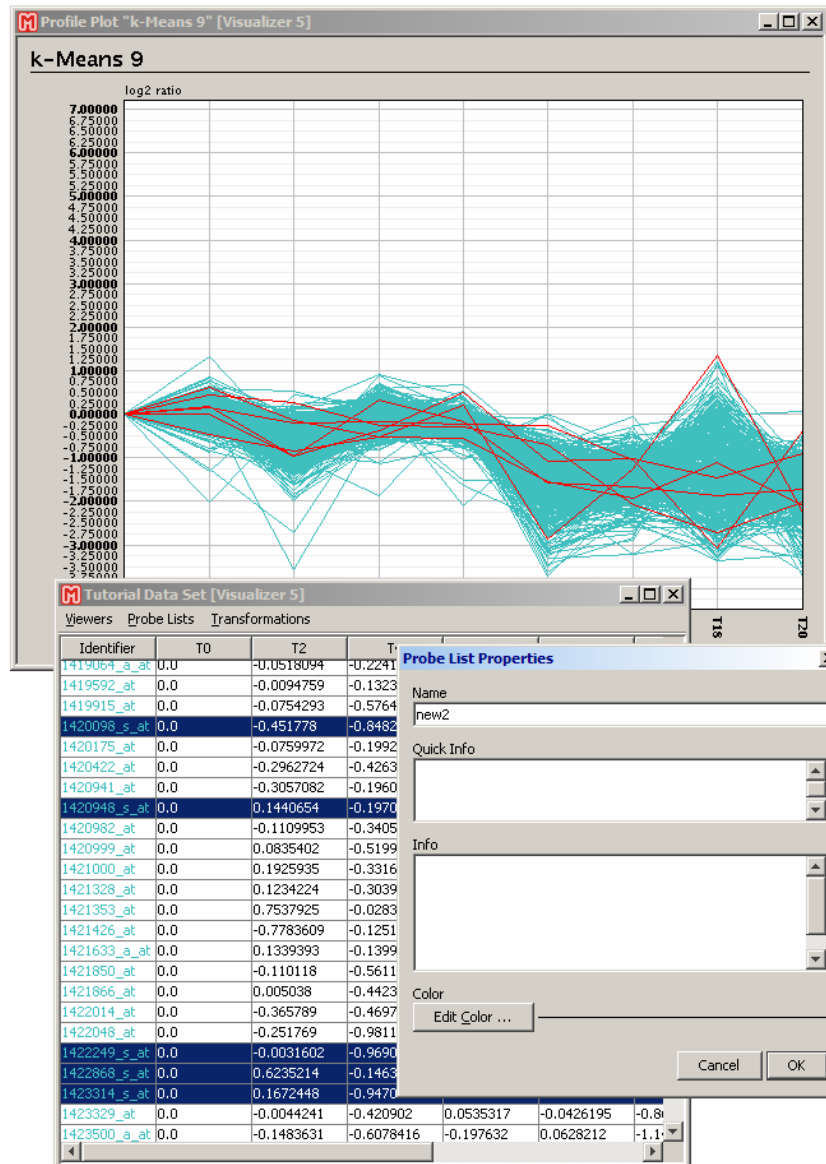
90



Select "Probe List From Selection ...".

Creating a probe list from selection

91

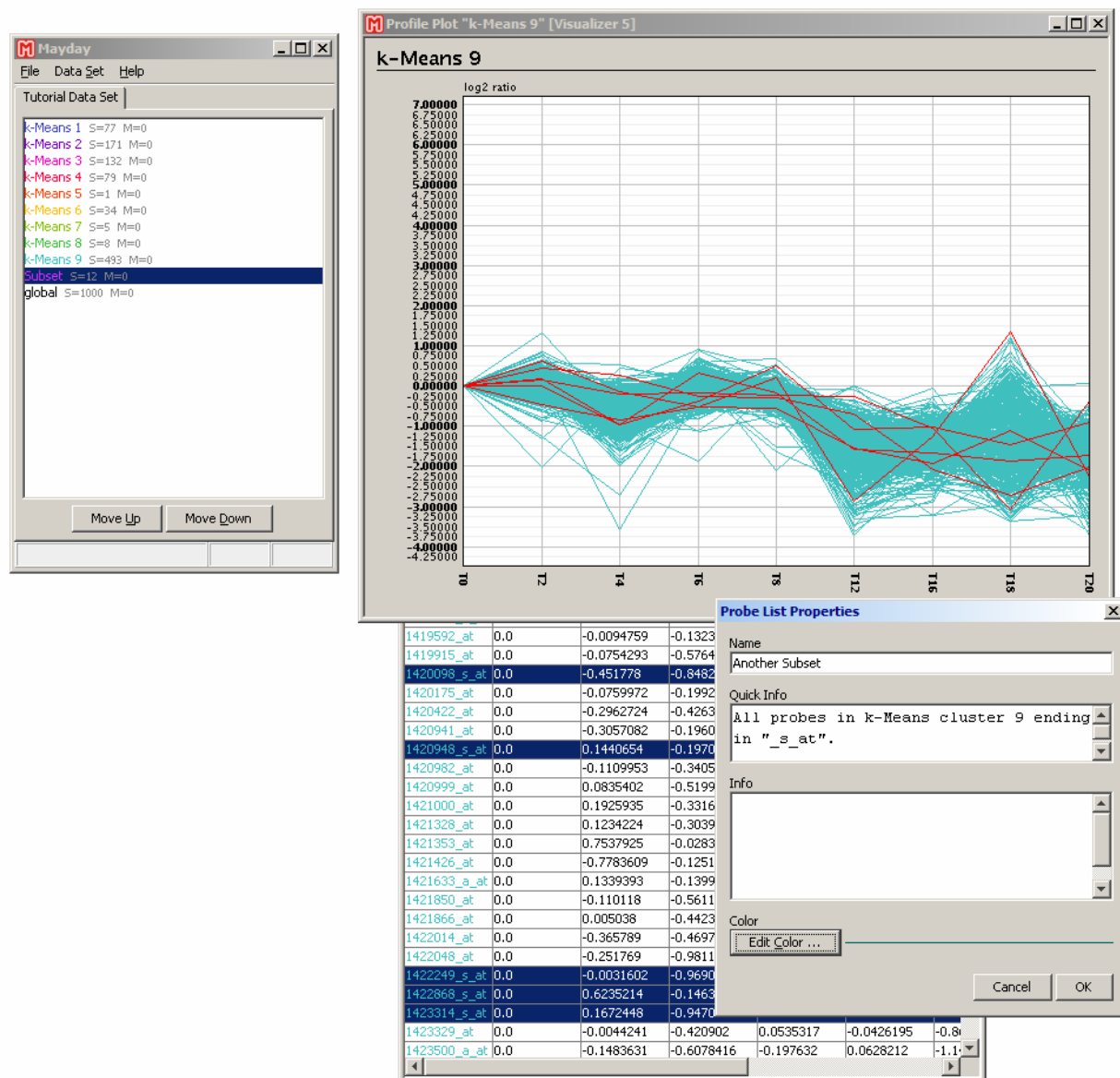


This is another way to create a probe list based on your selection.

Assign a name and a distinct color to the new probe list. You may enter additional information about the probe list as well.

Creating a probe list from selection

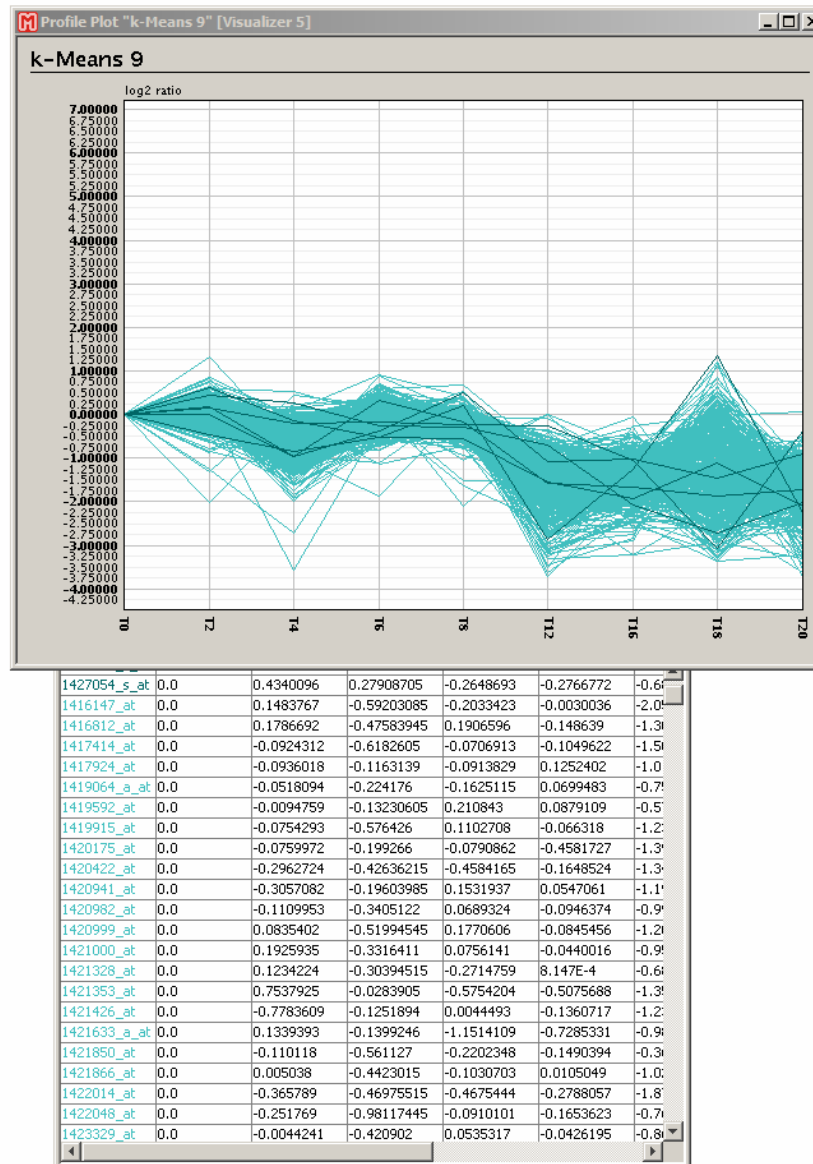
92



Click "OK" to confirm when you are done.

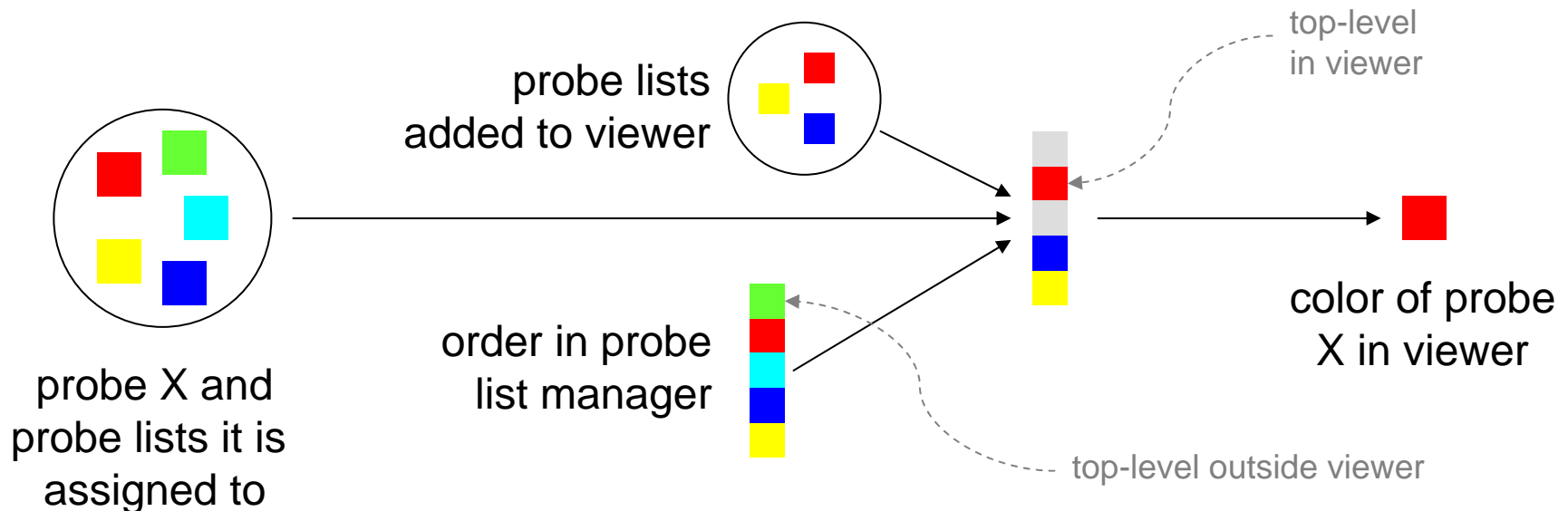
Creating a probe list from selection

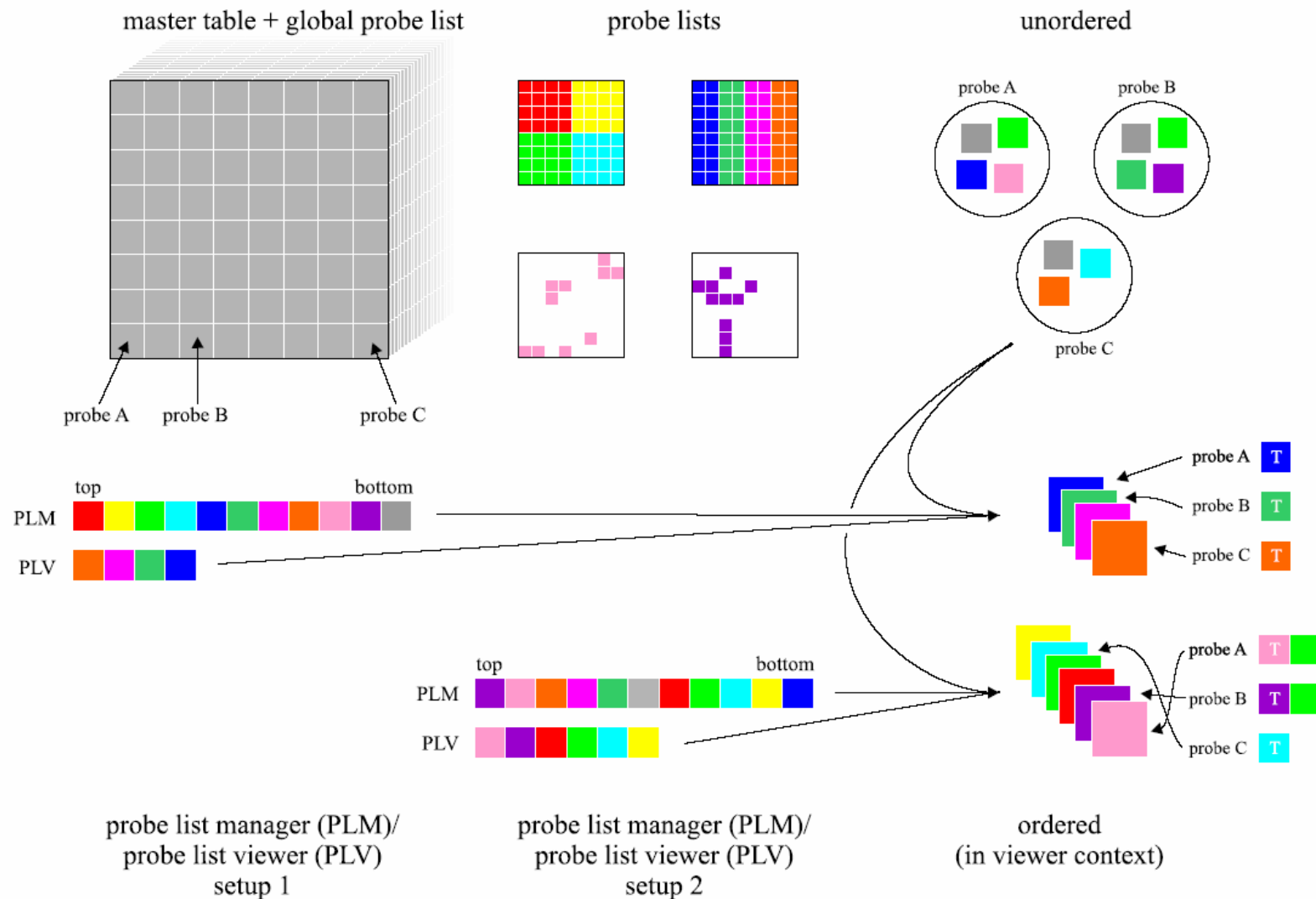
93



The probes contained in the new probe list appear in the color you have assigned to it. Note that the new probe list appears at the top of the probe list manager. The order of the probes in the probe list manager plays a crucial role in Mayday because is partly responsible for the color assigned to a probe in a viewer.

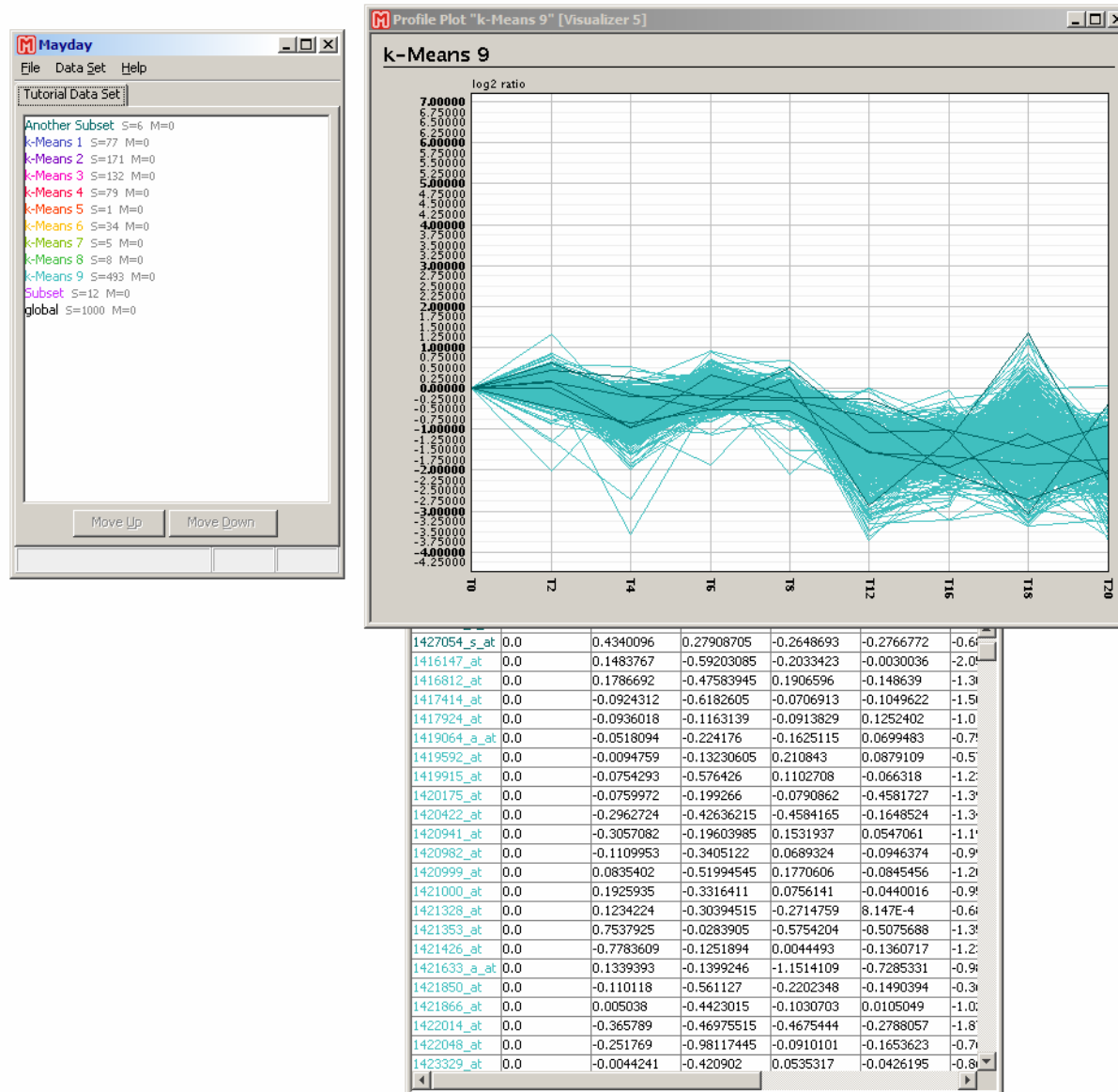
- factors that determine the color of a probe
 - colors of all probe lists the probe is contained in form the *basis*
 - probe lists that are contained in a viewer (visualizer) are a *filter*
 - order of probe lists in the probe list manager determines the *top-level probe list*
- color of a probe's top-level probe list with respect to the filters is the color of the probe in the viewer





Creating a probe list from selection

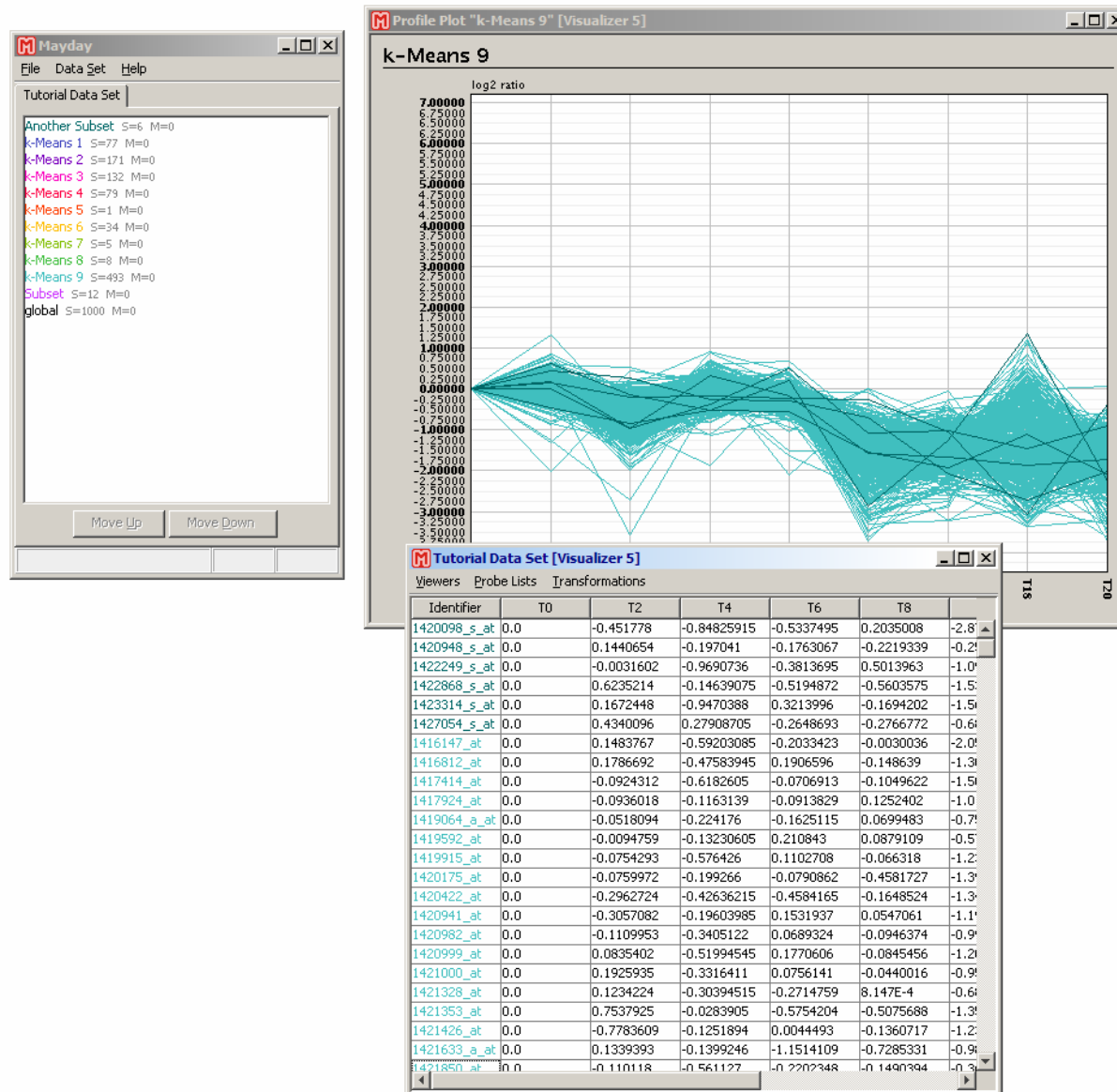
96



Bring the tabular viewer to the front.

Adding probe lists to a visualizer

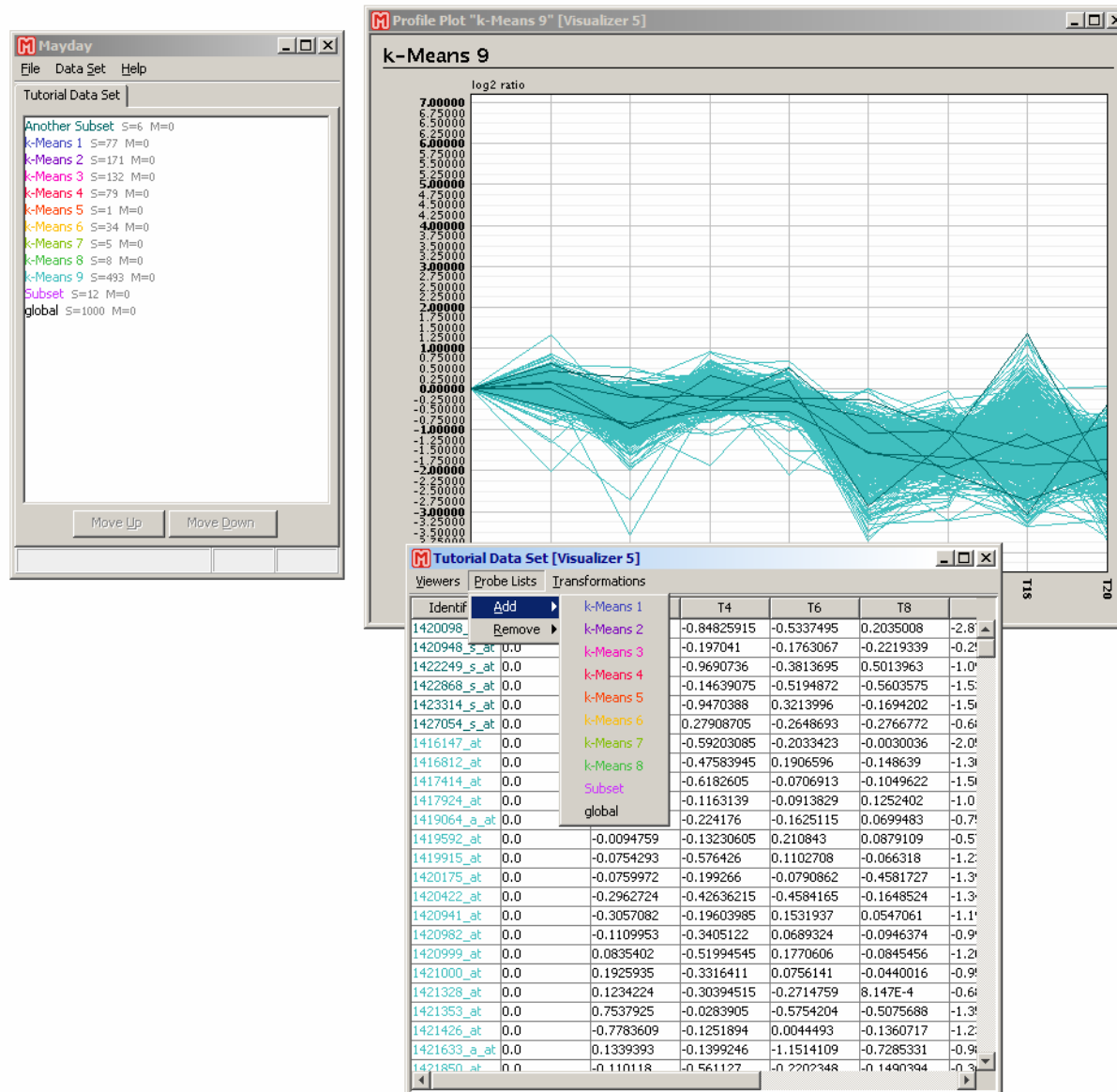
97



Select menu item
"Probe Lists" and open
submenu "Add".

Adding probe lists to a visualizer

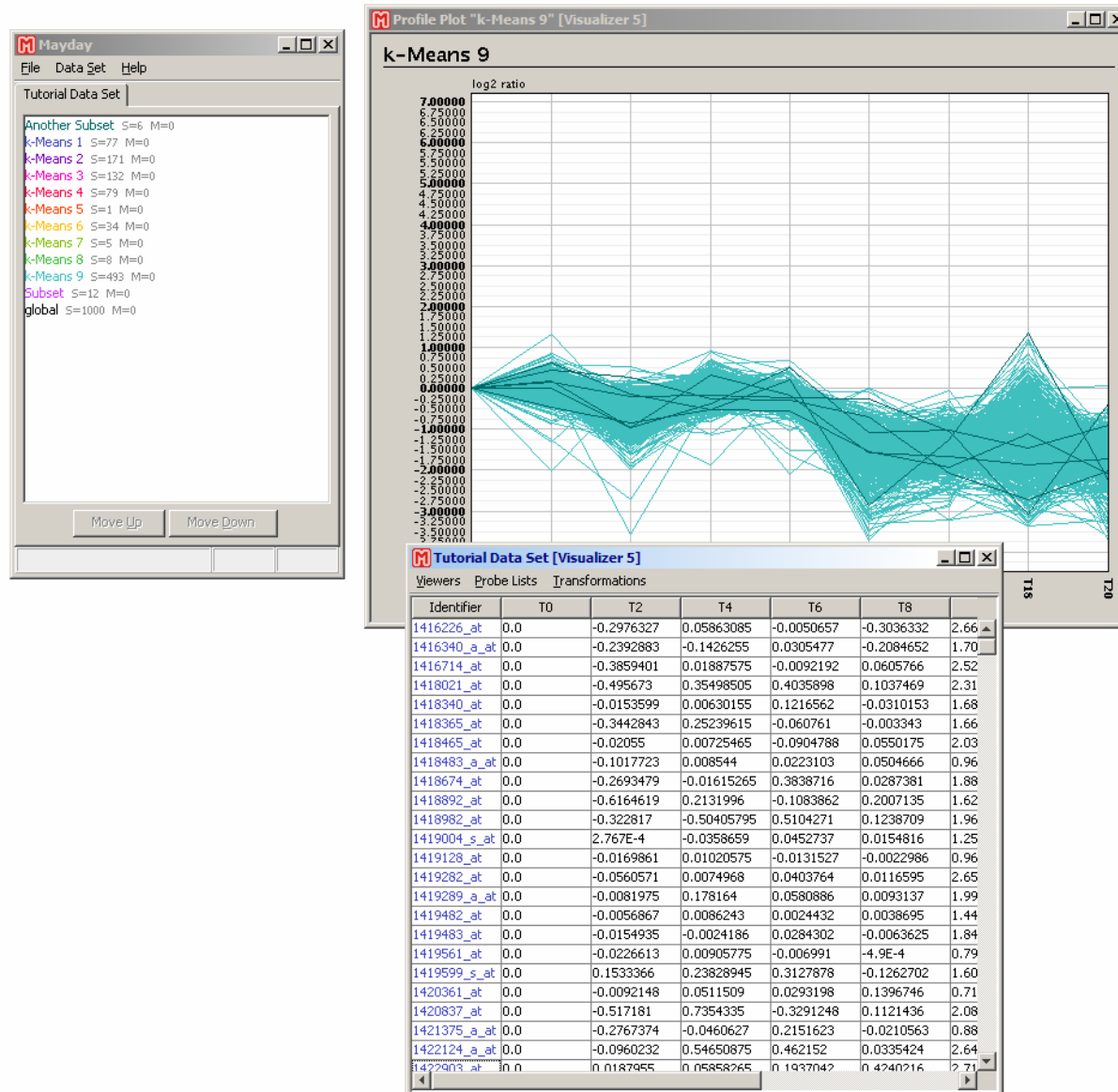
98



Select "k-Means 1".

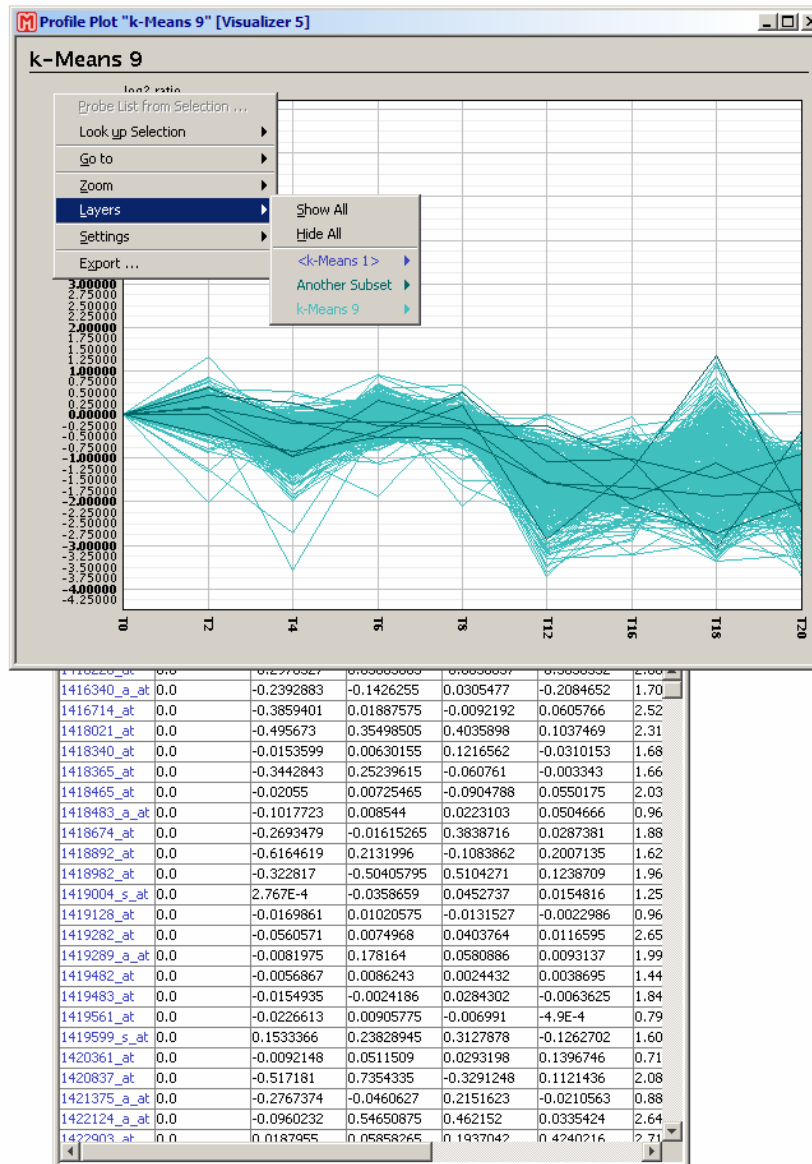
Adding probe lists to a visualizer

99



You can see the additional probes in the tabular viewer but not yet in the profile plot. You have to explicitly tell the profile plot to show the new probe list.

Open the context menu of the profile plot and select submenu "Layers".

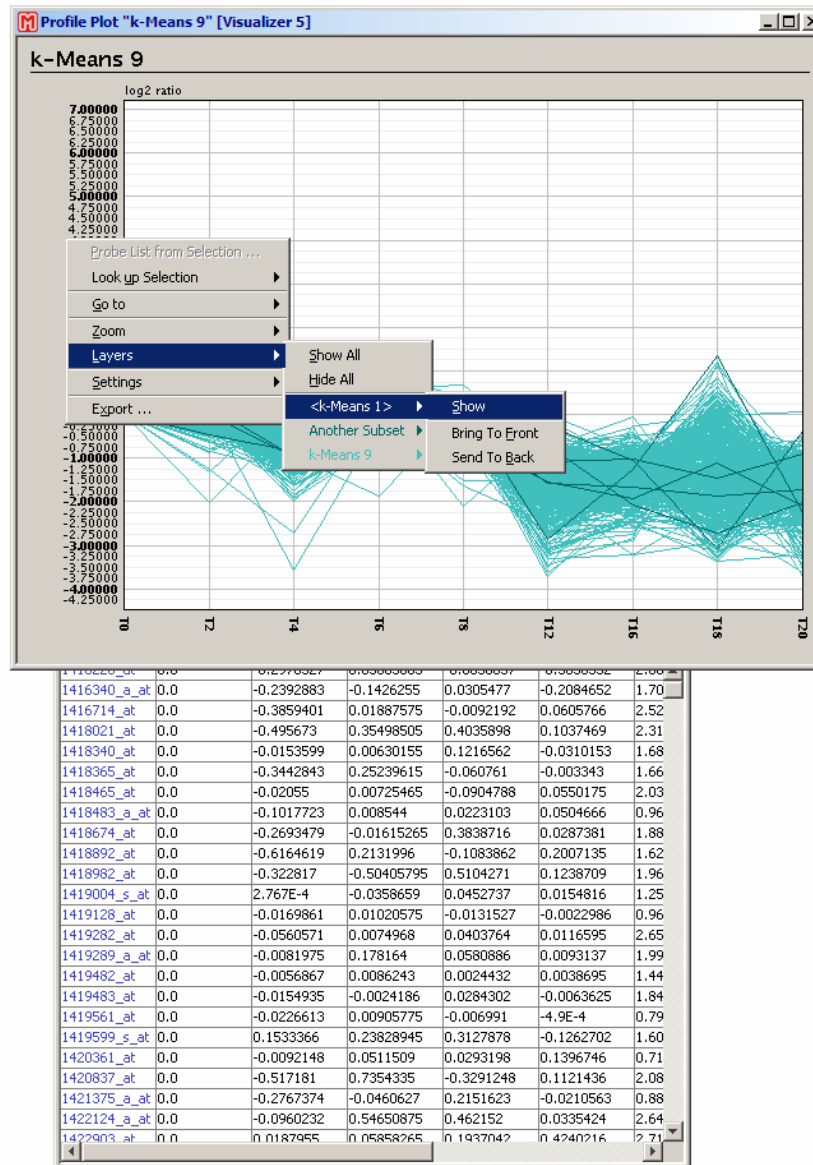


Each probe list is represented as a layer in the profile plot. You can think of the profile plot as a stack of transparencies, where each transparency has the profiles of one probe list printed on it.

Select "<k-Means 1>".

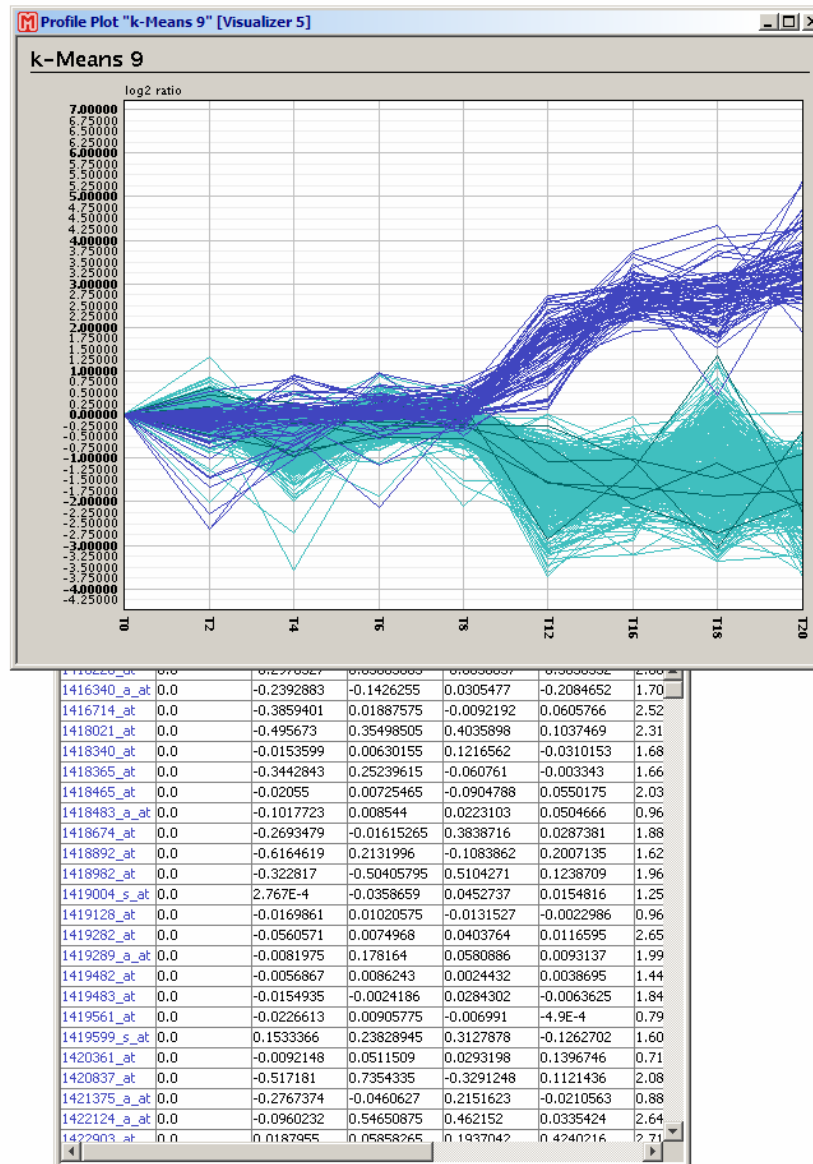
Making a layer visible

101

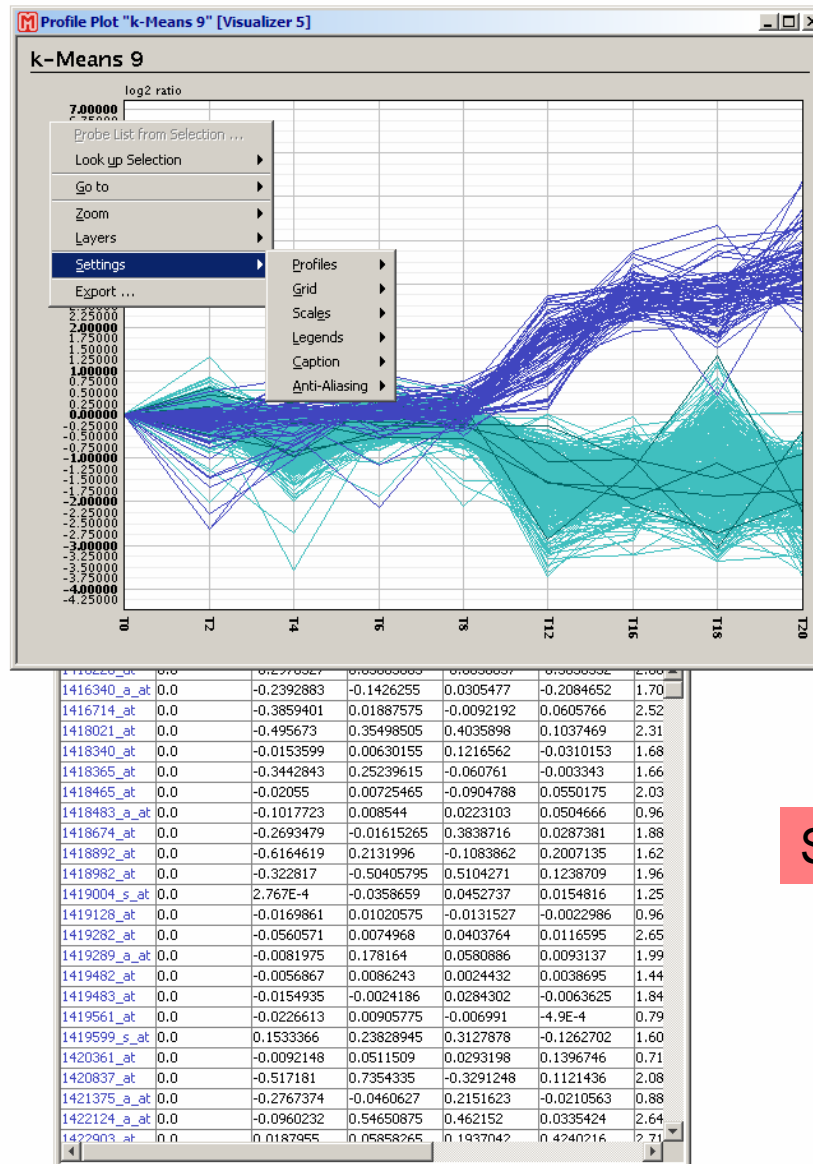


Layers can be hidden and their order can be rearranged. More on this later.

Click on "Show".



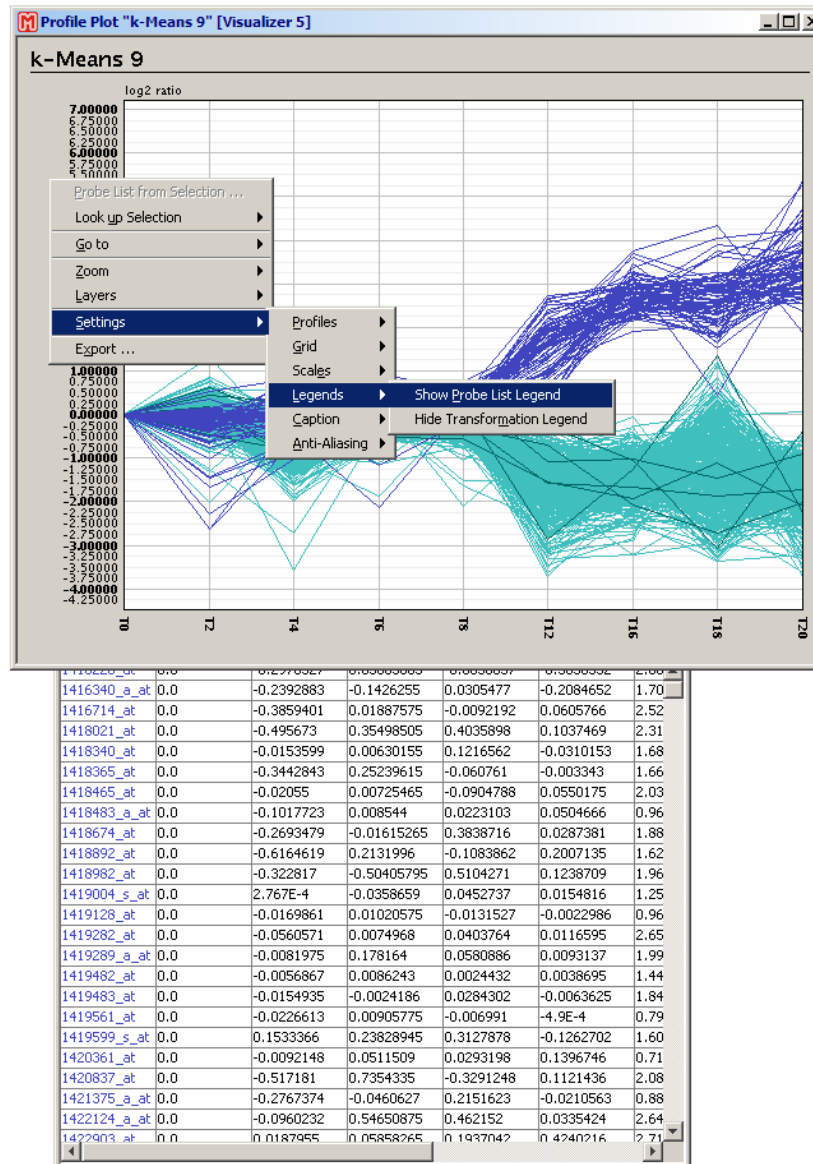
Open the profile plot's context menu and select submenu "Settings".



Select submenu “Legends”.

Adding a legend

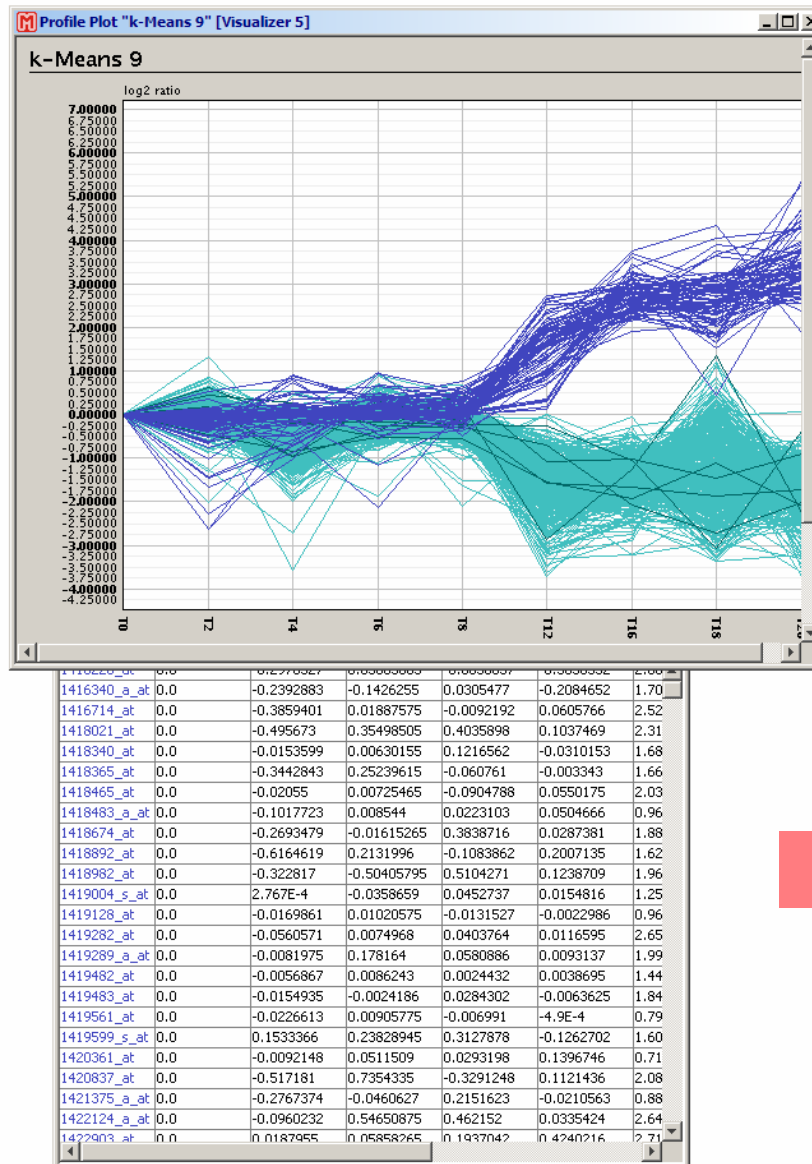
104



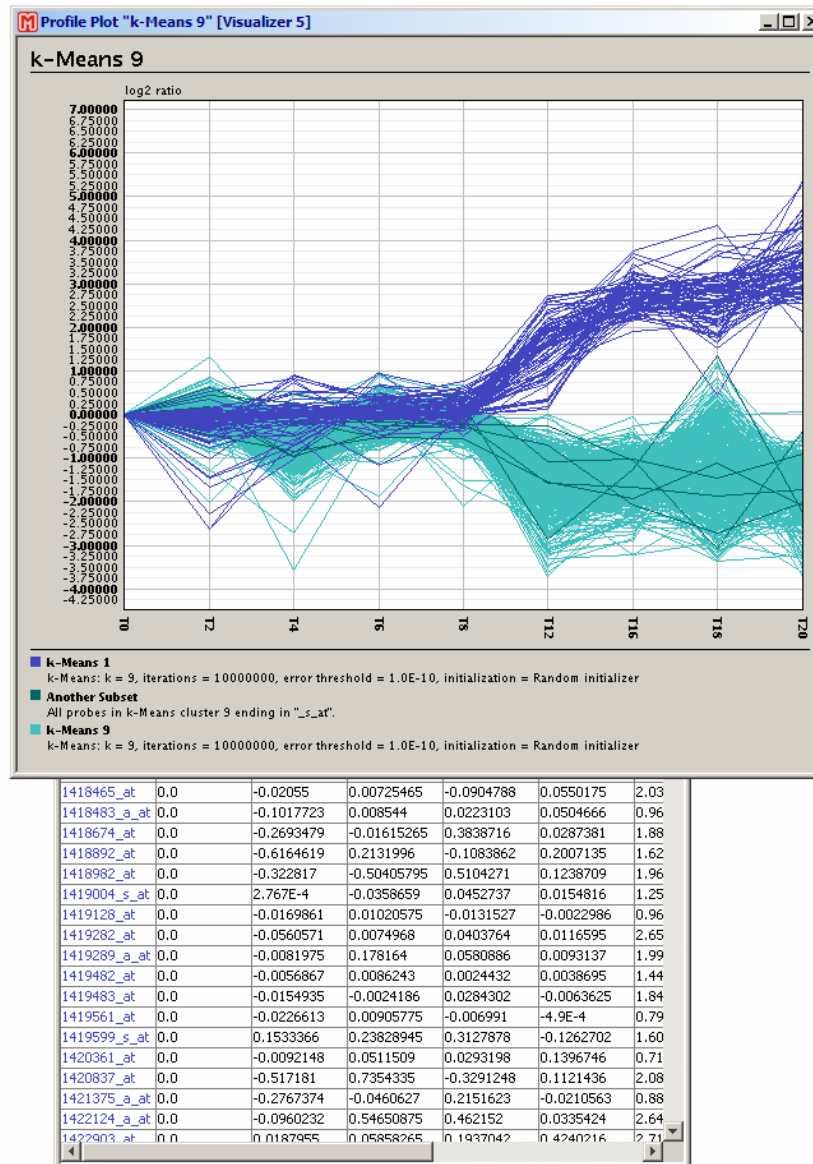
Select "Show Probe List Legend".

Adding a legend

105



Fit the profile plot's frame.

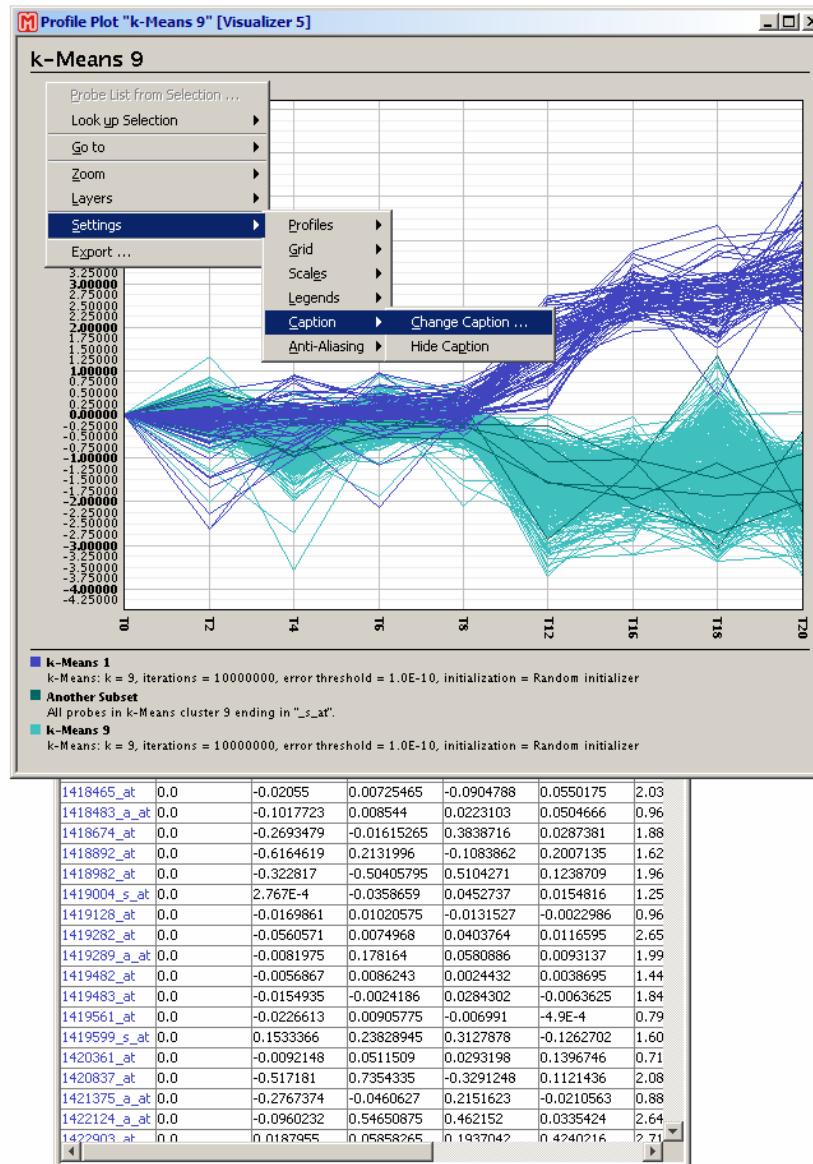


The legend helps you to keep track of the probe lists displayed in the viewer and the order of the layers. It also shows the “quick info” assigned to each probe list.

Open the profile plot's context menu.

Changing the caption of a viewer

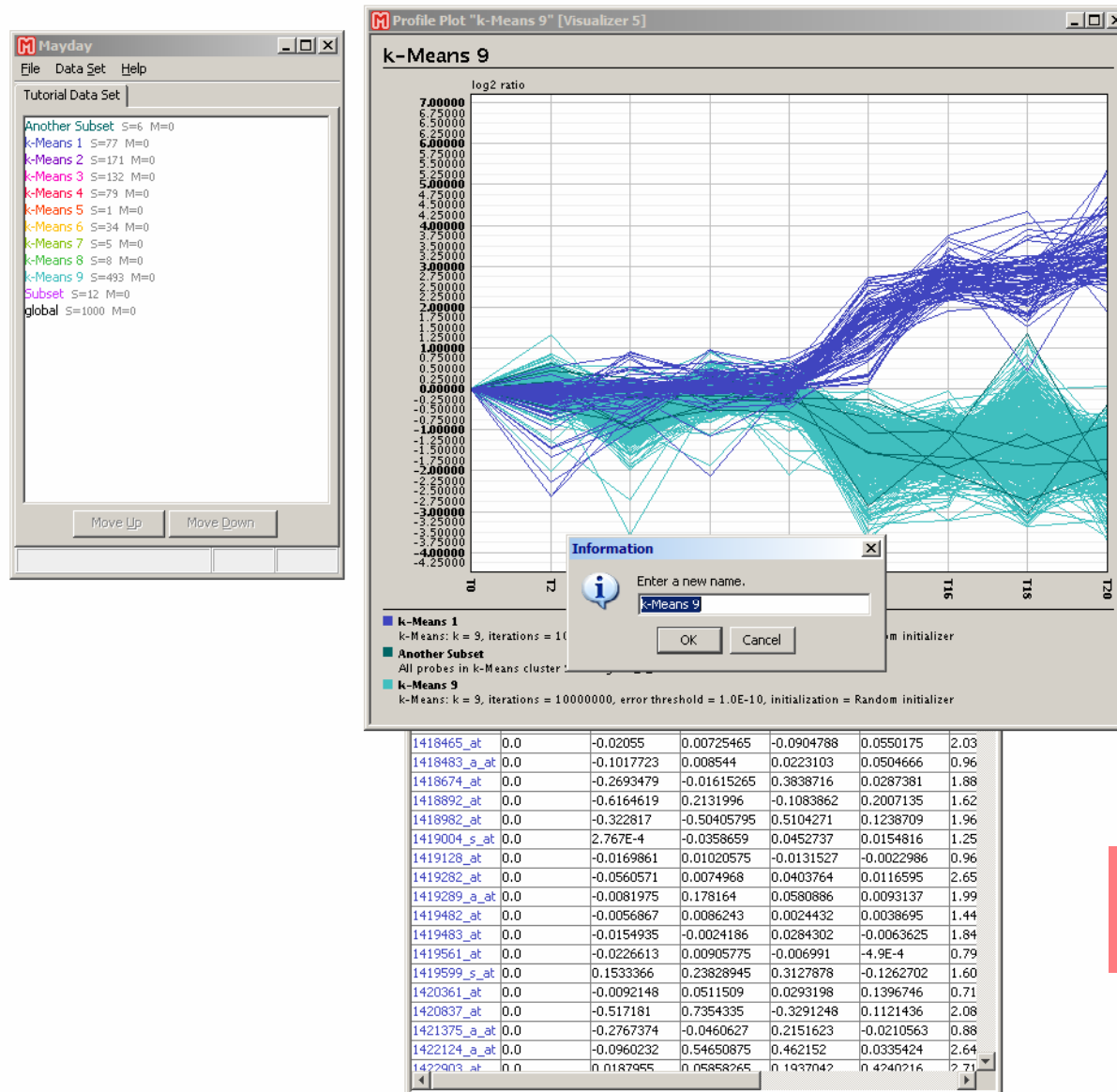
107



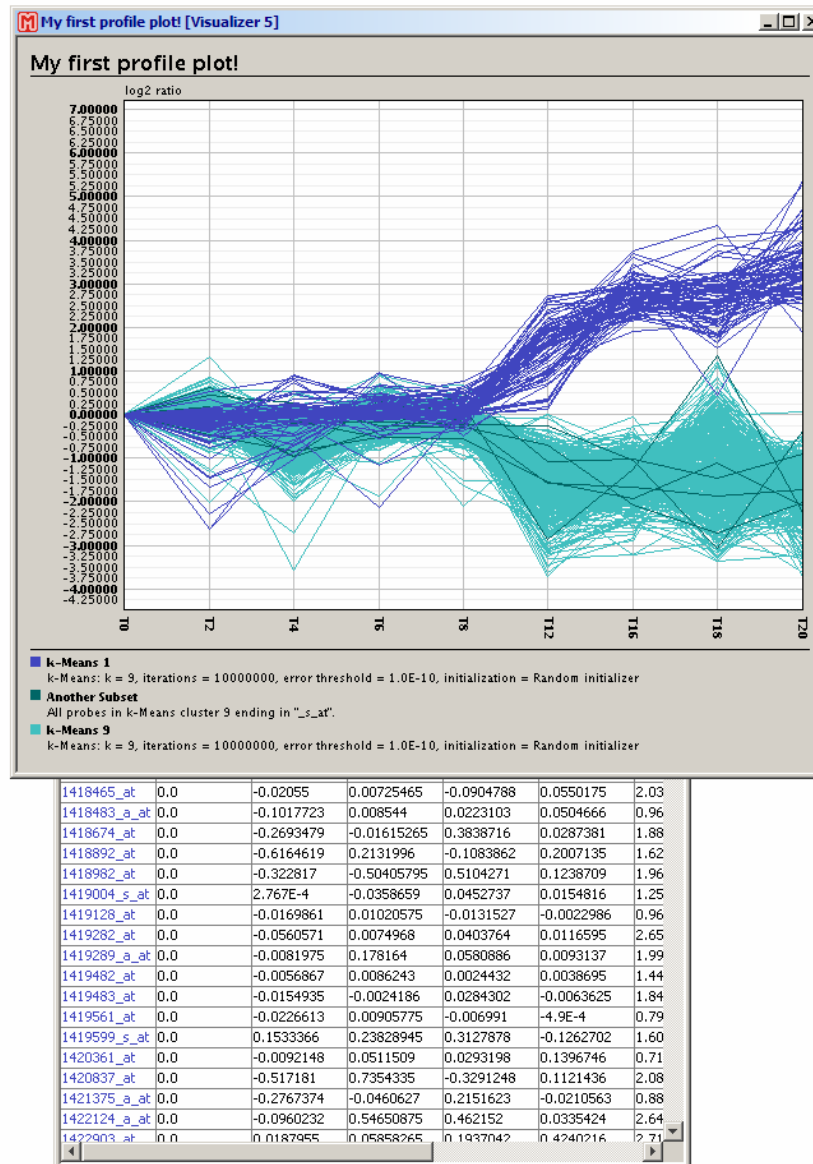
Select submenu
"Caption" and click
"Change caption ...".

Changing the caption of a viewer

108

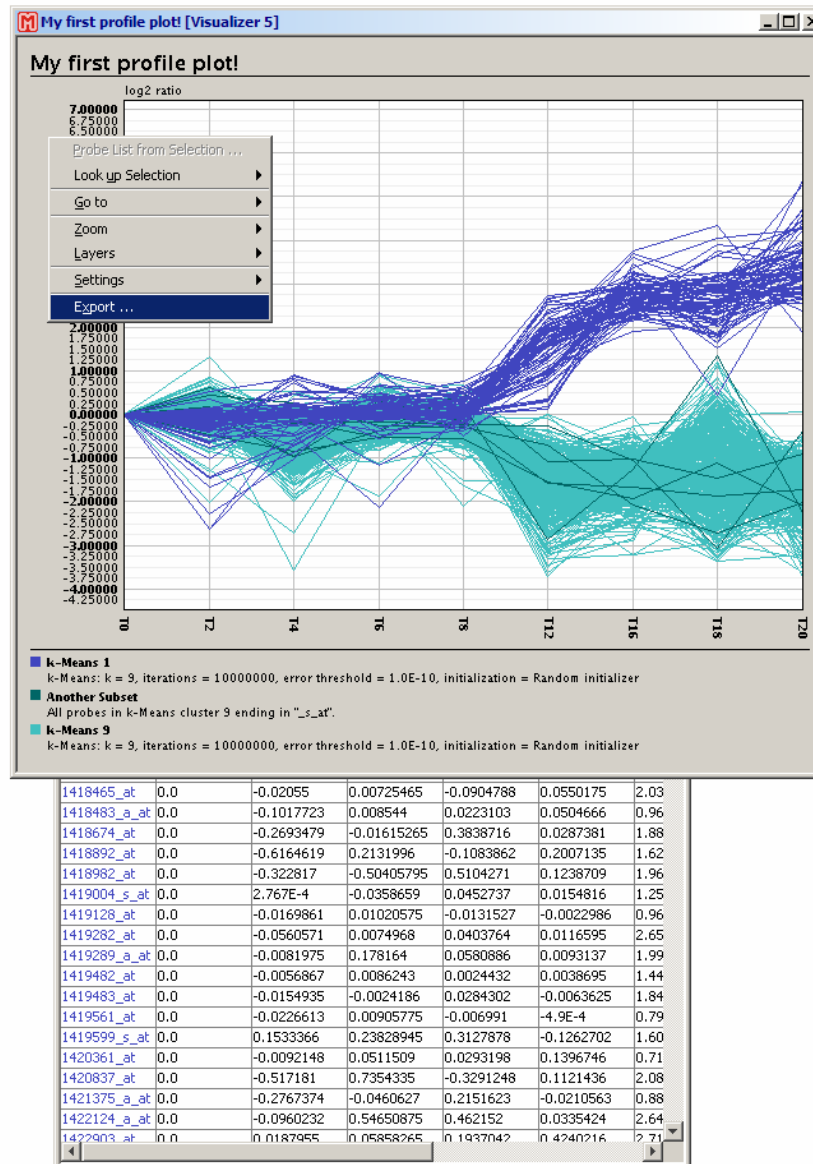


Type in a new caption
and click "OK".



Like the legend, changing the caption helps you to remember what you are looking at after you have exported the viewer to a graphics file format. This is what we will do next.

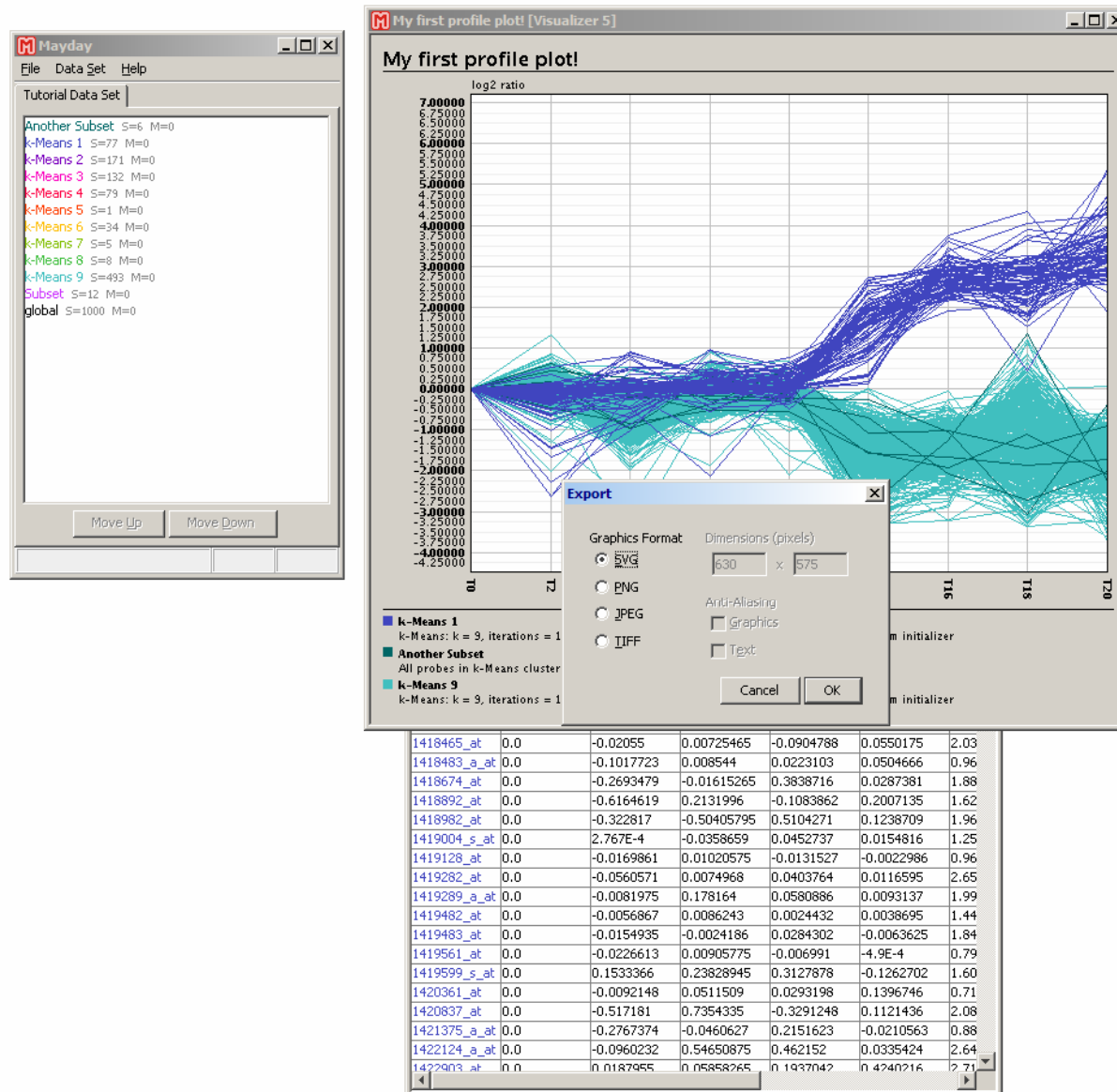
Open the profile plot's context menu.



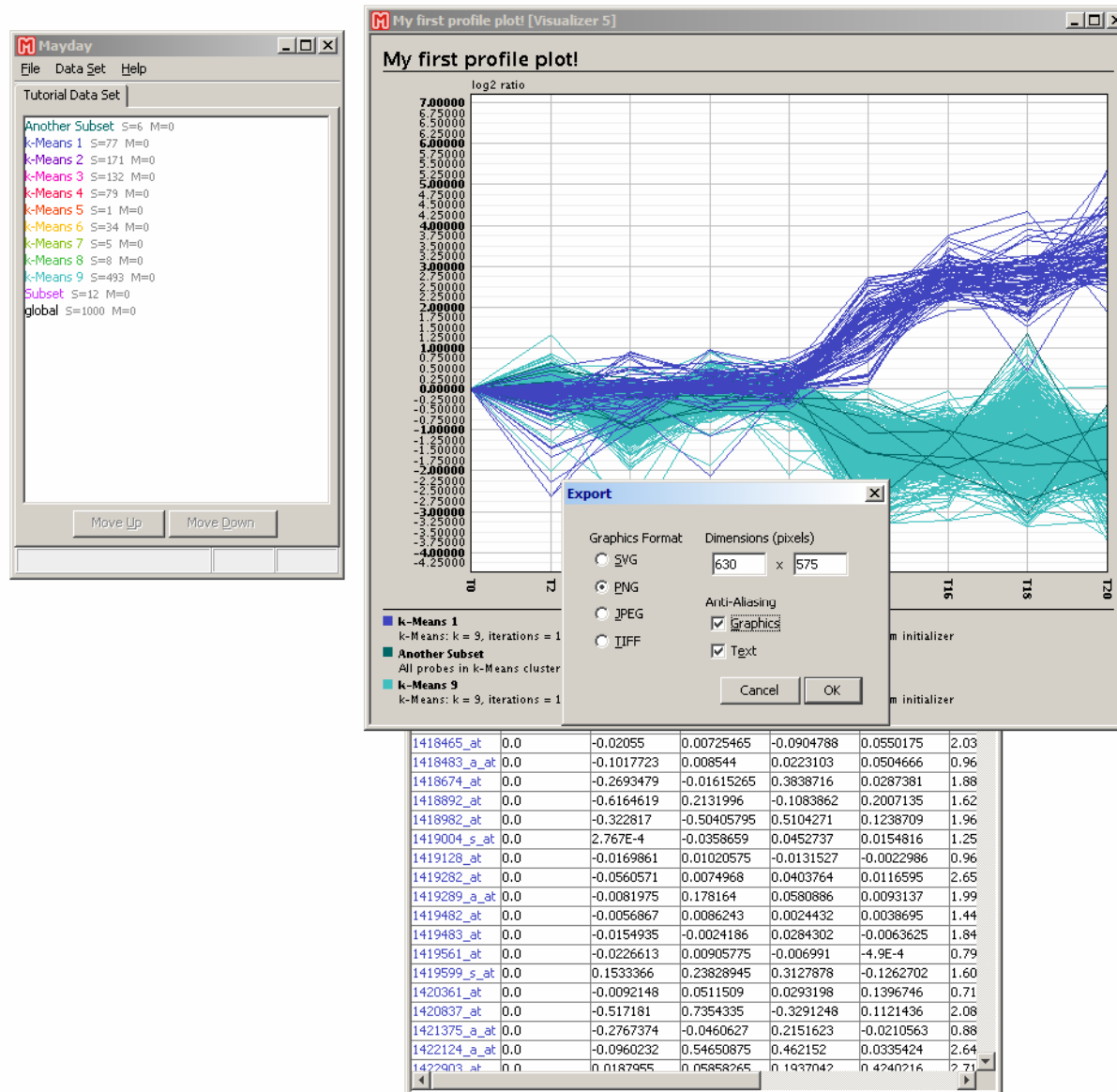
Select "Export".

Exporting a graphical viewer

111



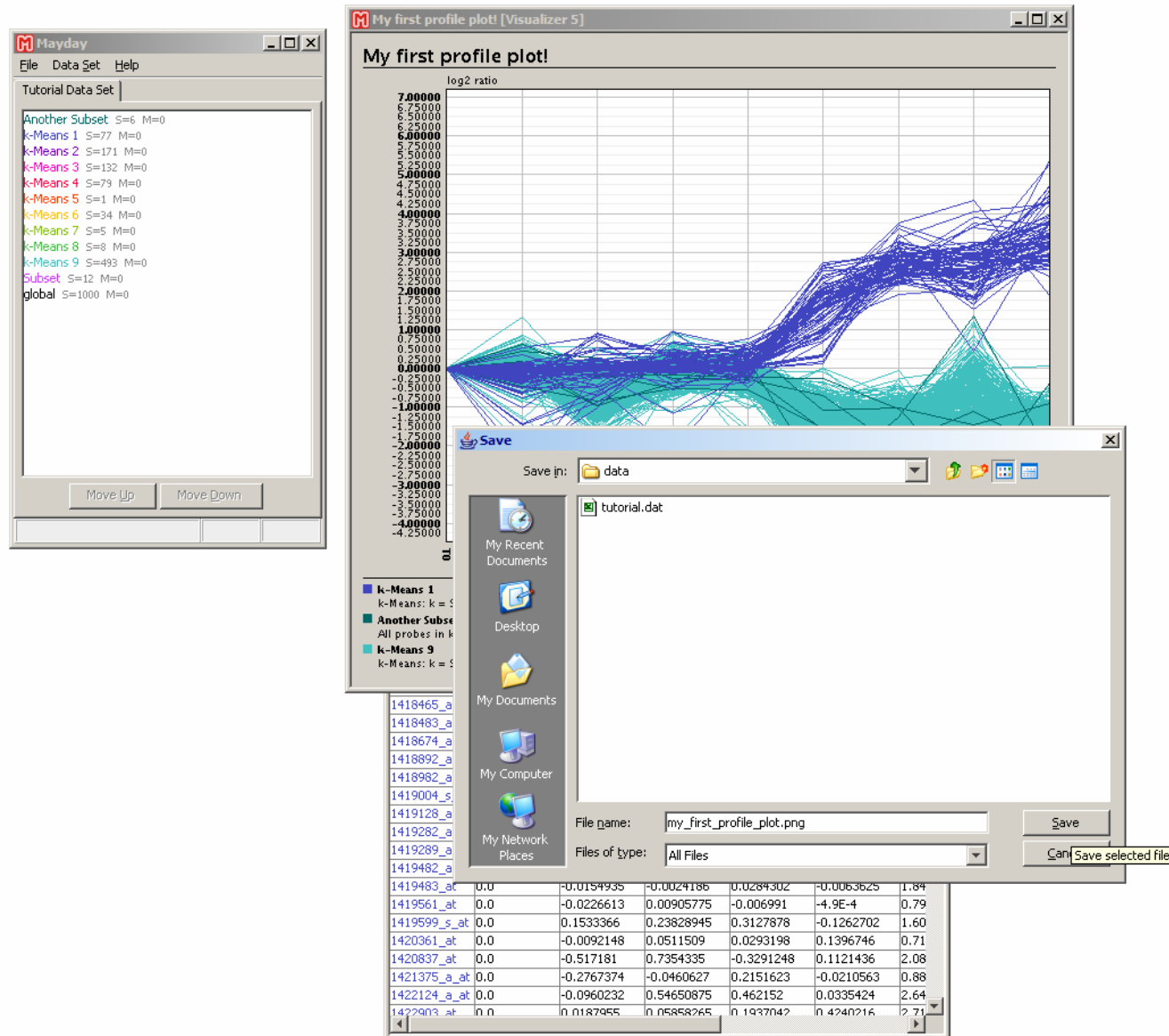
Select "PNG" and check graphics and text anti-aliasing.



Click "OK" to
export the
profile plot.

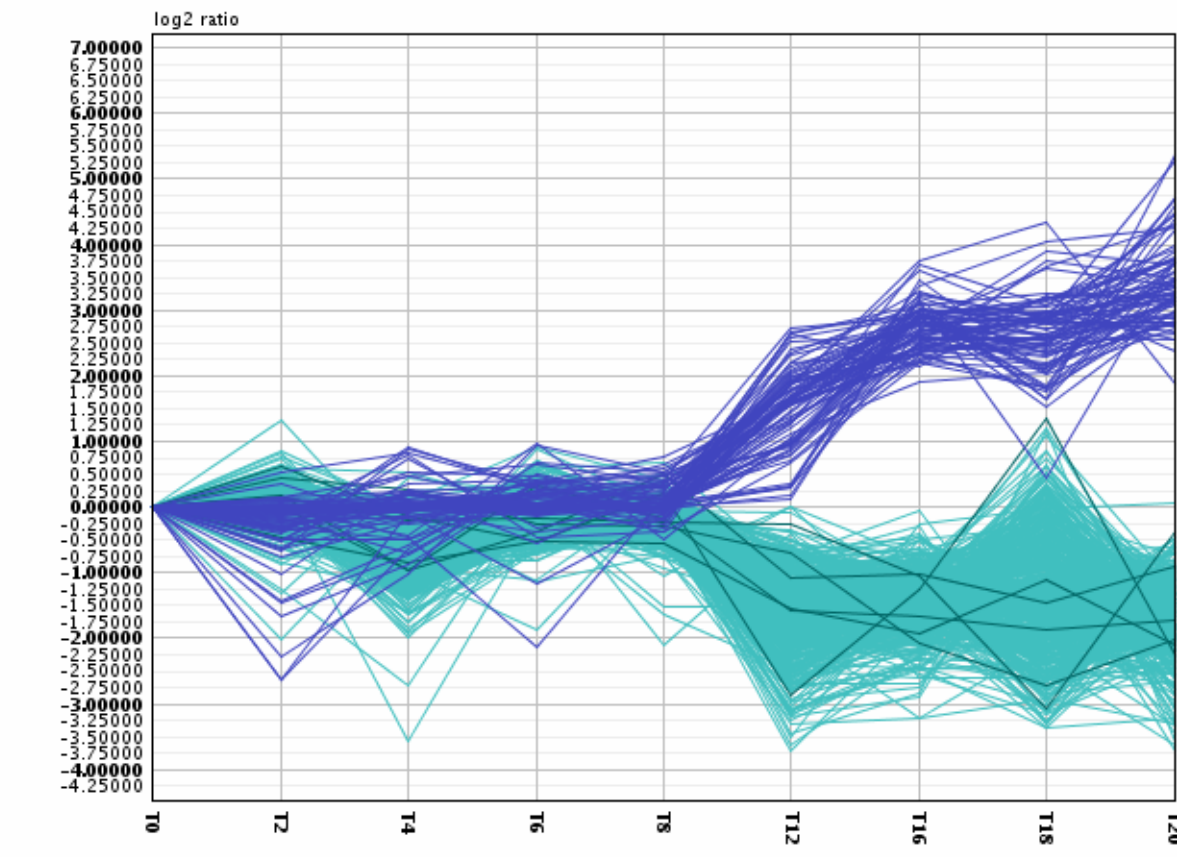
Exporting a graphical viewer

113



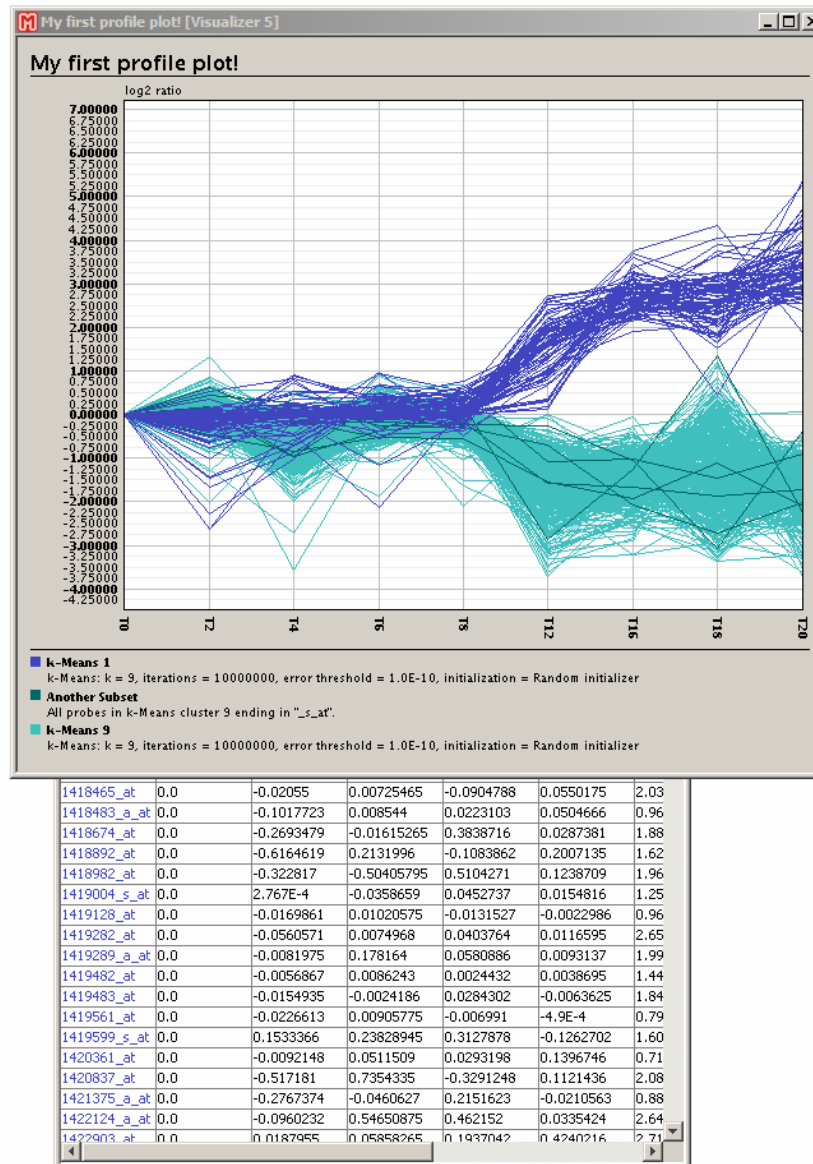
Enter a file name
and confirm.

My first profile plot!

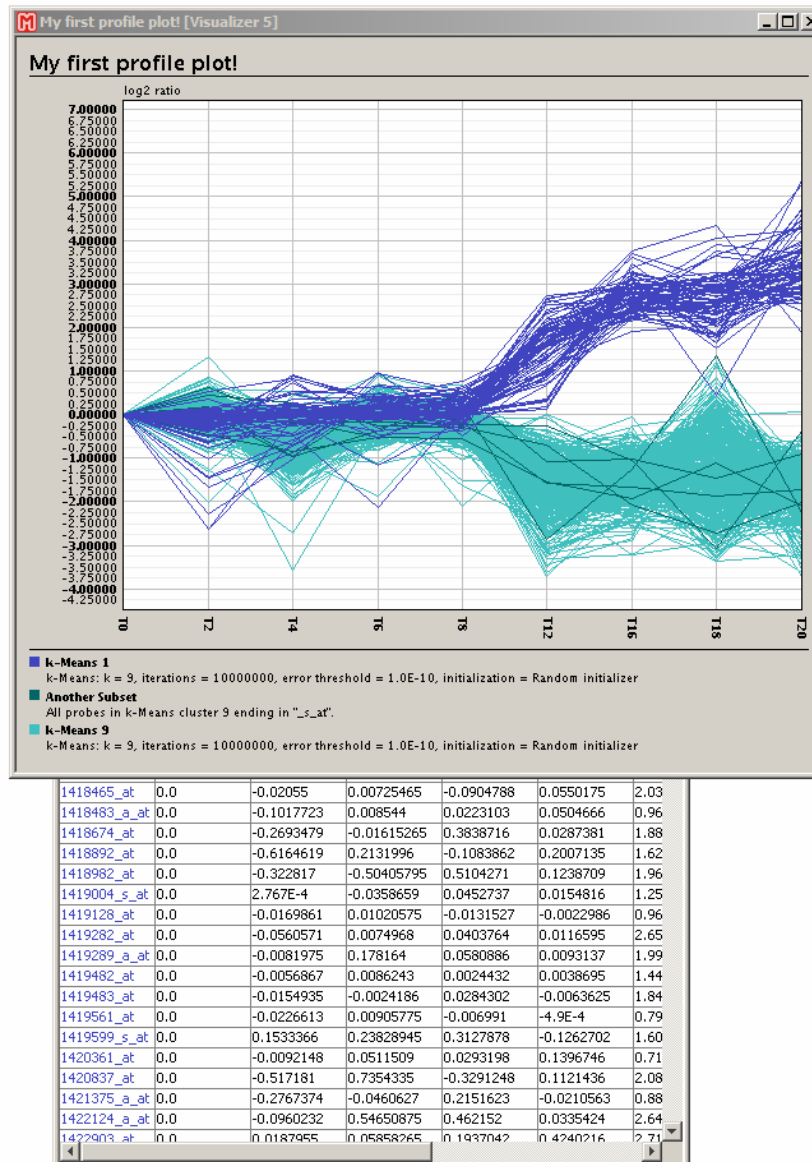
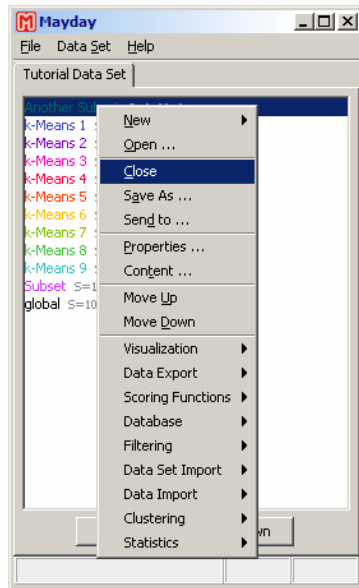


- **k-Means 1**
k-Means: k = 9, iterations = 10000000, error threshold = 1.0E-10, initialization = Random initializer
- **Another Subset**
All probes in k-Means cluster 9 ending in "_s_at".
- **k-Means 9**
k-Means: k = 9, iterations = 10000000, error threshold = 1.0E-10, initialization = Random initializer

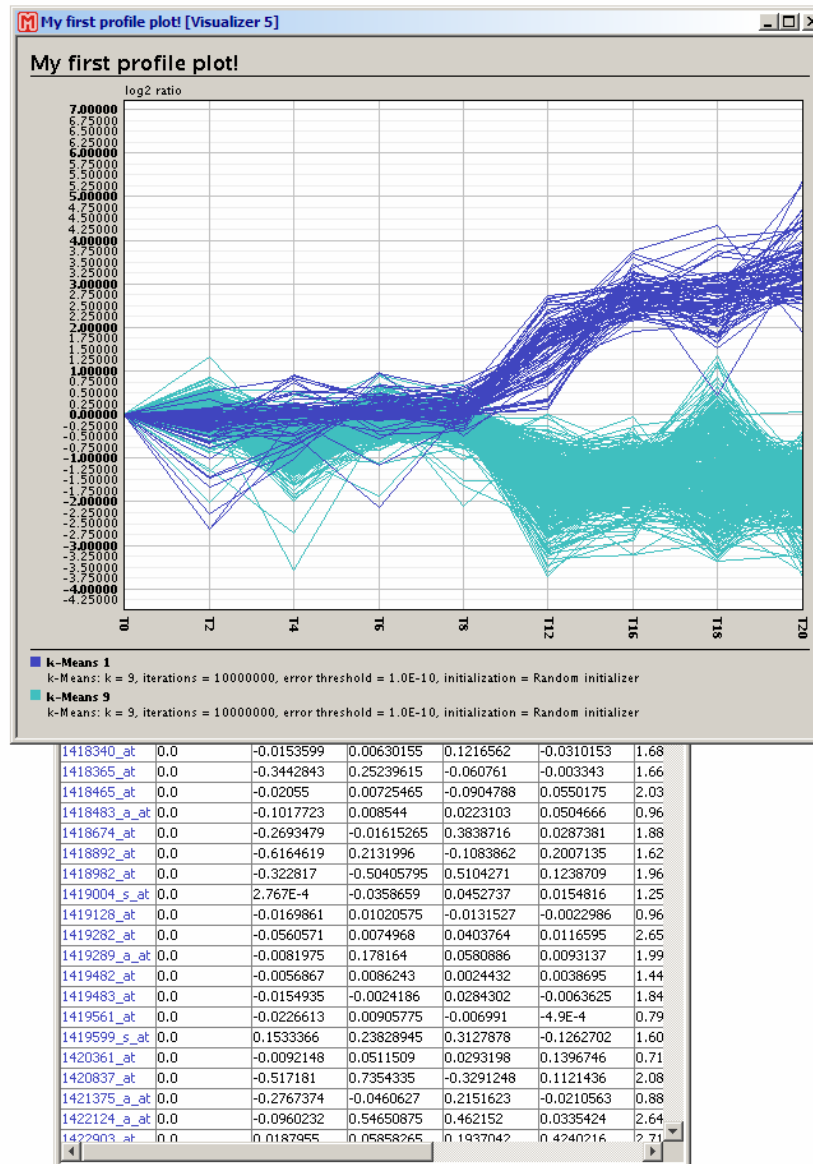
Here is the exported image of the profile plot. You can also export to SVG and then convert to PDF later. This helps a lot if you are going to publish your results.



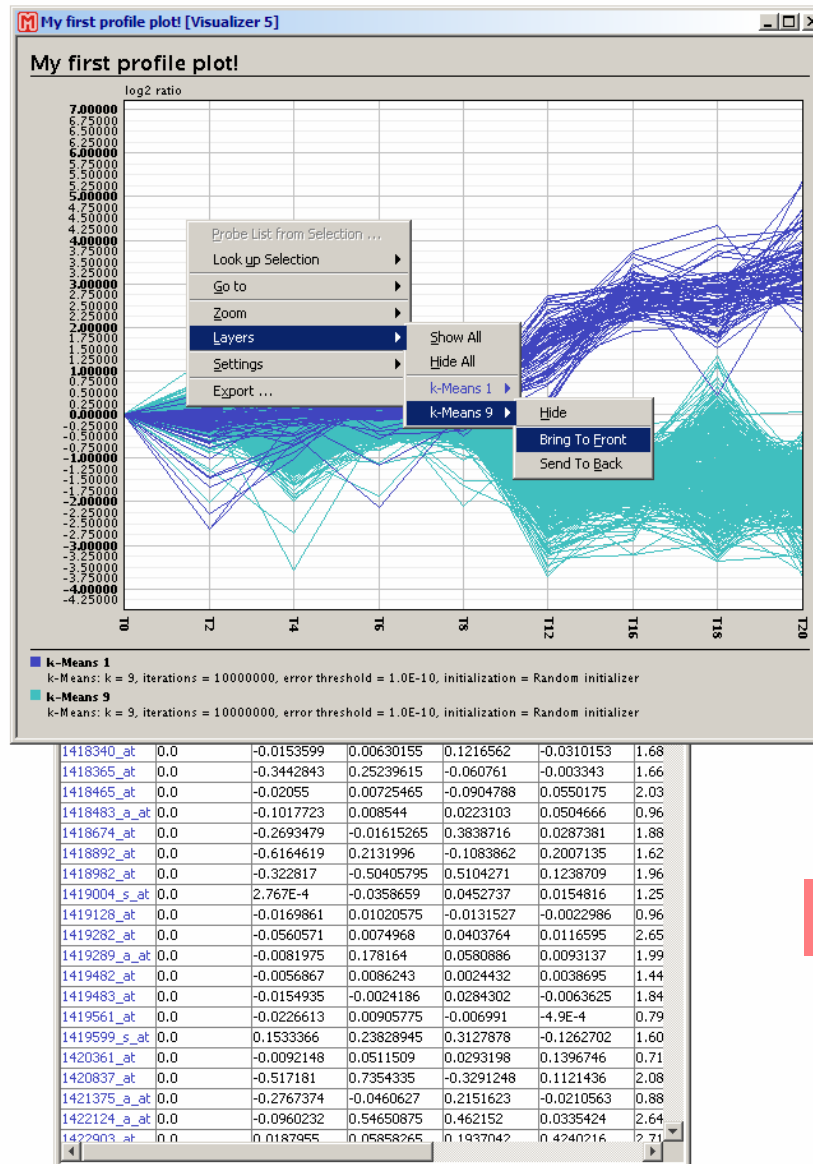
Select the probe list you have created earlier in the probe list manager and open the probe list managers context menu.



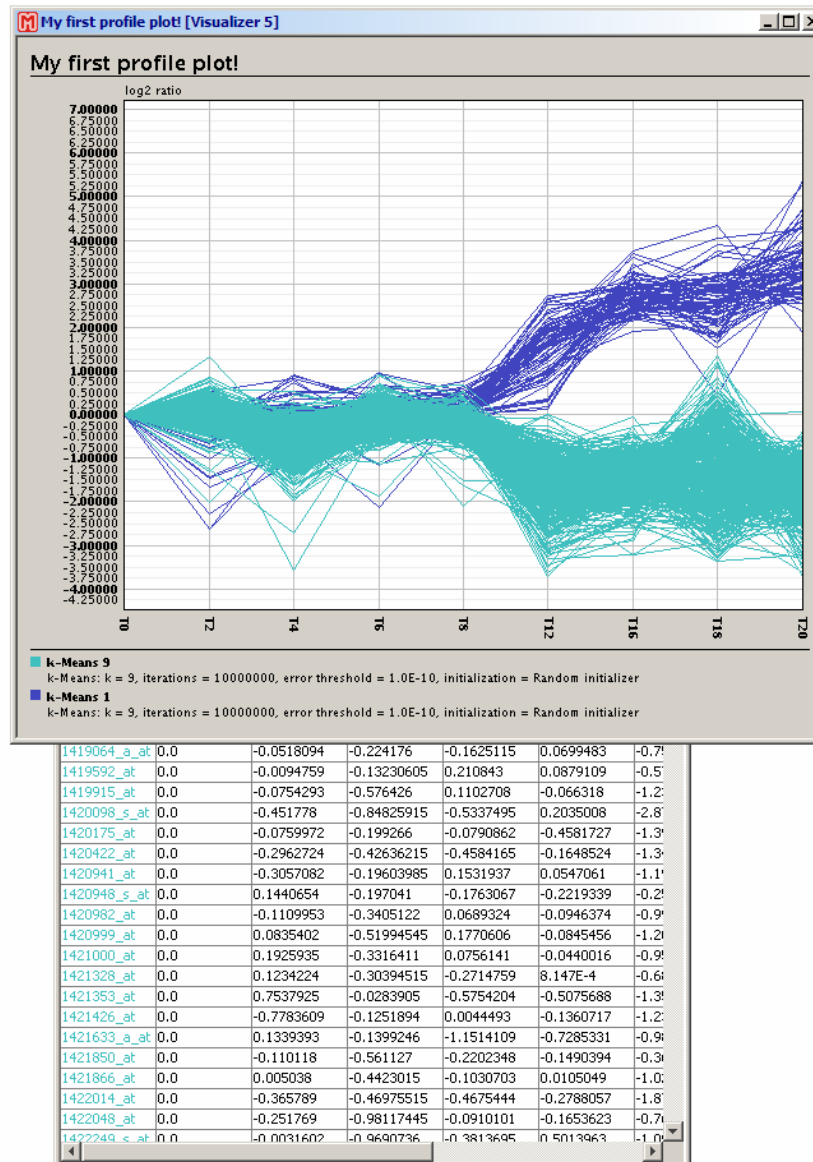
Select "Close" to remove the probe list.



Open the profile plot's context menu and select "Layers", then "k-Means 9".



Select "Bring to Front".

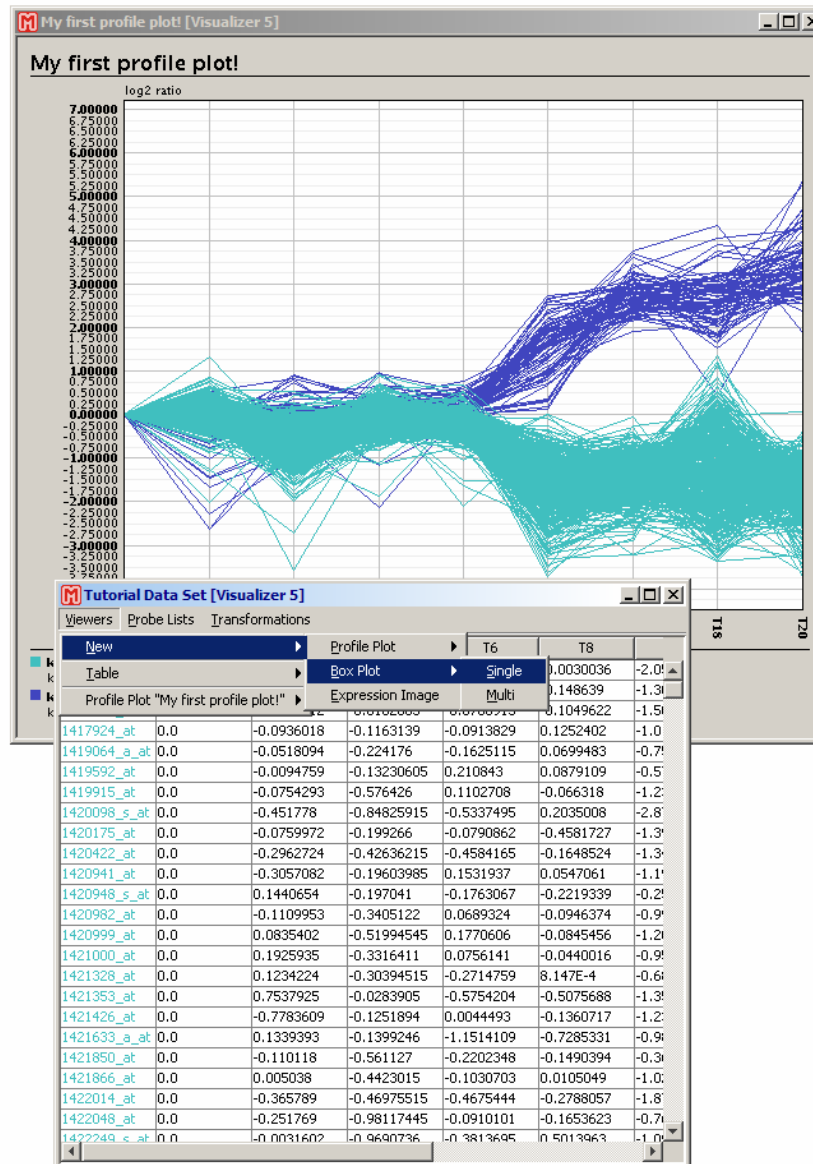


Rearranging the layers in a profile plot allows you to see profiles that would otherwise be hidden.

Bring the tabular viewer to the front, select menu item "Viewers", then "New", then "Box Plot".

Adding a box plot

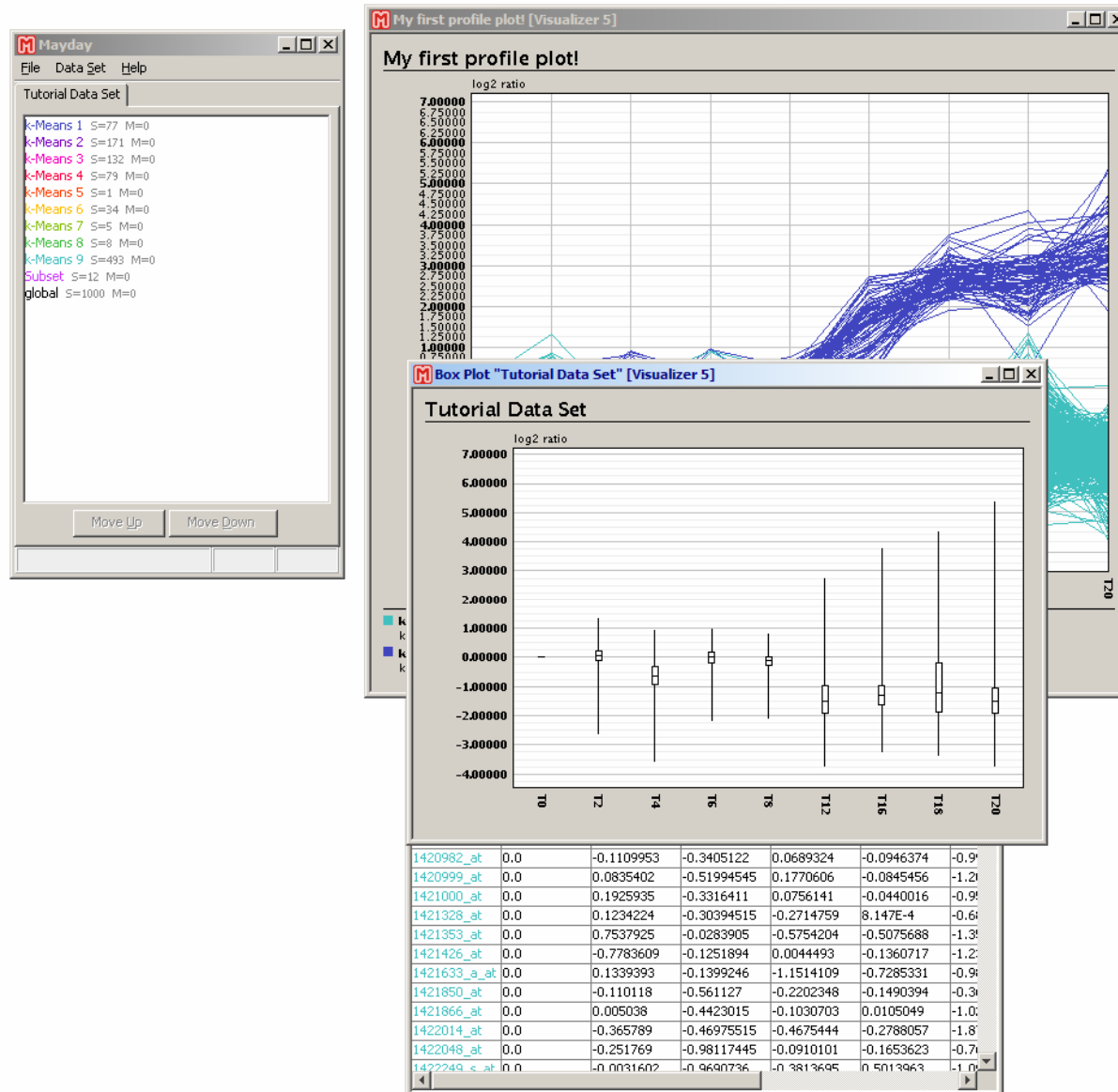
120



Click on "Single".

Adding a box plot

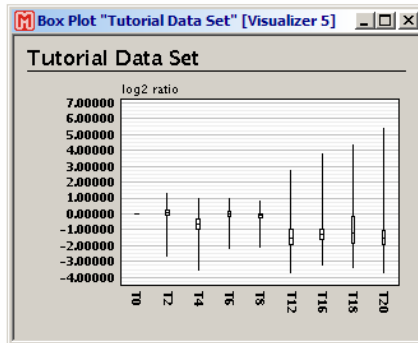
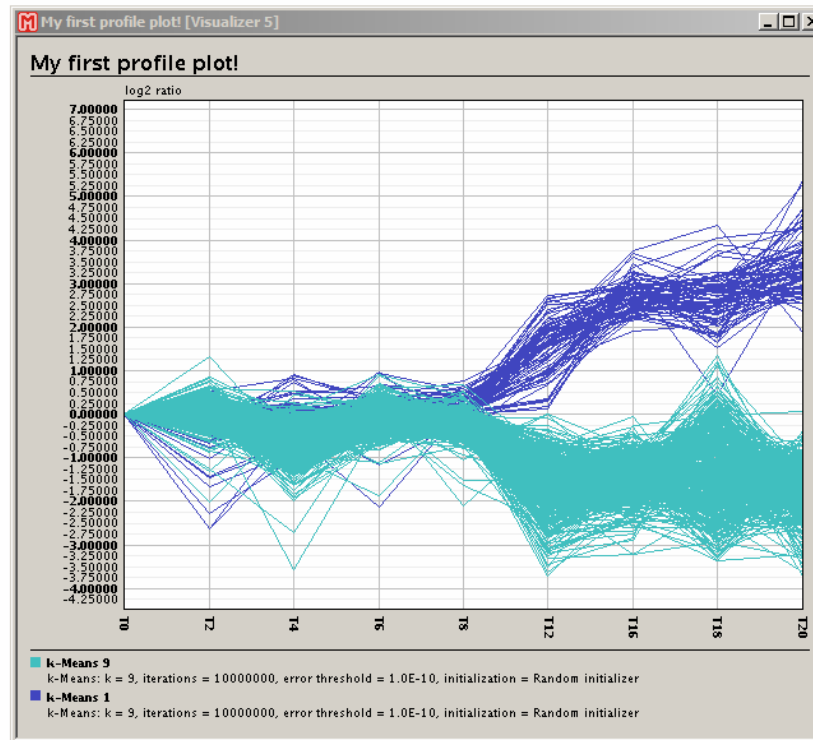
121



Zoom out using either the context menu or the keyboard short cuts.

Adding a box plot

122

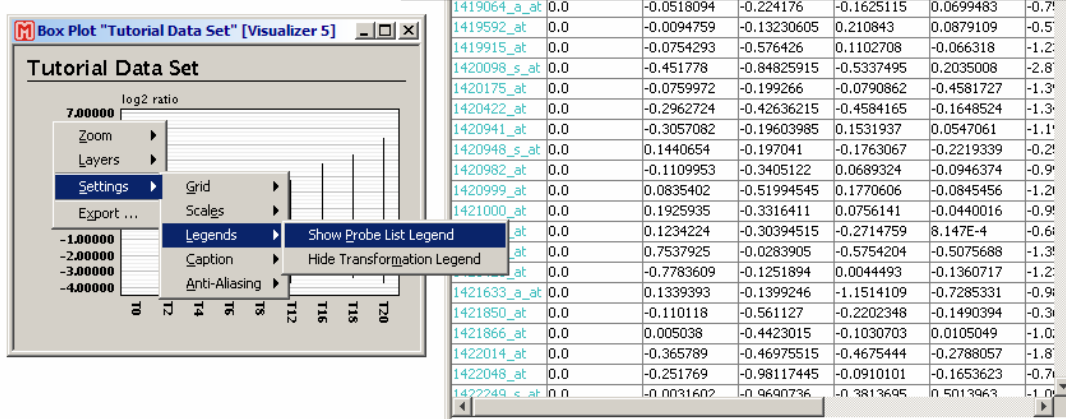
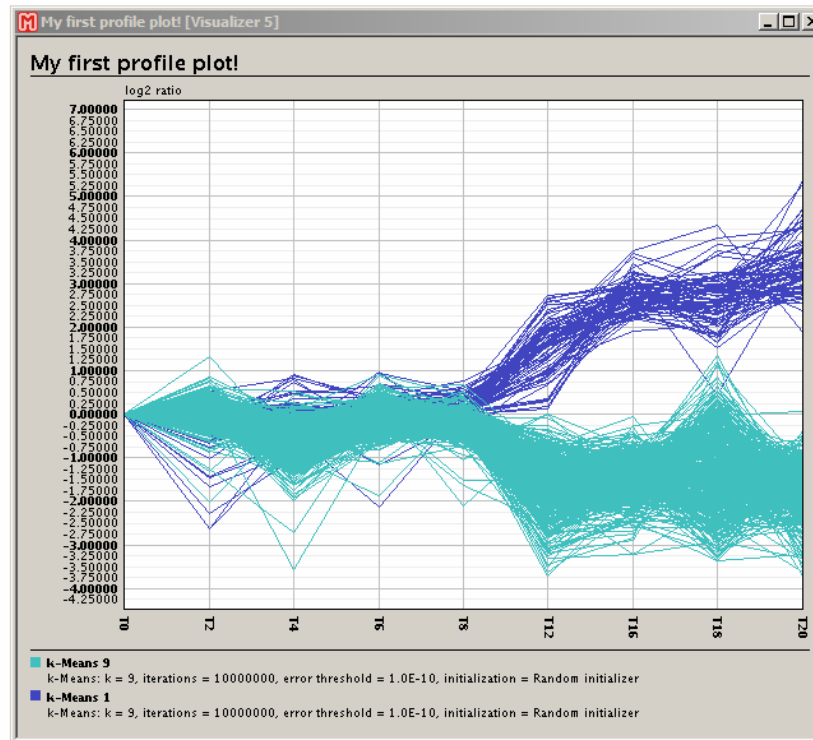


1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.74
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1770606	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

Open the box plot's context menu by right-clicking somewhere inside the window. Select "Settings" and then "Legends".

Adding a legend to a graphical viewer

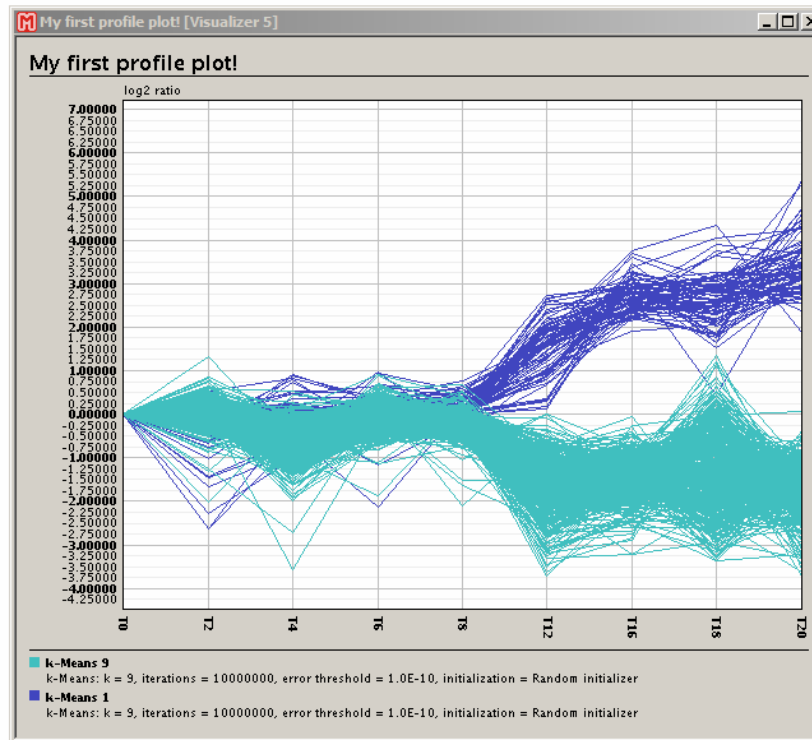
123



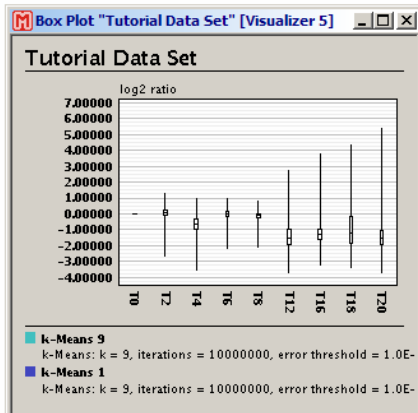
Click on "Show Probe List Legend".

Adding a legend to a graphical viewer

124

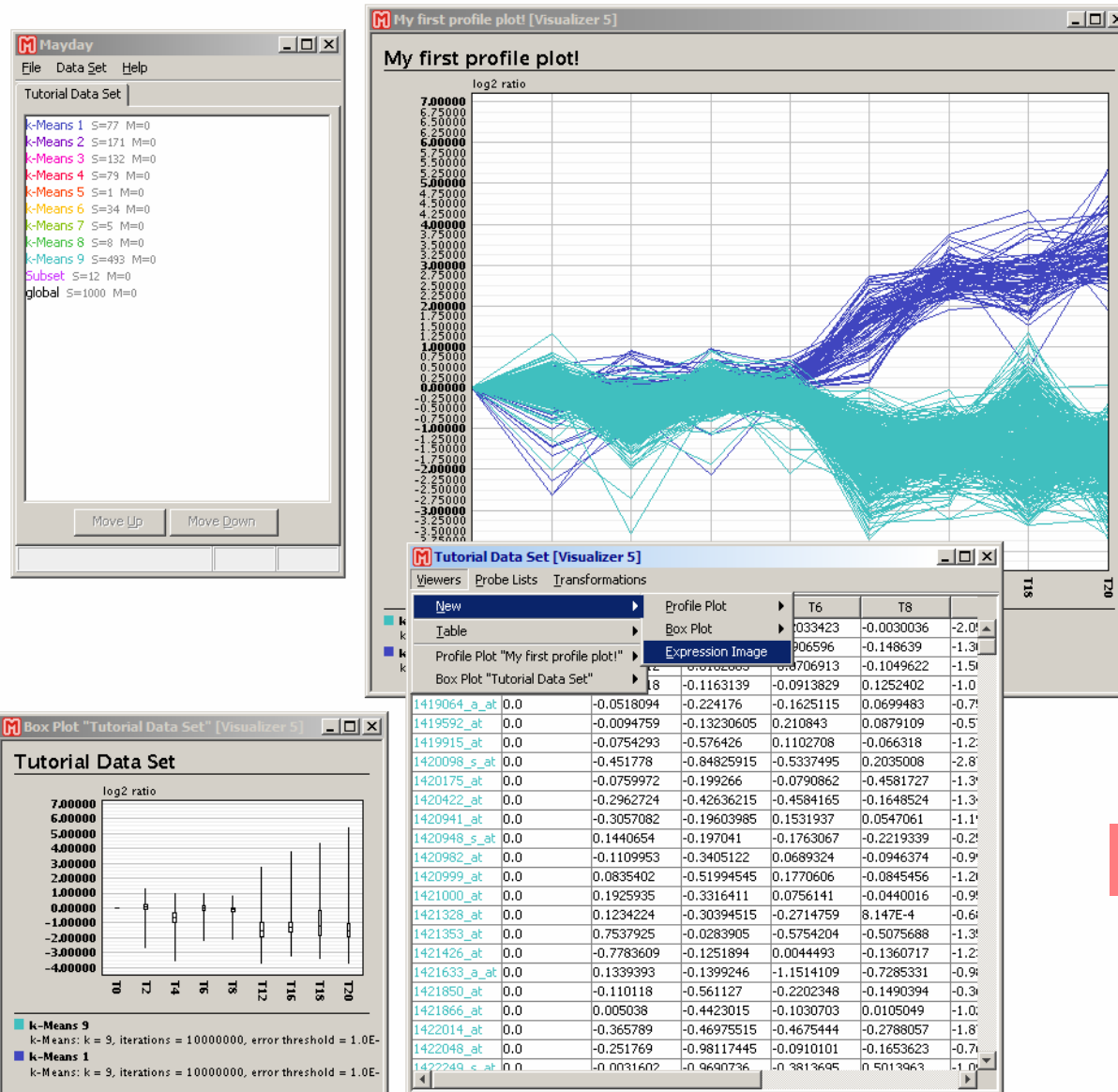


Adding a legend to a box plot will remind you of what you are actually looking at.



1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1770606	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

Bring the tabular viewer to the front, select menu item "Viewers" and then "New".

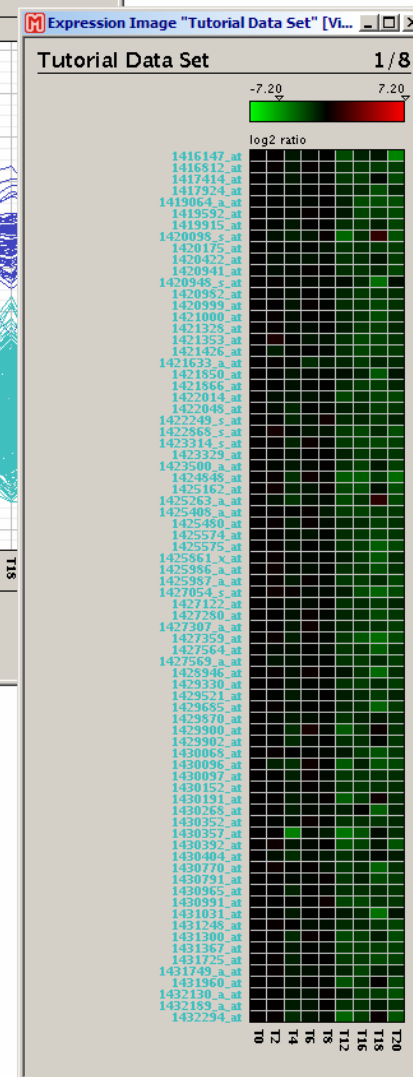
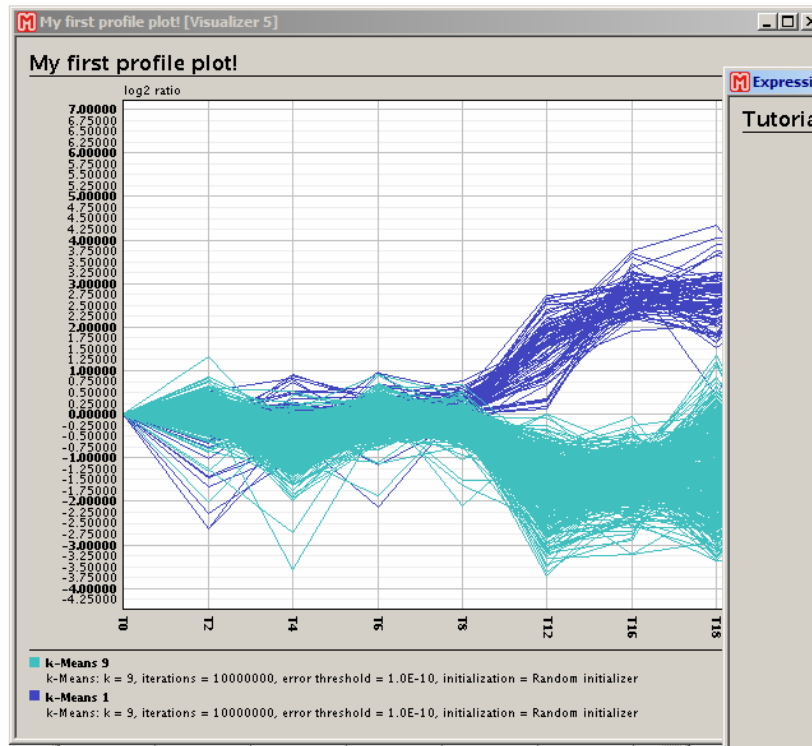


Using several viewers different at the same time will give you a better idea of the structure of your data.

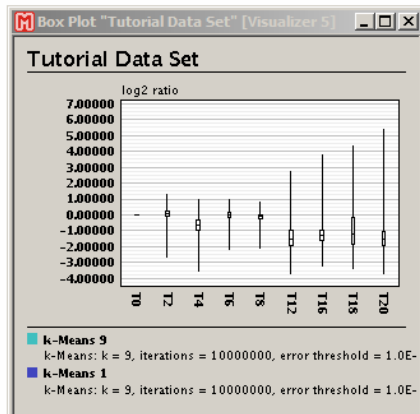
Select "Expression Image".

Adding a heatmap

126



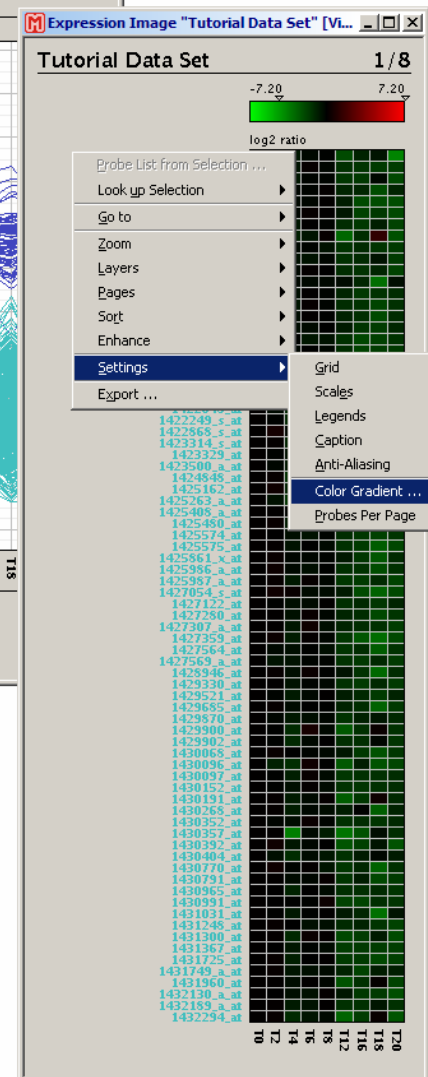
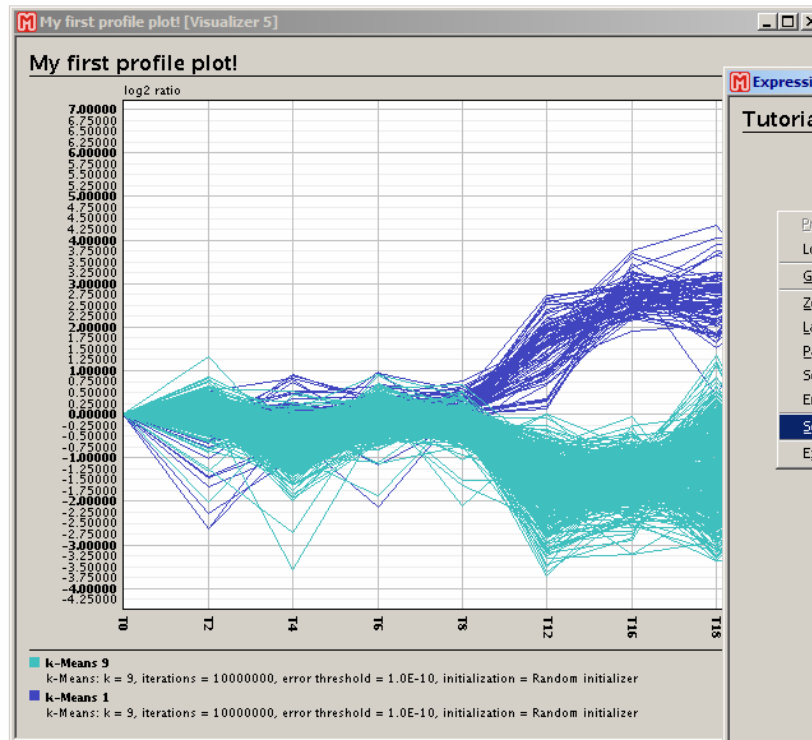
Right-click
on the
heatmap
to open its
context
menu.
Select
"Settings".



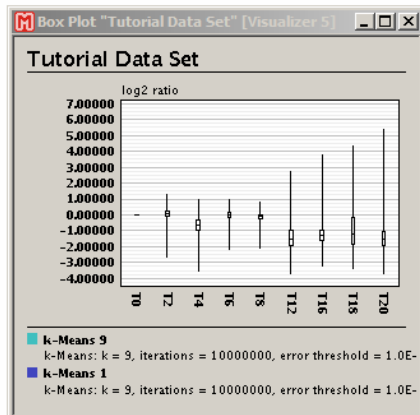
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1776006	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

Editing the color gradient

127



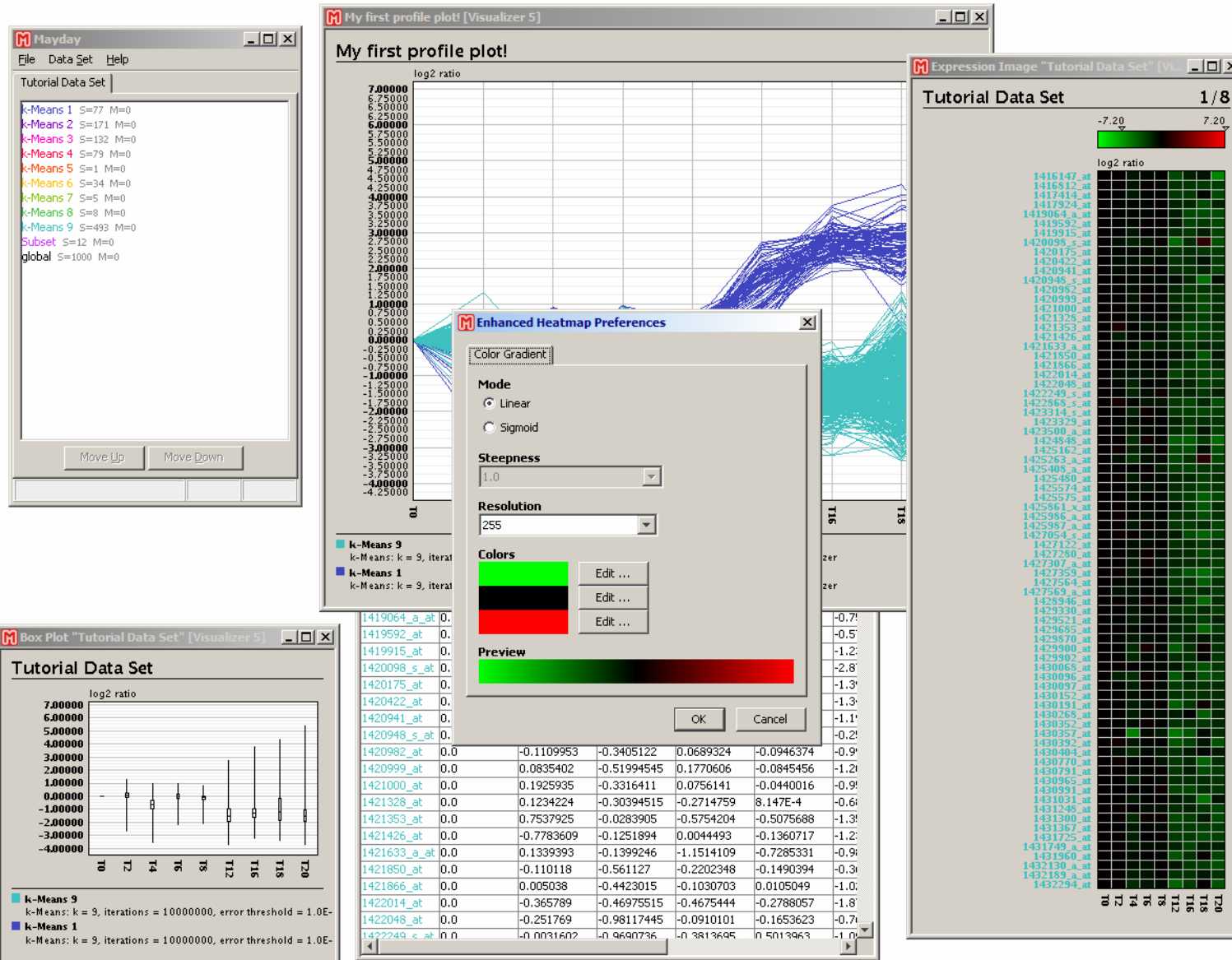
Click on
"Color
Gradient
..."



1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1776006	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

Editing the color gradient

128



Set mode to "Sigmoid" and steepness to "20".

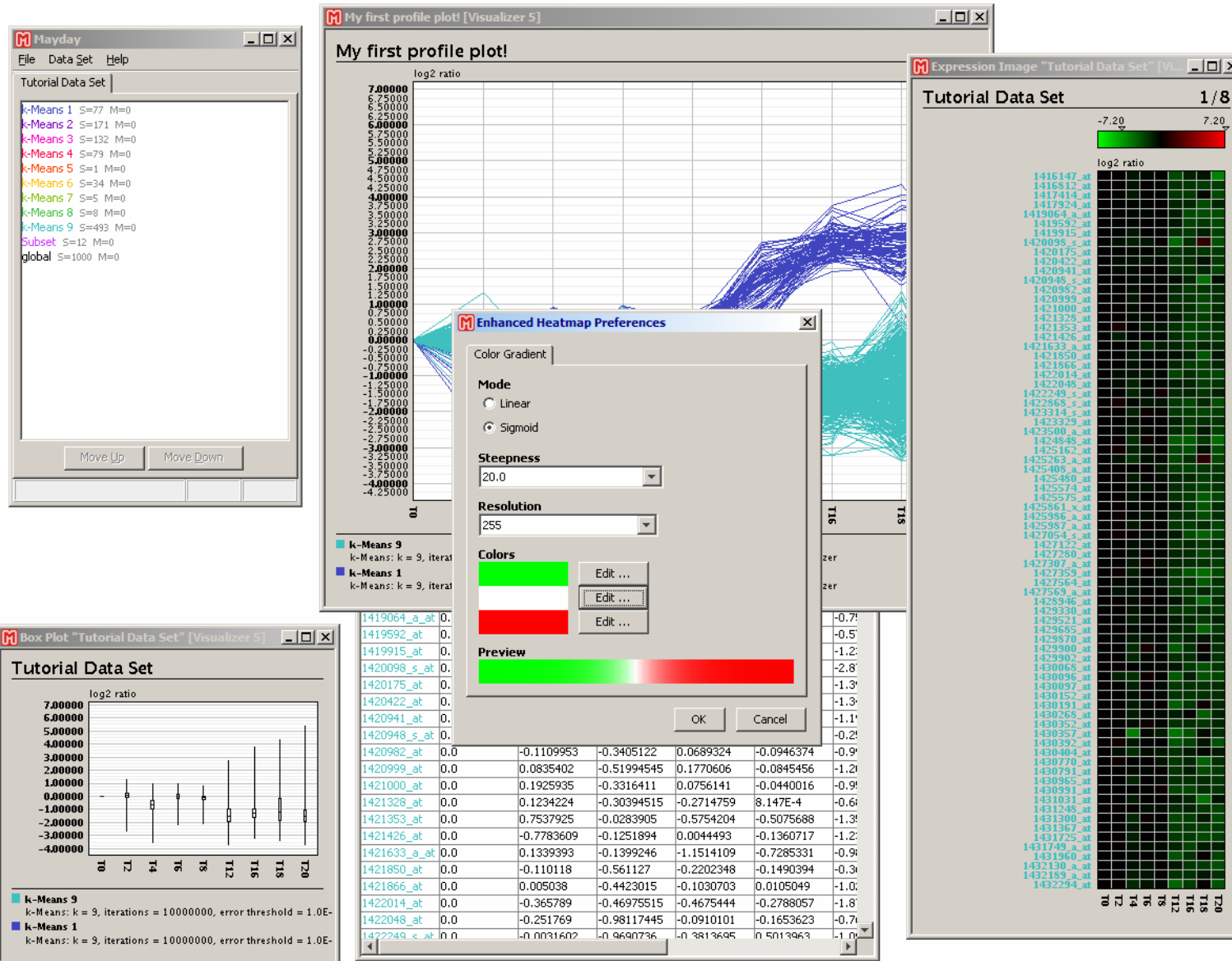
129



Change
the central
color to
white.

Editing the color gradient

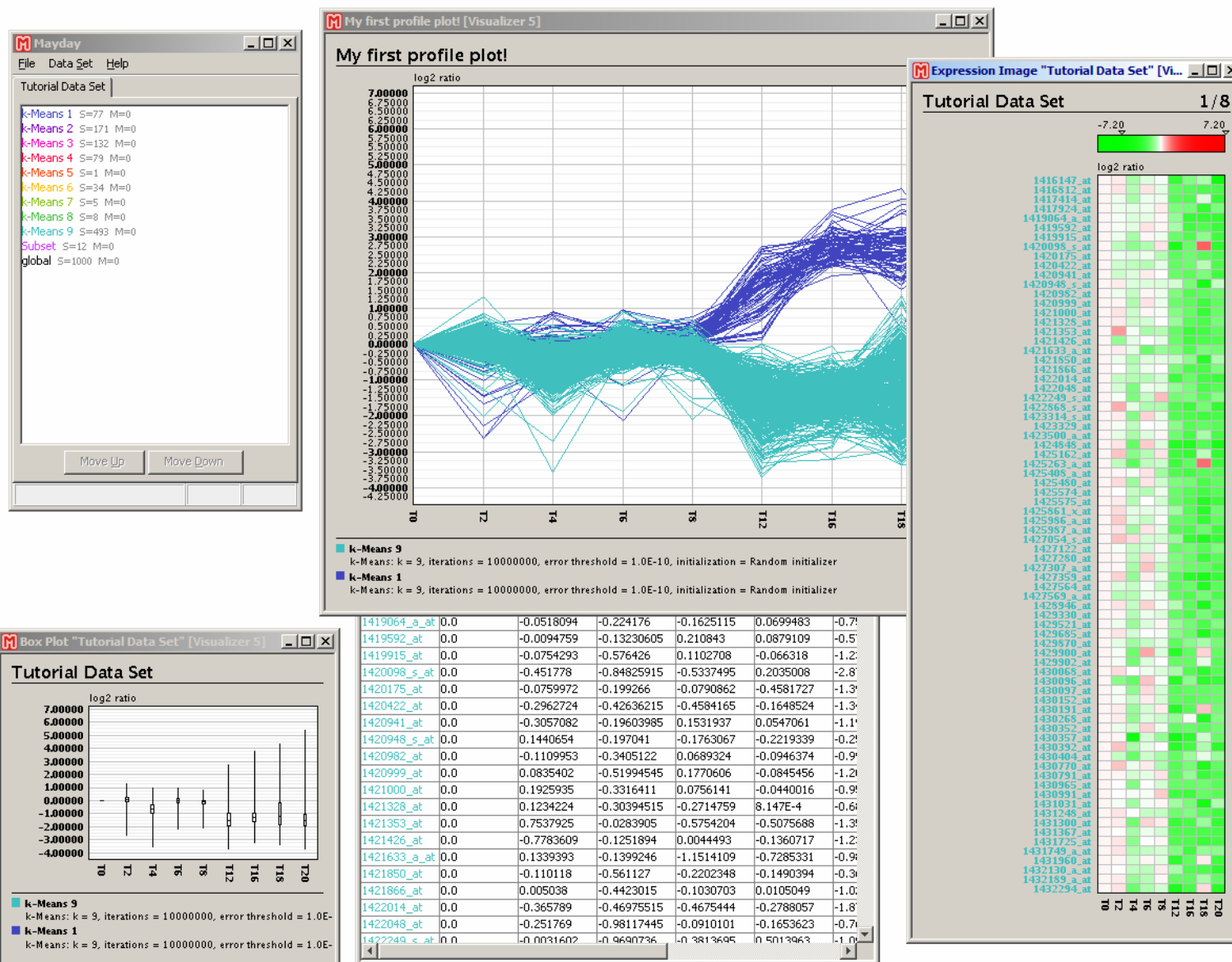
130



Click "OK"
to confirm
and update
the heatmap.

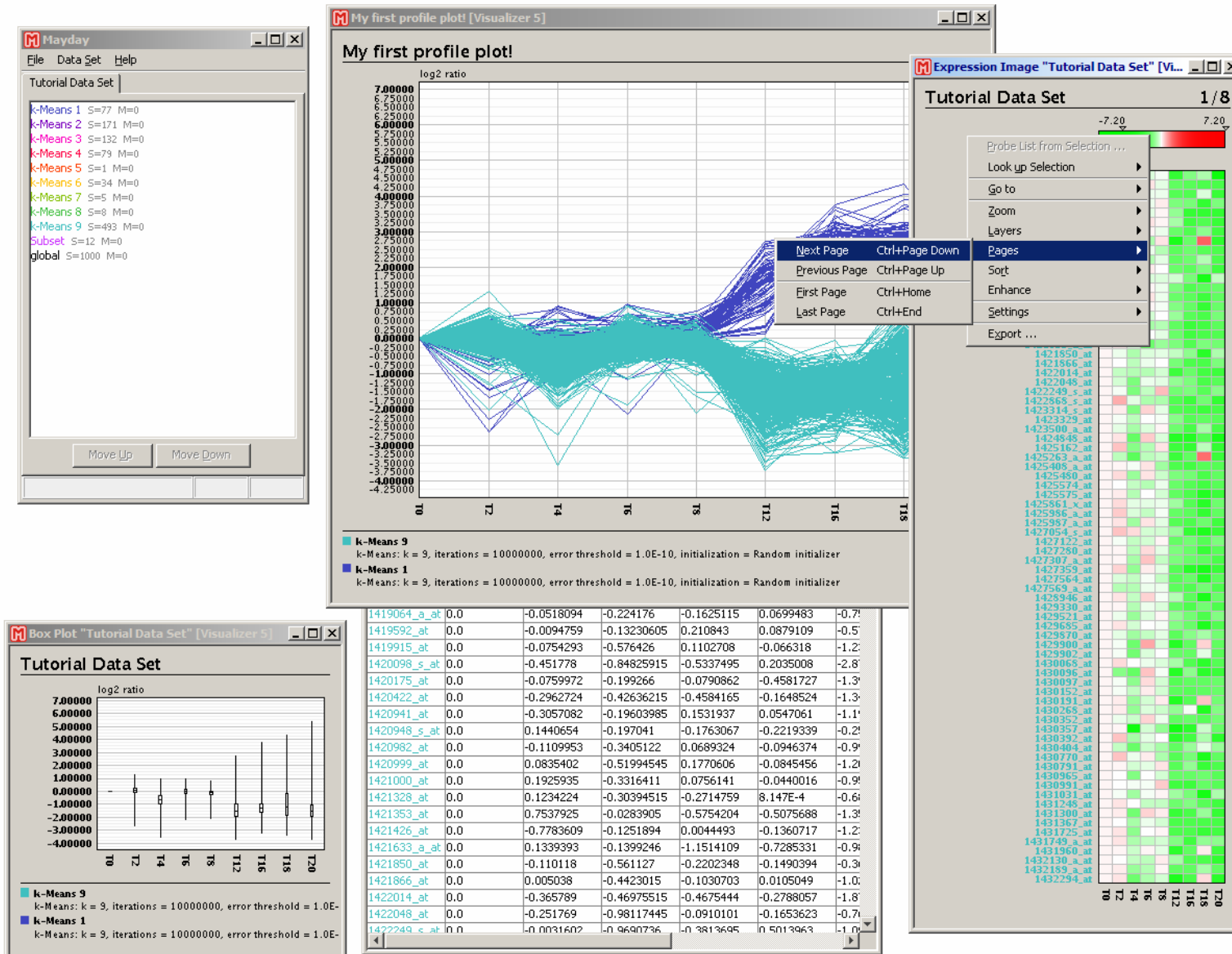
Editing the color gradient

131

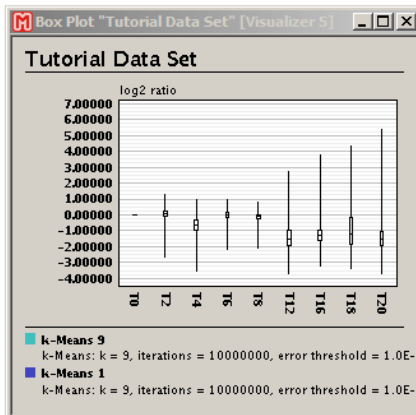
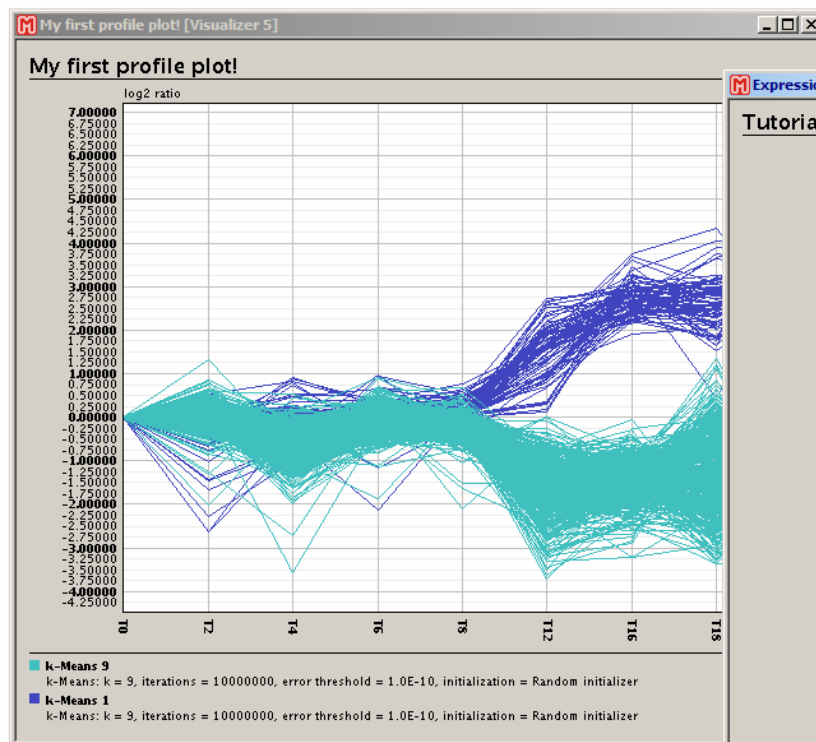


The new color gradient shows the features of the data much better.

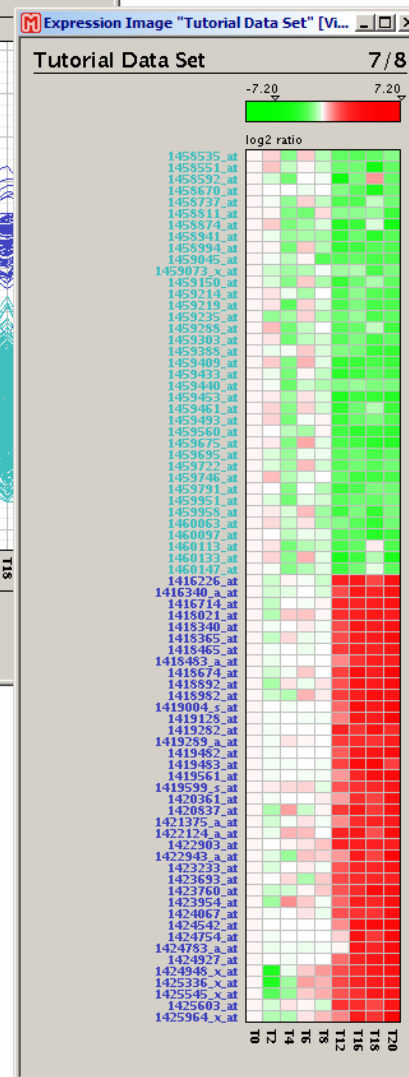
Open the context menu again and select submenu "Pages".



Click on
"Next
Page".
Repeat
this until
you reach
page 7.
You can
press
CTRL +
Page
Down
instead of
using the
menu.



1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1776006	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

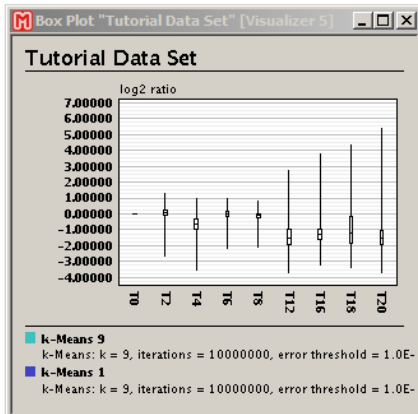
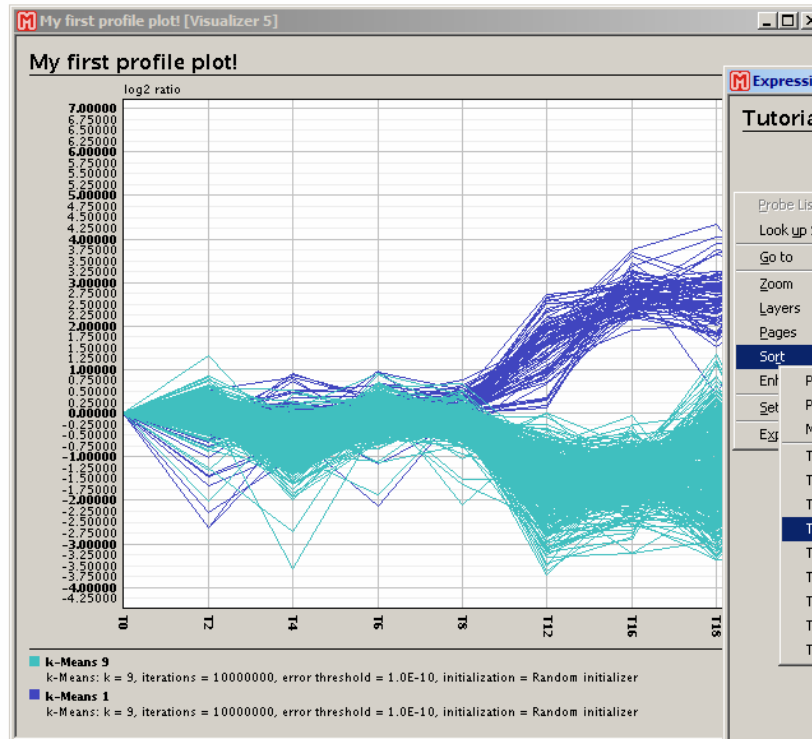


Open the context menu and select "Sort", then the "Descending" submenu.

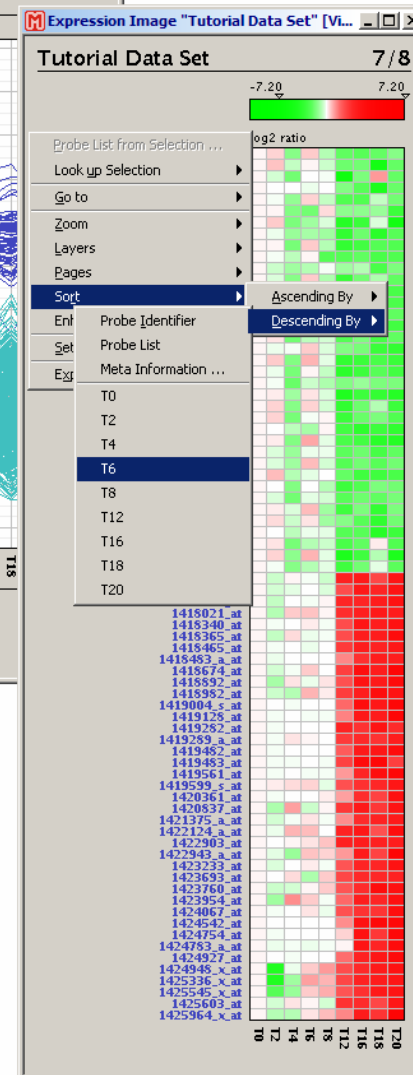
Sorting the rows of the heatmap

134

Click on
"T6".

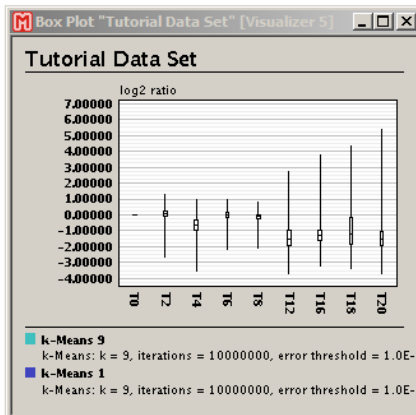
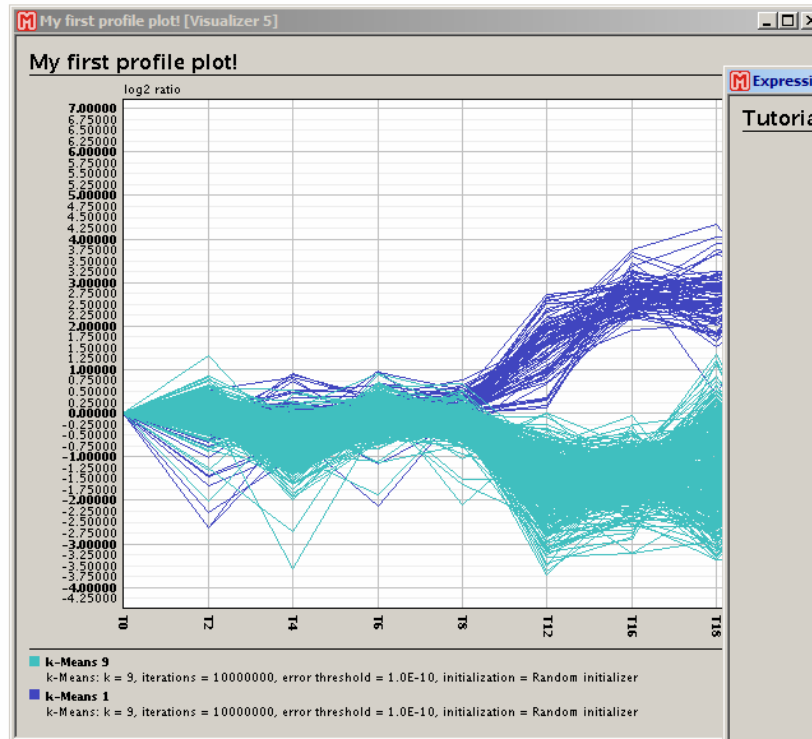


1419064_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1776006	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

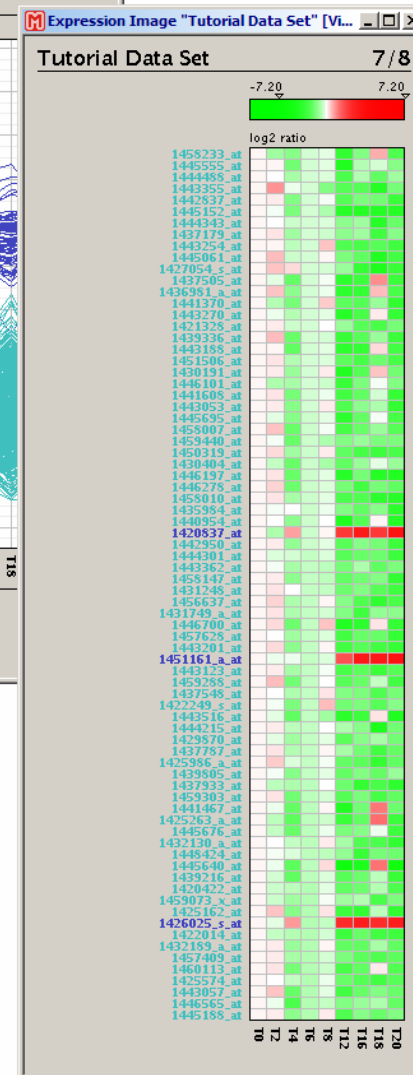


Sorting the rows of the heatmap

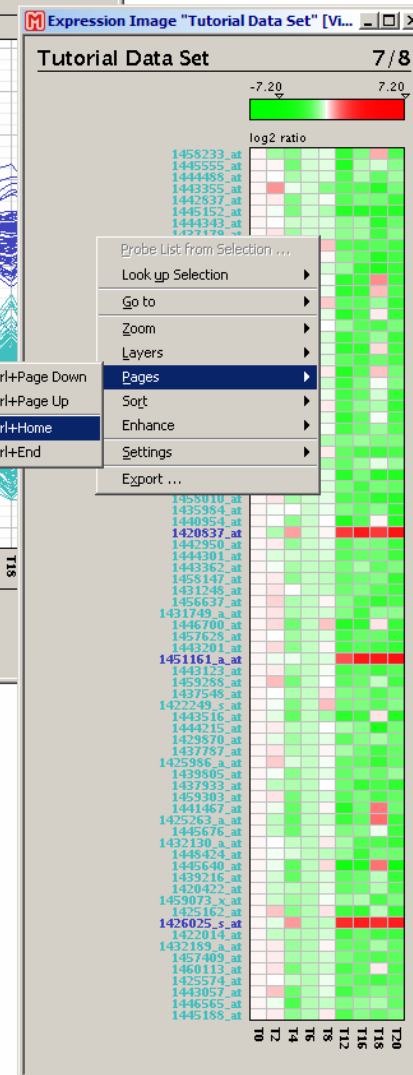
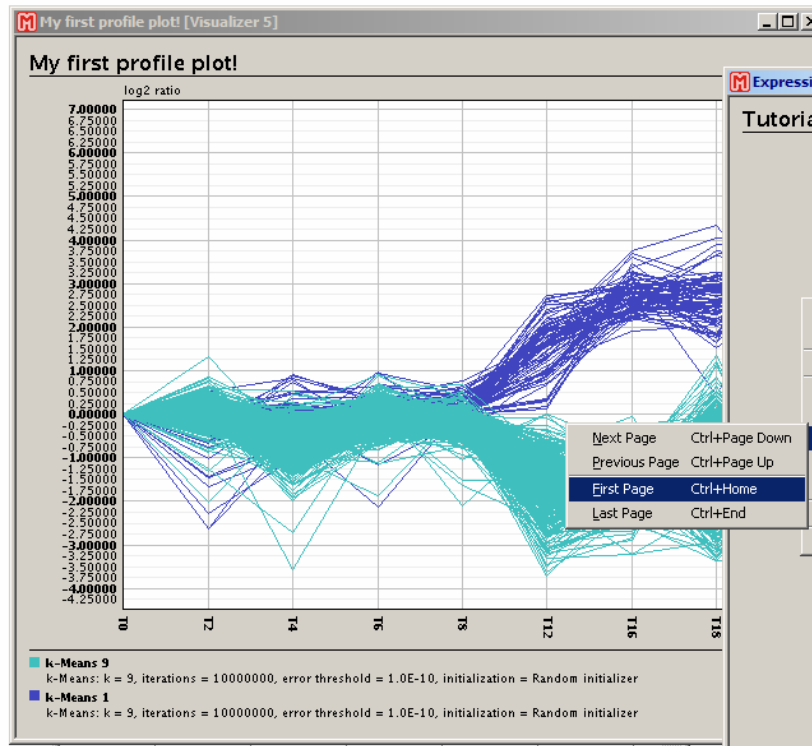
135



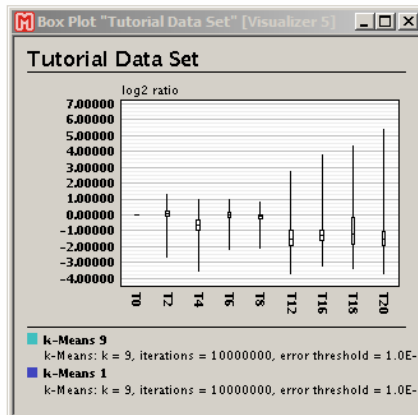
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1770606	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0



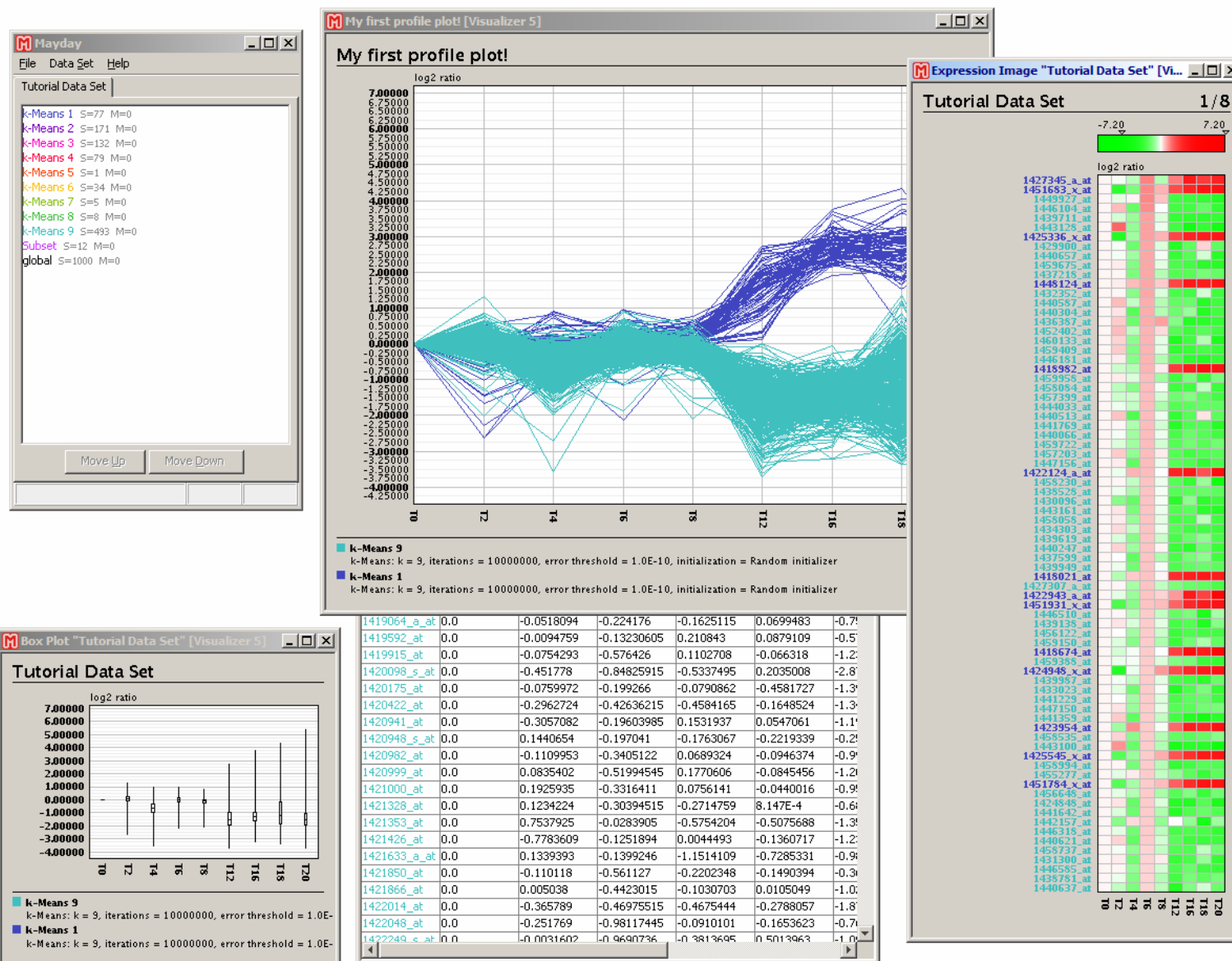
Open the context menu again and select submenu "Pages".



Click on
"First Page".



1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1776006	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_s_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

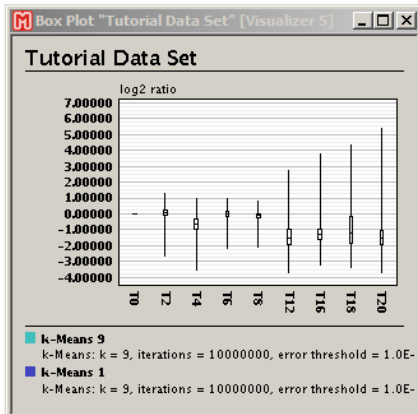
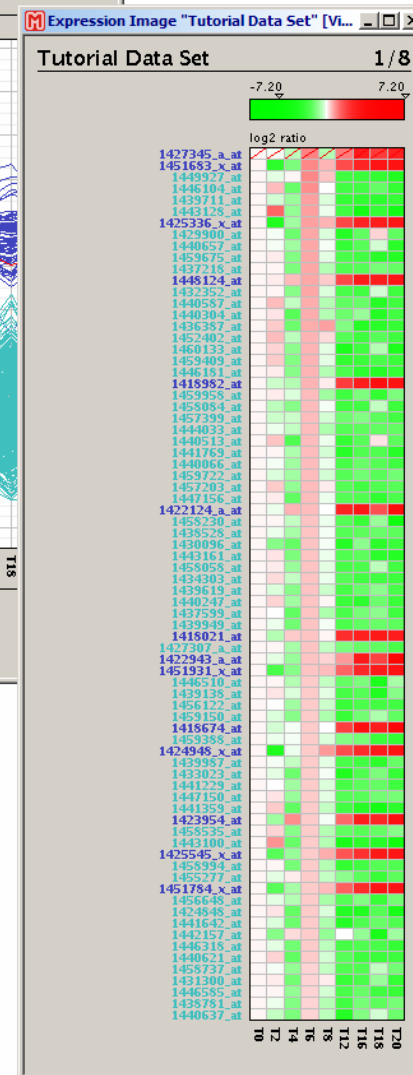
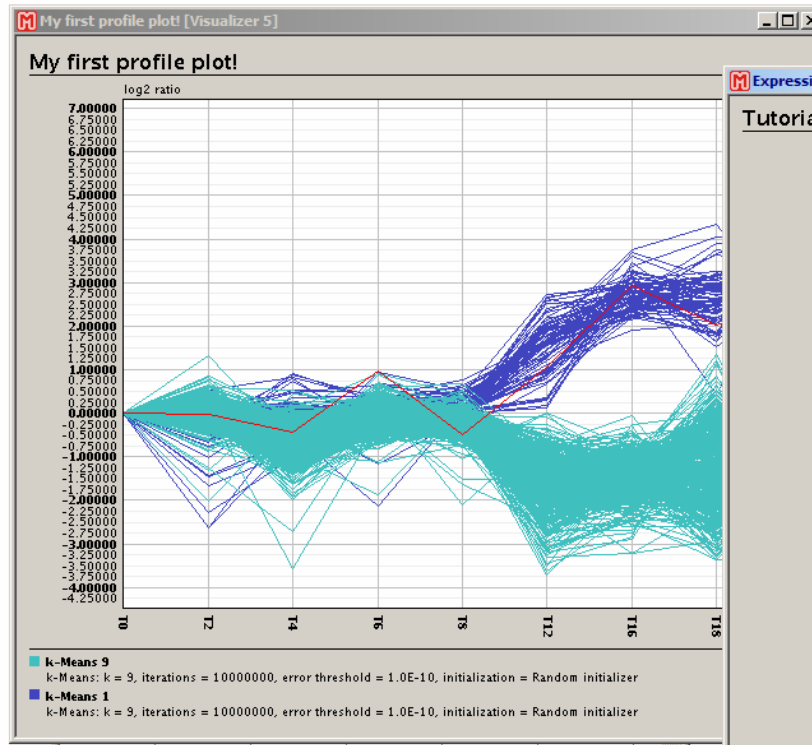


Profile plot and heatmap complement each other in this example.

Select the topmost probe by clicking on its row in the matrix.

Selecting probes across viewers

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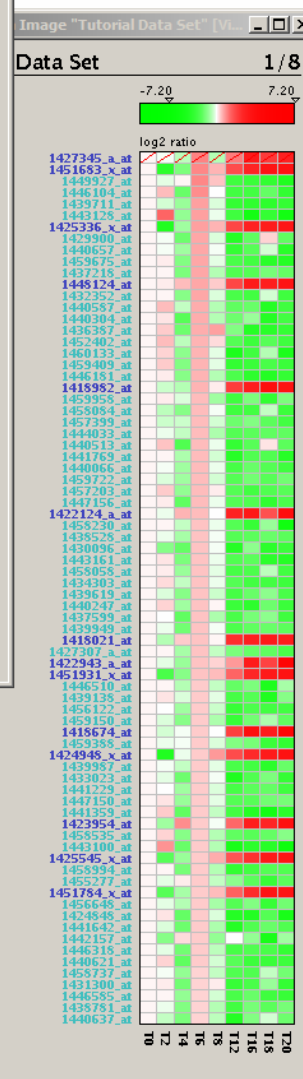
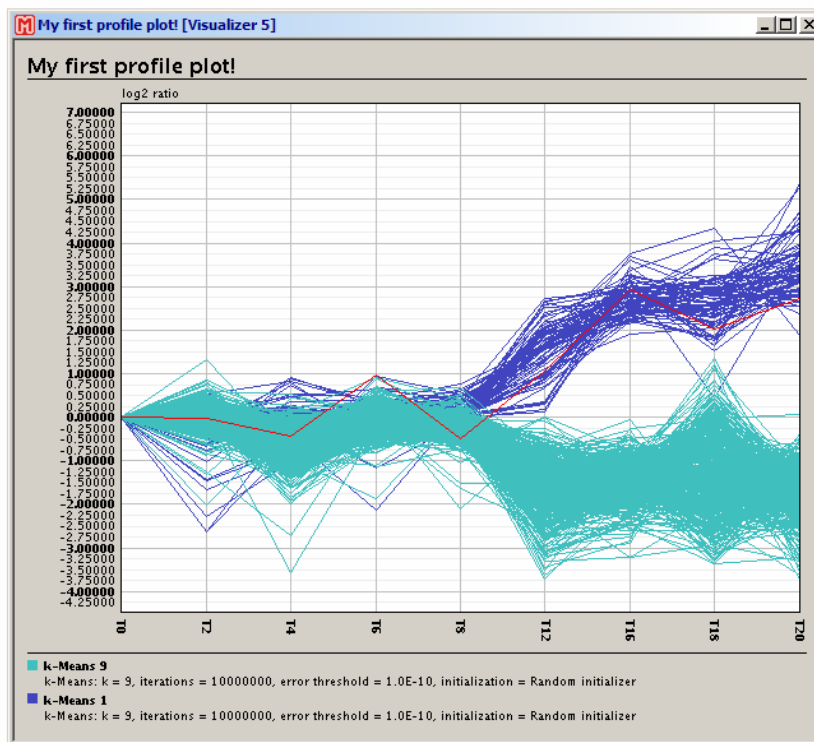
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1776006	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

Another example for linked viewers.

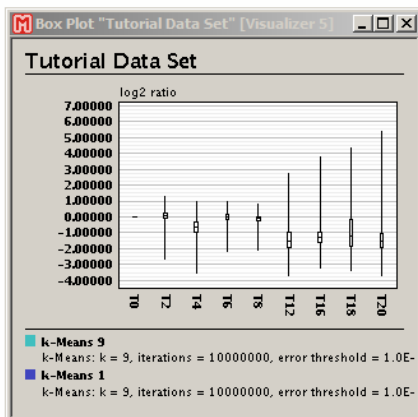
Bring the profile plot to the front.

Selecting probes across viewers

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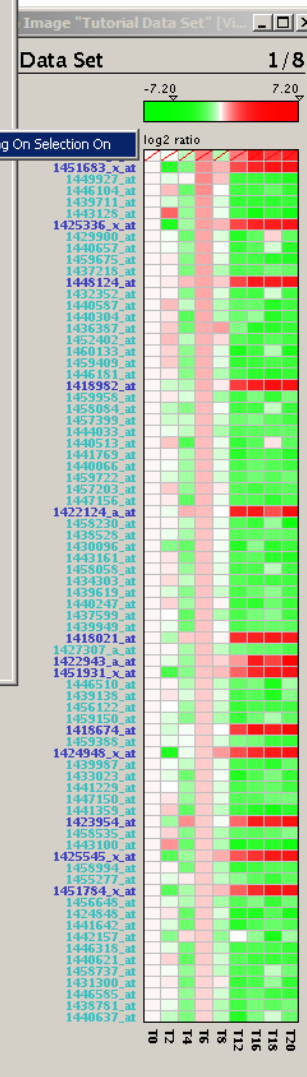
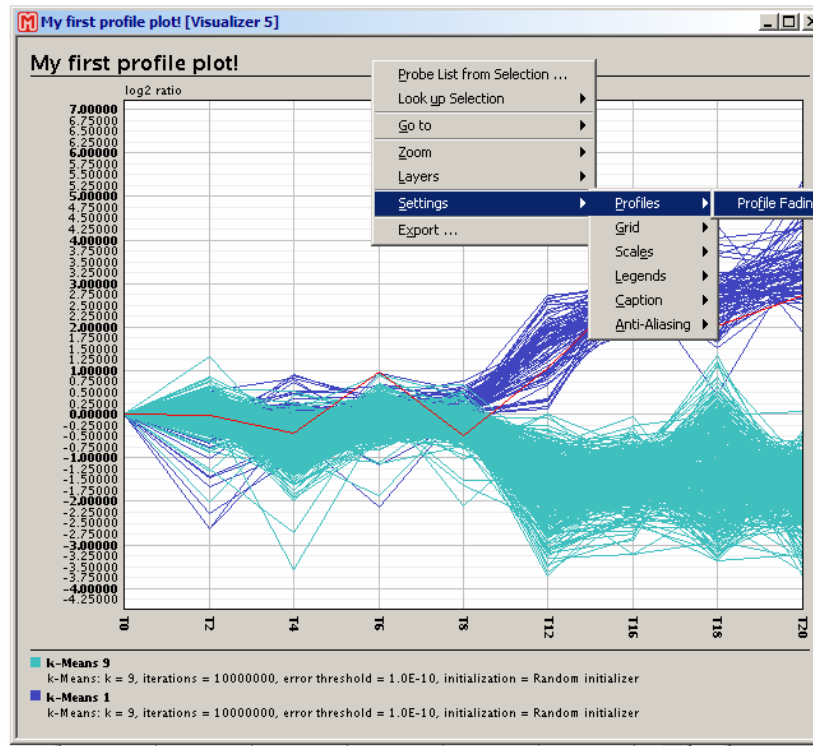
Right-click in the gray area of the profile plot window to open the context menu without clearing the selection. Select "Settings", then "Profiles".



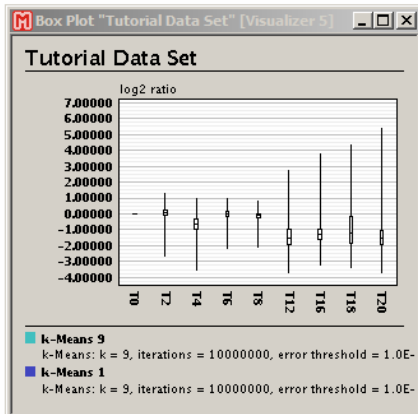
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1776006	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

Tweaking the profile plot

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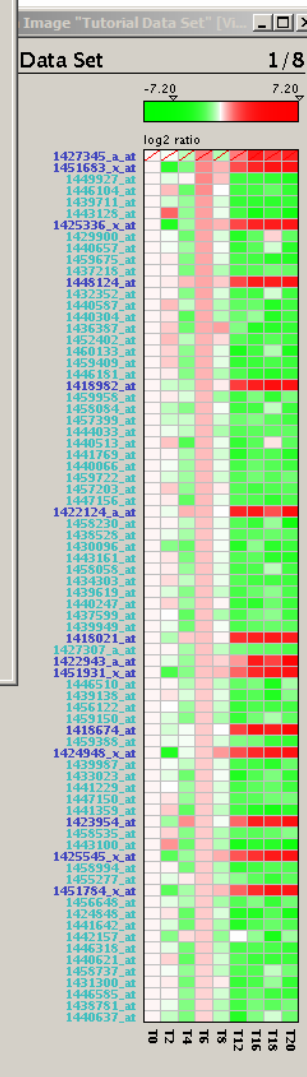
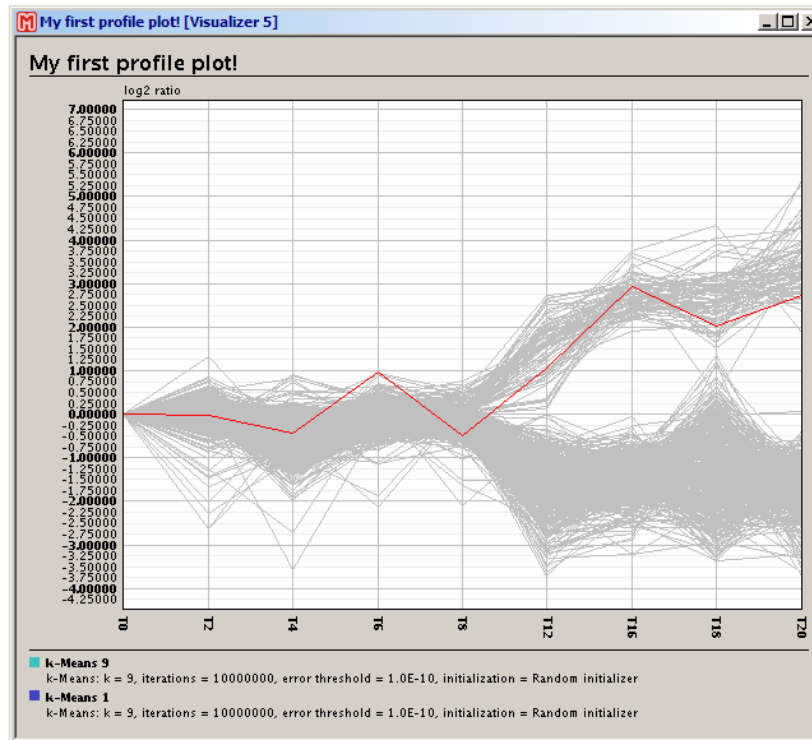
Click on
"Profile
Fading On
Selection
On".



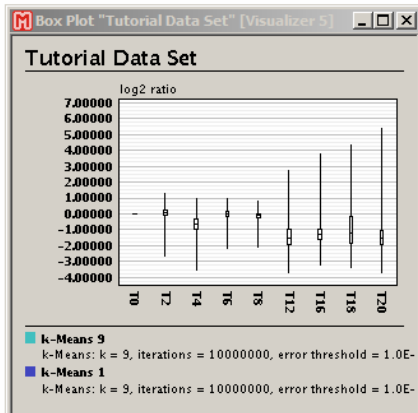
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	-0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1770606	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

Tweaking the profile plot

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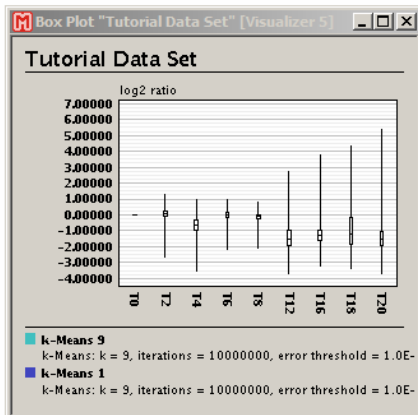
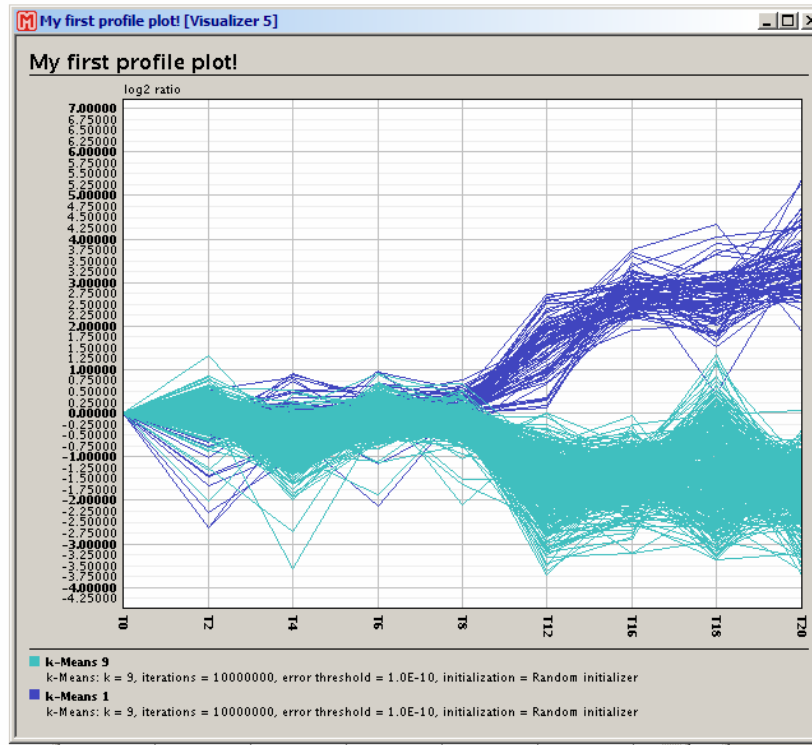
Click on the white area of the profile plot's window to clear the selection.



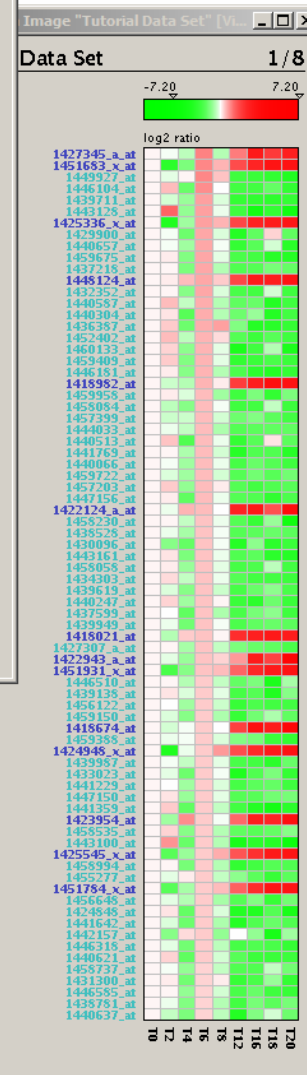
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1770606	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

Tweaking the profile plot

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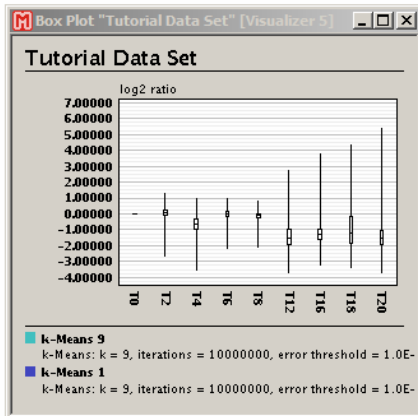
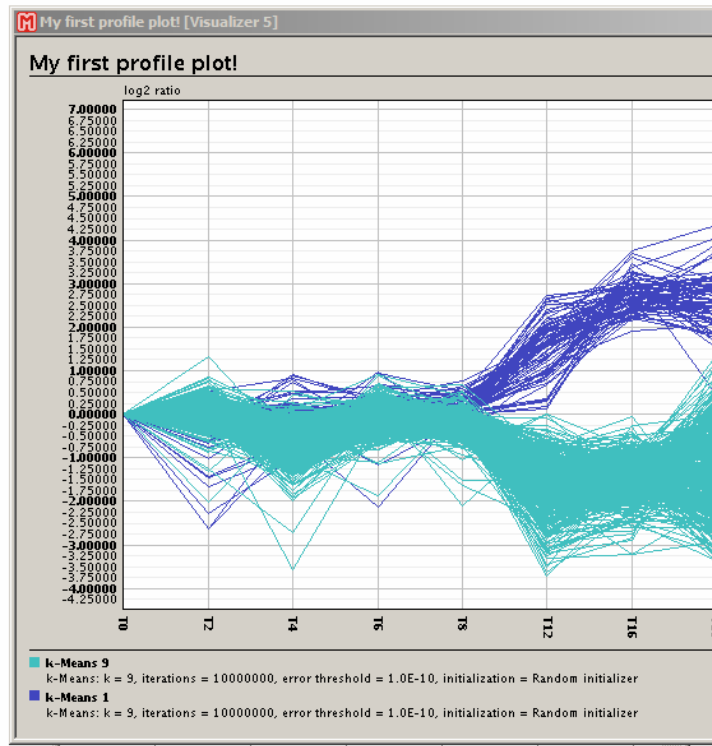
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.177606	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0



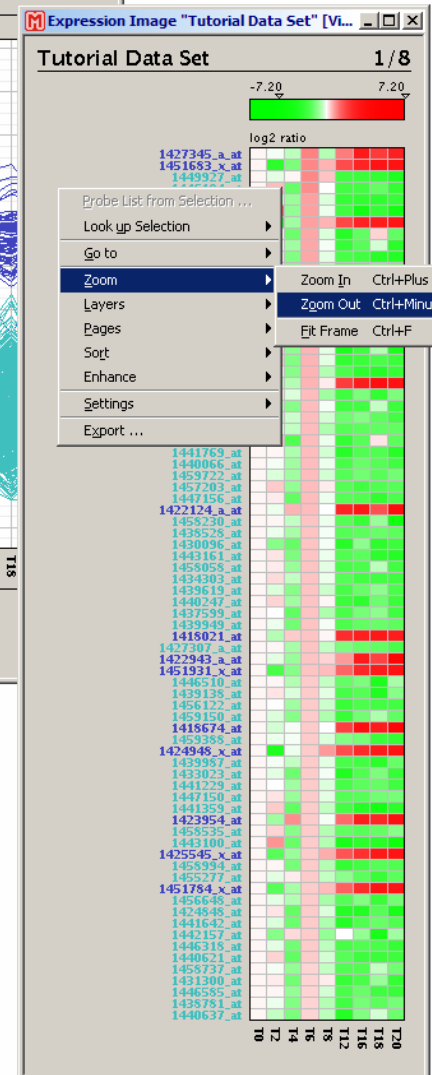
Right-click on the heatmap to open its context menu. Select "Settings". There select submenu "Zoom".

Tweaking the heatmap

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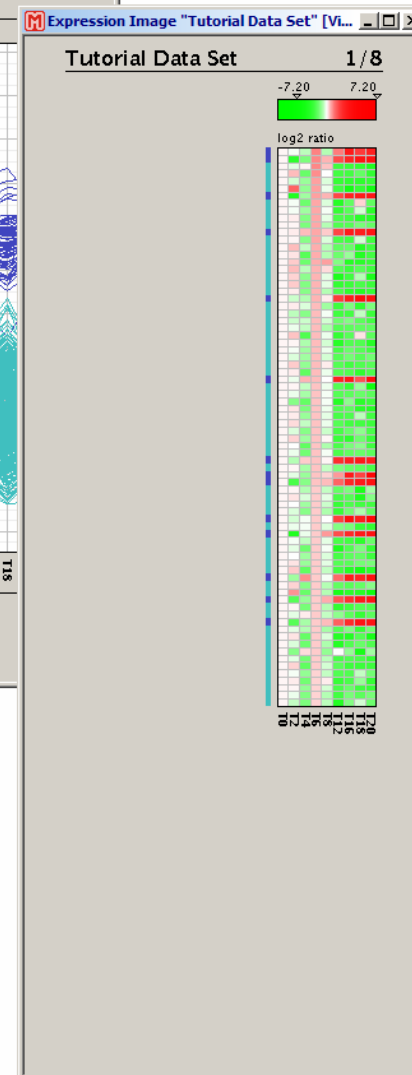
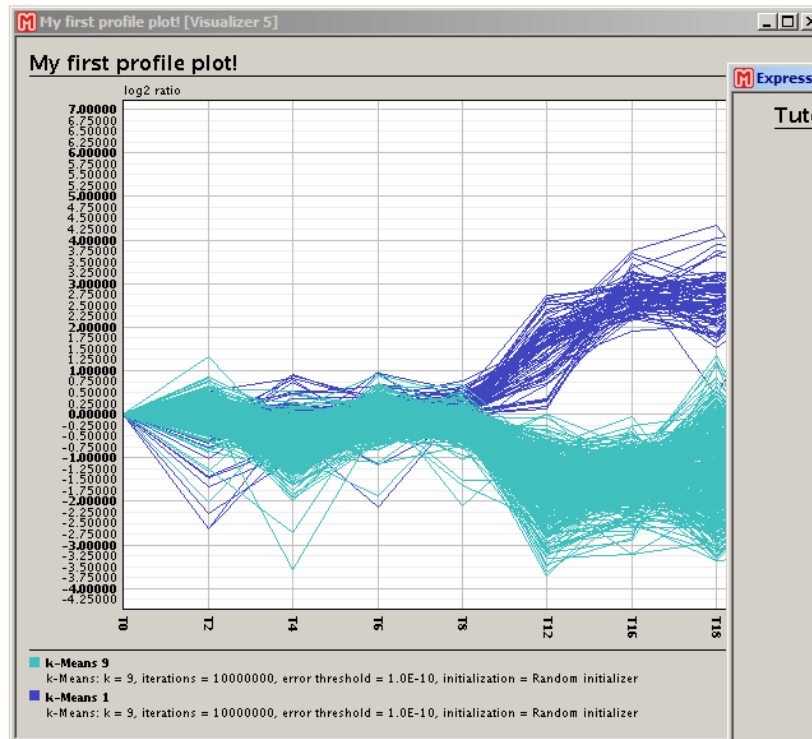
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1776006	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0



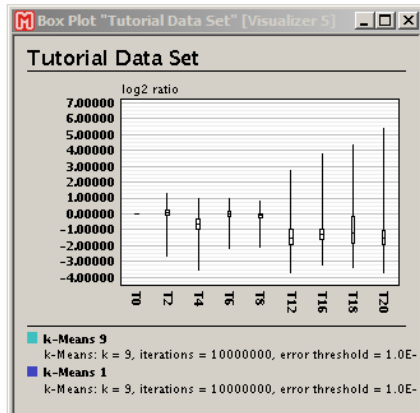
Click on
"Zoom
Out".
Repeat
this twice.

Tweaking the heatmap

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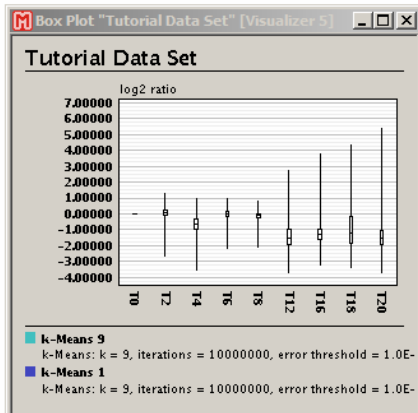
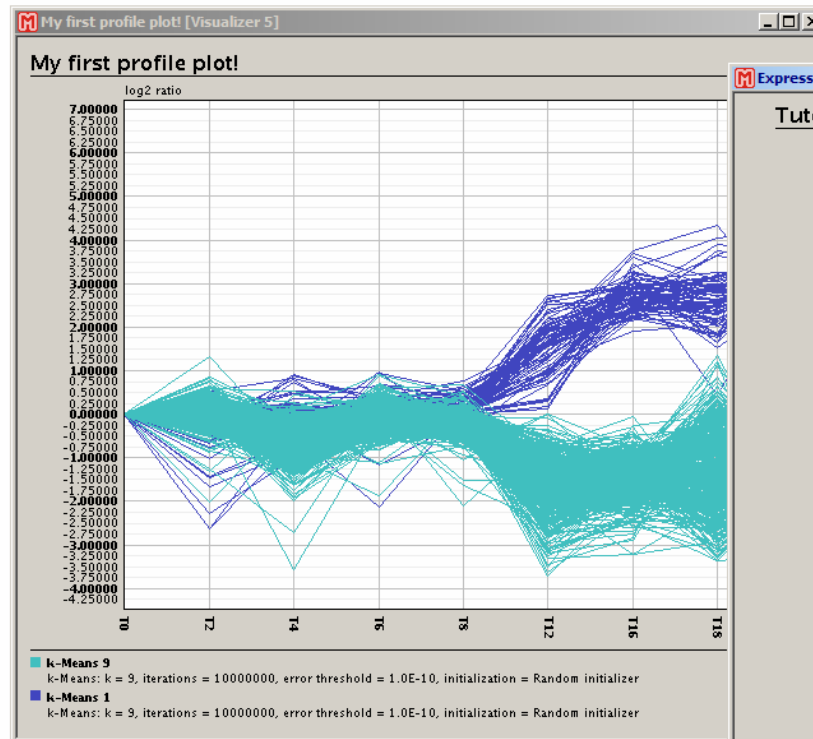
Open the context menu once again, select submenu "Settings" and then "Probes per Page".



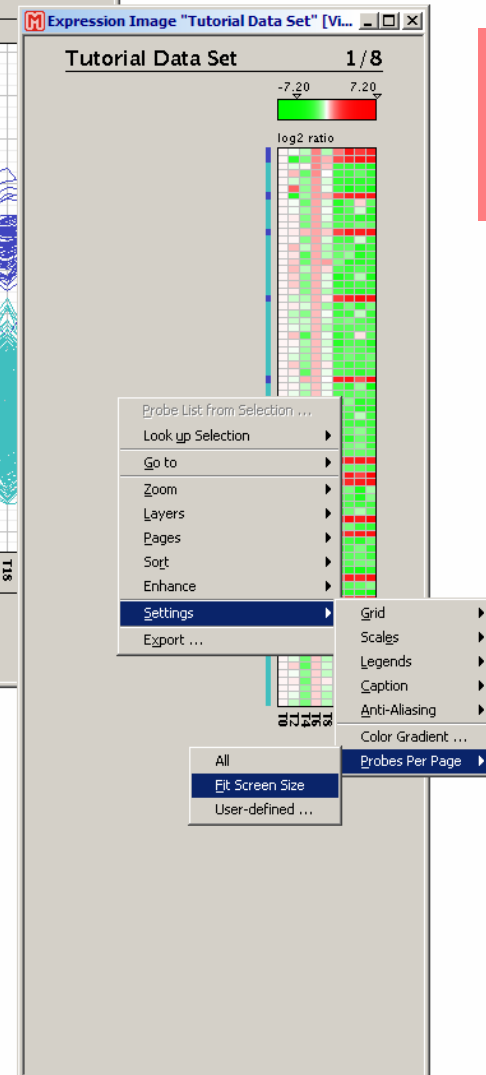
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.74
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1770606	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

Tweaking the heatmap

145



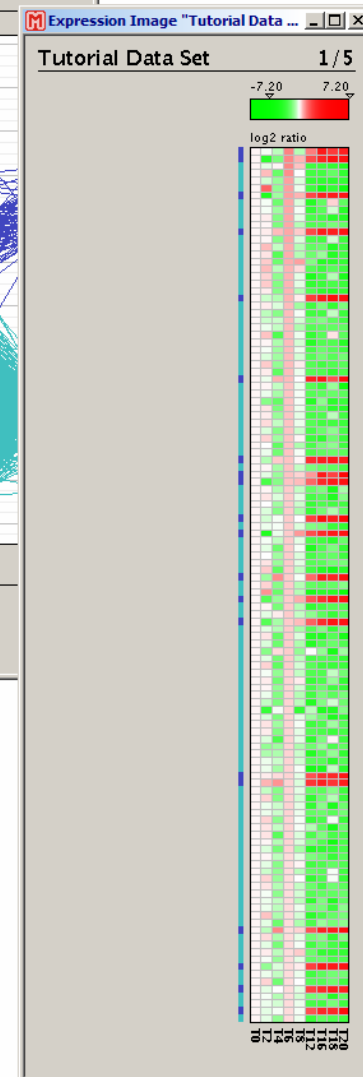
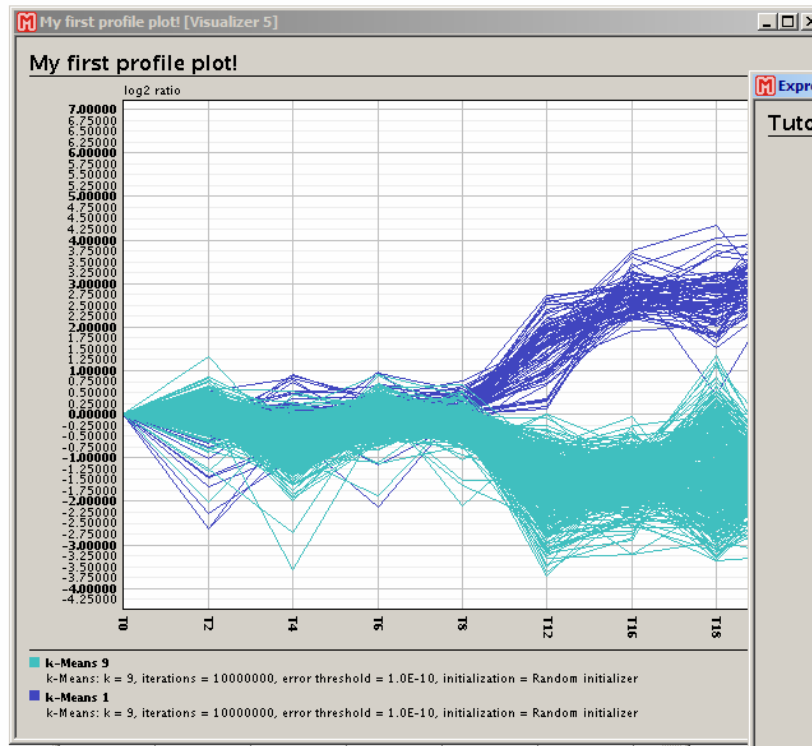
1419064_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.177606	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0



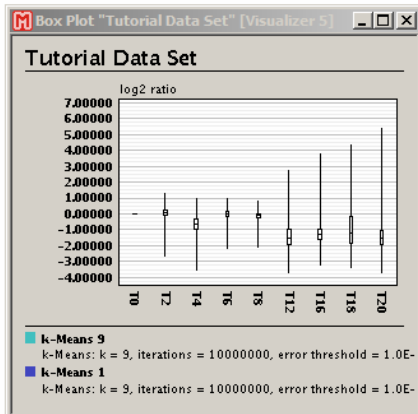
Click "Fit Screen Size".

Tweaking the heatmap

146



Zooming allows you to get a better overview of the data.

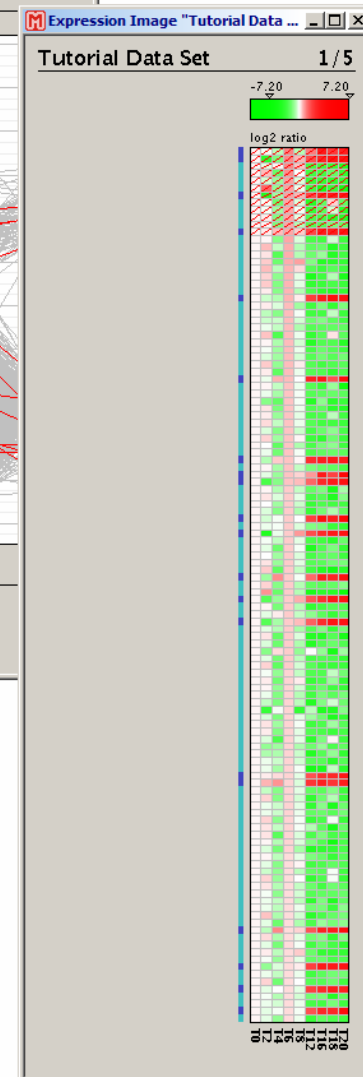
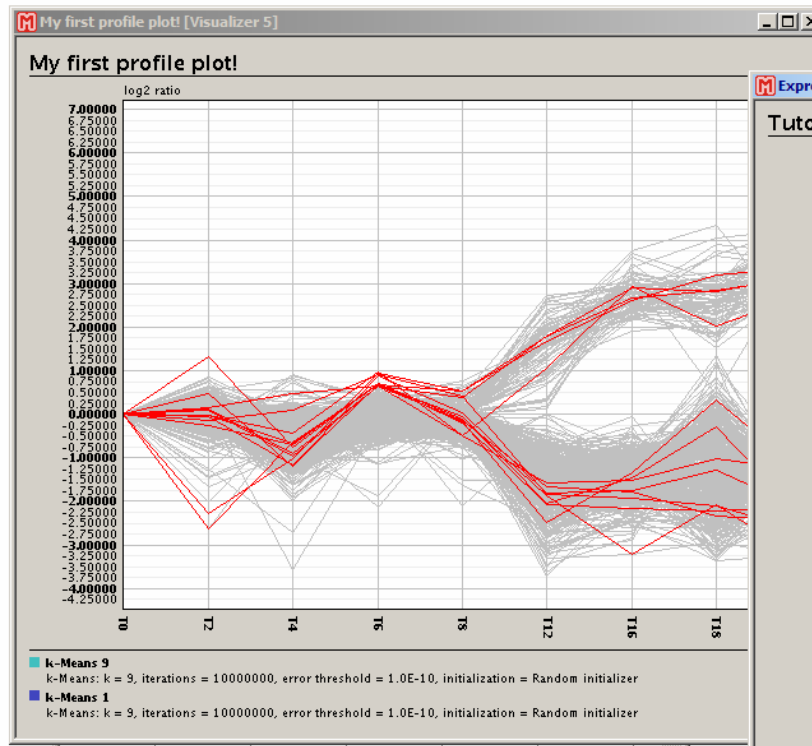


1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1770606	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

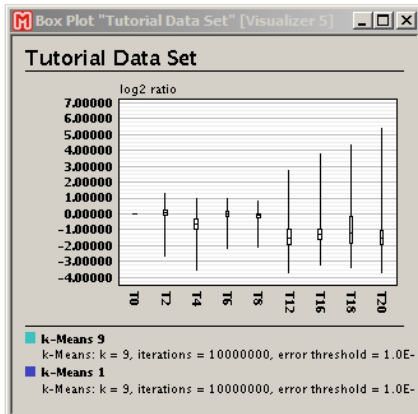
Hold down the CTRL key and select the 12 topmost probes in the heatmap.

Selecting multiple probes across viewers

147



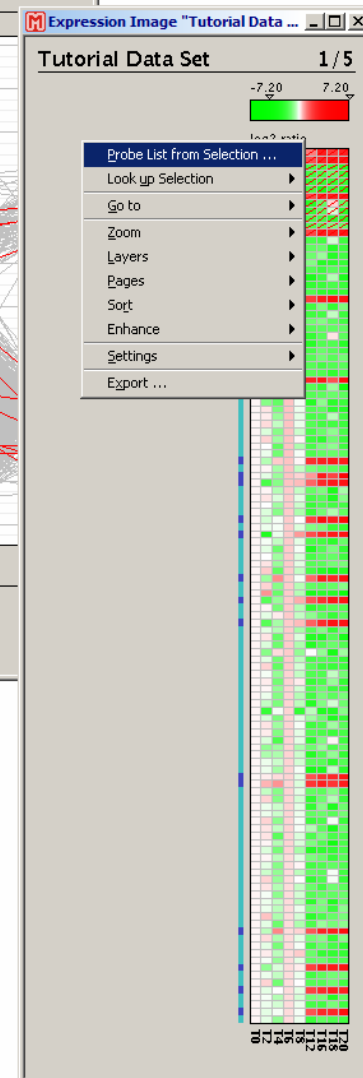
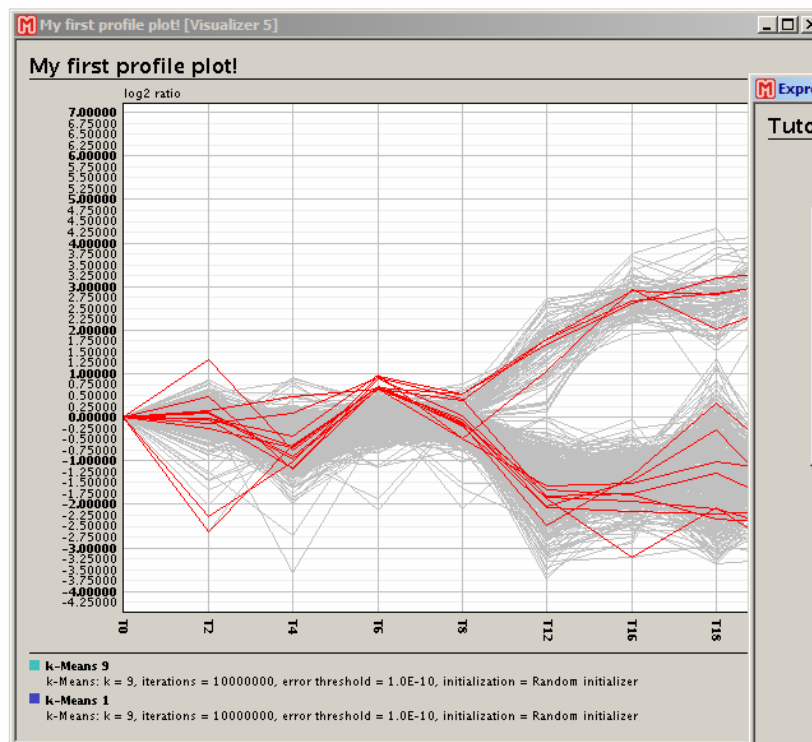
Right-click
on the
heatmap to
open its
context
menu and
select
"Probe List
From
Selection".



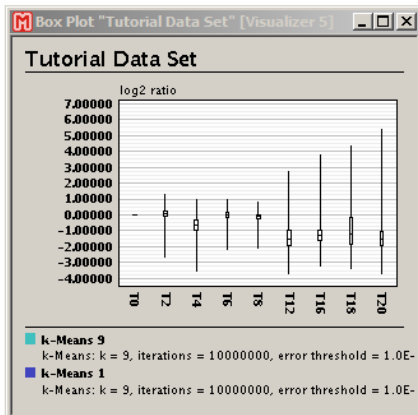
1419064_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1776006	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

Creating a probe list from selection

148



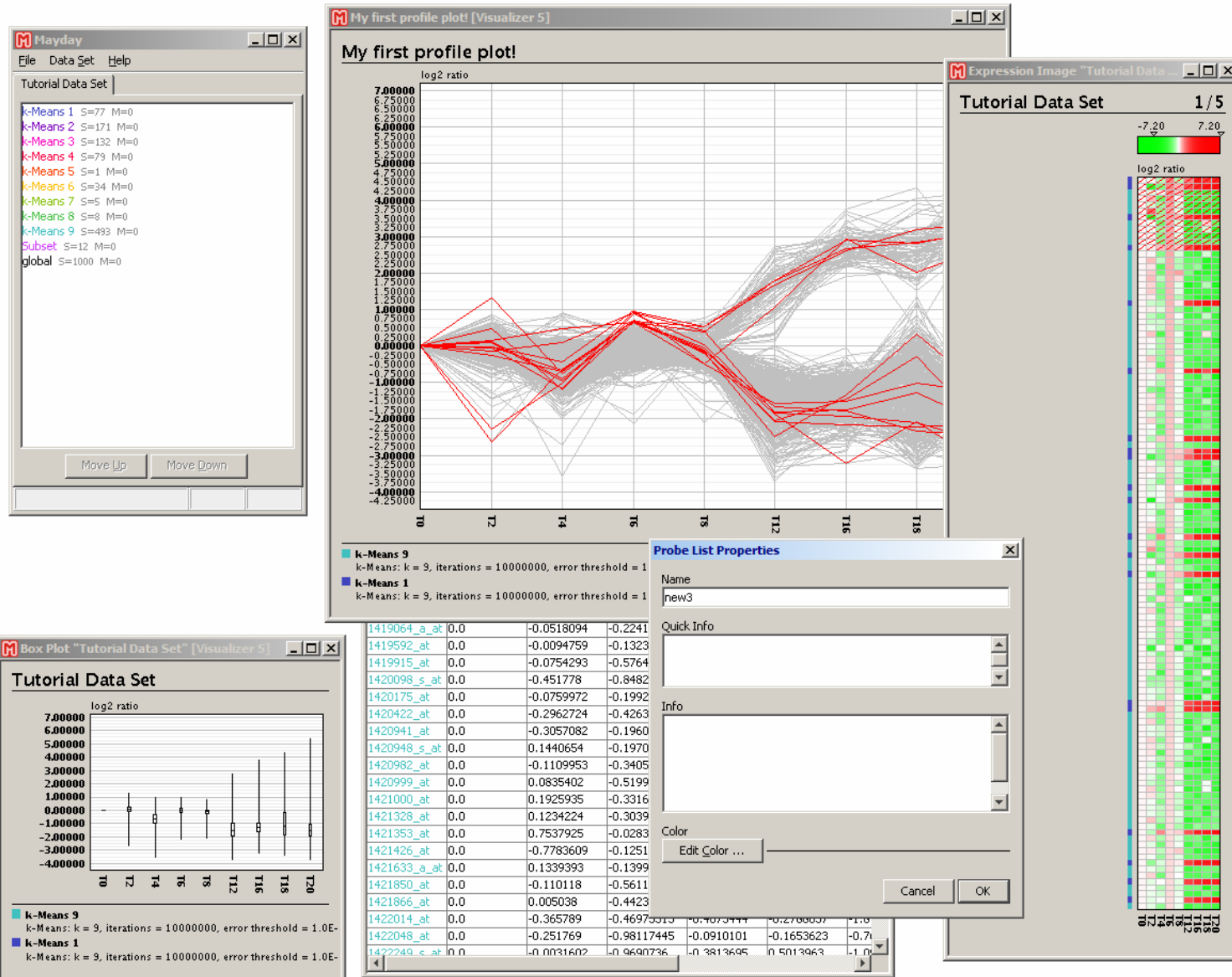
Right-click
on the
heatmap
to open its
context
menu.
Select
"Settings".



1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.71
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_s_at	0.0	0.1440654	-0.197041	-0.1763067	-0.2219339	-0.2
1420982_at	0.0	-0.1109953	-0.3405122	0.0689324	-0.0946374	-0.9
1420999_at	0.0	0.0835402	-0.51994545	0.1770606	-0.0845456	-1.2
1421000_at	0.0	0.1925935	-0.3316411	0.0756141	-0.0440016	-0.9
1421328_at	0.0	0.1234224	-0.30394515	-0.2714759	8.147E-4	-0.6
1421353_at	0.0	0.7537925	-0.0283905	-0.5754204	-0.5075688	-1.3
1421426_at	0.0	-0.7783609	-0.1251894	0.0044493	-0.1360717	-1.2
1421633_a_at	0.0	0.1339393	-0.1399246	-1.1514109	-0.7285331	-0.9
1421850_at	0.0	-0.110118	-0.561127	-0.2202348	-0.1490394	-0.3
1421866_at	0.0	0.005038	-0.4423015	-0.1030703	0.0105049	-1.0
1422014_at	0.0	-0.365789	-0.46975515	-0.4675444	-0.2788057	-1.8
1422048_at	0.0	-0.251769	-0.98117445	-0.0910101	-0.1653623	-0.7
1422249_c_at	0.0	-0.0031602	-0.9690736	-0.3813695	0.5013963	-1.0

Creating a probe list from selection

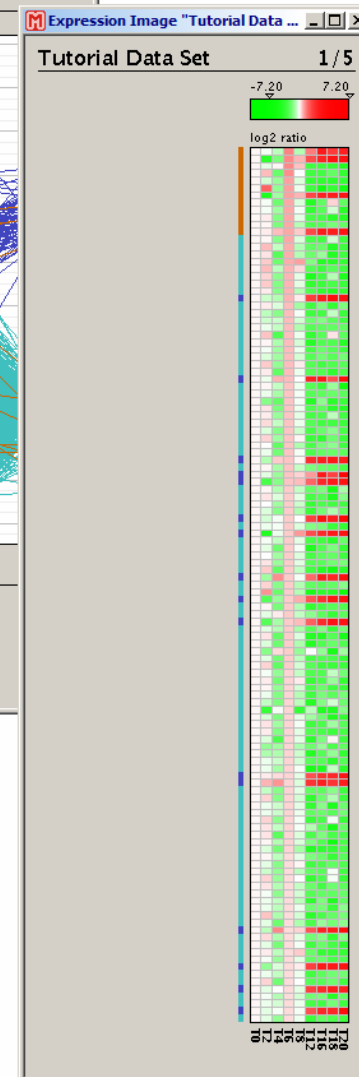
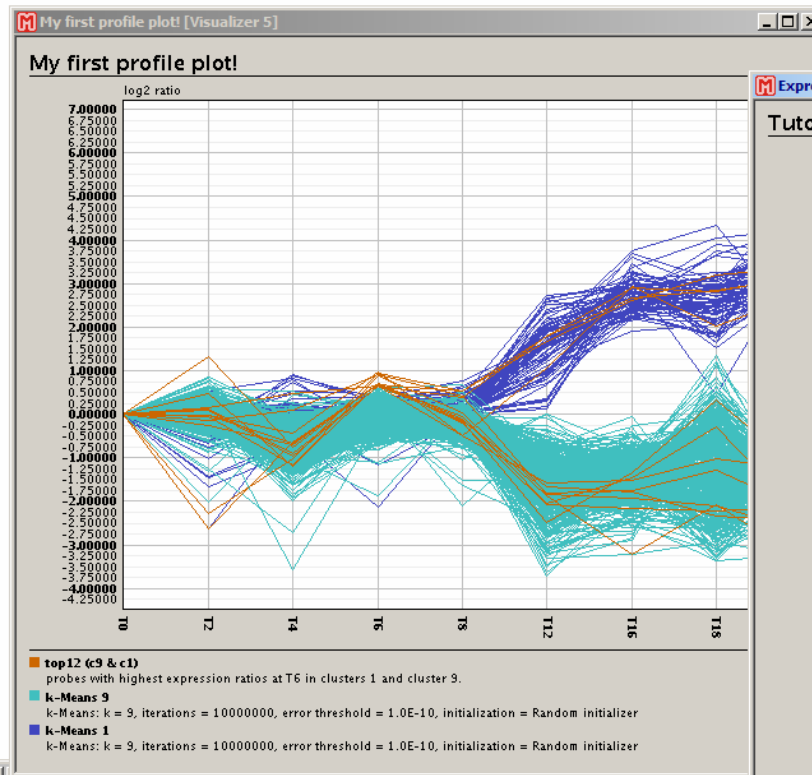
149



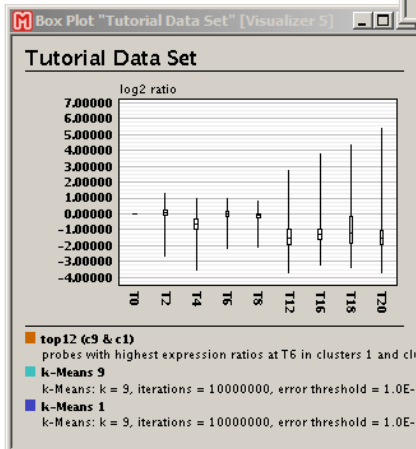
Assign a name and a distinct color to the new probe list. You may enter additional information about the probe list as well.

Creating a probe list from selection

150



Bring the tabular viewer to the front. Select menu item "Probe Lists" and open submenu "Remove".

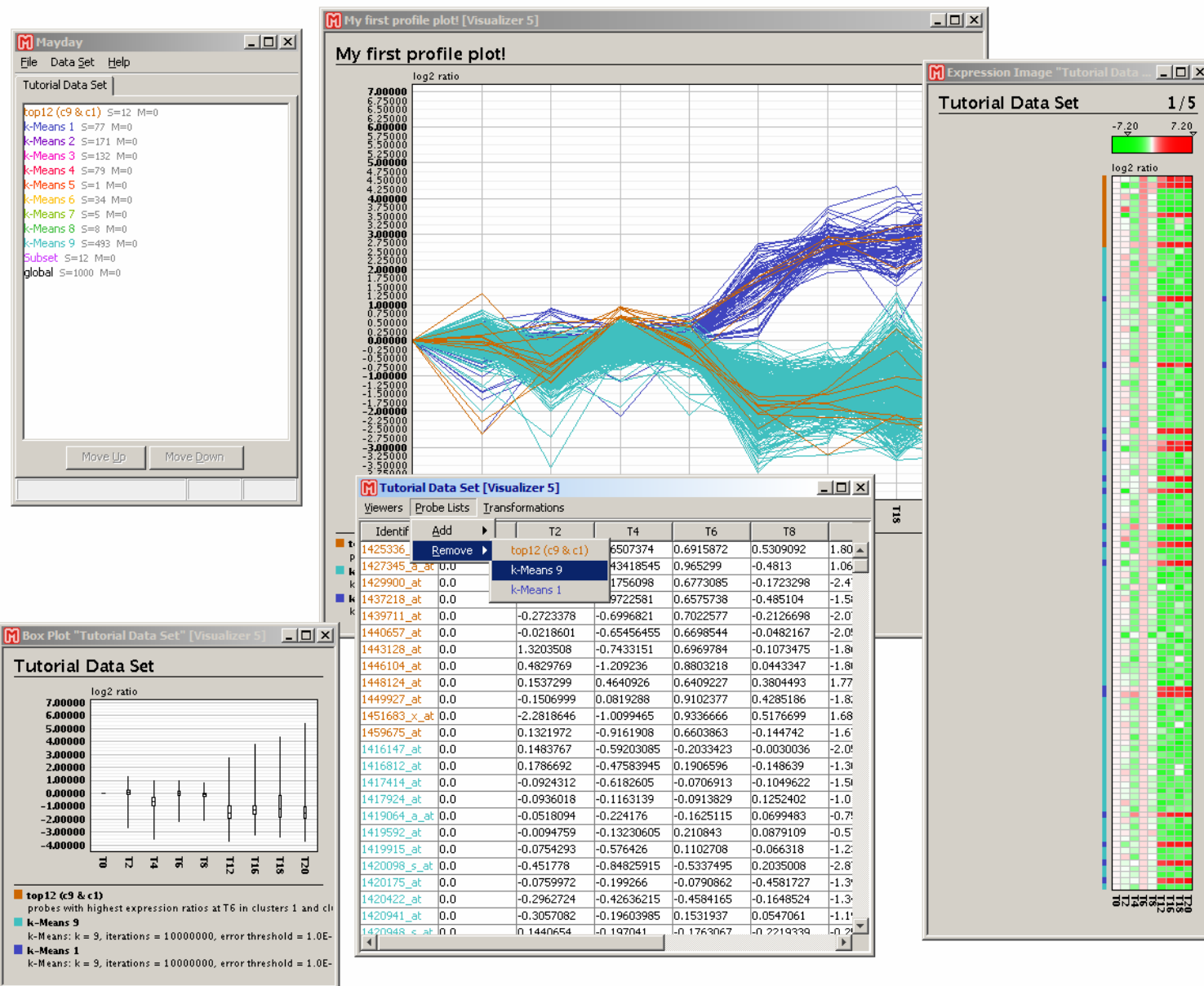


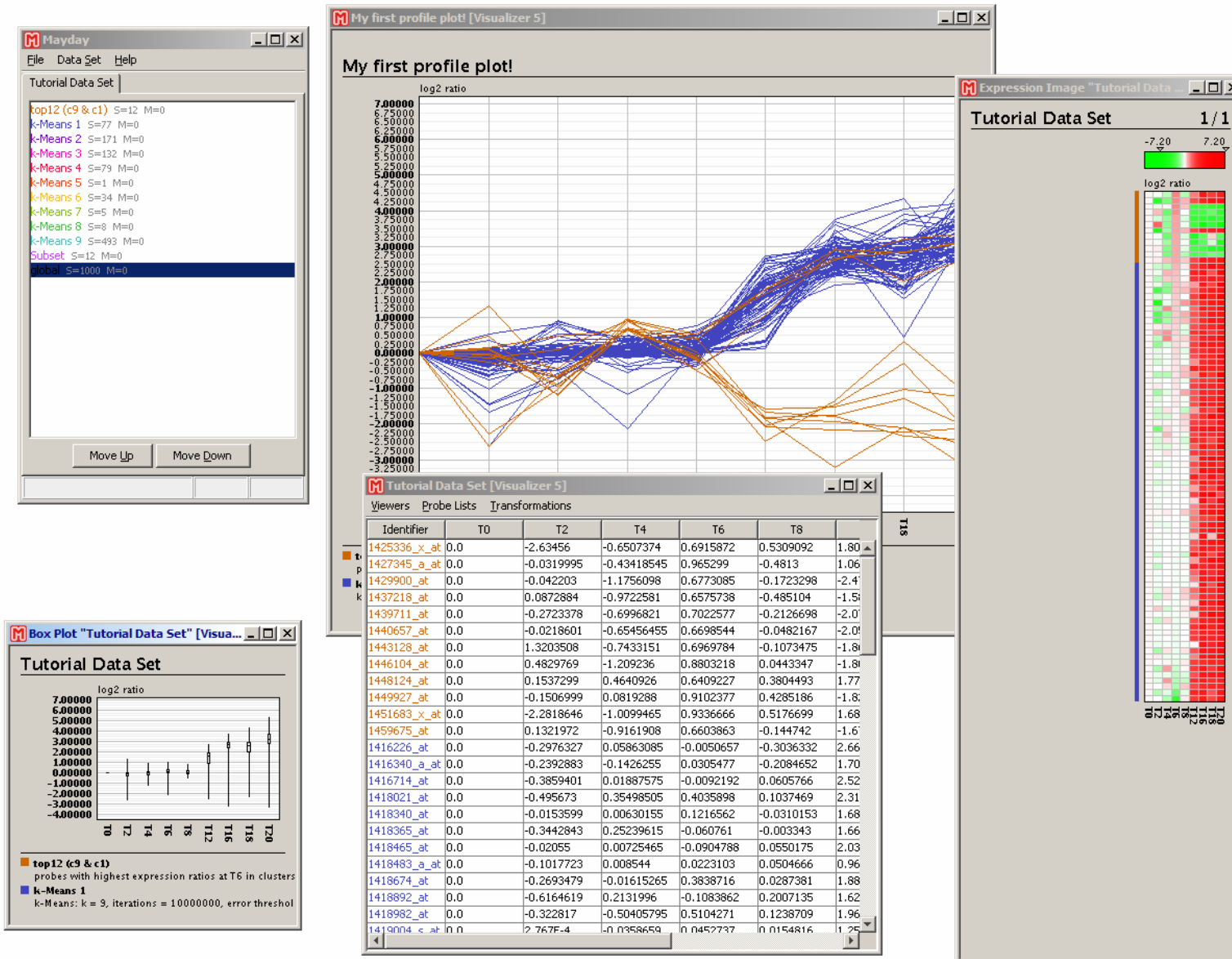
1443126_at	0.0	1.3203508	-0.7433151	0.6969784	-0.1073475	-1.8
1446104_at	0.0	0.4829769	-1.209236	0.8803218	0.0443347	-1.8
1448124_at	0.0	0.1537299	0.4640926	0.6409227	0.3804493	1.77
1449927_at	0.0	-0.1506999	0.0819288	0.9102377	0.4285186	-1.8
1451683_x_at	0.0	-2.2818646	-1.0099465	0.9336666	0.5176699	1.68
1459675_at	0.0	0.1321972	-0.9161908	0.6603863	-0.144742	-1.6
1416147_at	0.0	0.1483767	-0.59203085	-0.2033423	-0.0030036	-2.0
1416812_at	0.0	0.1786692	-0.47583945	0.1906596	-0.148639	-1.3
1417414_at	0.0	-0.0924312	-0.6182605	-0.0706913	-0.1049622	-1.5
1417924_at	0.0	-0.0936018	-0.1163139	-0.0913829	0.1252402	-1.0
1419064_a_at	0.0	-0.0518094	-0.224176	-0.1625115	0.0699483	-0.7
1419592_at	0.0	-0.0094759	-0.13230605	0.210843	0.0879109	-0.5
1419915_at	0.0	-0.0754293	-0.576426	0.1102708	-0.066318	-1.2
1420098_s_at	0.0	-0.451778	-0.84825915	-0.5337495	0.2035008	-2.8
1420175_at	0.0	-0.0759972	-0.199266	-0.0790862	-0.4581727	-1.3
1420422_at	0.0	-0.2962724	-0.42636215	-0.4584165	-0.1648524	-1.3
1420941_at	0.0	-0.3057082	-0.19603985	0.1531937	0.0547061	-1.1
1420948_c_at	n	n	1440654	-0.197041	-0.1763067	-0.219339

Remember how the color of a probe is determined!

Removing a probe list from the visualizer

151



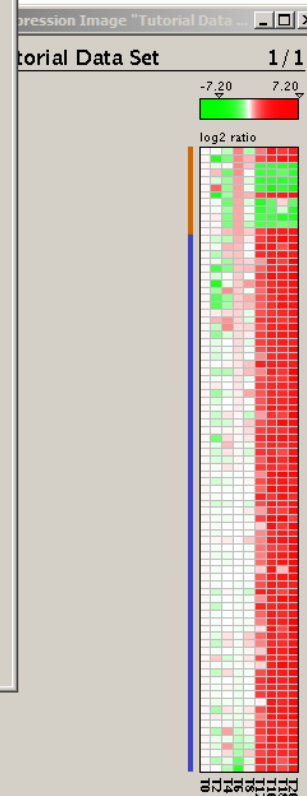
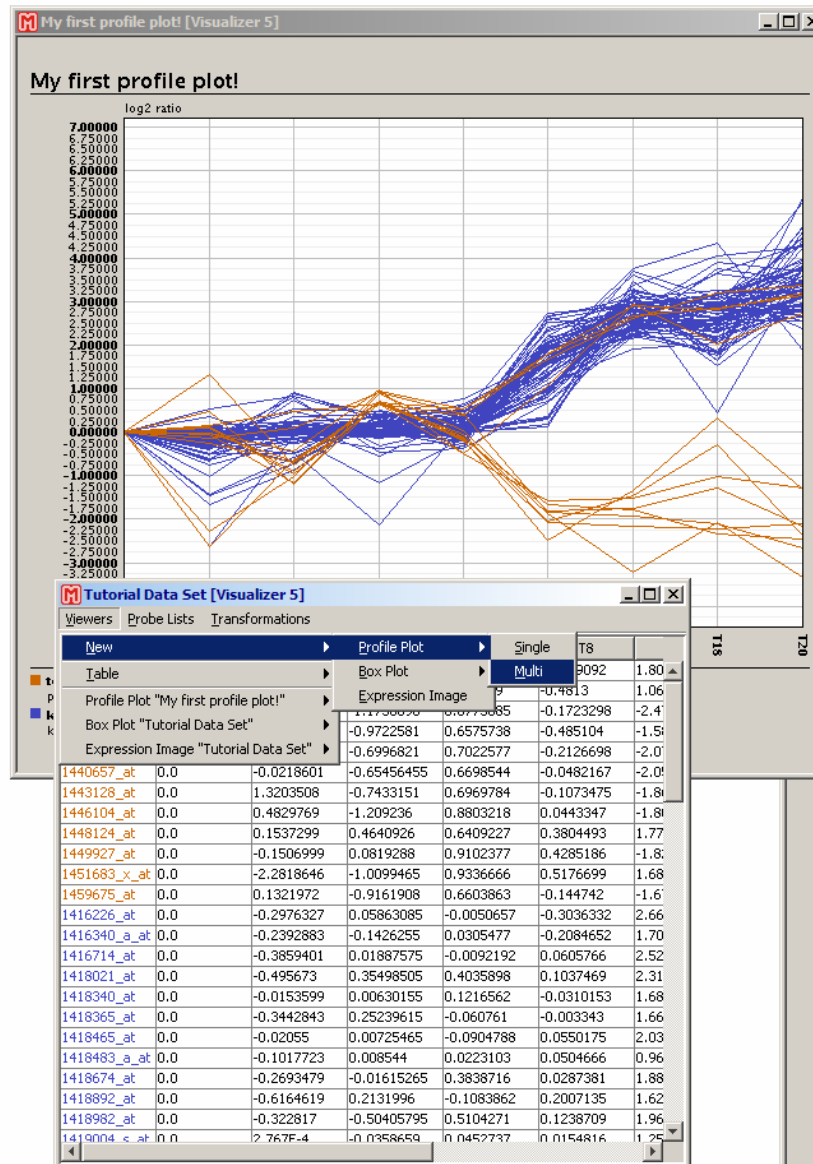
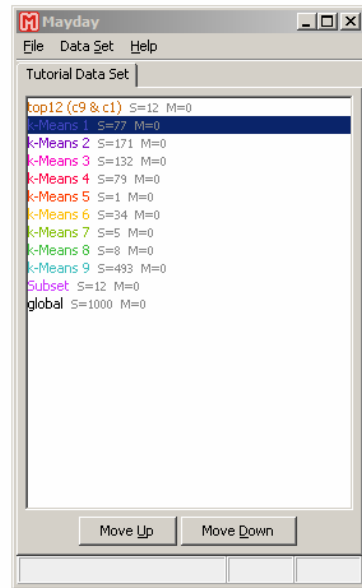


Bring the tabular viewer to the front, select menu item "Viewers", then "New" and "Profile Plot".

Removing uninteresting probe lists gives you a better view on the details.

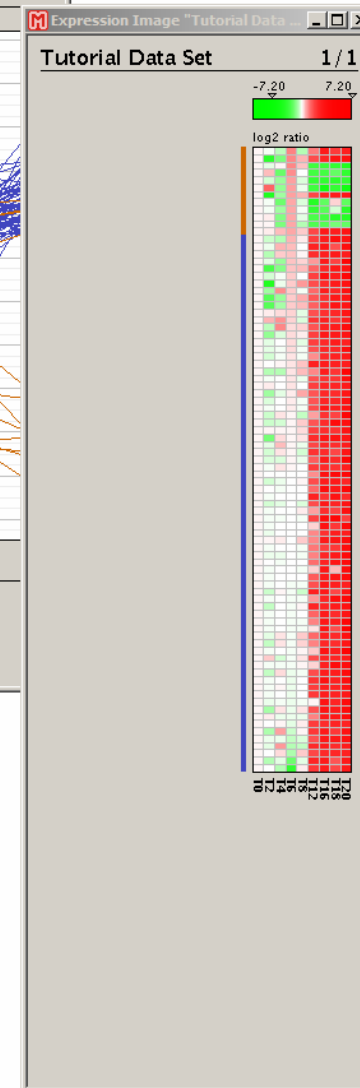
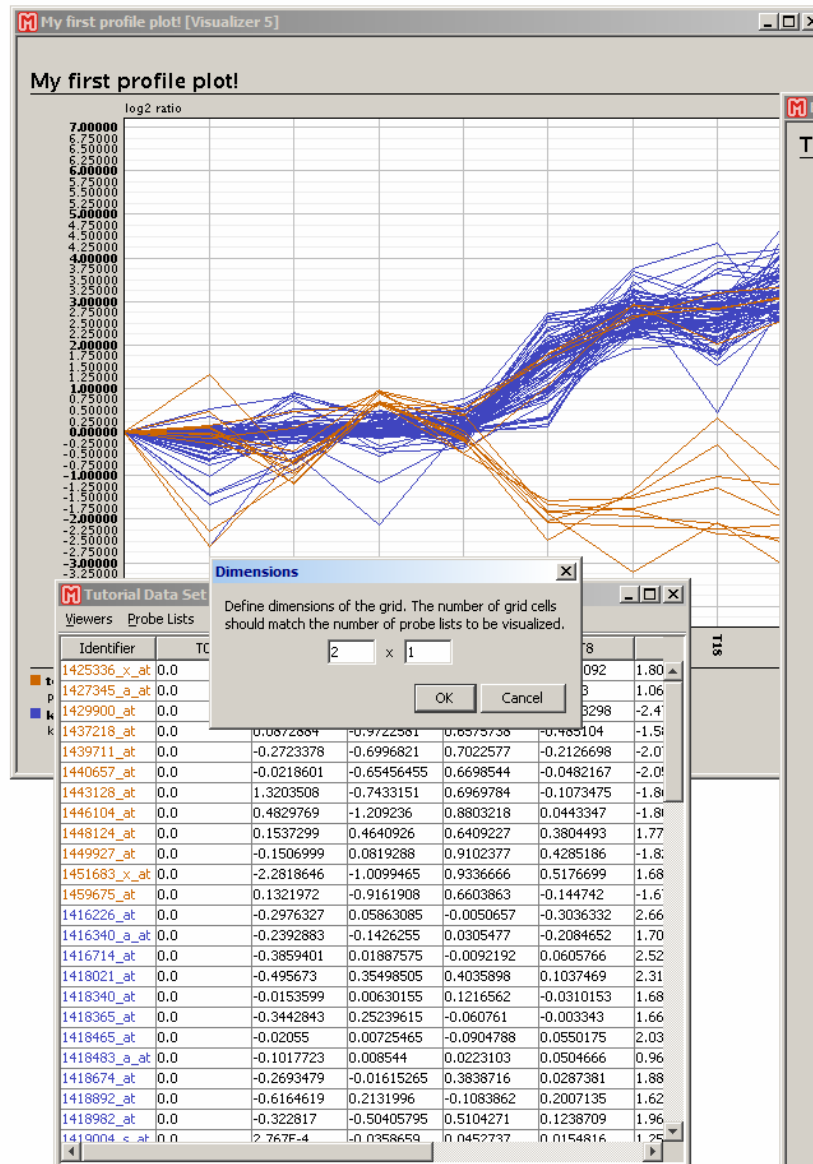
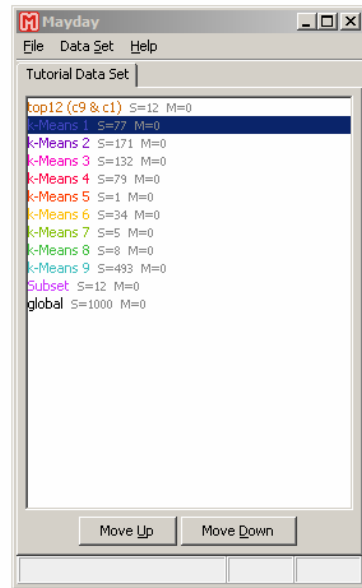
Adding a multi profile plot

153

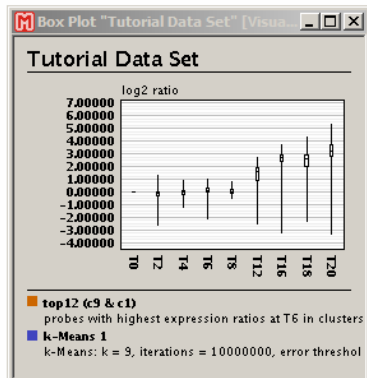


Adding a multi profile plot

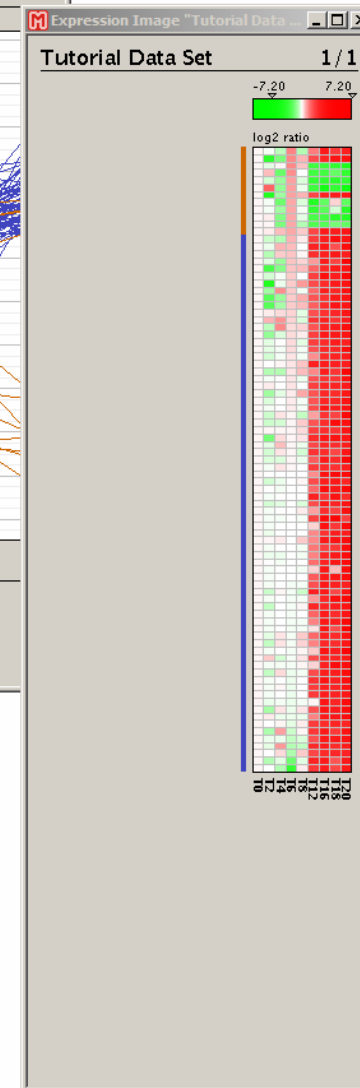
154



Enter the dimensions of the grid and confirm by clicking "OK".



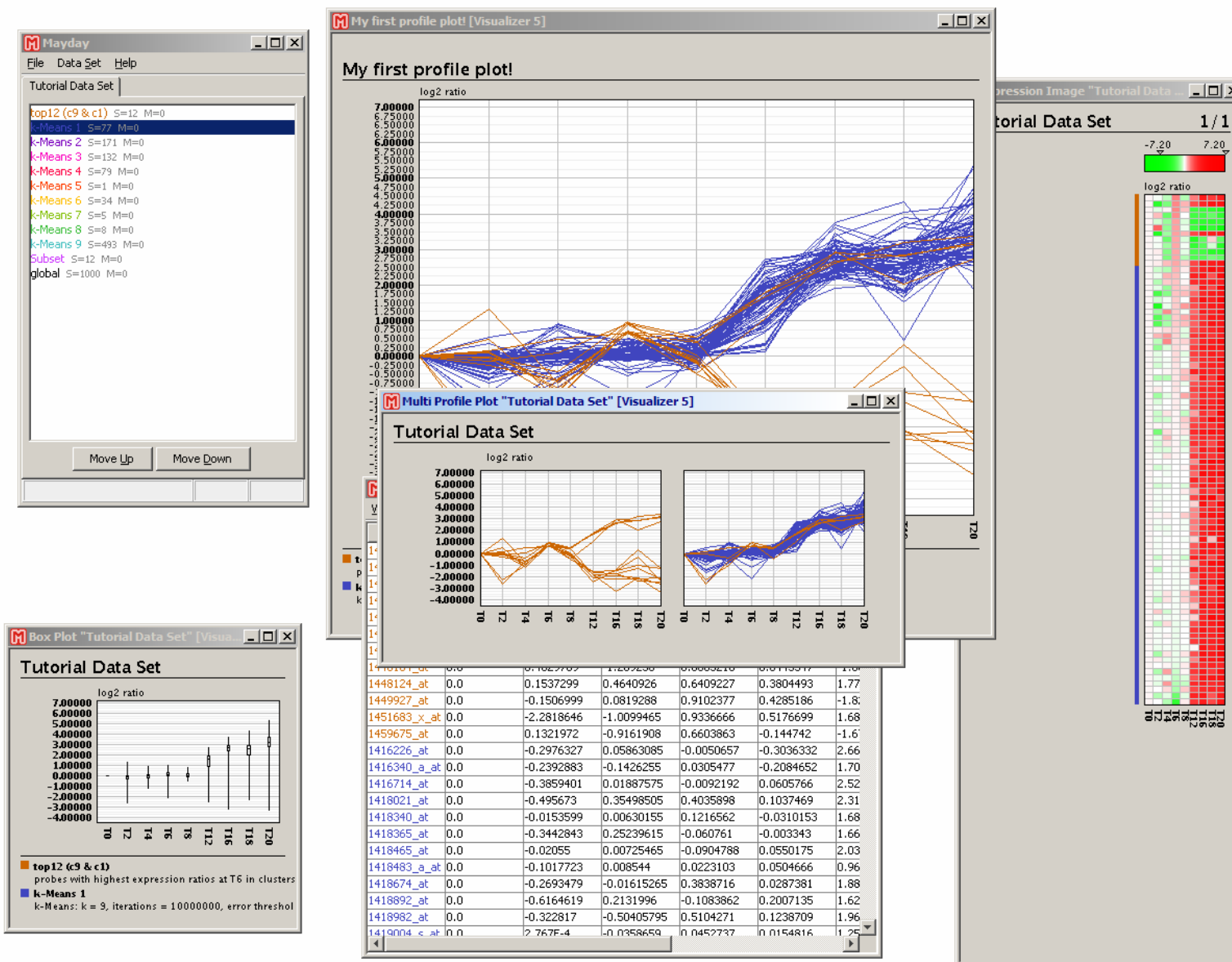
155



Assign
probe lists
to the
cells of
the grid
and
confirm by
clicking
“OK”.

Adding a multi profile plot

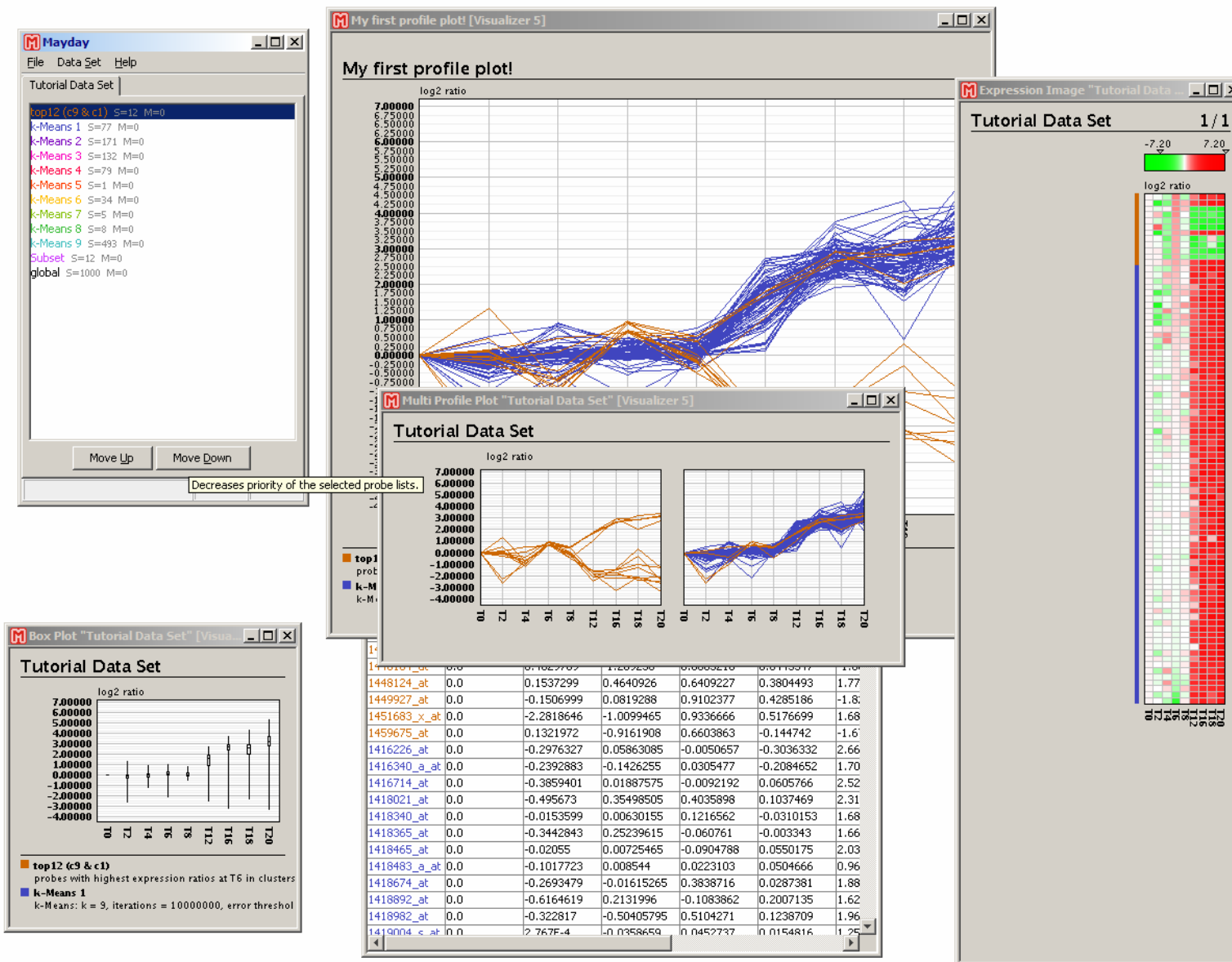
156



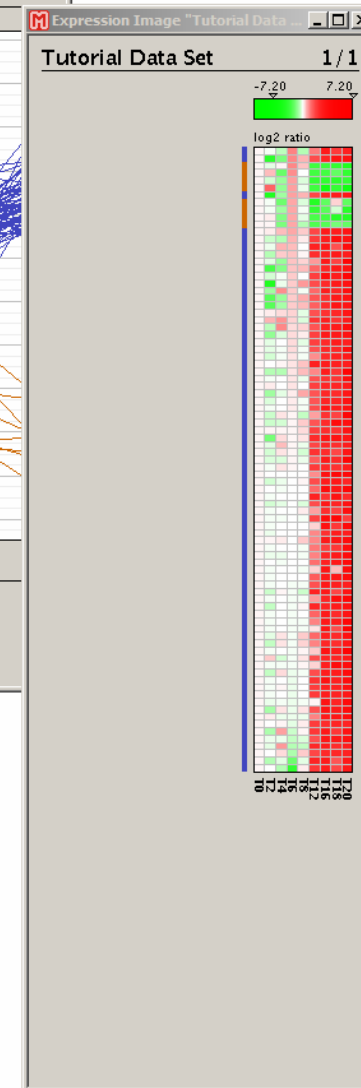
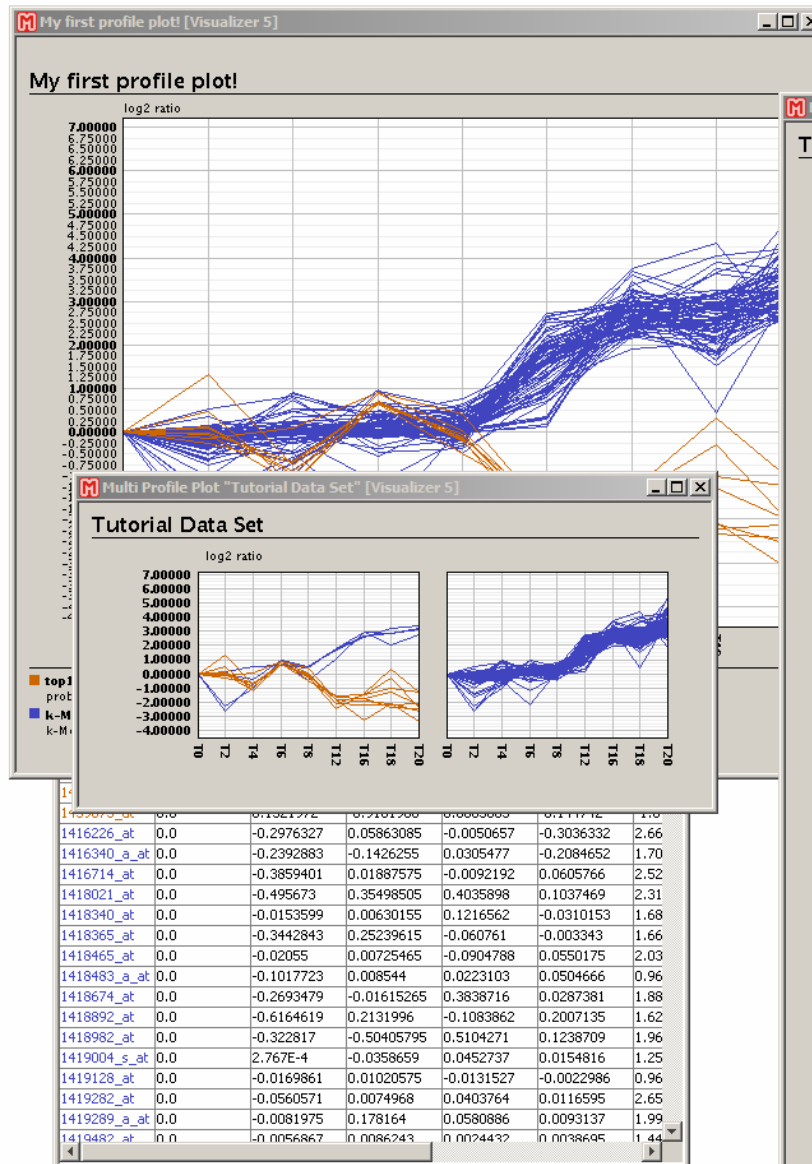
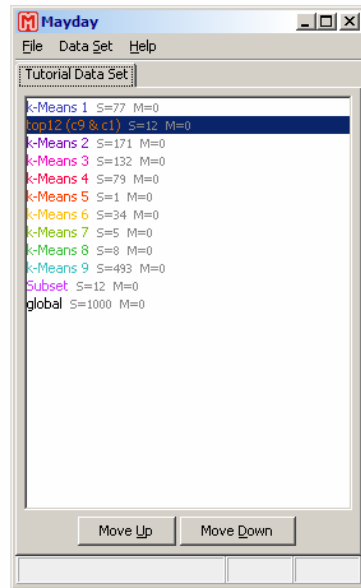
Select the probe list you have created from the selection in the heatmap in the probe list manager.

Reassigning probe list priorities

157

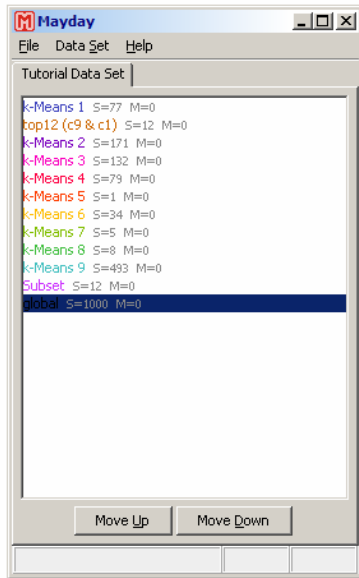


Click
"Move
Down"
in the probe
list
manager.

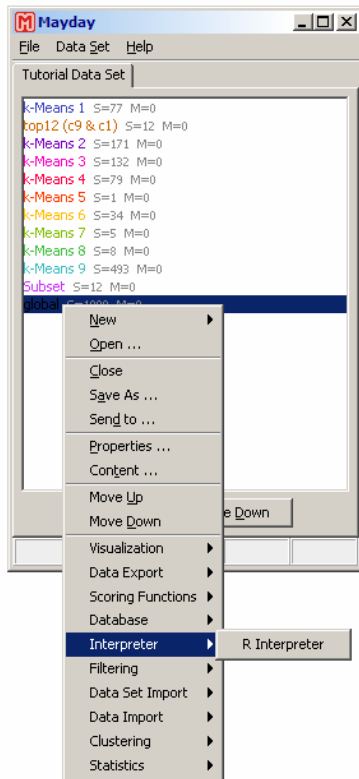


Reassigning probe list priorities allows you to see what is most interesting at the current stage of data exploration. This particular case also features overlapping probe lists.

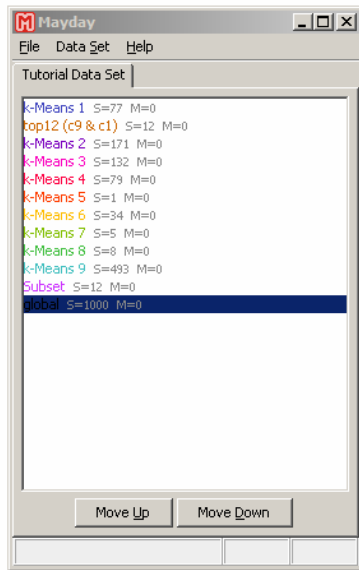
Using R in Mayday



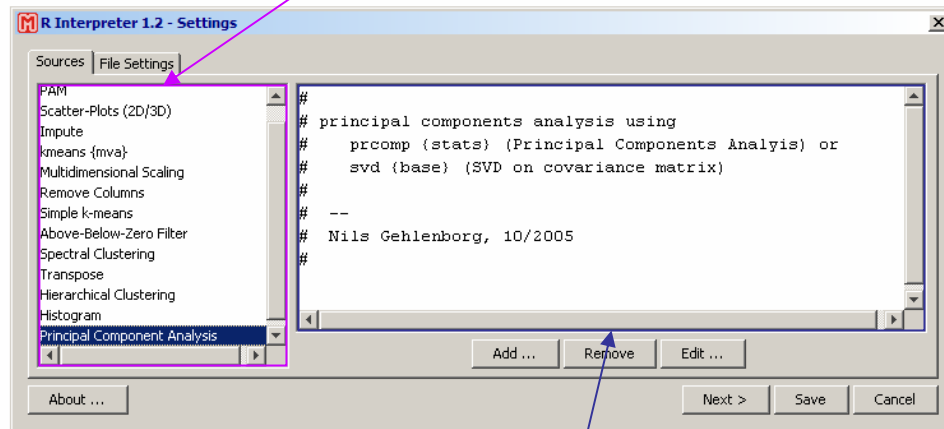
Select the global
probe list.



Open the probe list manager's context menu and select submenu "Interpreter". Then click on "R Interpreter".



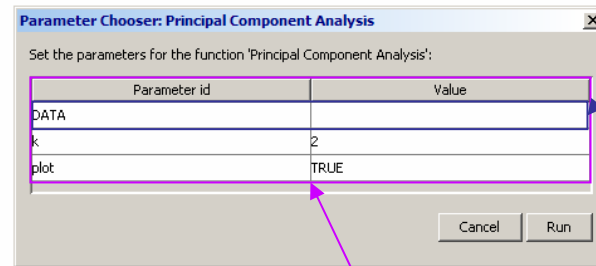
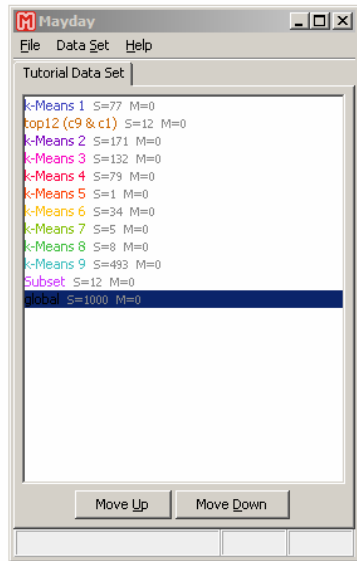
list of R scripts available



description of the selected script

Select
“Principal
Component
Analysis” in
the column
on the left.
Click on
“Next >”.

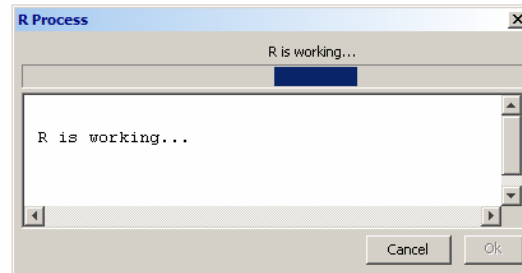
The main window of the R interpreter plug-in. You can run loaded scripts on the probe lists you selected or on the current data set (depends on the script). You can also add new scripts (press “Save” after you have done this) or set up the Mayday for your R installation in the “File Settings” tab.



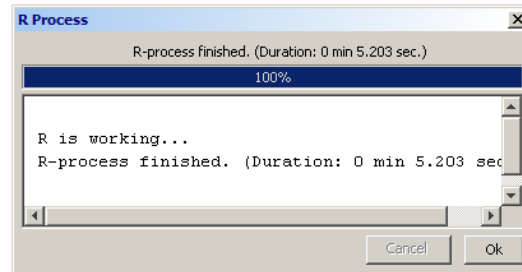
Mayday will automatically fill in your selected data structures for transfer to R

parameters of the selected R script

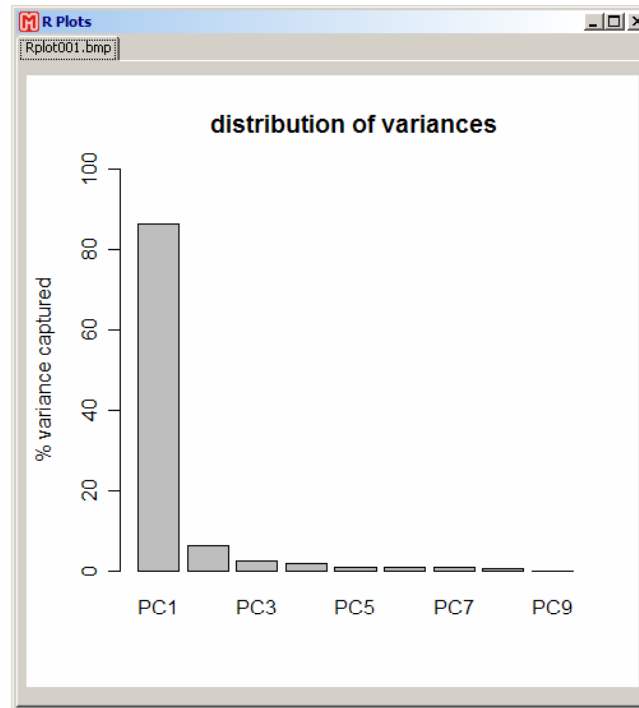
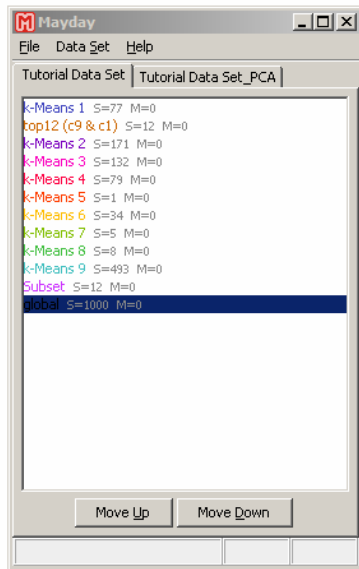
Leave all parameters at their default values. Click “Run”.



Wait until R has finished.

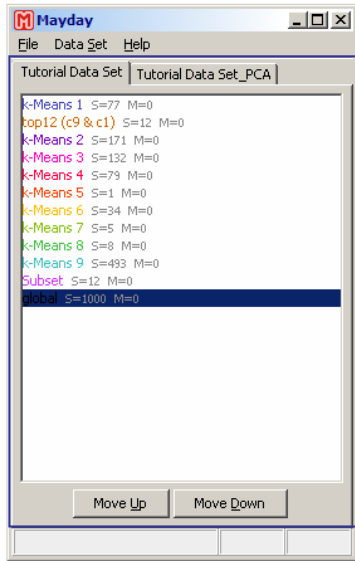


When R has finished click on “OK”.



Plots created by R are not interactive
as the ones provided by Mayday itself.

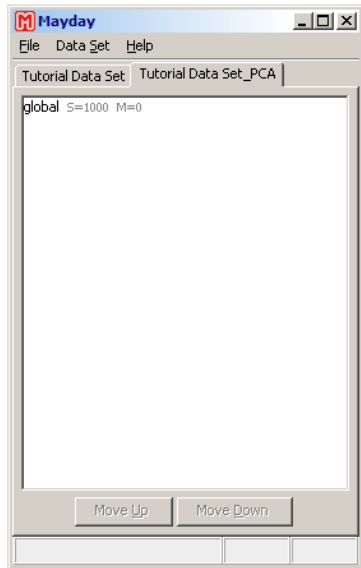
Close the plot or
send it to the back.



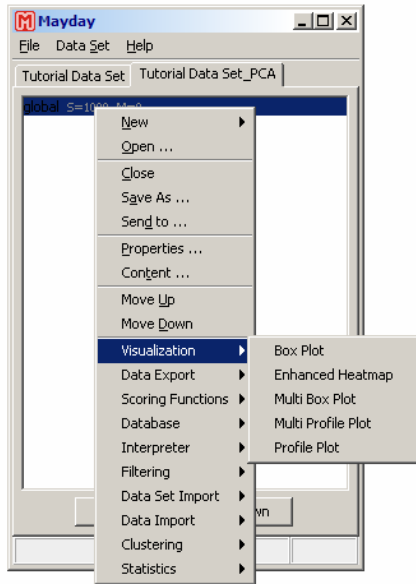
Data Set Manager

Now you have two data sets loaded. You can switch back and forth between them using the tabs in the data set manager. Data sets are completely separated from each other, i.e. they don't share any resources such as probe lists or probes.

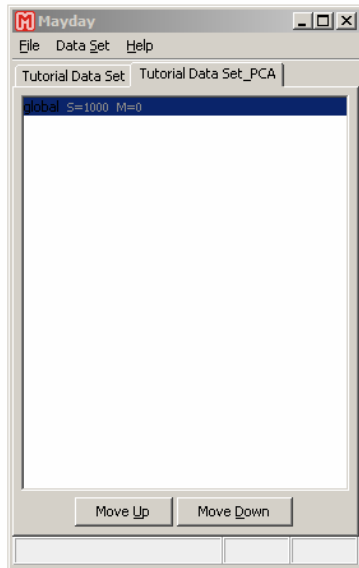
Select the new tab
"Tutorial Data Set_PCA"
in the data set manager.



Select the global probe list of the new data set. Open the probe list managers context menu and go to submenu "Visualization".

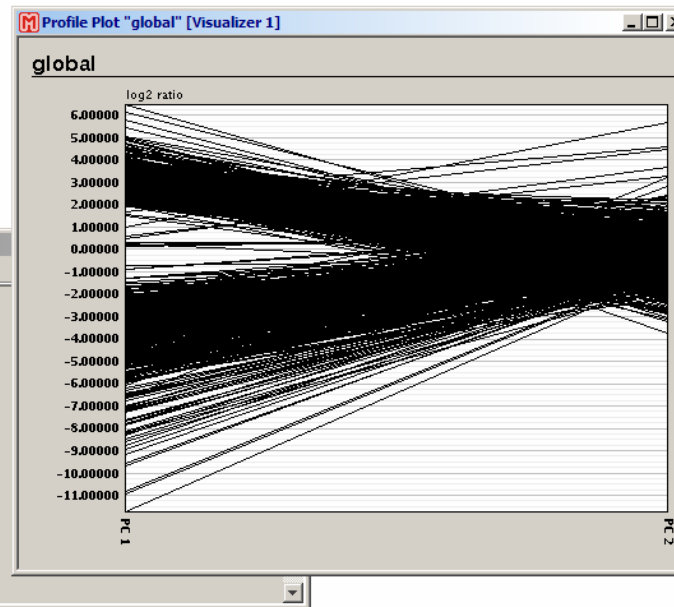


Select “Profile Plot”.

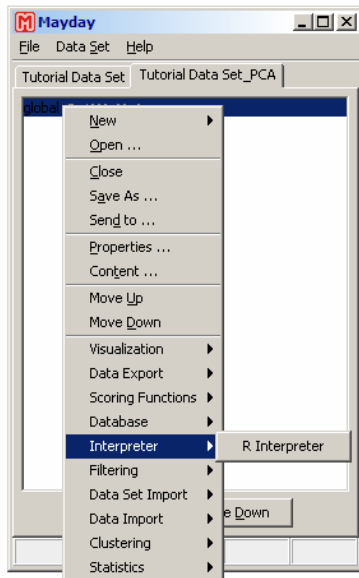


The 'Tutorial Data Set_PCA [Visualizer 1]' window displays a table with three columns: 'Identifier', 'PC 1', and 'PC 2'. The table contains 15 rows of data, showing the principal component analysis results for the tutorial data set.

Identifier	PC 1	PC 2
1415677_at	-3.0001465...	-0.6117308...
1415798_at	-2.7133788...	0.11014872...
1415859_at	-2.6467042...	-0.1333248...
1415893_at	-2.1872769...	-0.8997491...
1415983_at	-3.7651645...	-0.3263843...
1416111_at	-2.9462300...	-0.0129683...
1416147_at	3.82628475...	-1.2170567...
1416164_at	-2.9672984...	-0.4711573...
1416226_at	-5.3089522...	0.60019056...
1416239_at	-2.3655459...	0.80913071...
1416340_a_at	-5.3095986...	-0.5463194...
1416382_at	-3.1111417...	-0.1532741...
1416451_s_at	-3.8128561...	0.38159540...
1416529_at	-3.0825433...	-0.4610965...
1416554_at	-3.3081400...	0.34001600...



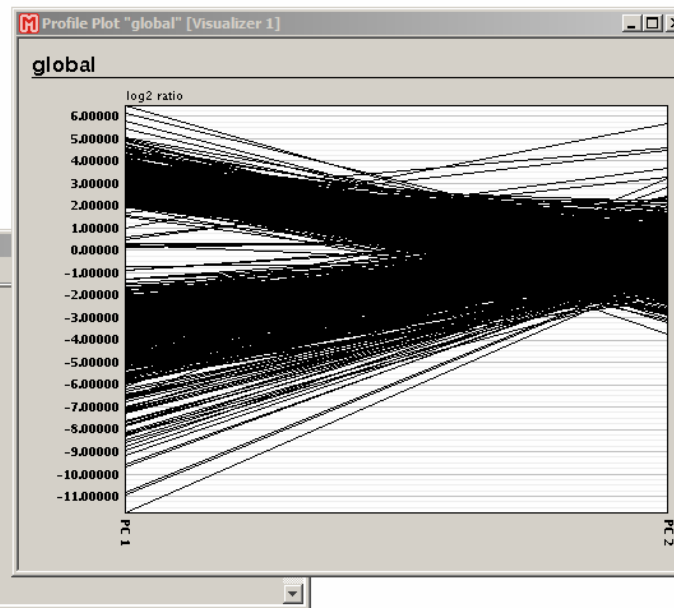
Select the global probe list
and open the probe list
manager's context menu.
Go to submenu "Interpreter".



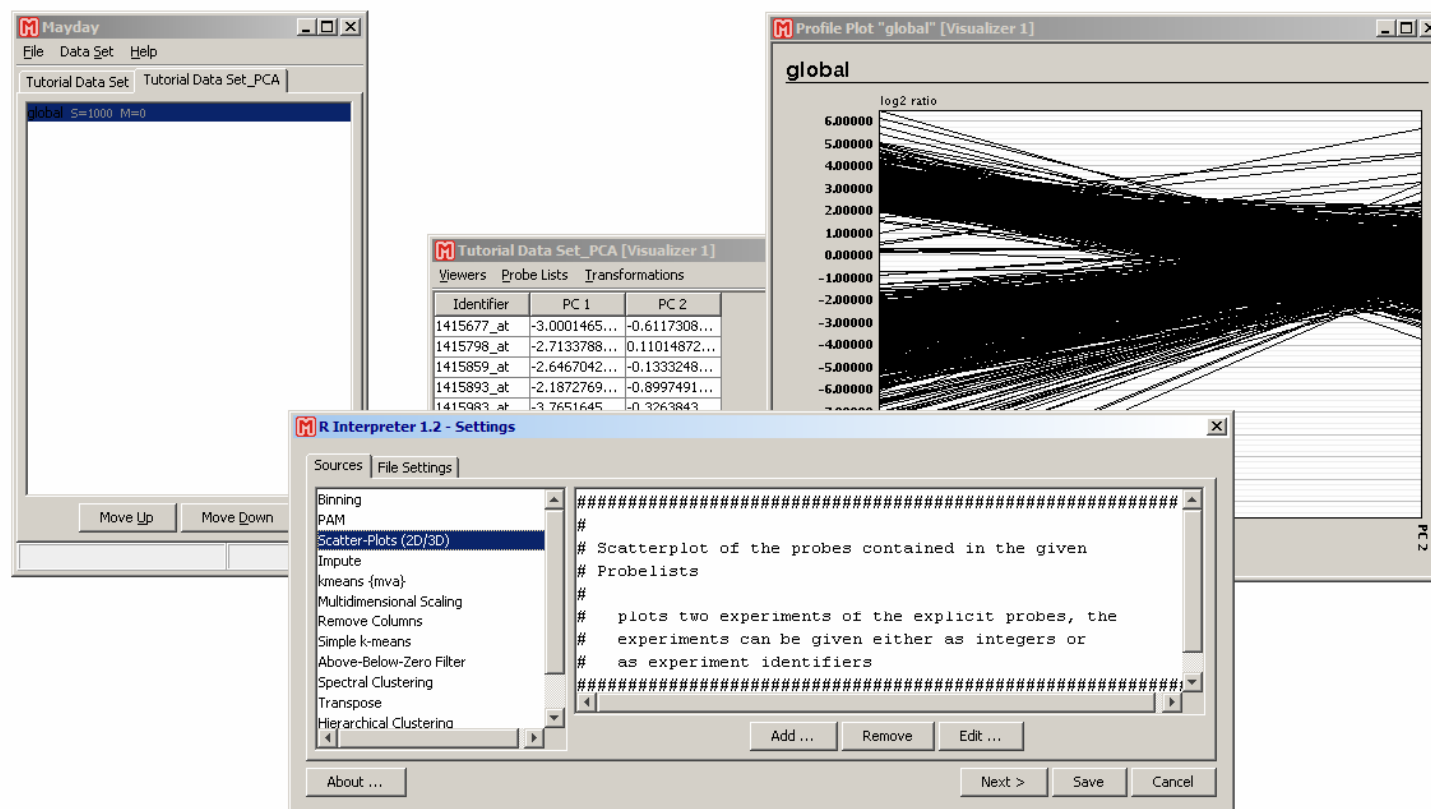
Tutorial Data Set_PCA [Visualizer 1]

Viewers Probe Lists Transformations

Identifier	PC 1	PC 2
1415677_at	-3.0001465...	-0.6117308...
1415798_at	-2.7133788...	0.11014872...
1415859_at	-2.6467042...	-0.1333248...
1415893_at	-2.1872769...	-0.8997491...
1415983_at	-3.7651645...	-0.3263843...
1416111_at	-2.9462300...	-0.0129683...
1416147_at	3.82628475...	-1.2170567...
1416164_at	-2.9672984...	-0.4711573...
1416226_at	-5.3089522...	0.60019056...
1416239_at	-2.3655459...	0.80913071...
1416340_a_at	-5.3095986...	-0.5463194...
1416382_at	-3.1111417...	-0.1532741...
1416451_s_at	-3.8128561...	0.38159540...
1416529_at	-3.0825433...	-0.4610965...
1416554_at	-3.3087400...	0.34001600...



Select "R Interpreter".



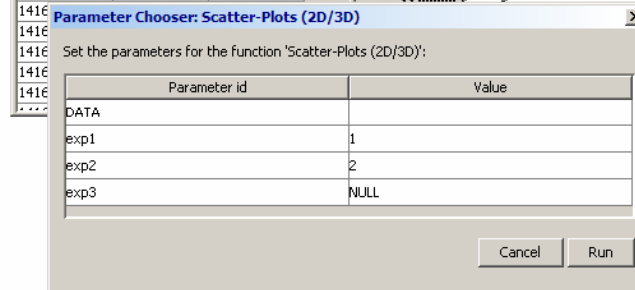
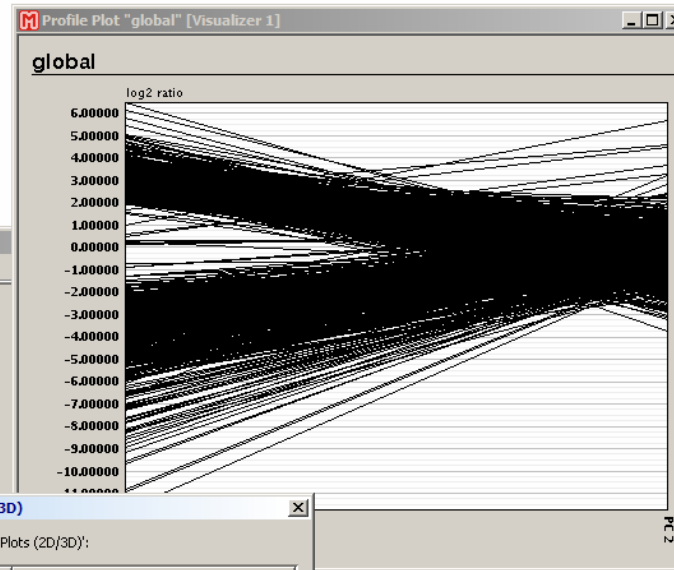
Select "Scatter Plots (2D/3D)" from the list of available R scripts.



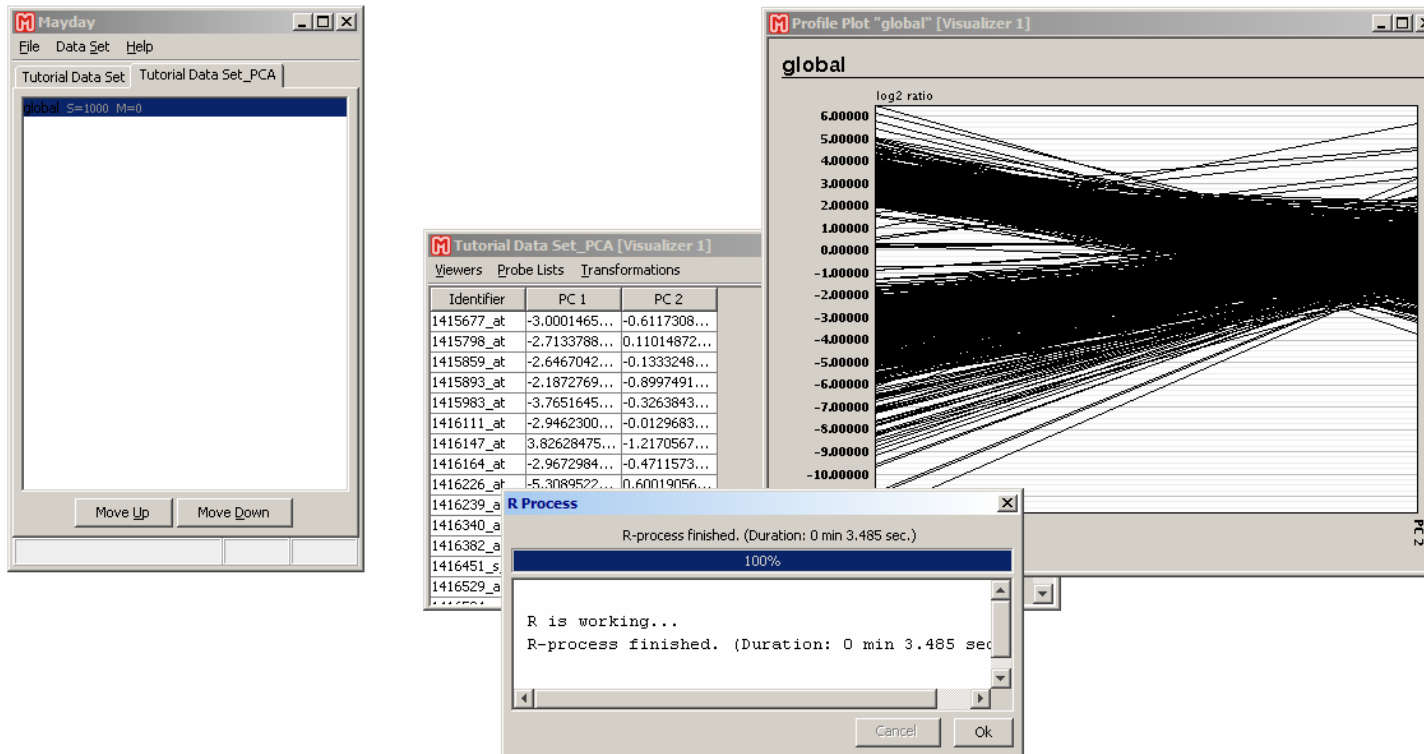
Tutorial Data Set_PCA [Visualizer 1]

Viewers Probe Lists Transformations

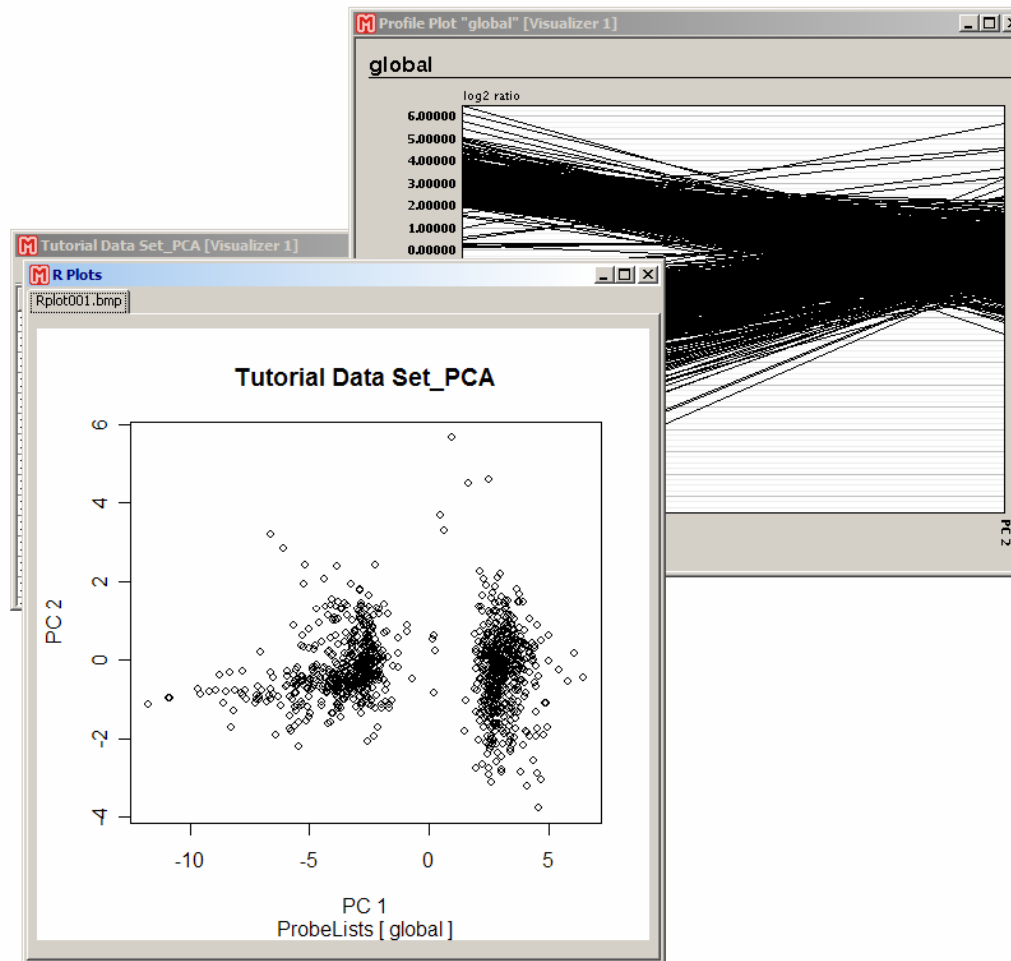
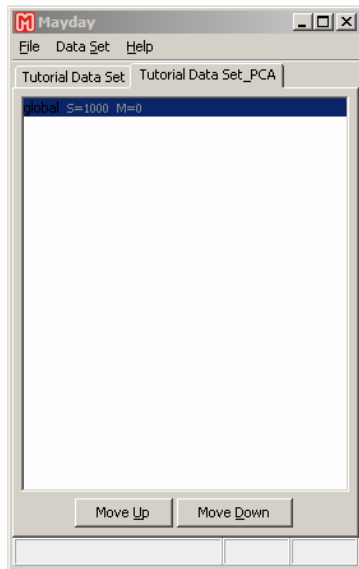
Identifier	PC 1	PC 2
1415677_at	-3.0001465...	-0.6117308...
1415798_at	-2.7133788...	0.11014872...
1415859_at	-2.6467042...	-0.1333248...
1415893_at	-2.1872769...	-0.8997491...
1415983_at	-3.7651645...	-0.3263843...
1416111_at	-2.9462300...	-0.0129683...
1416147_at	3.82628475...	-1.2170567...
1416164_at	-2.9672984...	-0.4711573...
1416226_at	-5.3089522...	0.60019056...



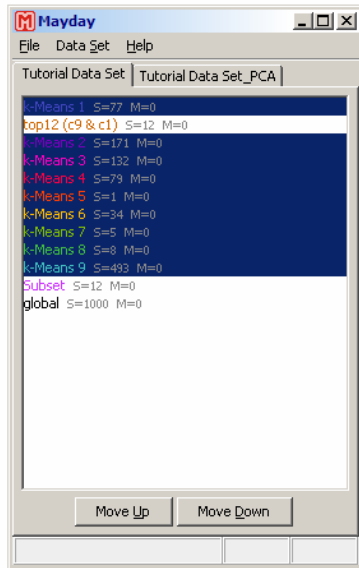
Leave all parameters at their default values. Click "Run".



Click "OK" when R has finished running.



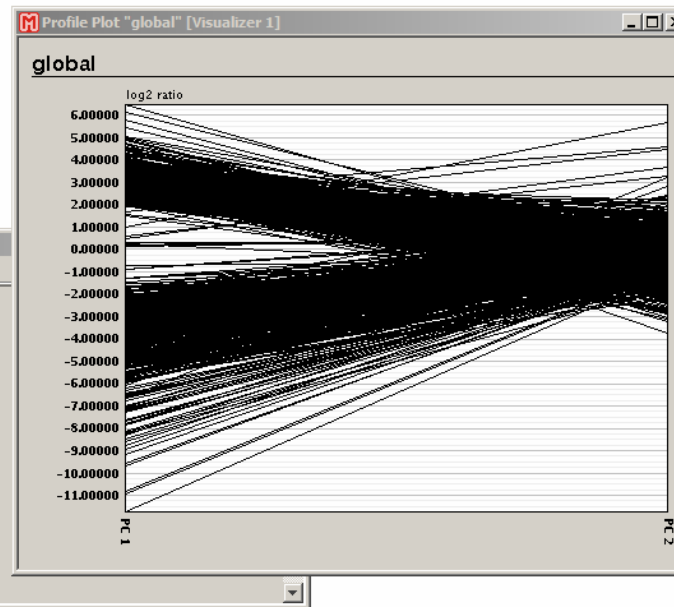
Close the plot or send it to the background.



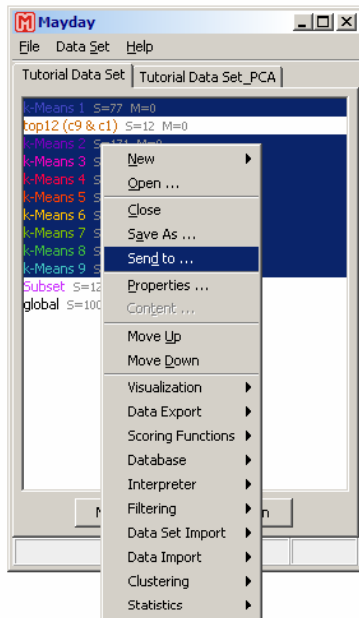
Tutorial Data Set_PCA [Visualizer 1]

Viewers Probe Lists Transformations

Identifier	PC 1	PC 2
1415677_at	-3.0001465...	-0.6117308...
1415798_at	-2.7133788...	0.11014872...
1415859_at	-2.6467042...	-0.1333248...
1415893_at	-2.1872769...	-0.8997491...
1415983_at	-3.7651645...	-0.3263843...
1416111_at	-2.9462300...	-0.0129683...
1416147_at	3.82628475...	-1.2170567...
1416164_at	-2.9672984...	-0.4711573...
1416226_at	-5.3089522...	0.60019056...
1416239_at	-2.3655459...	0.80913071...
1416340_a_at	-5.3095986...	-0.5463194...
1416382_at	-3.1111417...	-0.1532741...
1416451_s_at	-3.8128561...	0.38159540...
1416529_at	-3.0825433...	-0.4610965...

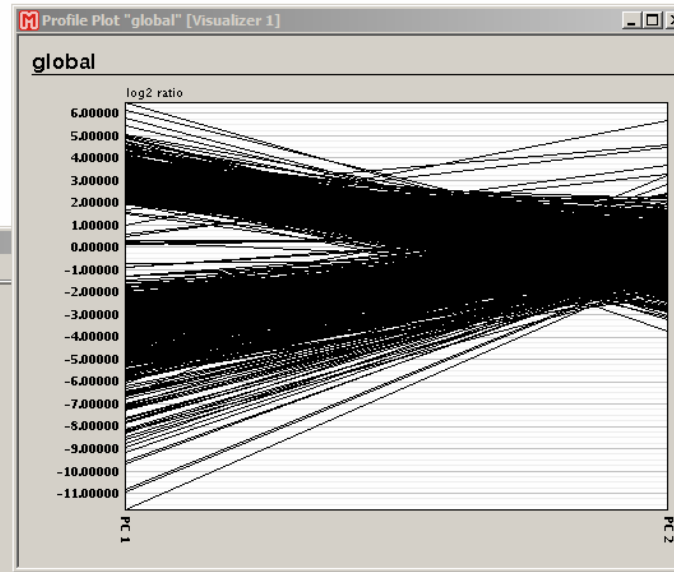


Go back to the original data set.
Select the 9 k-means clusters.

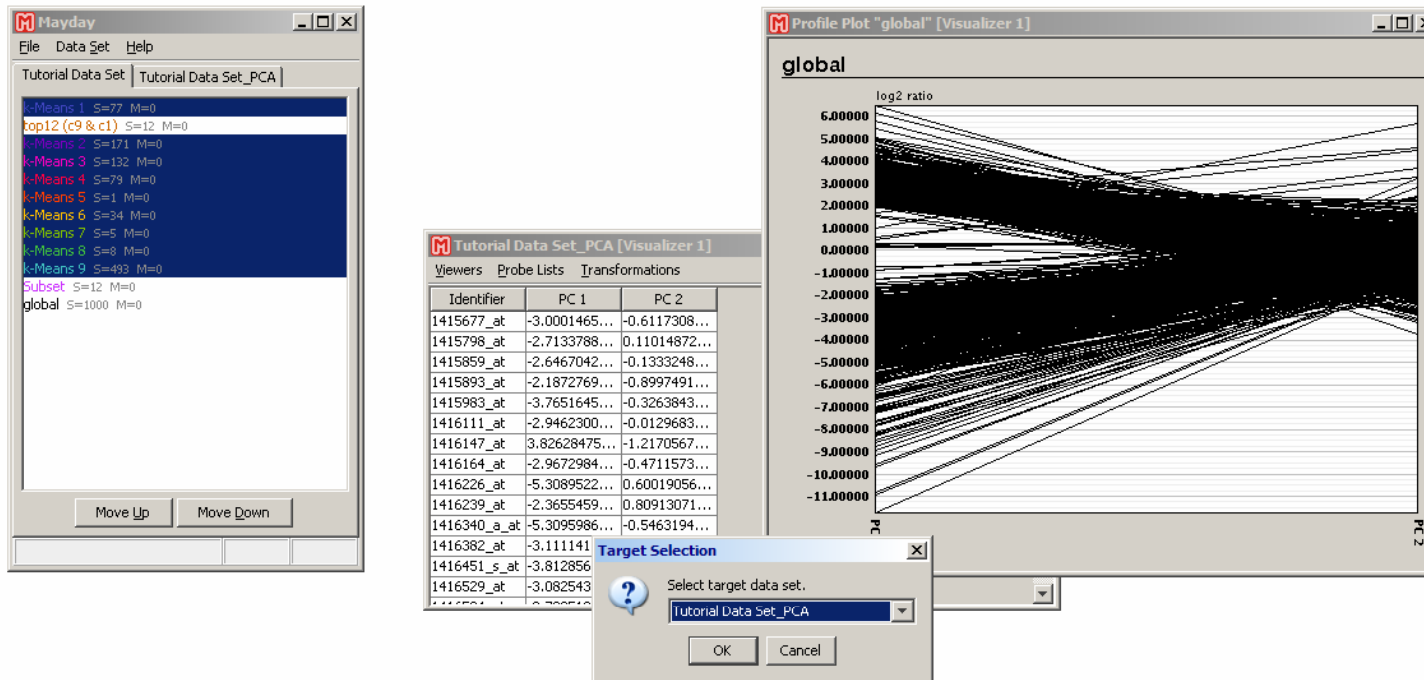


The screenshot shows the 'Tutorial Data Set_PCA [Visualizer 1]' window. It displays a table with three columns: 'Identifier', 'PC 1', and 'PC 2'. The table contains 15 rows of data, representing different probe lists and their corresponding PC 1 and PC 2 values.

Identifier	PC 1	PC 2
1415677_at	-3.0001465...	-0.6117308...
1415798_at	-2.7133788...	0.11014872...
1415859_at	-2.6467042...	-0.1333248...
1415893_at	-2.1872769...	-0.8997491...
1415983_at	-3.7651645...	-0.3263843...
1416111_at	-2.9462300...	-0.0129683...
1416147_at	3.82628475...	-1.2170567...
1416164_at	-2.9672984...	-0.4711573...
1416226_at	-5.3089522...	0.60019056...
1416239_at	-2.3655459...	0.80913071...
1416340_a_at	-5.3095986...	-0.5463194...
1416382_at	-3.1111417...	-0.1532741...
1416451_s_at	-3.8128561...	0.38159540...
1416529_at	-3.0825433...	-0.4610965...
1416554_at	-3.3081400...	0.34001000...



Open the probe list manager's context menu and select "Send to ...".

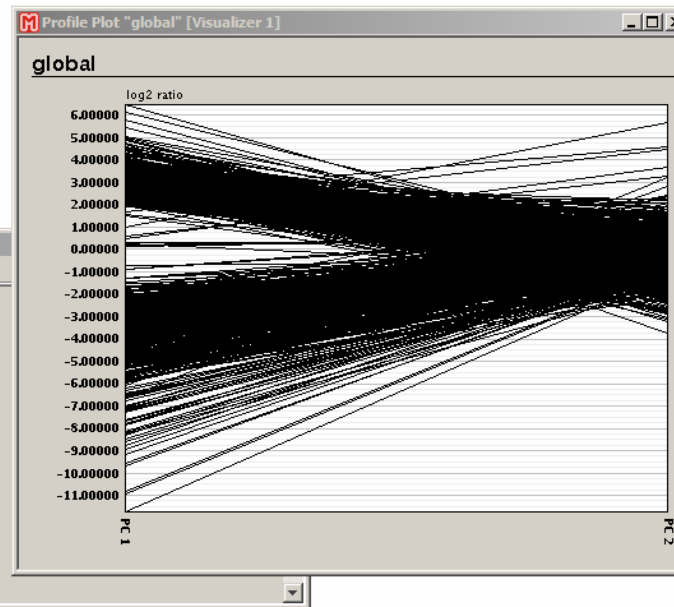


Select "Tutorial Data Set_PCA" as target and confirm by clicking "OK". Go back to new data set.



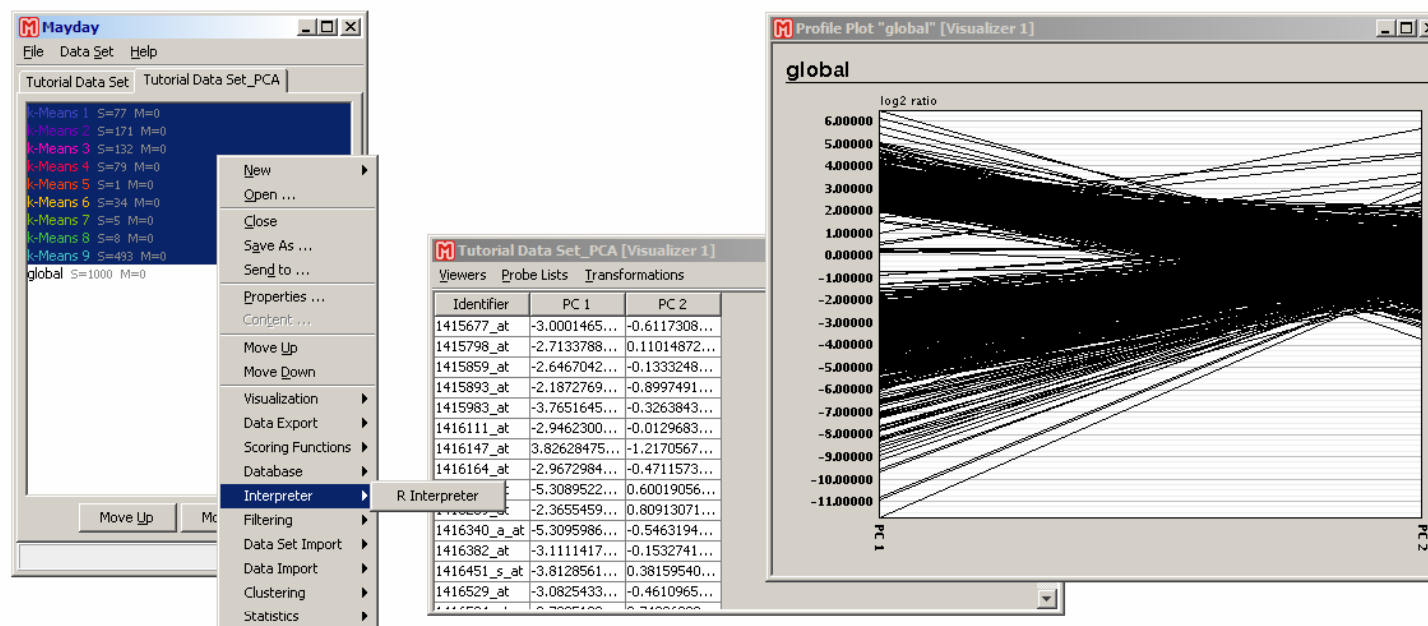
The 'Tutorial Data Set_PCA [Visualizer 1]' window displays a table with the following data:

Identifier	PC 1	PC 2
1415677_at	-3.0001465...	-0.6117308...
1415798_at	-2.7133788...	0.11014872...
1415859_at	-2.6467042...	-0.1333248...
1415893_at	-2.1872769...	-0.8997491...
1415983_at	-3.7651645...	-0.3263843...
1416111_at	-2.9462300...	-0.0129683...
1416147_at	3.82628475...	-1.2170567...
1416164_at	-2.9672984...	-0.4711573...
1416226_at	-5.3089522...	0.60019056...
1416239_at	-2.3655459...	0.80913071...
1416340_a_at	-5.3095986...	-0.5463194...
1416382_at	-3.1111417...	-0.1532741...
1416451_s_at	-3.8128561...	0.38159540...
1416529_at	-3.0825433...	-0.4610965...

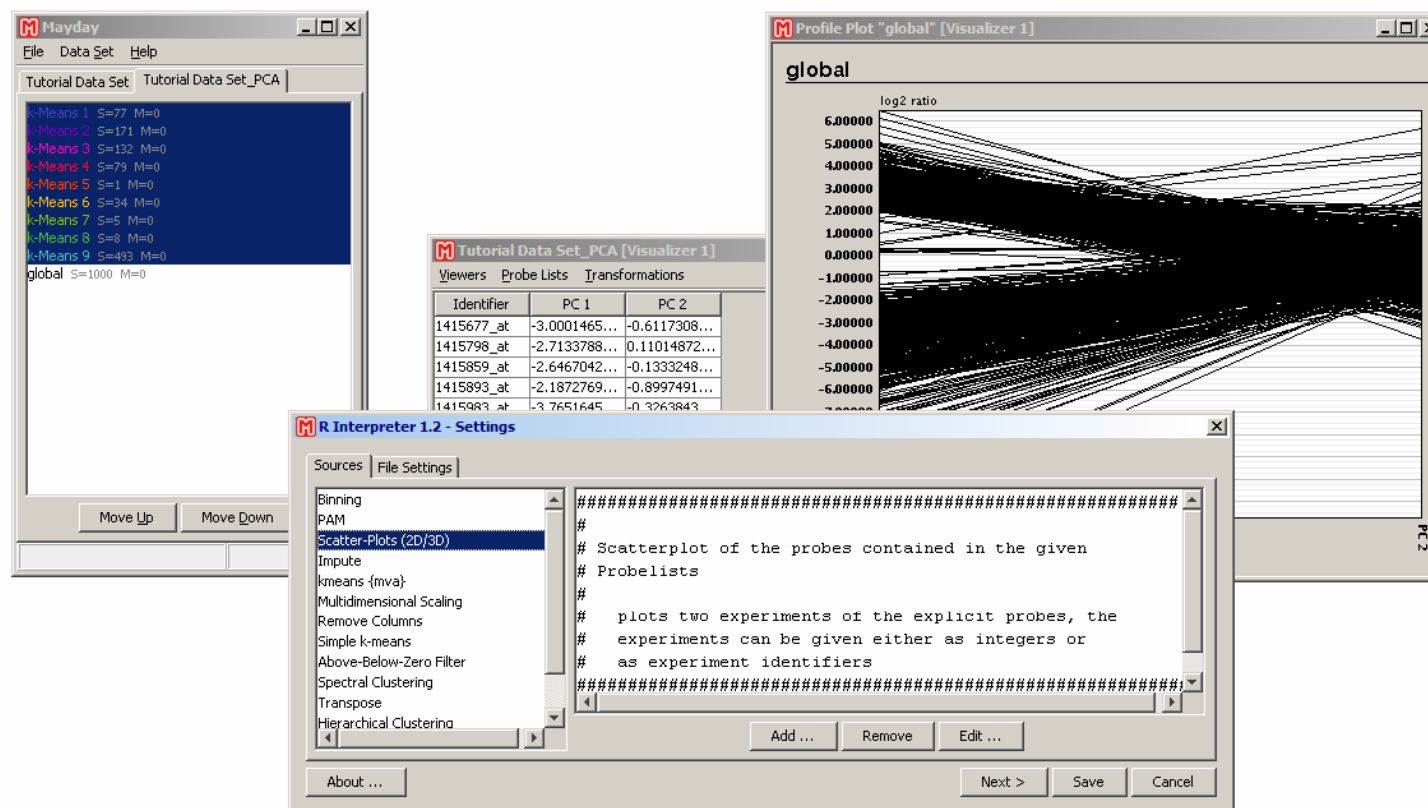


This is an example how you can share information between two data sets. Please note that the probe identifiers have to be the same in both data set for the probe list transfer to work.

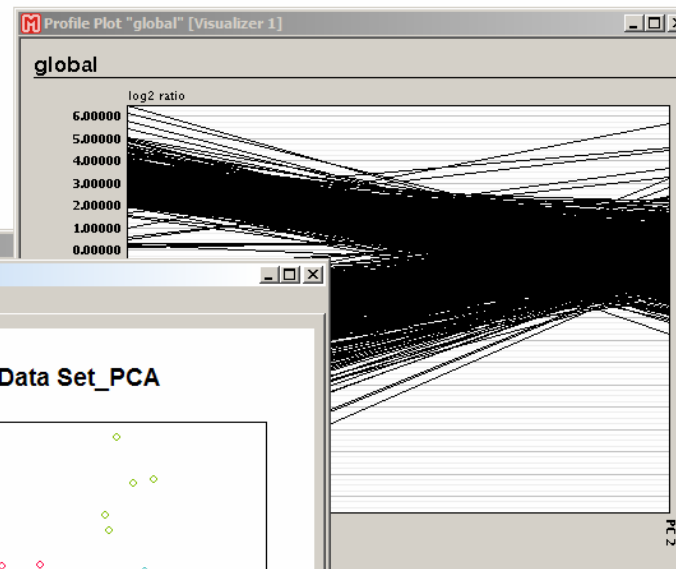
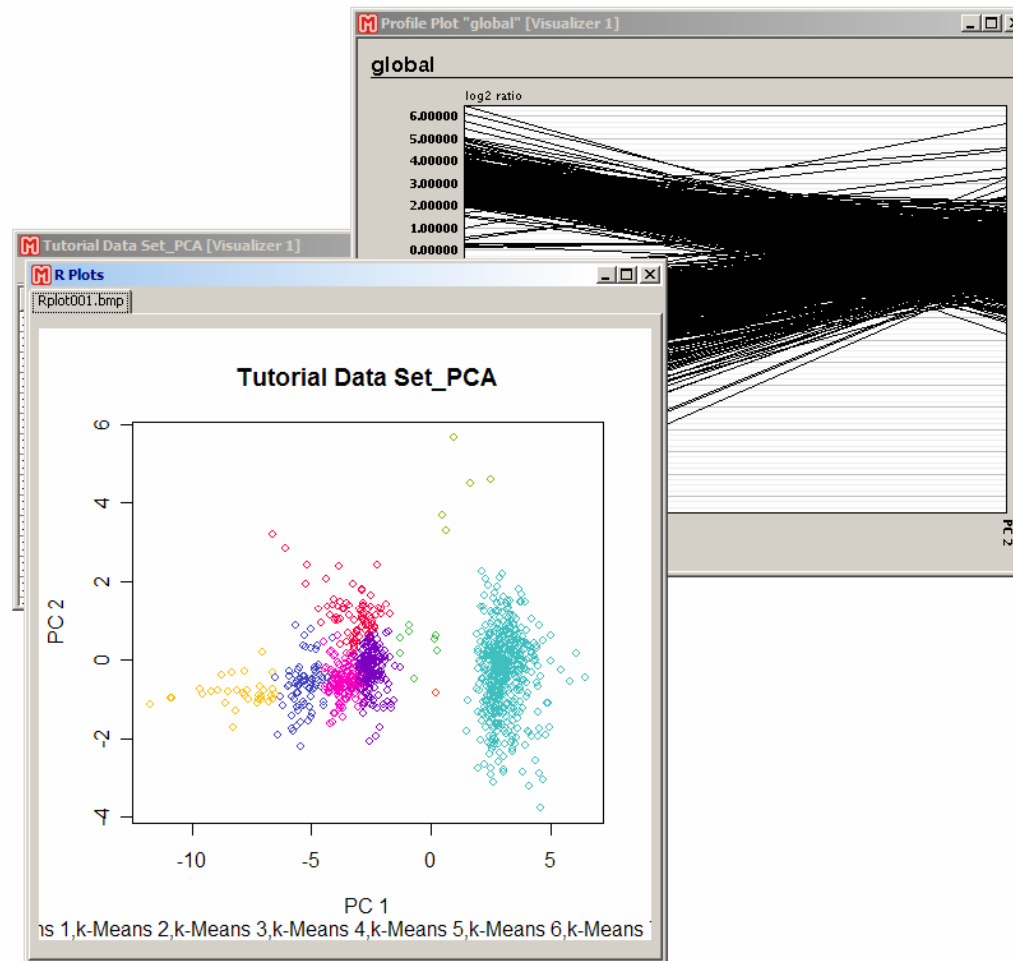
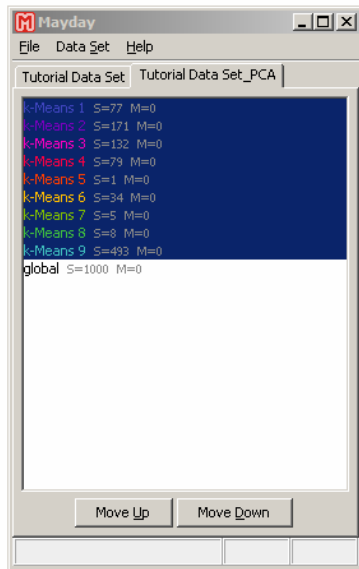
Select the transferred probe lists.



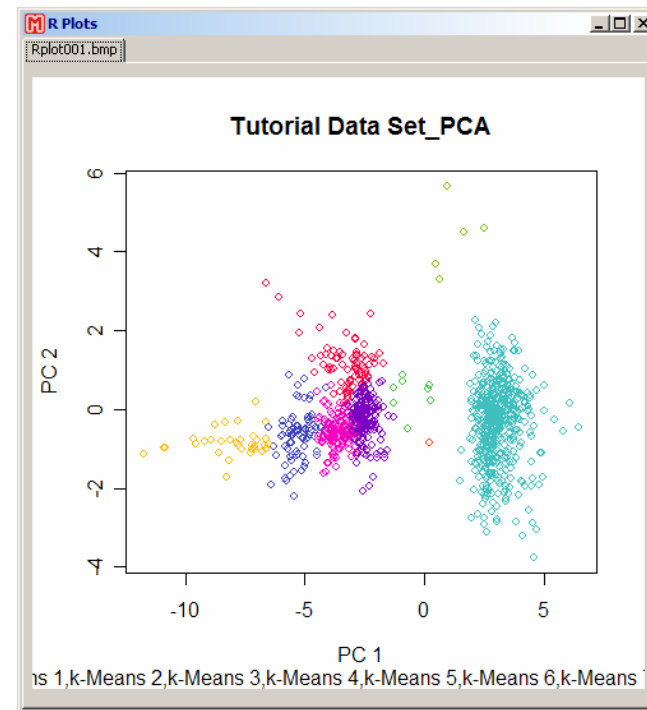
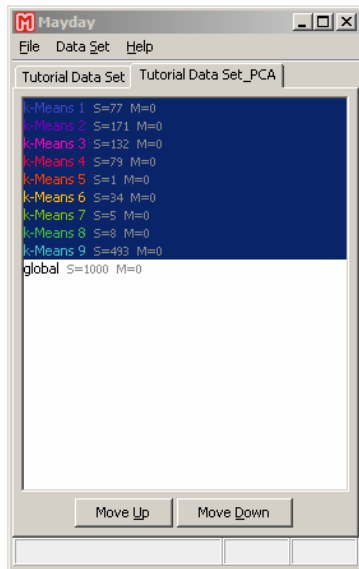
Open the probe list manager's context menu and go to submenu "Interpreter". Select "R Interpreter".



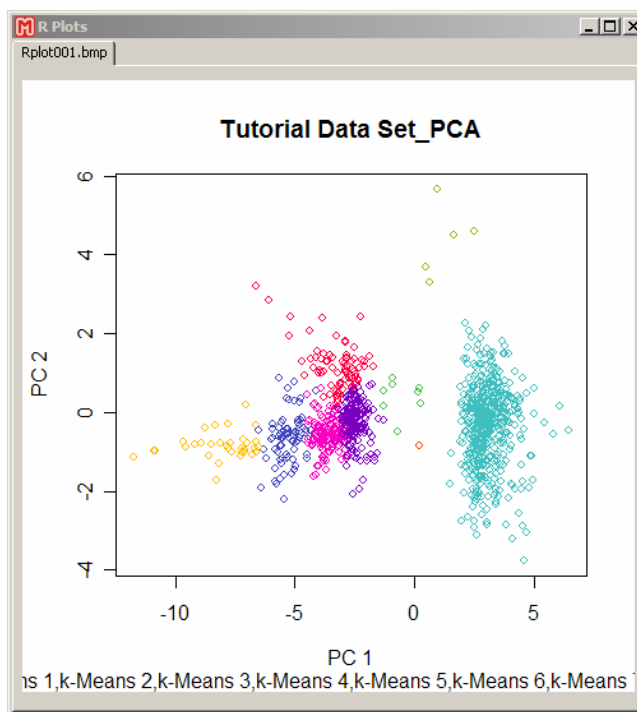
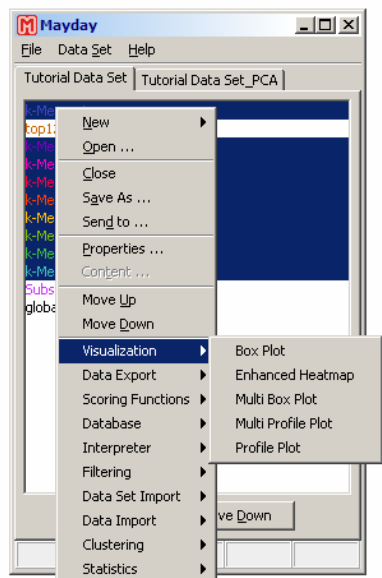
Select "Scatter Plots (2D/3D)" and run with default values.



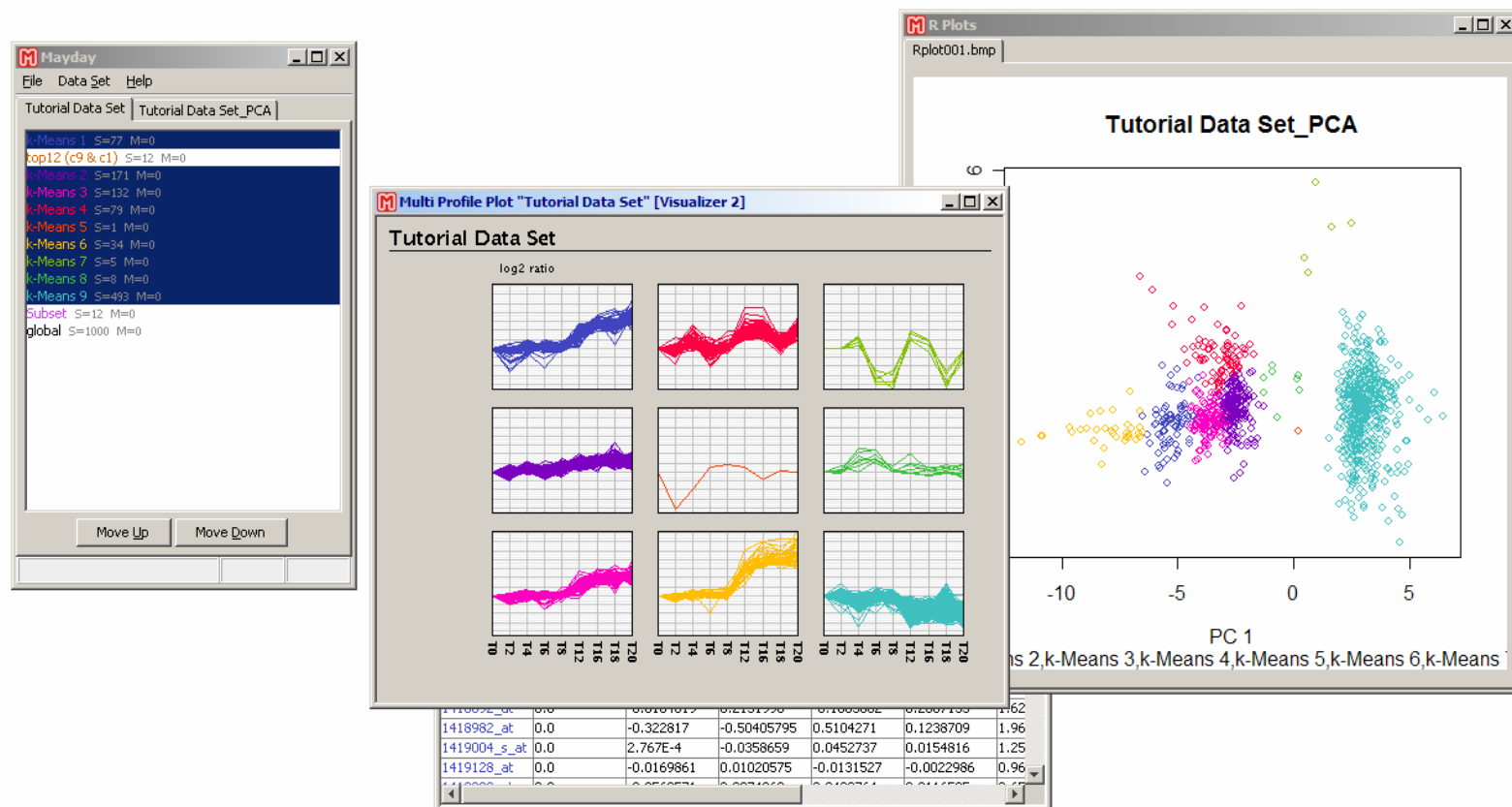
Close the profile plot
and the tabular viewer.



Select all k-means clusters and open the probe list manager's context menu.

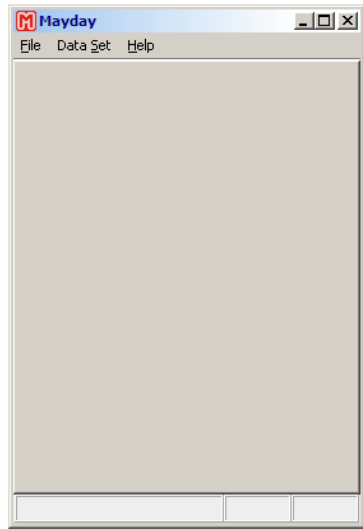


Go to submenu visualization, select “Multi Profile Plot” and create a 3x3 multi profile plot. Don’t change the automatic assignment of probe lists to grid positions.

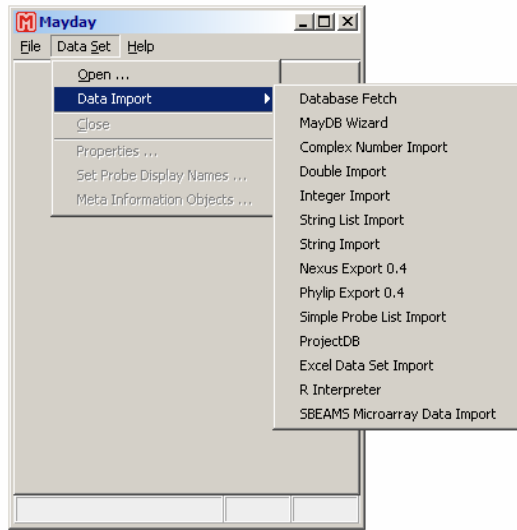


Close both data sets by opening the “Data Set” menu in the main window, then select “Close”. Alternatively you can right-click on the tabs of the corresponding data set and select “Close” in the context menu.

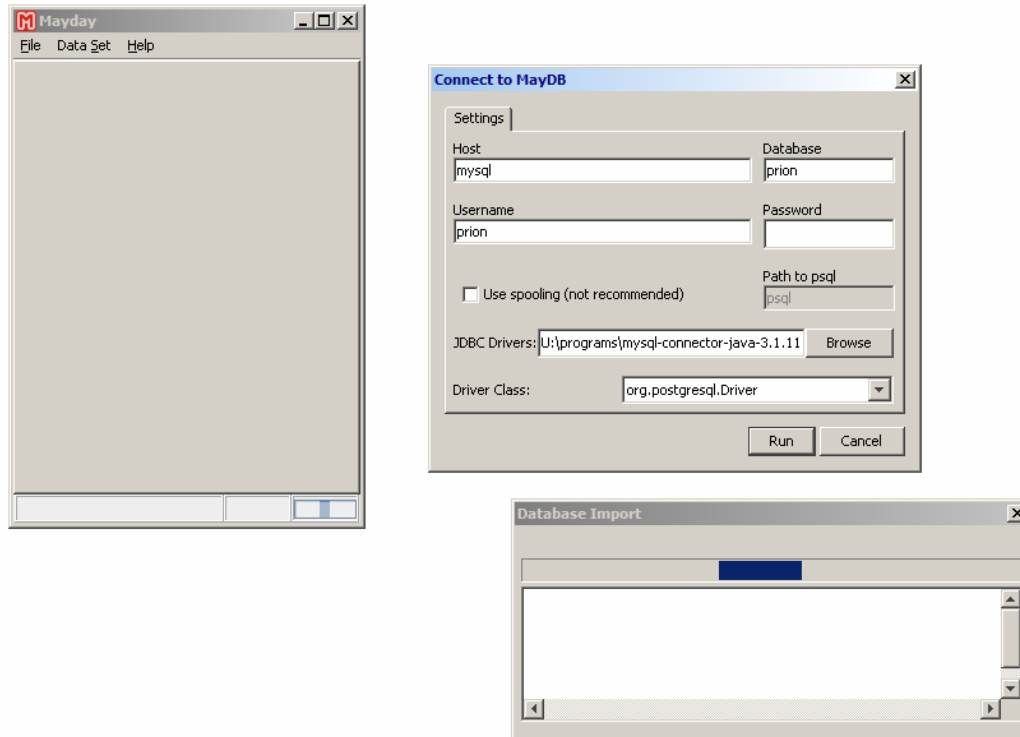
Loading Data From MayDB



Open the “Data Set” menu and go to submenu “Data Import”.

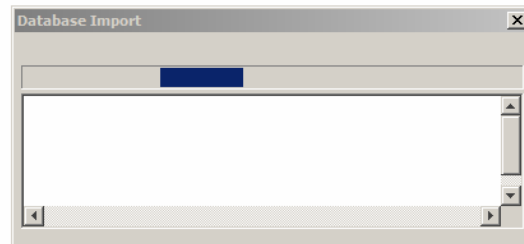
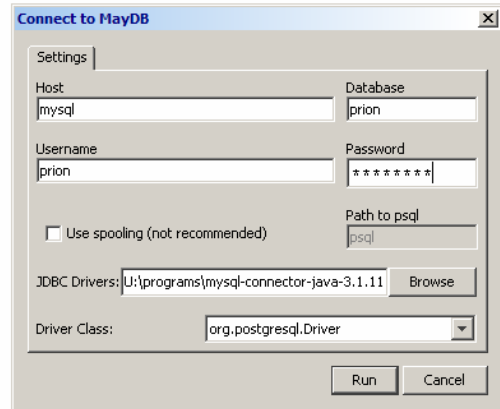
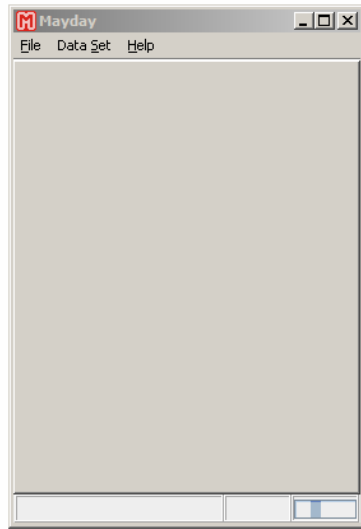


Select “Database Fetch”.



Enter your database host, database name and username. Then enter your password.

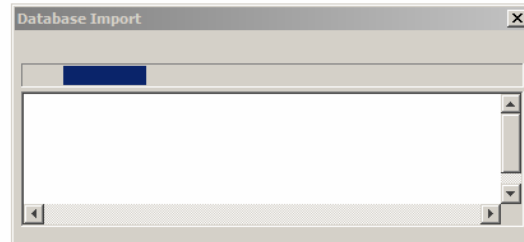
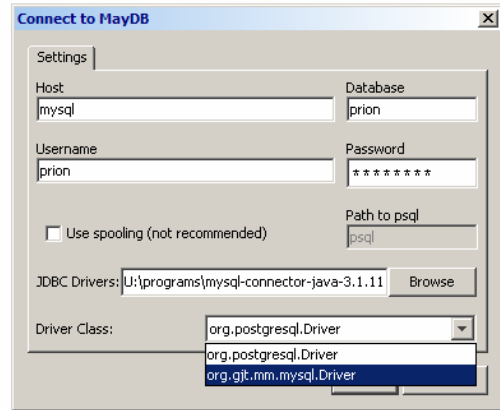
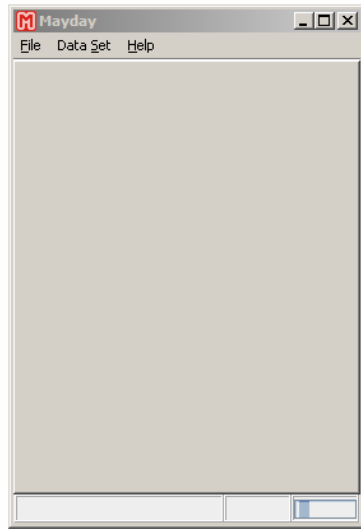
This is the database connection dialog. You have to enter information about the database and your account. This information will be stored for future use. The password has to be entered every time for security reason. The JDBC drivers have to match the selected driver class and both have to match the database you are running MayDB on. This is either MySQL or PostgreSQL. In both cases the names for JDBC driver and driver class are mostly self-explaining.



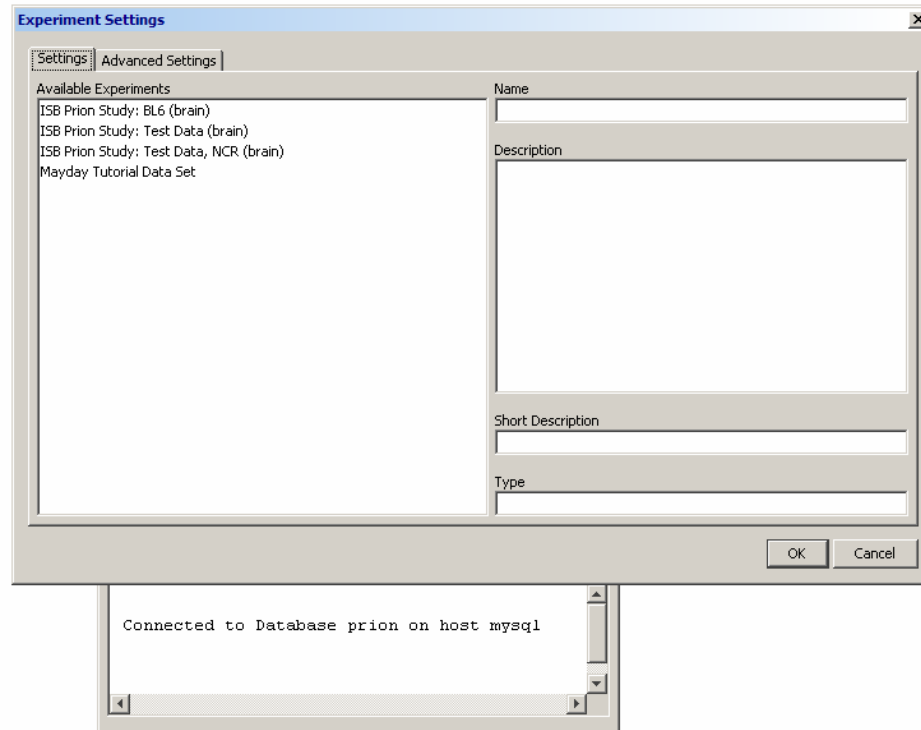
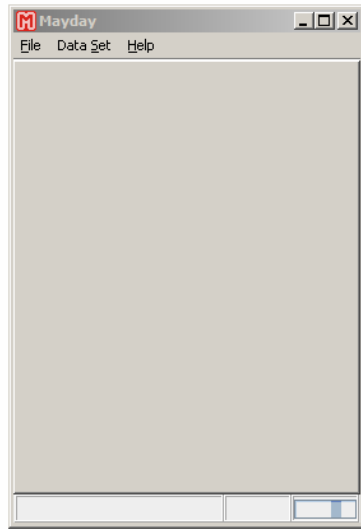
Enter the path to the JDBC drivers
or click “Browse” to select.

Fetching a data set

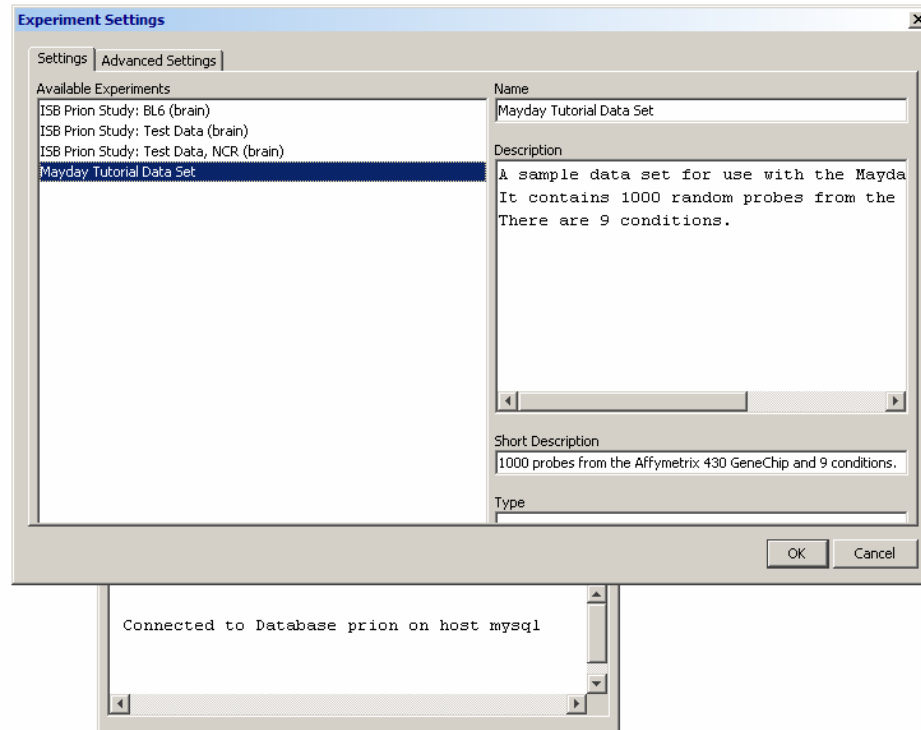
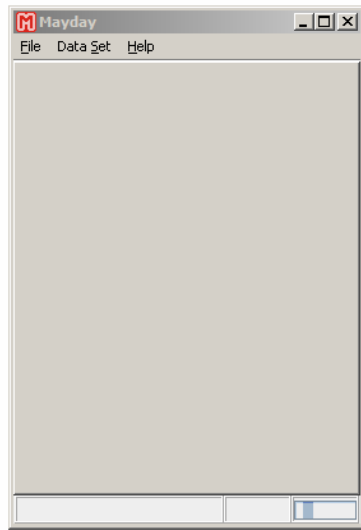
191



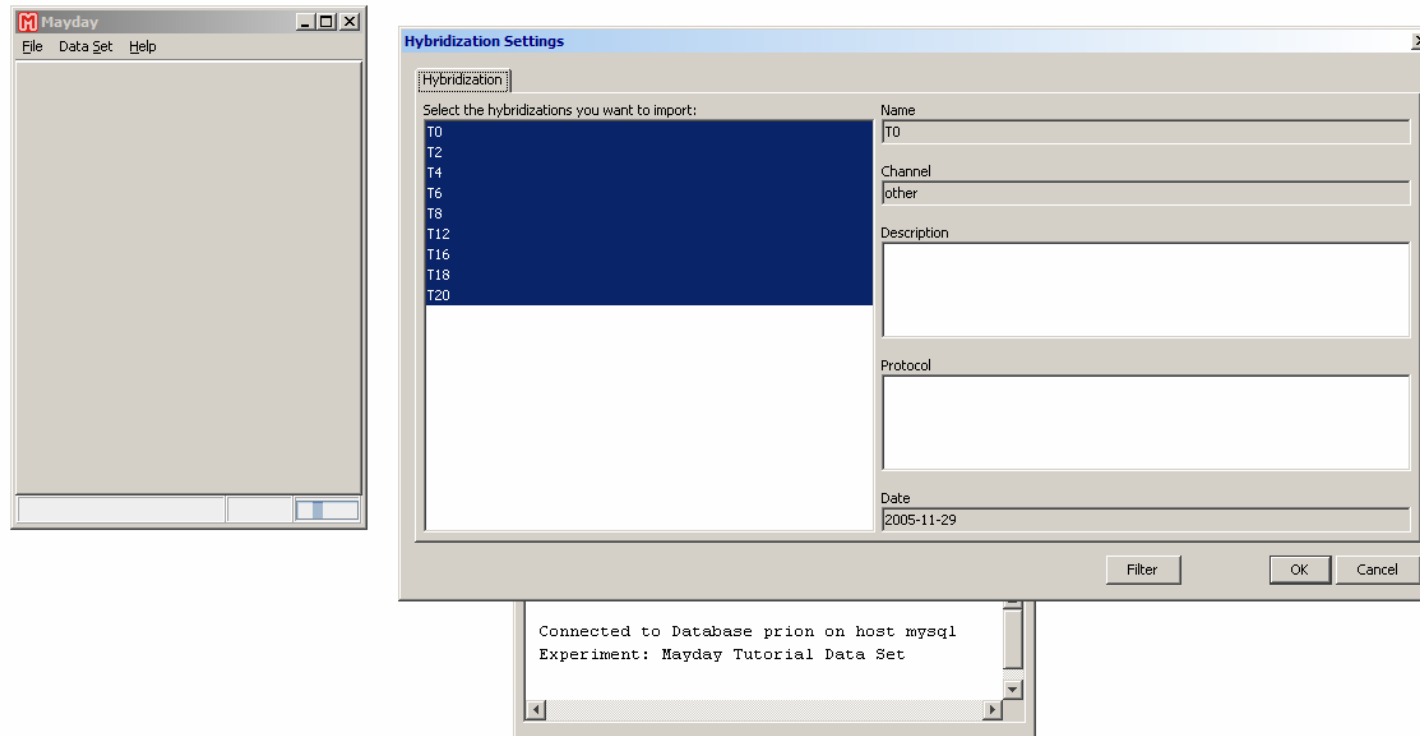
Select the correct driver class for the JDBC driver and click “OK” to connect to the database.



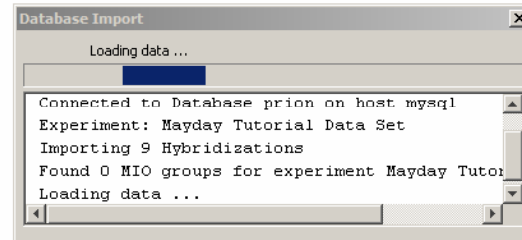
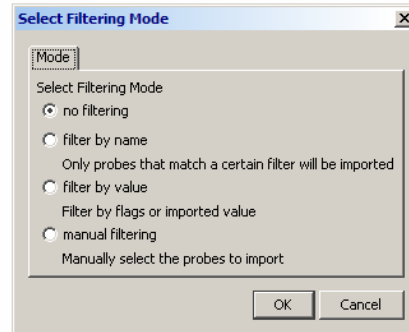
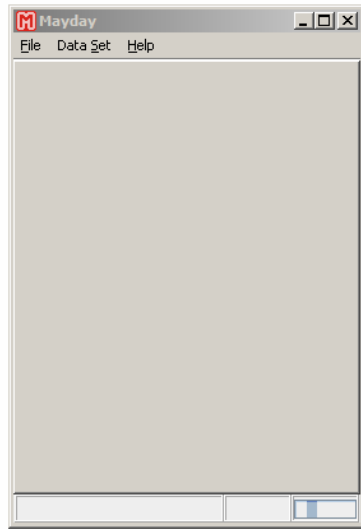
Select "Mayday Tutorial Data Set" from the list of available experiments.



Review the information and click “OK”
when you are done.

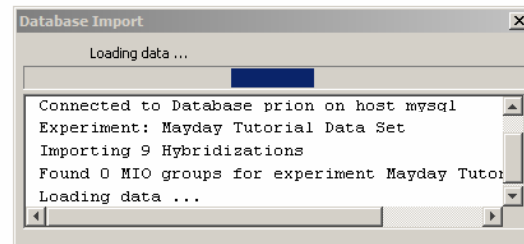
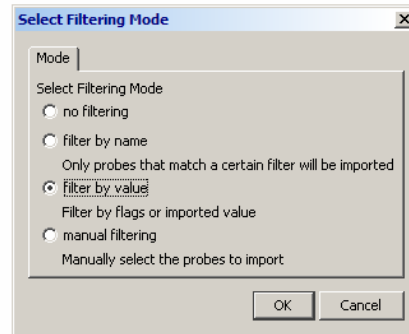
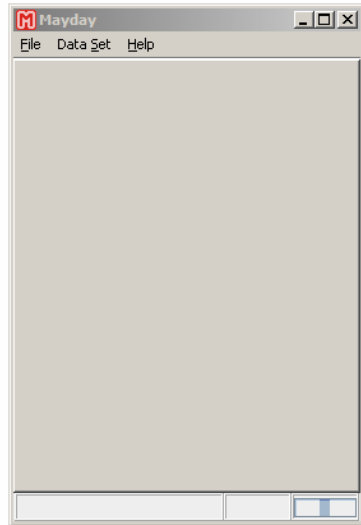


Select all hybridizations. Use the CTRL key or the SHIFT key to select multiple hybridizations. Click “OK” to confirm.

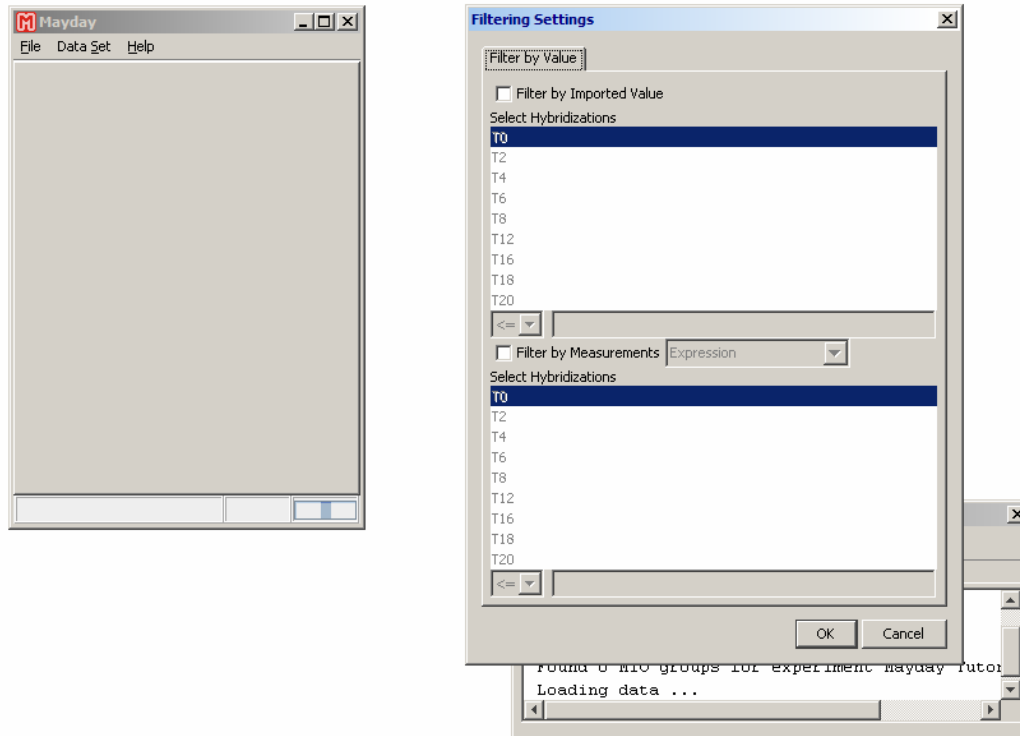


All probes of the selected experiment will be imported no matter what filter you choose. However, filtering data will create an additional probe list of all probes that have passed the filter.

Select a the “filter by value” mode.

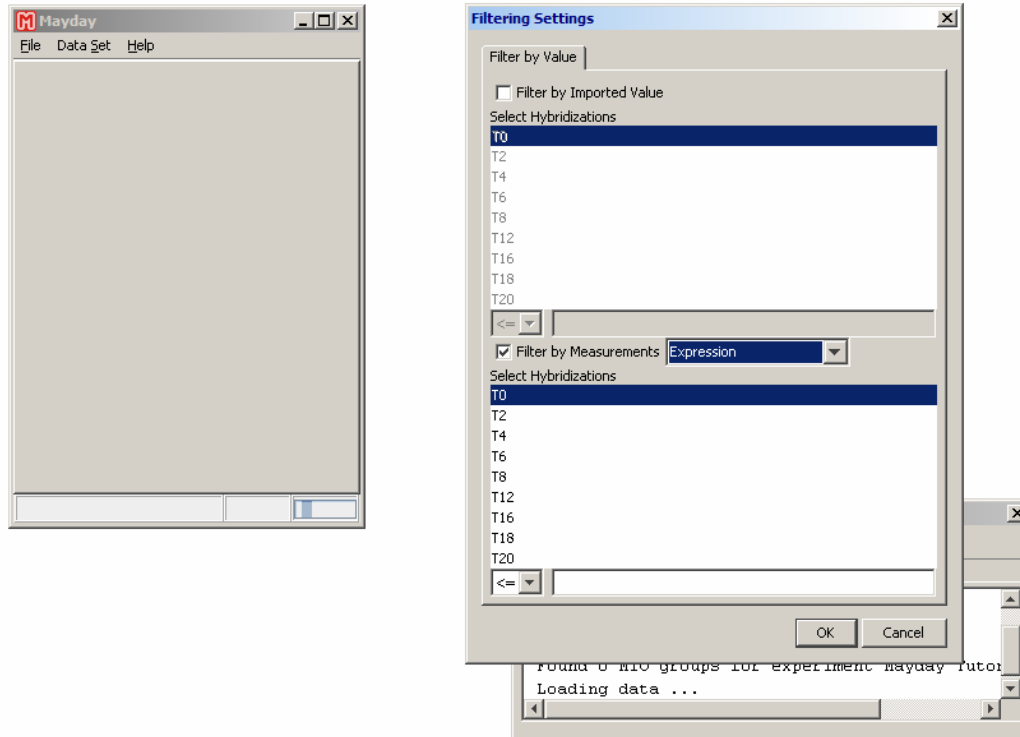


Click "OK" to confirm.

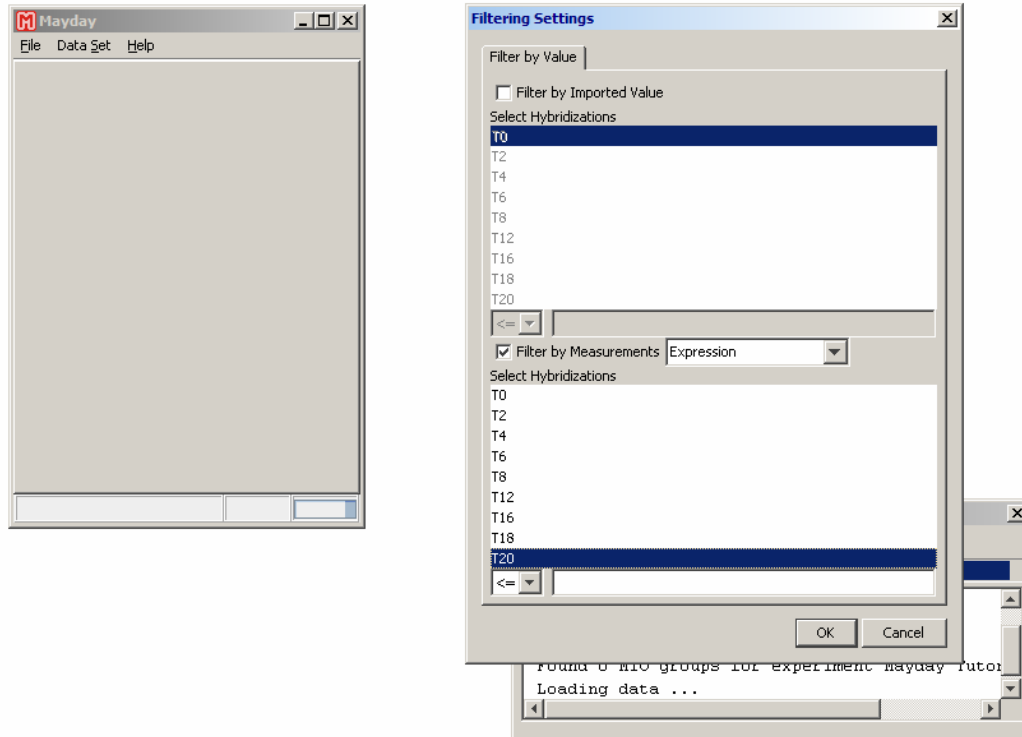


Probes can be filtered based on the value that will be imported. The value that will be imported maybe different from the one stored in the database. This depends on the data import mode, which will be discussed later. For the tutorial we filter by the values stored in the database, the so-called measurements.

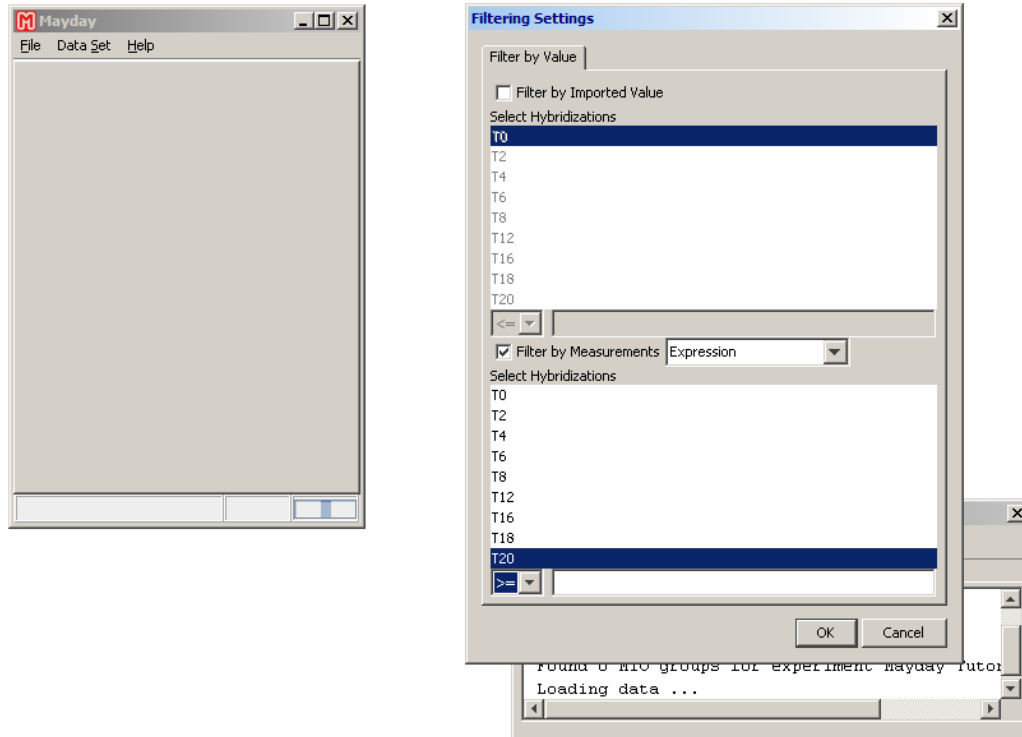
Check “Filter by Measurements”.



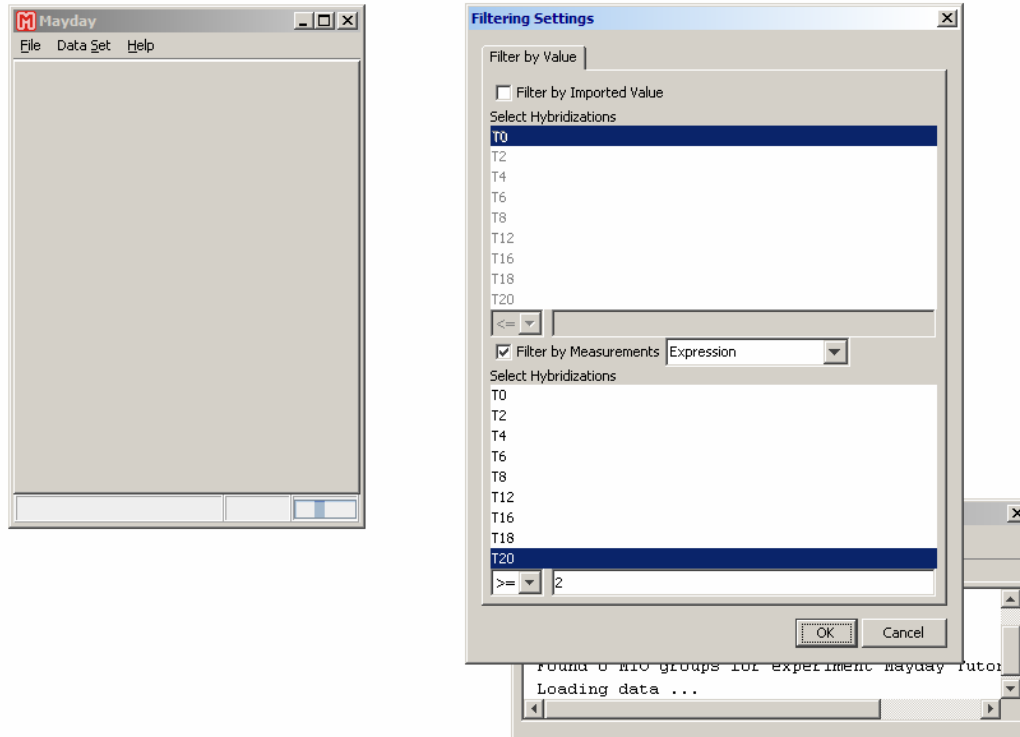
Select “Expression” as measurements.



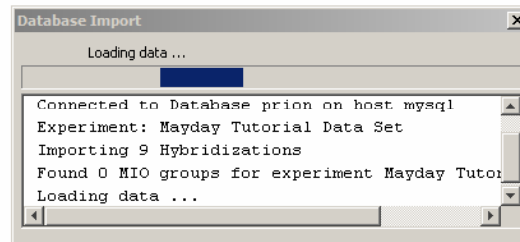
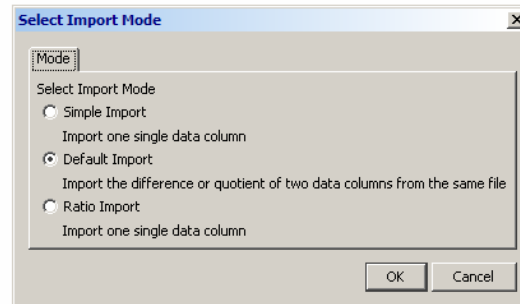
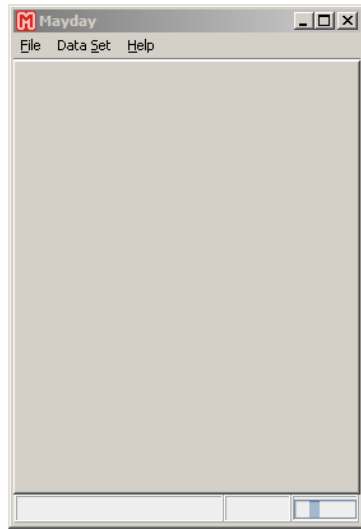
Select Hybridization “T20”.



Change "<=" to ">=".



Enter “2” as threshold value.

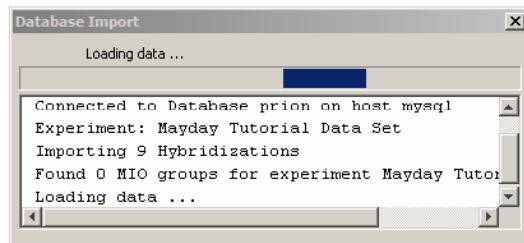
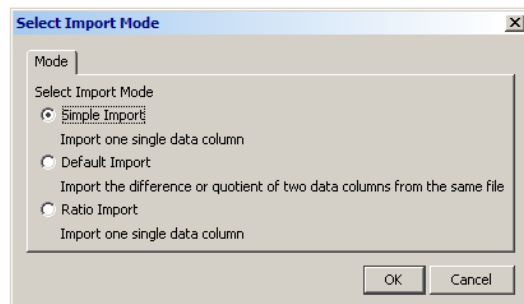
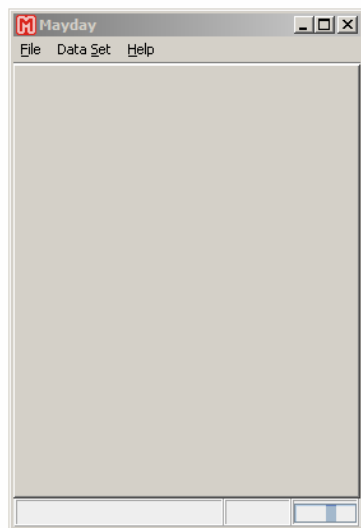


MayDB can also manage individual channels (e.g. from cDNA array scans). “Default , Import” mode can be used to compute the ratio between such channels. The tutorial data set is already preprocessed and doesn’t need any special treatment. Thus “Simple Import” is the right choice.

Select “Simple Import” as import mode.

Setting an import mode

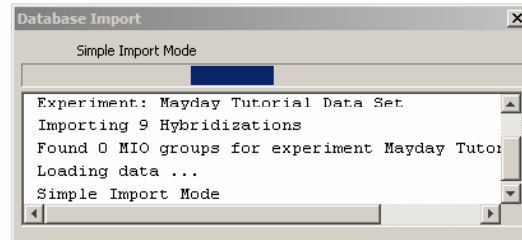
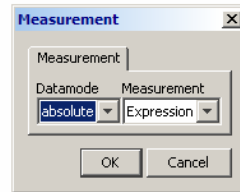
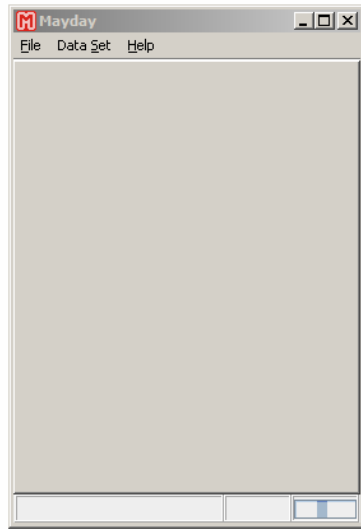
203



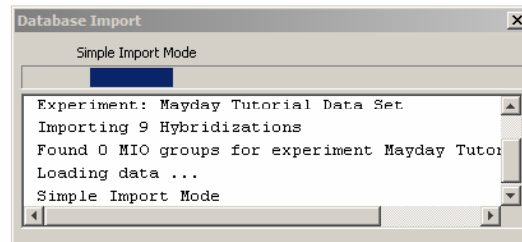
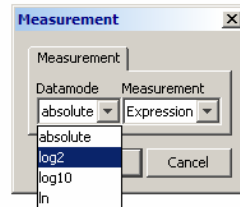
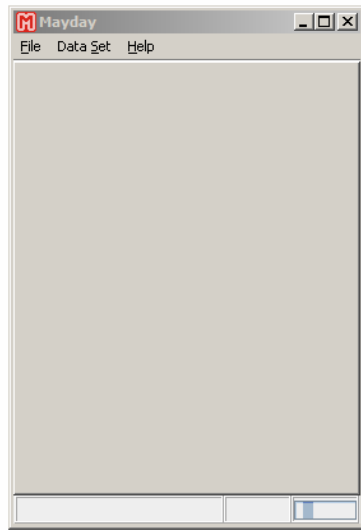
Click "OK" to confirm.

Setting an import mode

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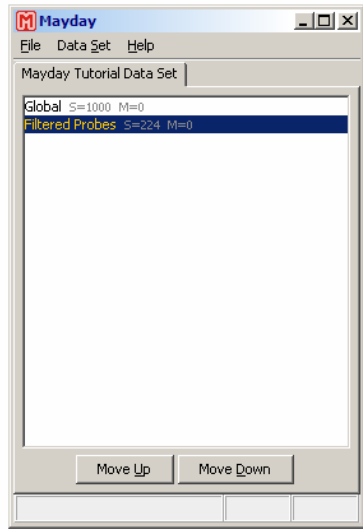
Select the correct data mode.



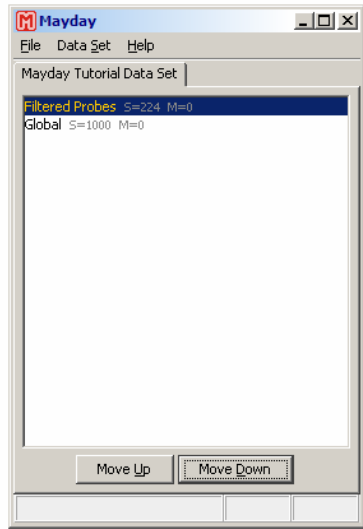
Select "log2" as data mode and click "OK" to confirm.



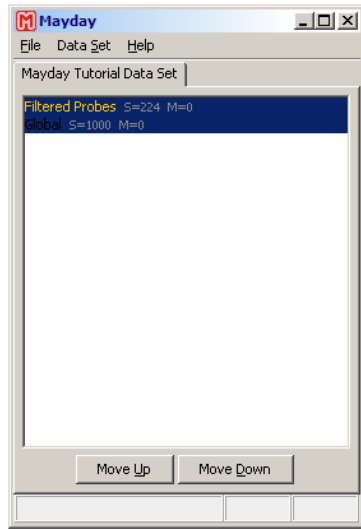
Select probe list
“Filtered Probes”.



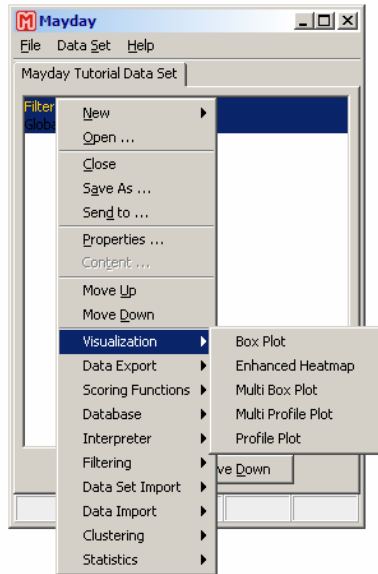
Click “Move Up” in the probe list manager.



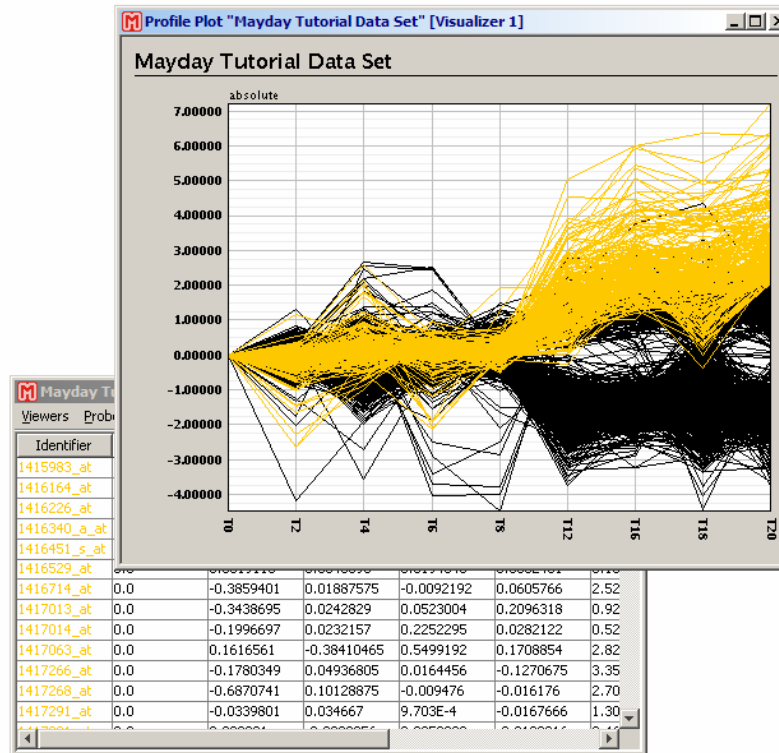
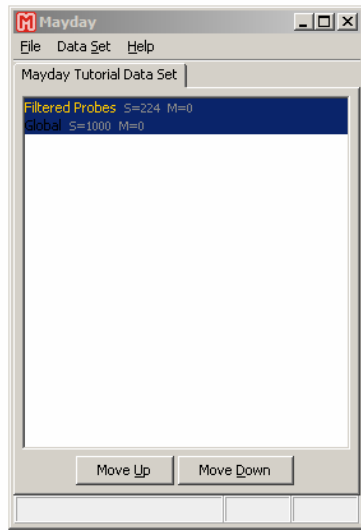
Select both probe lists in the probe list manager.



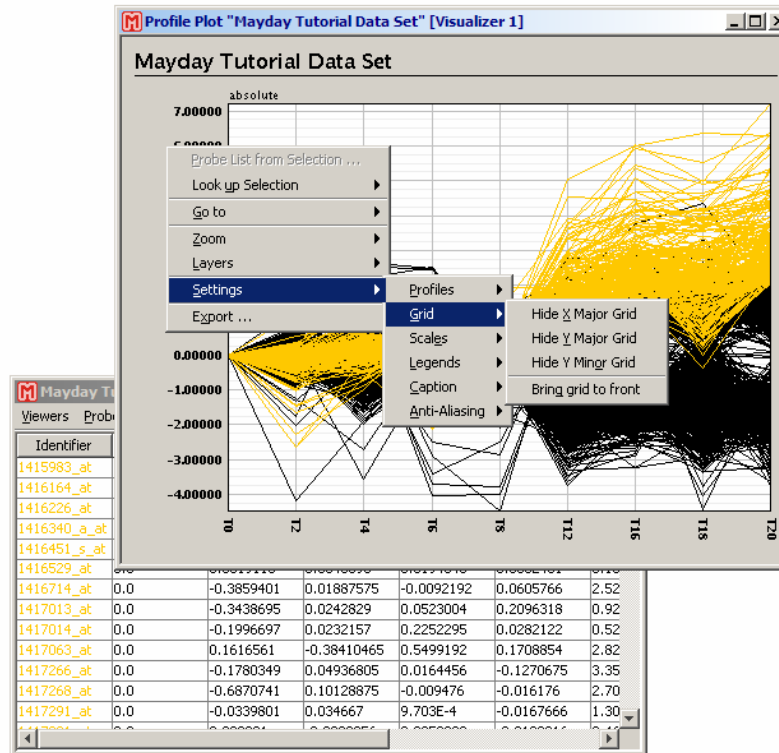
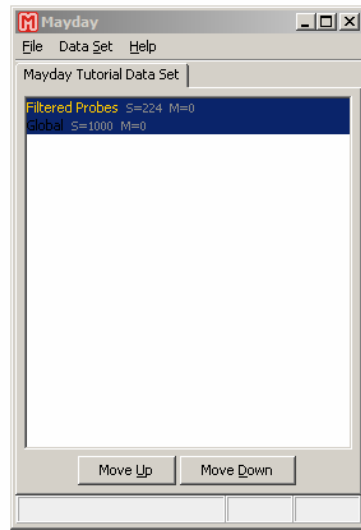
Open the probe list manager's context menu and go to submenu "Visualization".



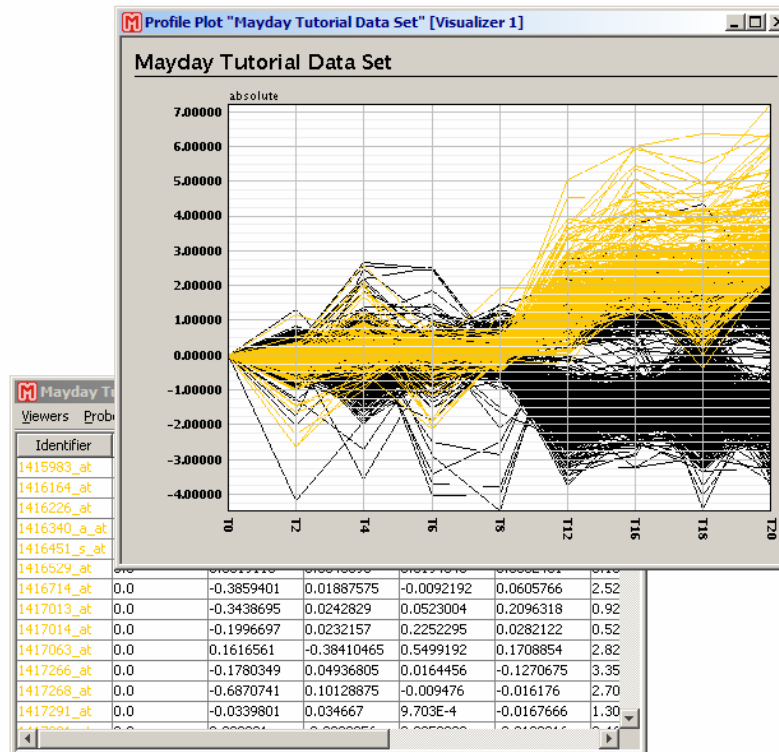
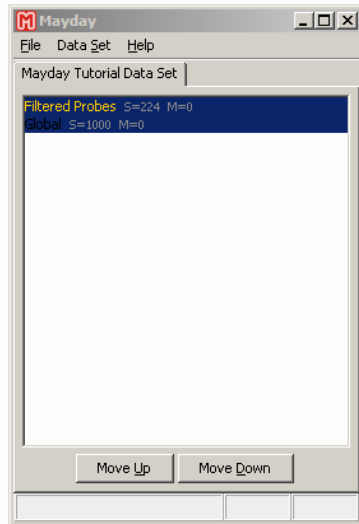
Select "Profile Plot".



Open the context menu of the profile plot, go to submenu "Settings" and then "Grid".



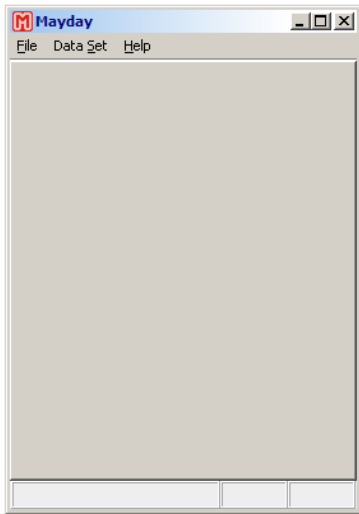
Select "Bring grid to front".



Close the data set.

Bringing the grid to front allows you to better determine the actual expression ratios. In this case it is a good way to verify the results of the filter.

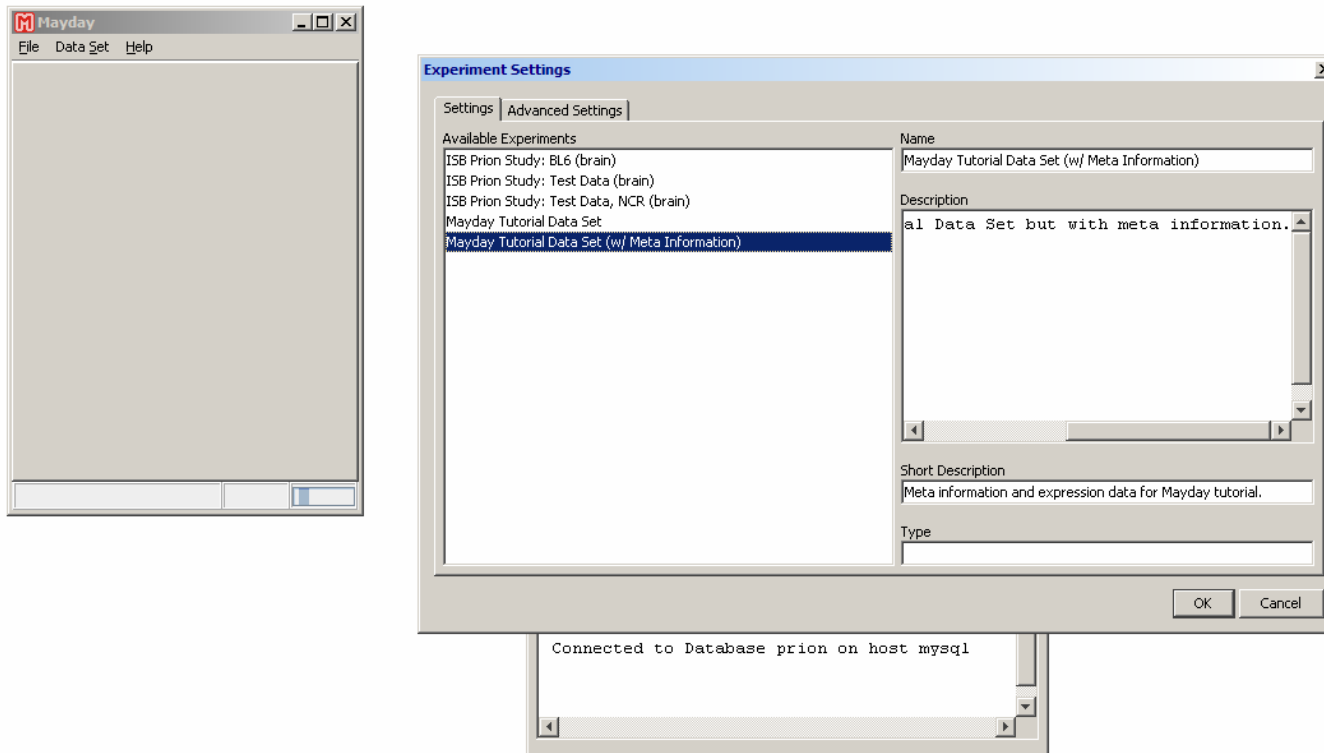
Working with Meta Information



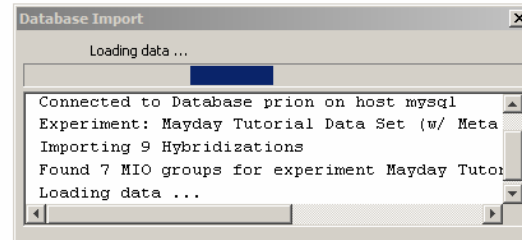
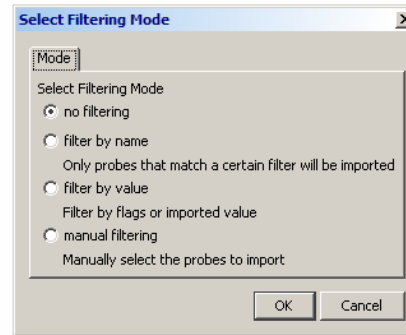
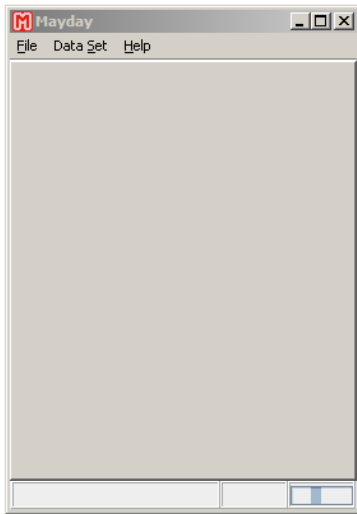
Connect to MayDB
as explained in the
previous section.

Loading a data set with meta information

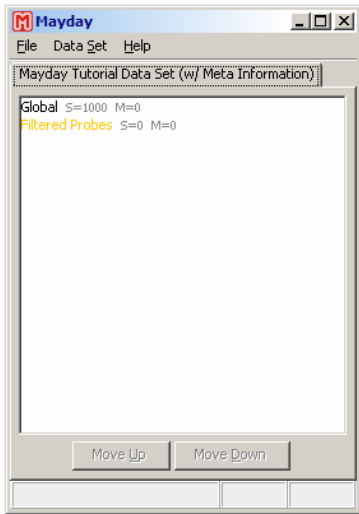
216



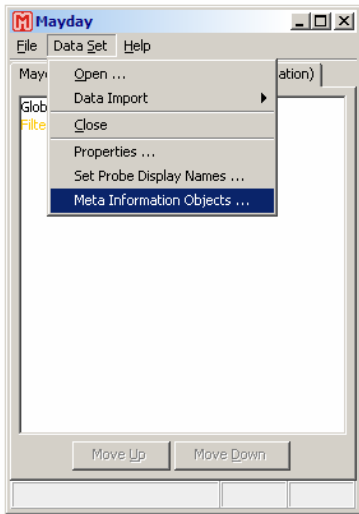
Select experiment
“Mayday Tutorial
Data Set (w/ meta
information).”



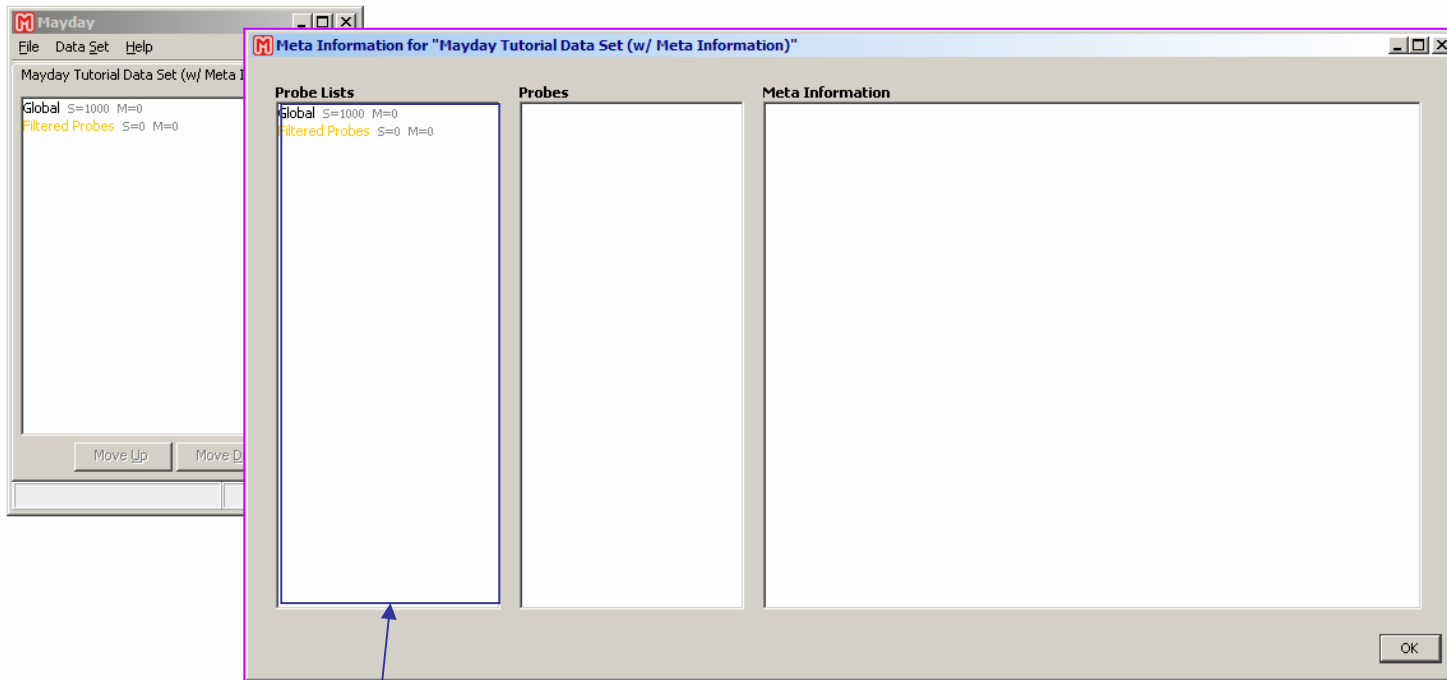
Do not choose a filter.
Click "OK" to confirm.



Open the “Data Set”
menu.



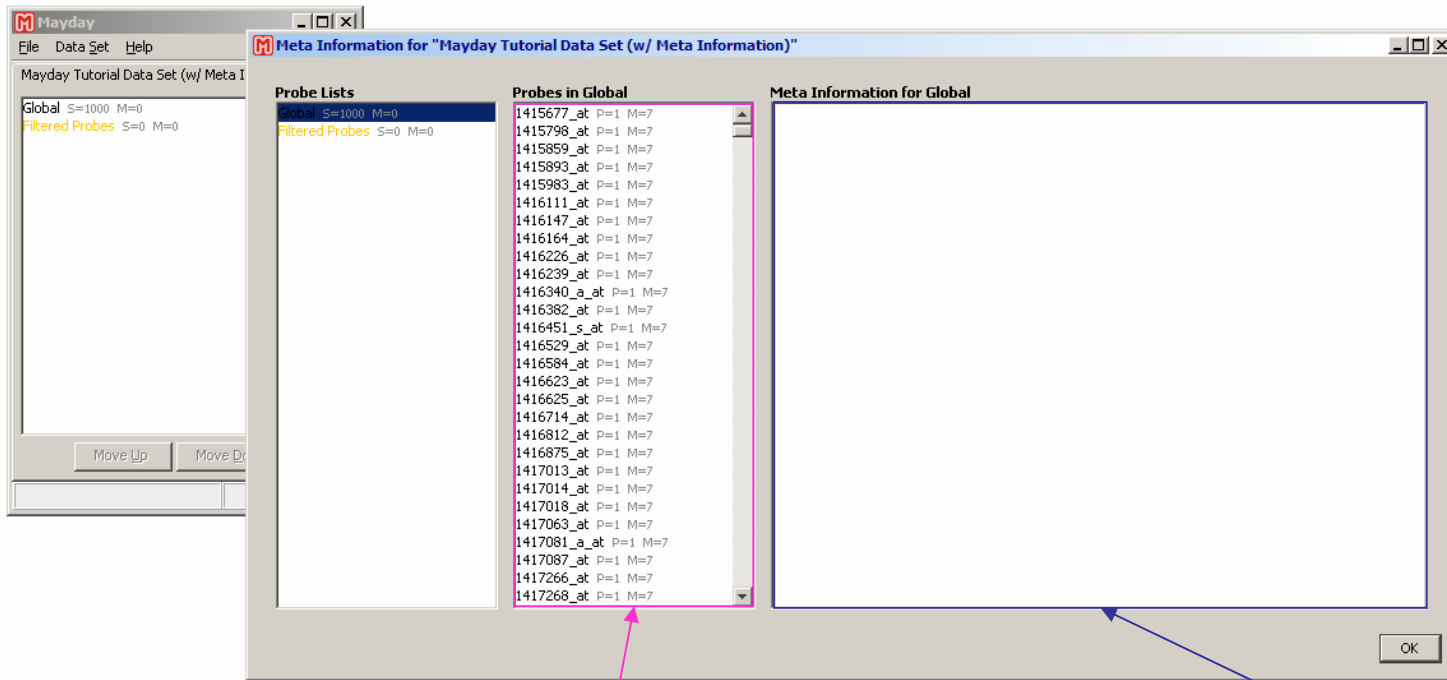
Select “Meta Information Objects ...” to open the meta information manager.



*list of probe lists in the
selected data set*

meta information manager

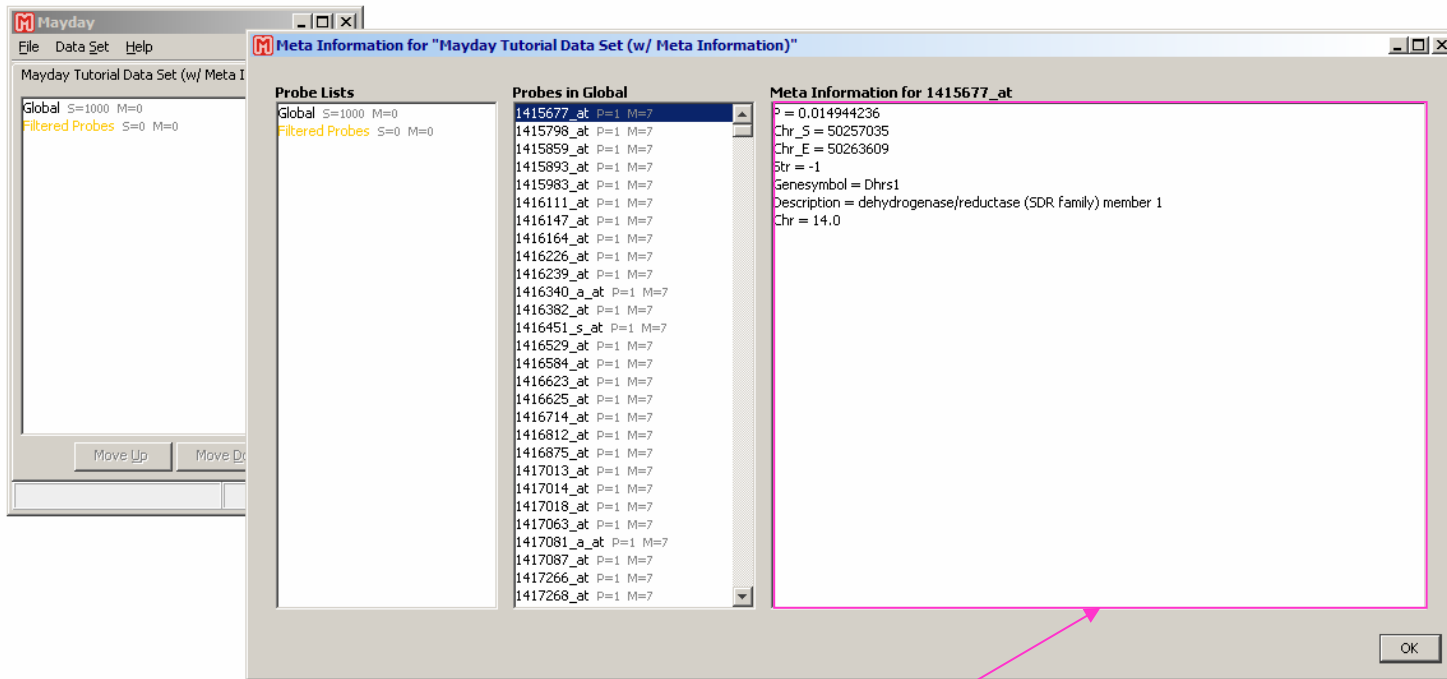
Select "Global" in the
list of probe lists.



*list of probe lists in the
selected probe list*

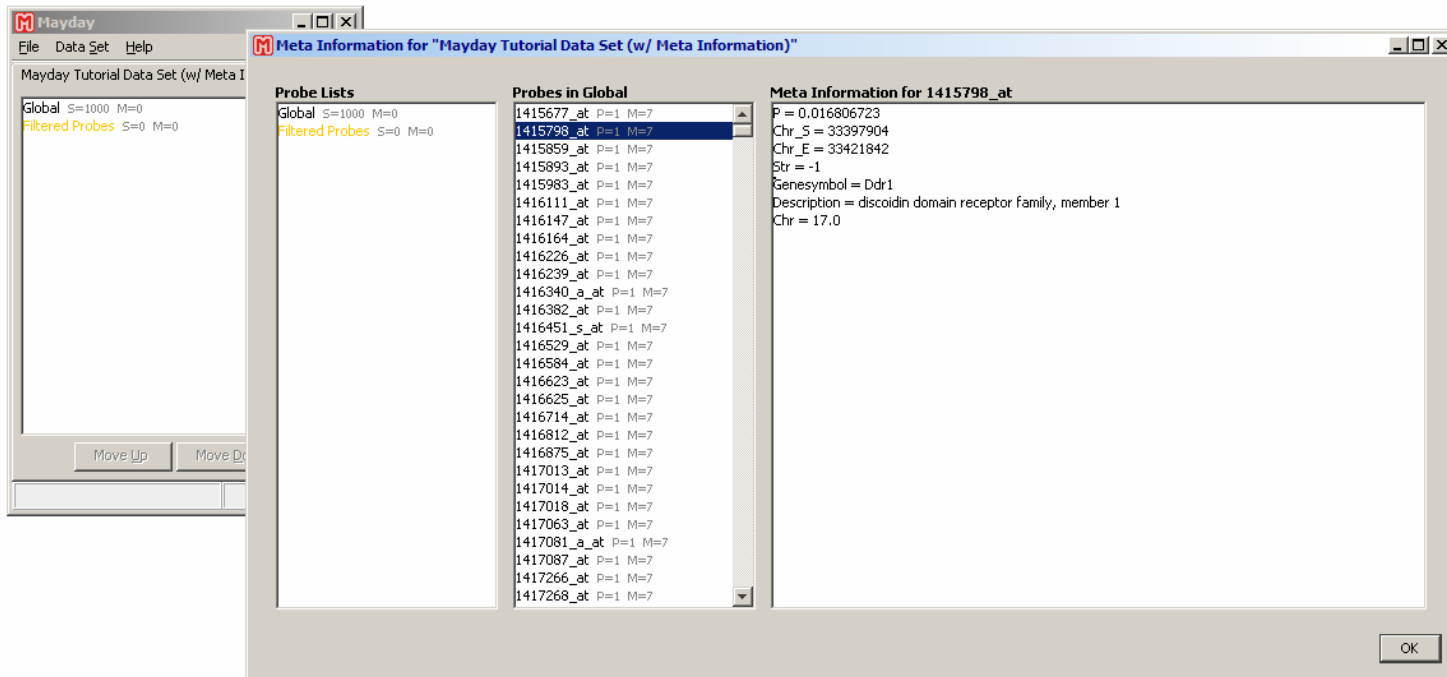
*meta information associated with
the selected probe list*

Select the topmost
probe in the list of
probes.

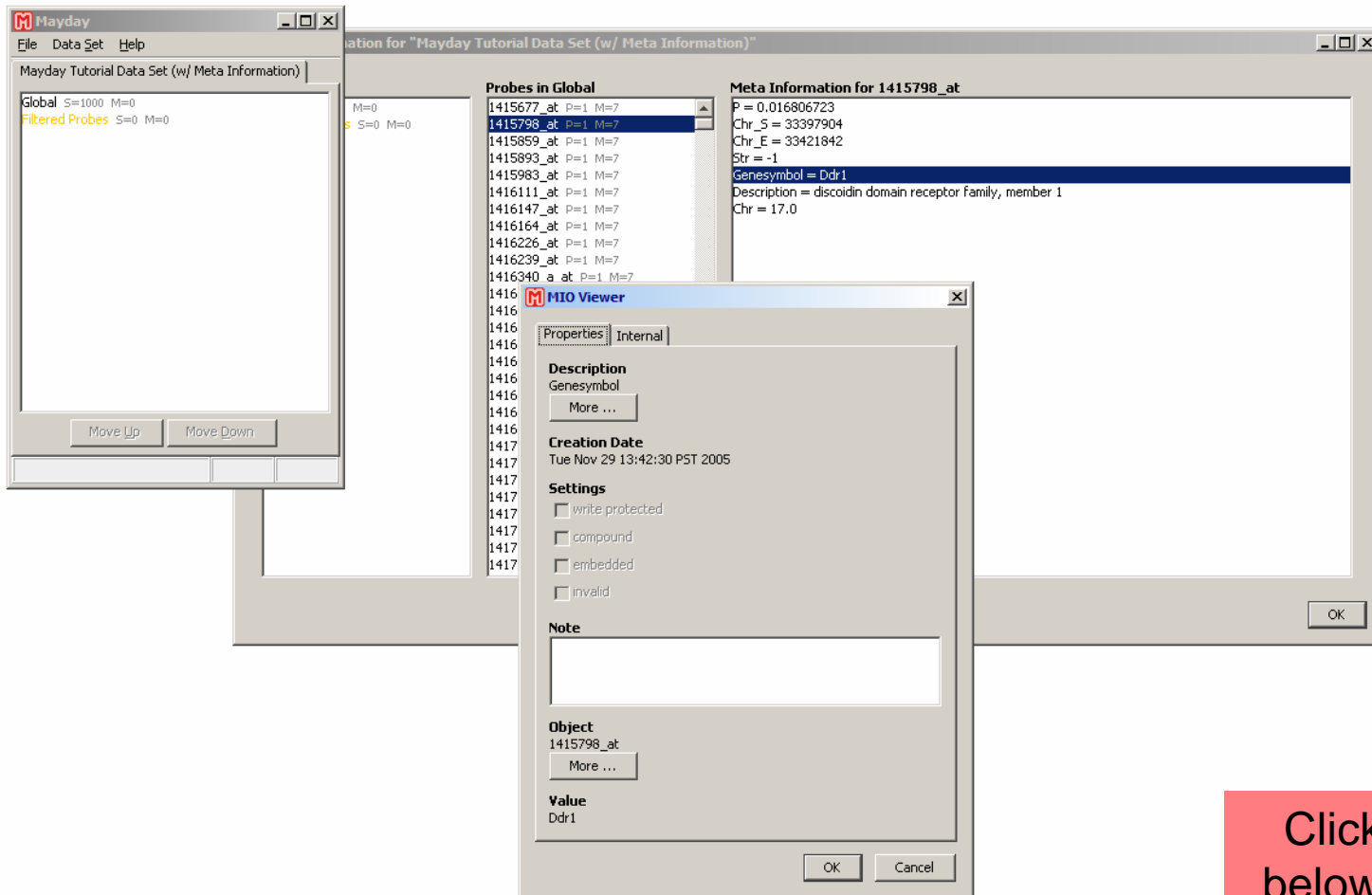


*meta information associated with
the selected probe*

Review the
information. Select
another probe.

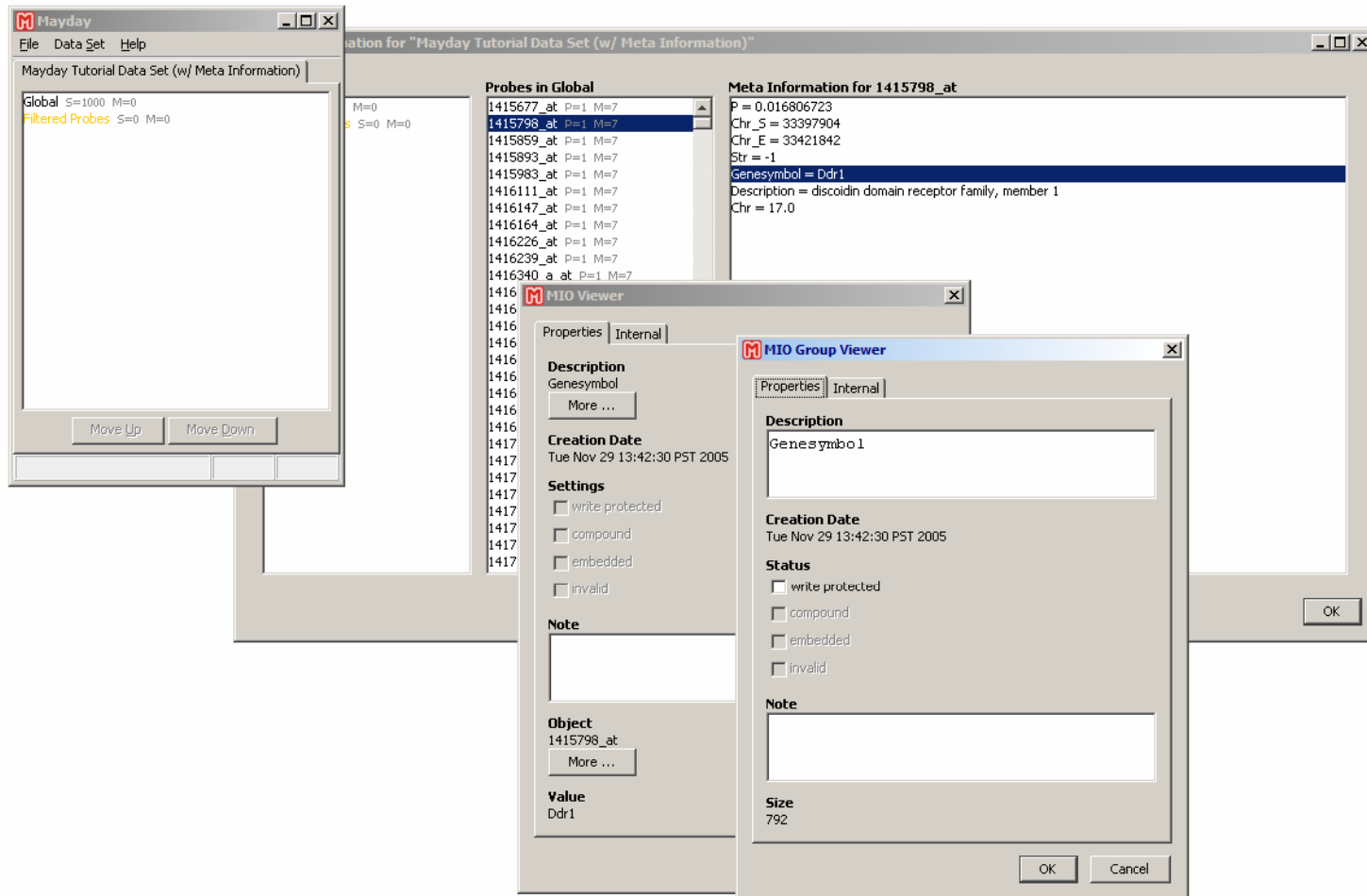


Review the information. Double-click on "Genesymbol" in the list of meta information objects.

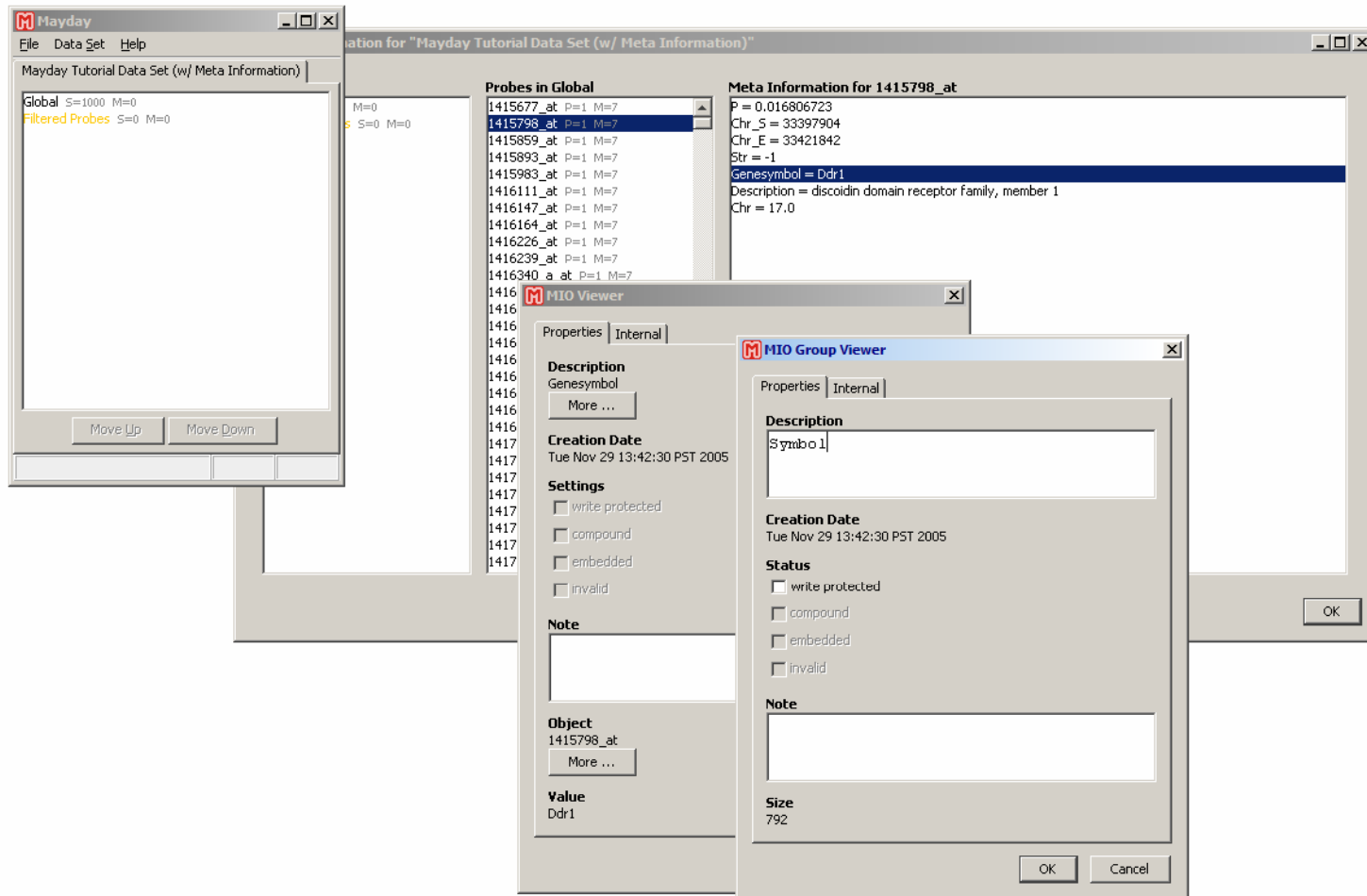


Click on "More ..."
below "Description".

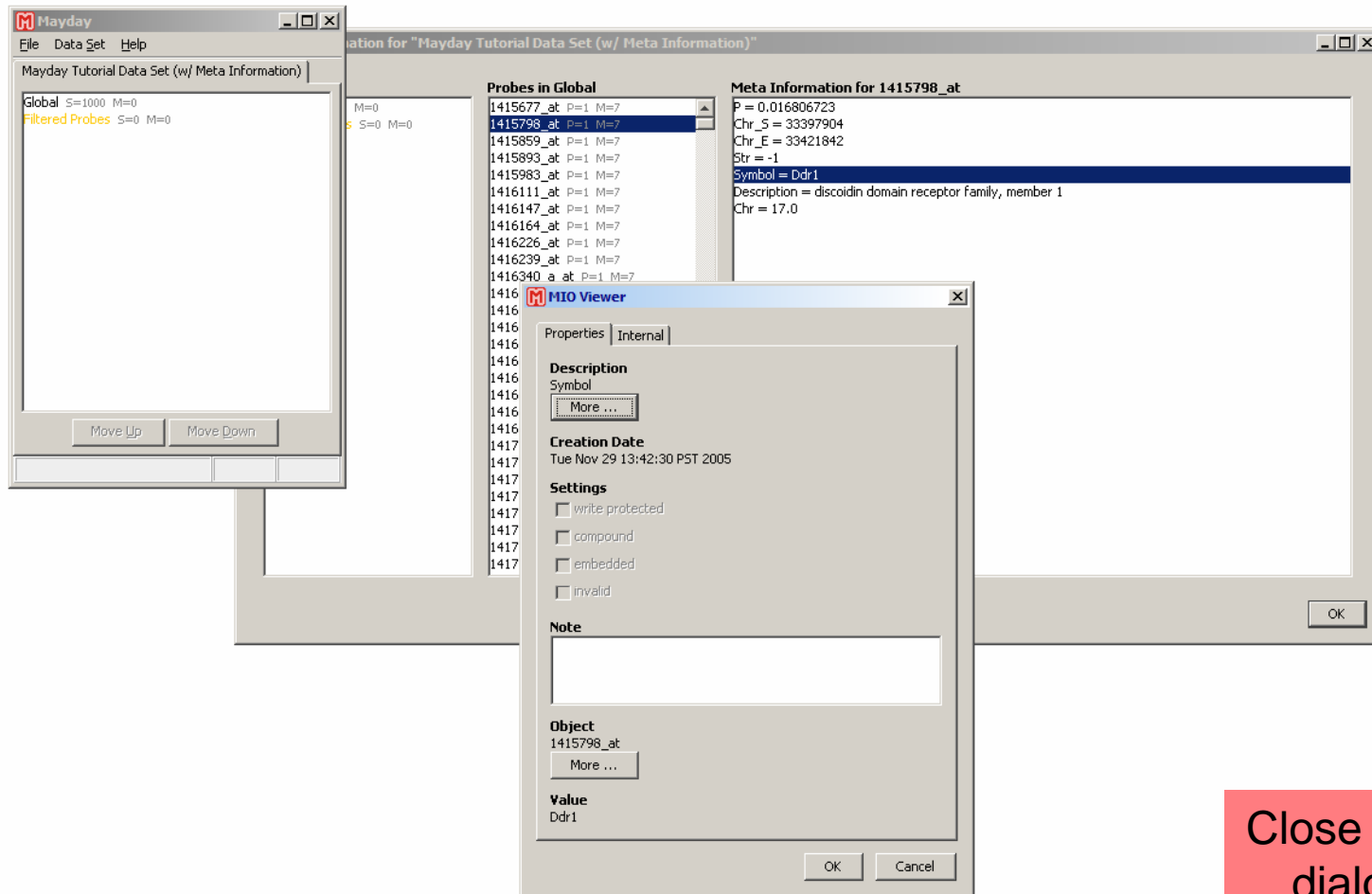
The description of the meta
information can be changed.



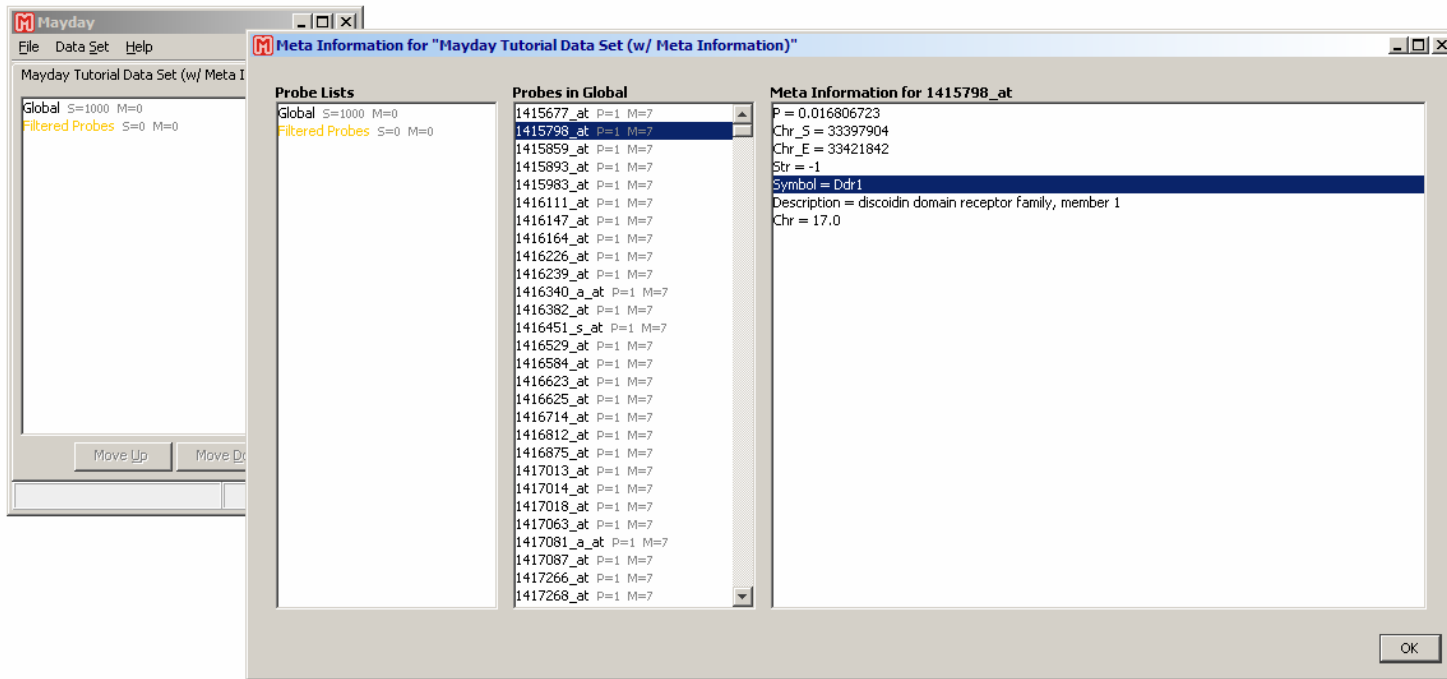
Change
"Genesymbol" to
"Symbol".



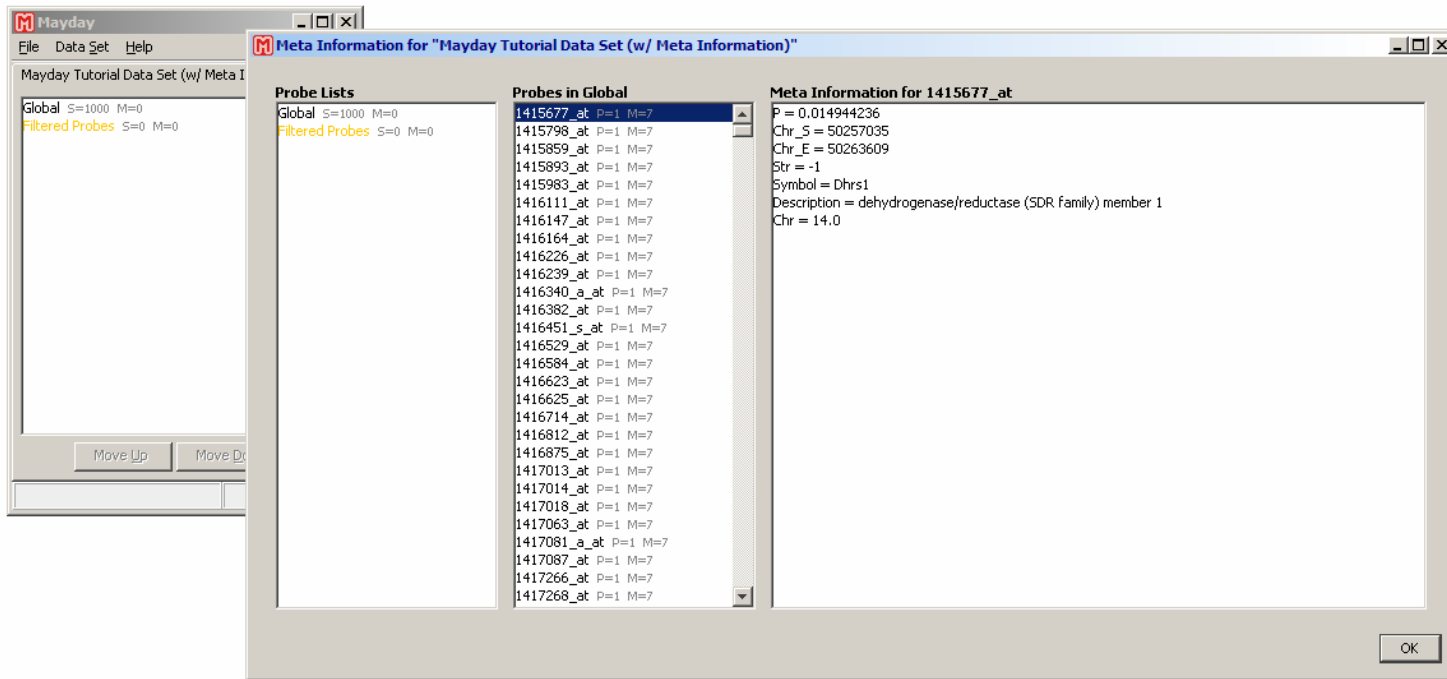
Click "OK" to confirm.



Close the MIO viewer dialog by clicking "OK" or "Cancel".

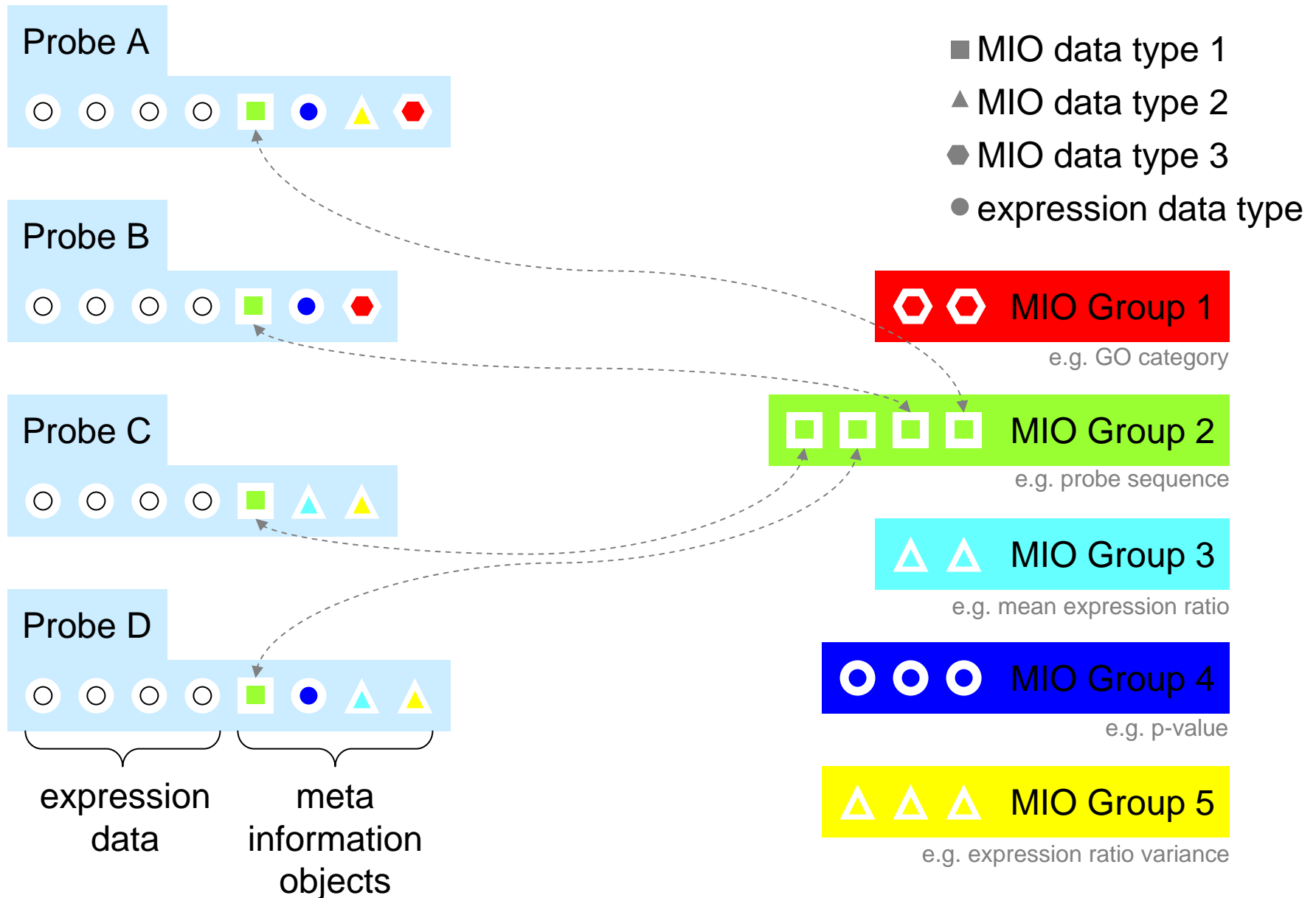


Select another probe.

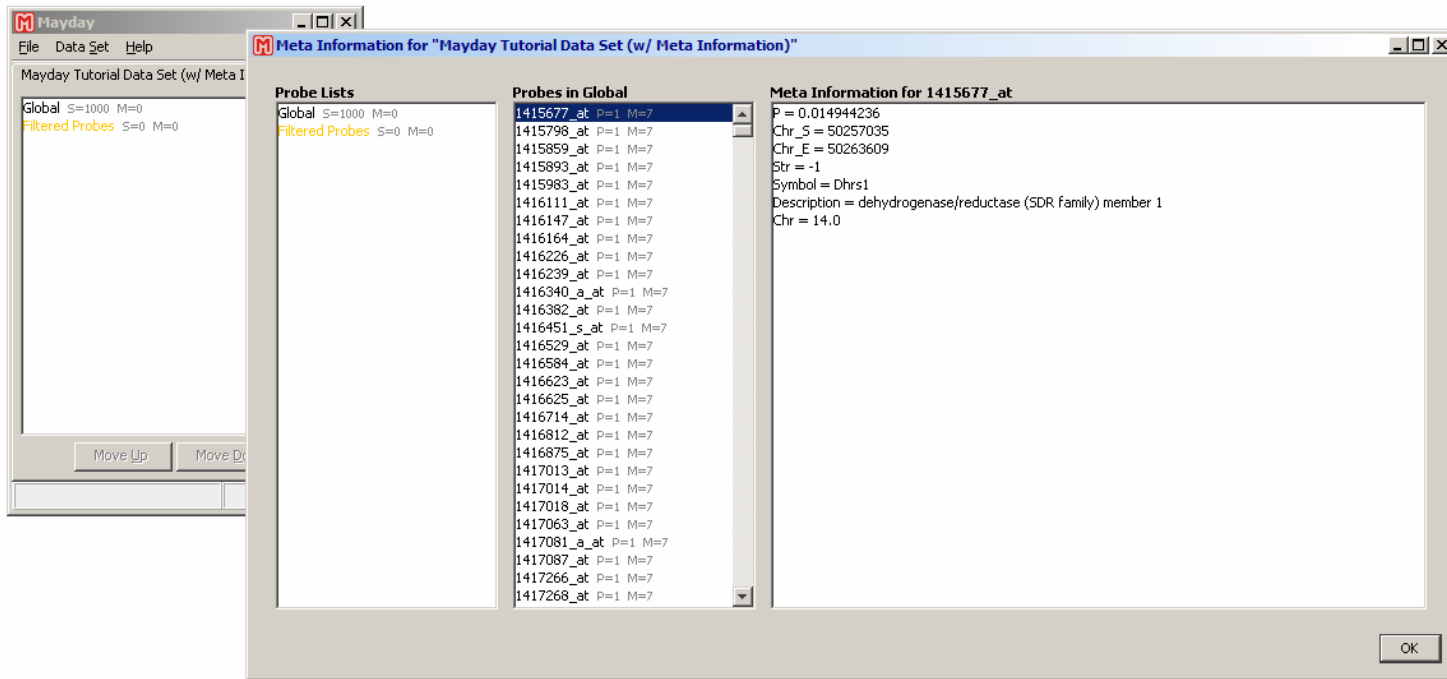


The meta information that used to be named "Genesymbol" is now named "Symbol" for all probes.

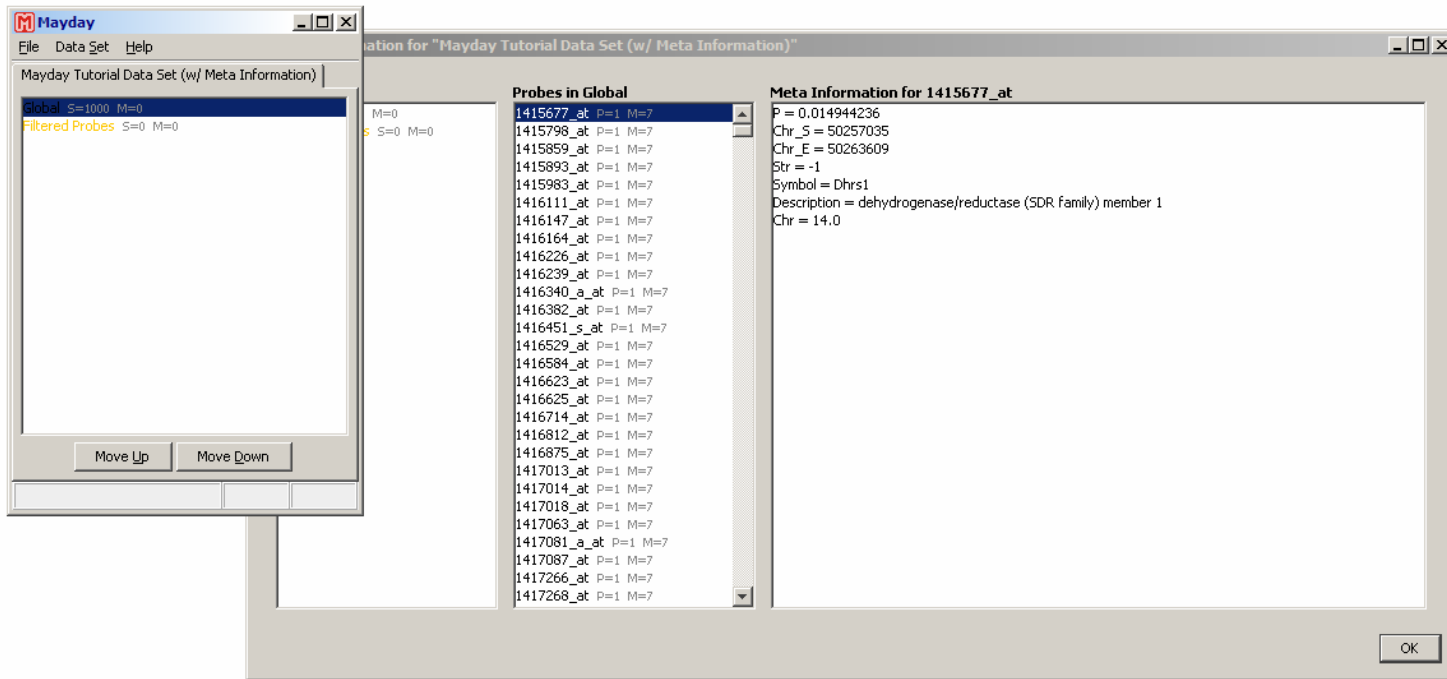
- meta information stored in so-called meta information objects (MIOs)
- multiple MIOs and MIO types per probe or probe list
- MIOs for probes or probe lists that are created by the same process (loading, algorithm, ...) are stored in a joint MIO group for future access
 - else one would have to select MIOs for 1000s of probes individually
- MIO groups contain only one MIO per probe or probe list
- probes or probe lists contain only one MIO per MIO group



- all MIO groups managed by a meta information manager
- one meta information manager per data set

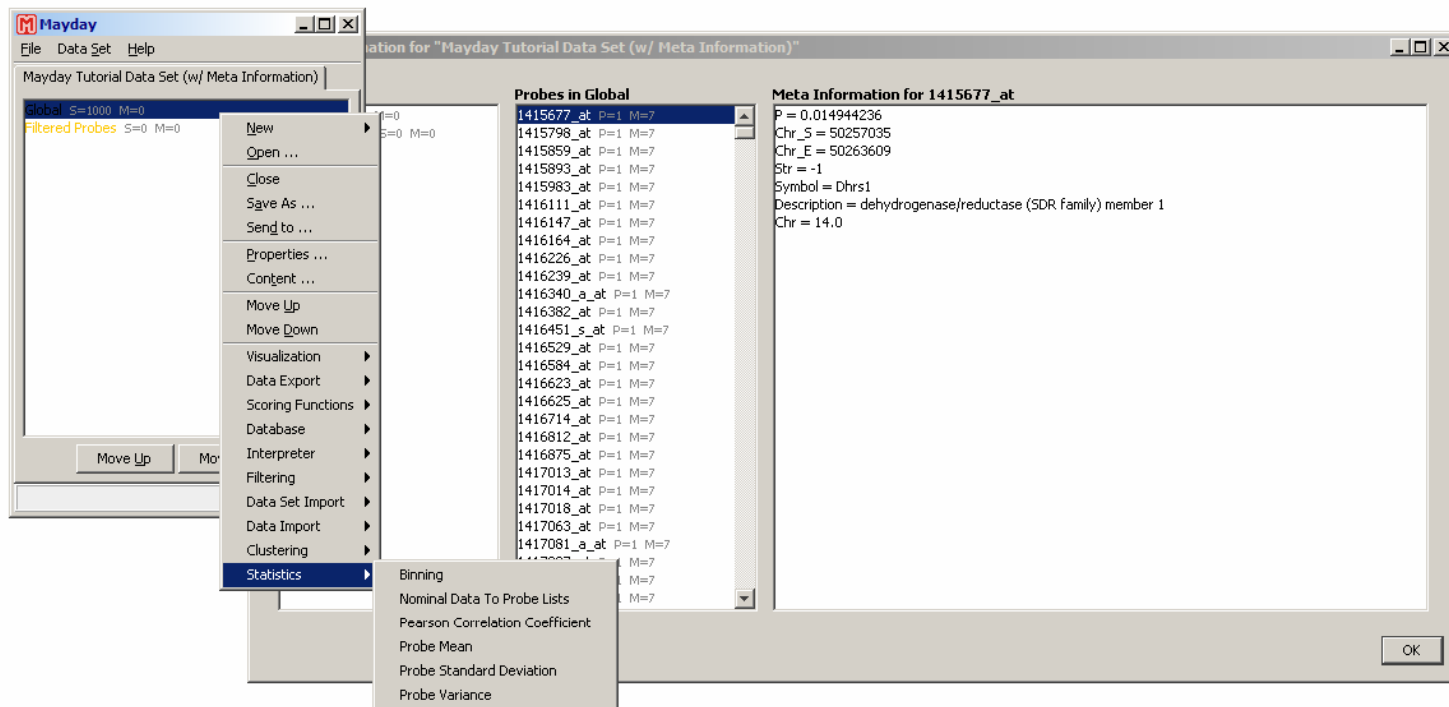


Bring the main window to the front.
Leave the meta information manager open.

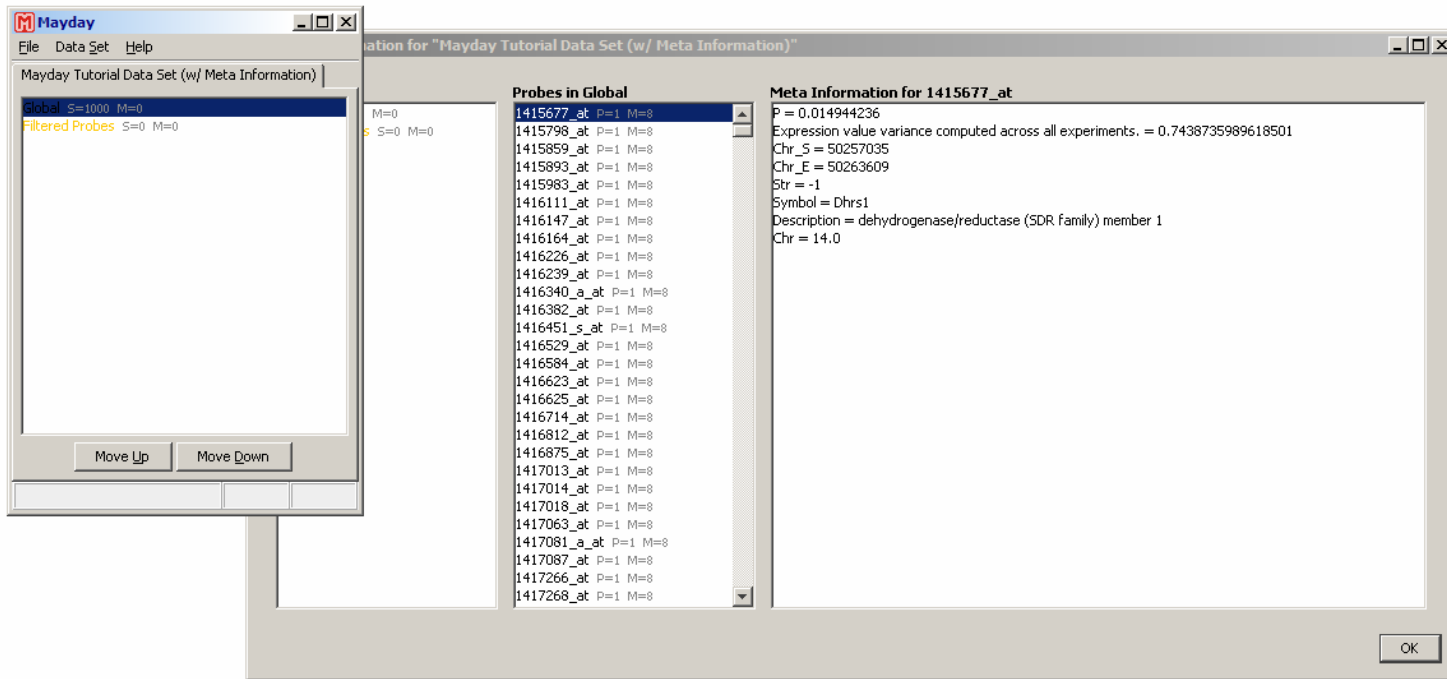


The meta information manager will automatically update to changes you make to meta information groups or objects. More about that on the following slides.

Select the global probe list and open the probe list manager's context menu. Go to submenu "Statistics".

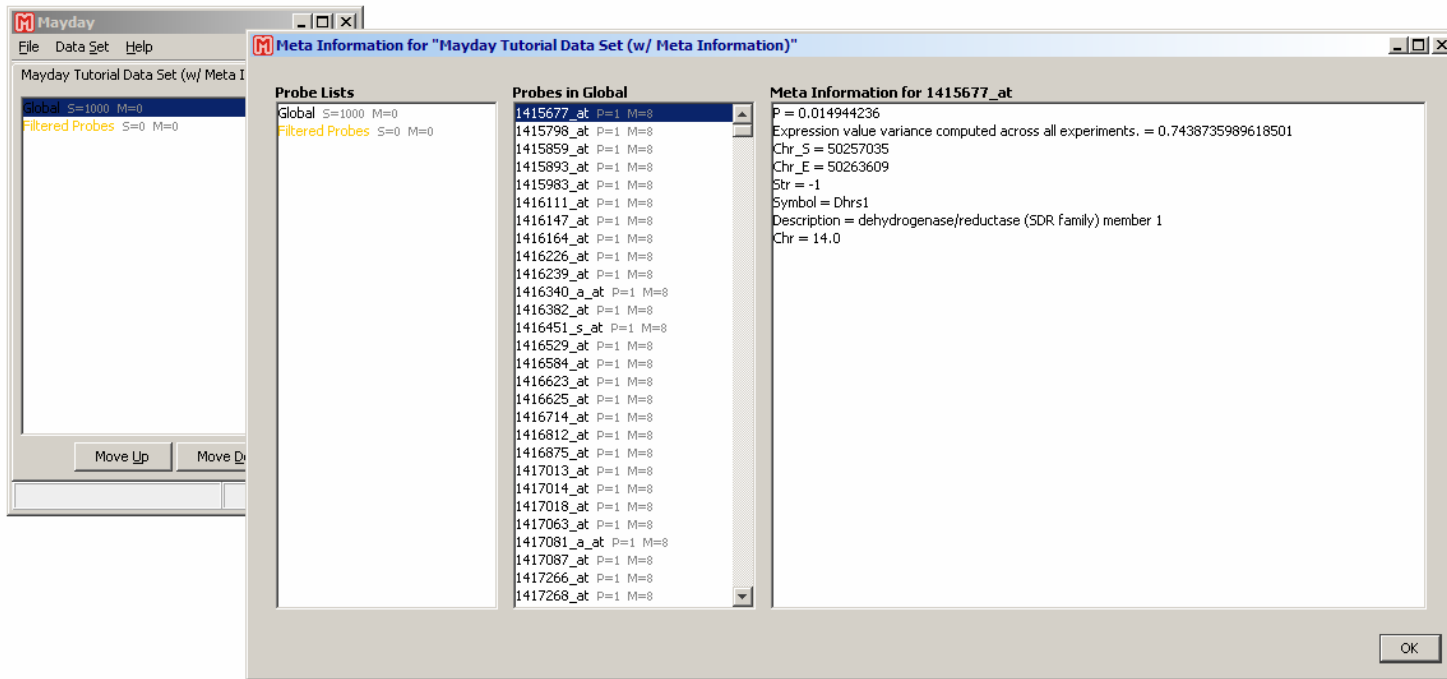


Select "Probe Variance".



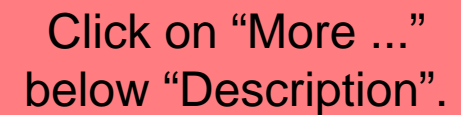
A new meta information object has been added in the list on the right.

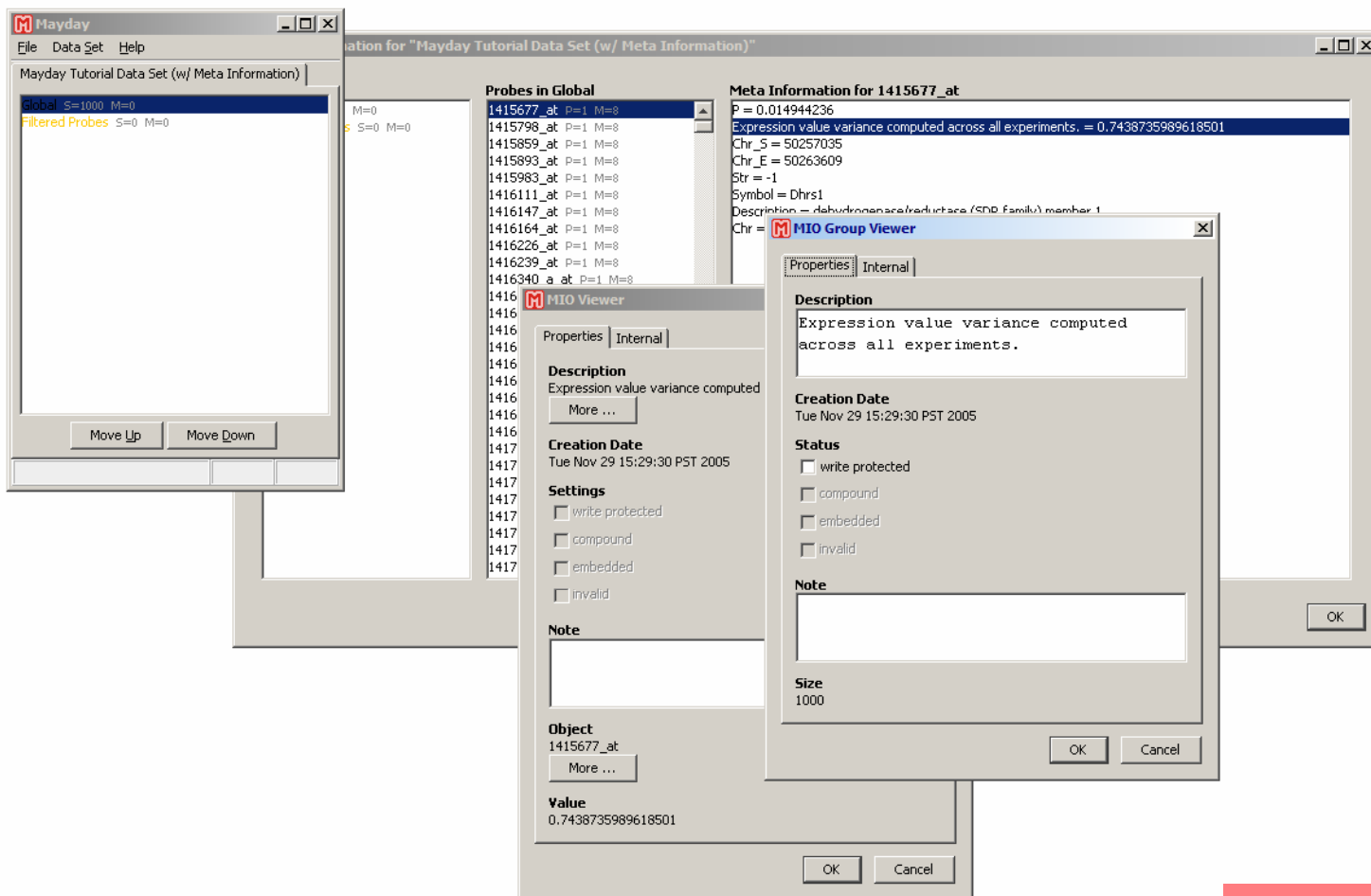
Bring the meta information manager to the front.



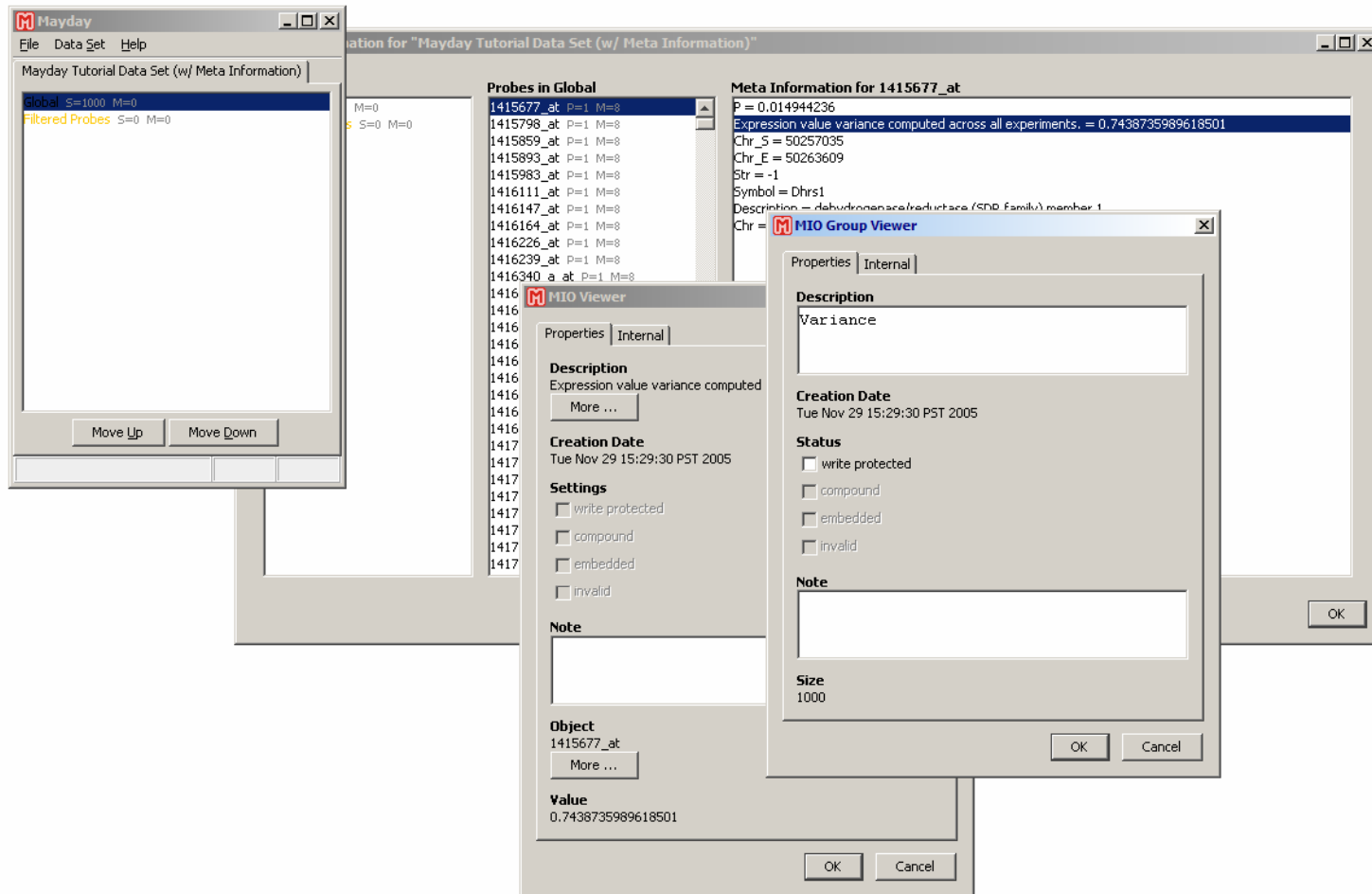
Double-click the entry
“Expression value
variance [...]” in the list
of MIOs on the right.

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Change the description of the MIO group to "Variance".

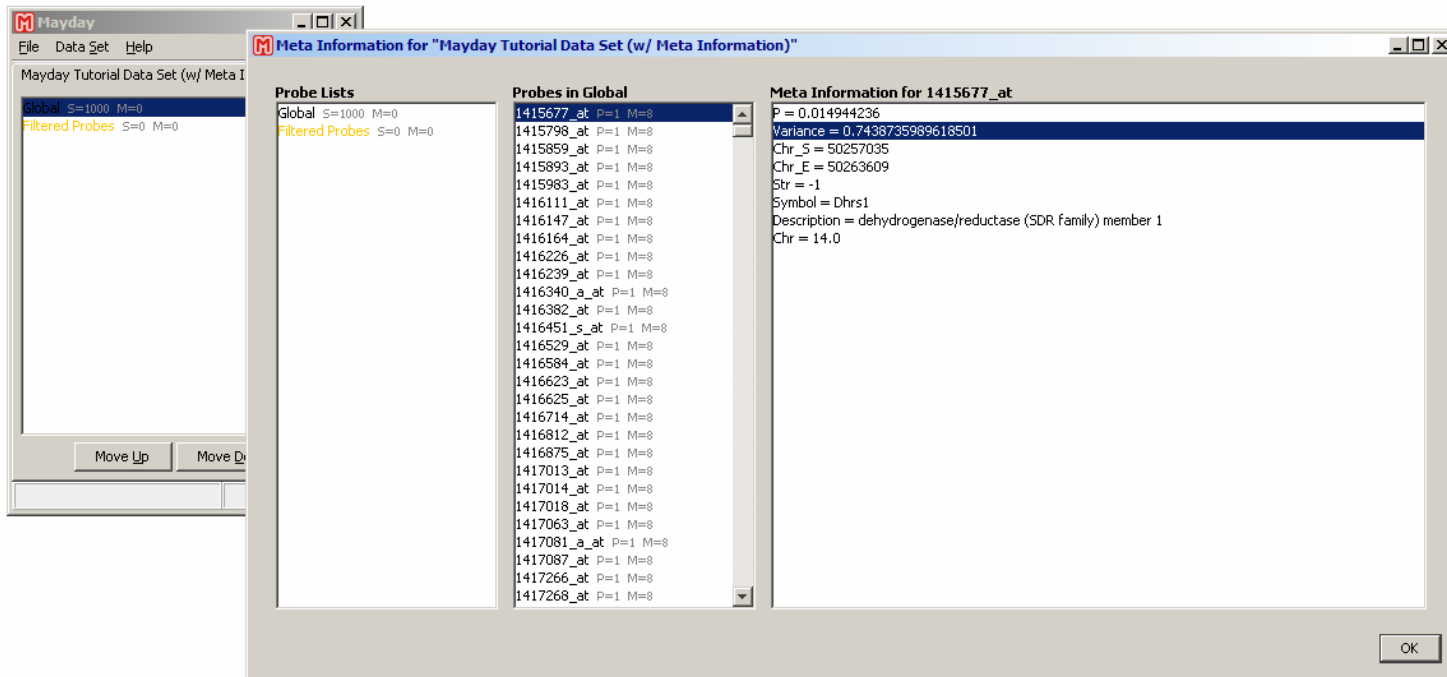


.....
..... Descriptions should be clear and concise.
.....

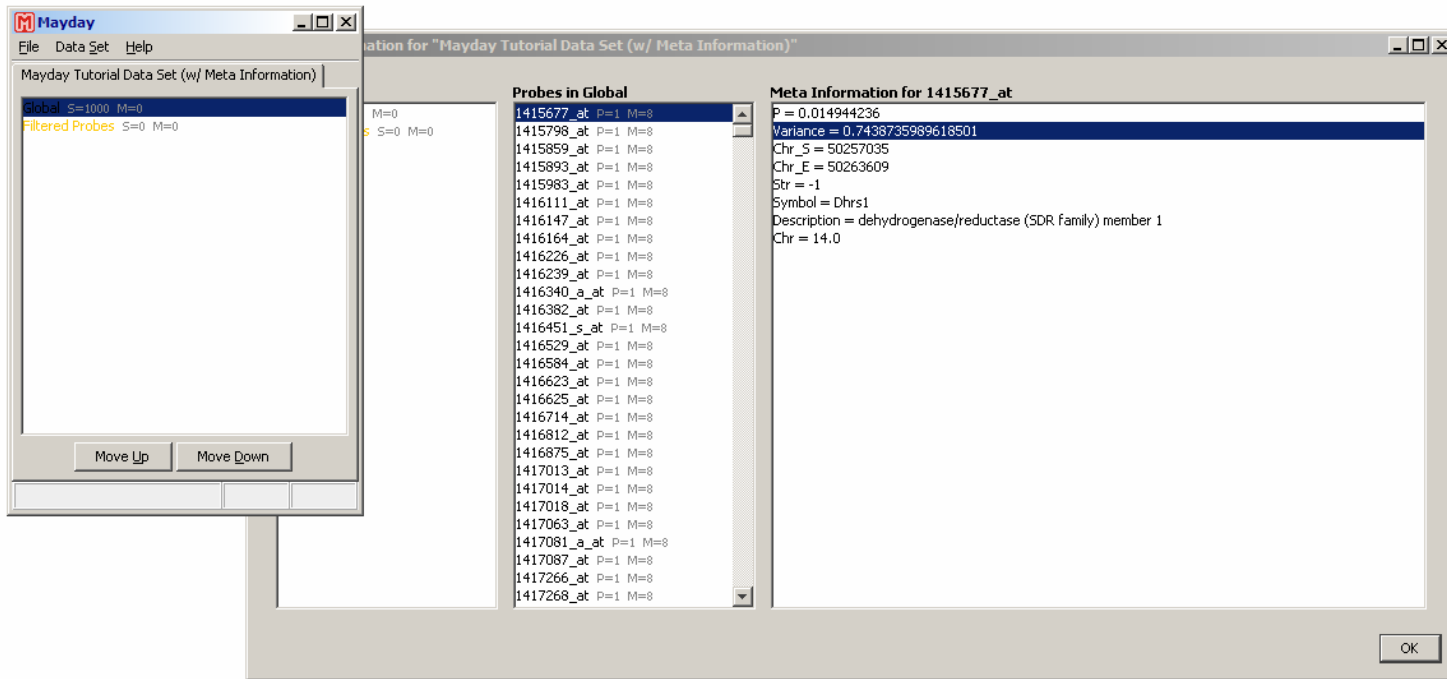
Click "OK" to confirm.

Creating meta information

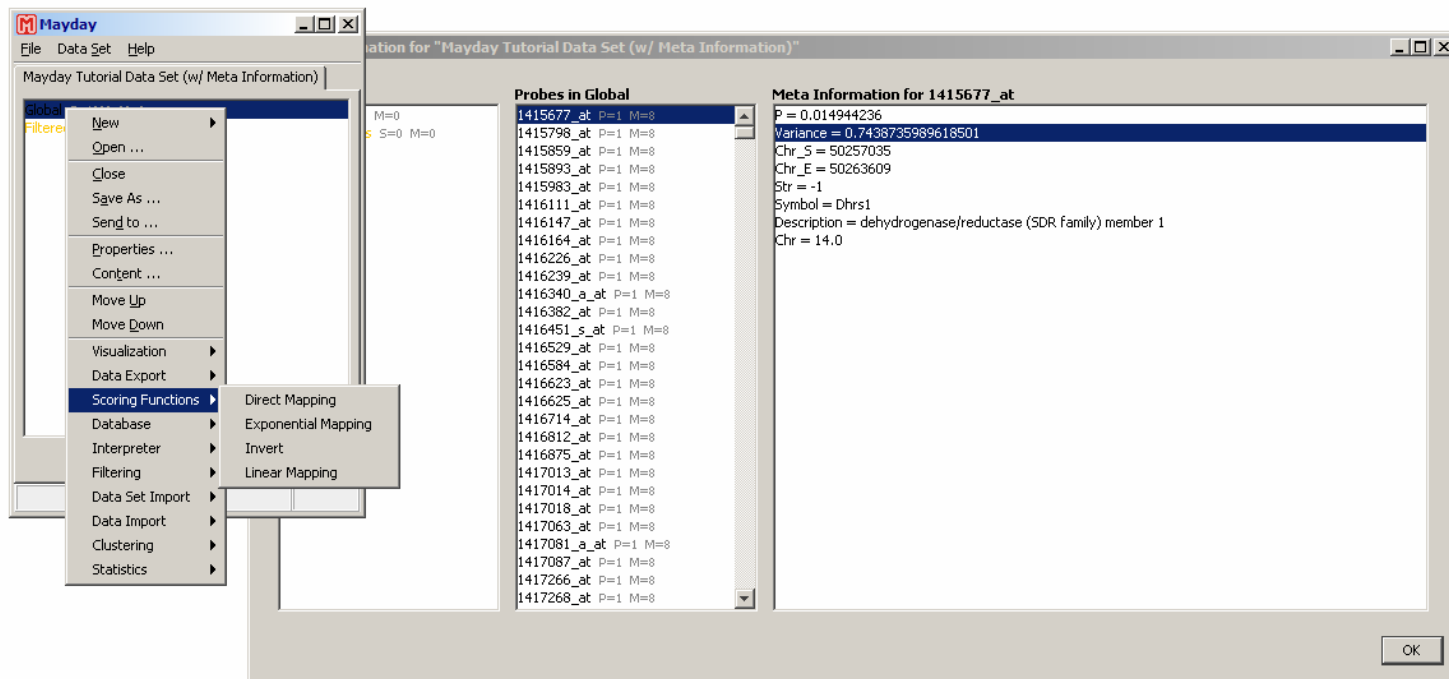
241



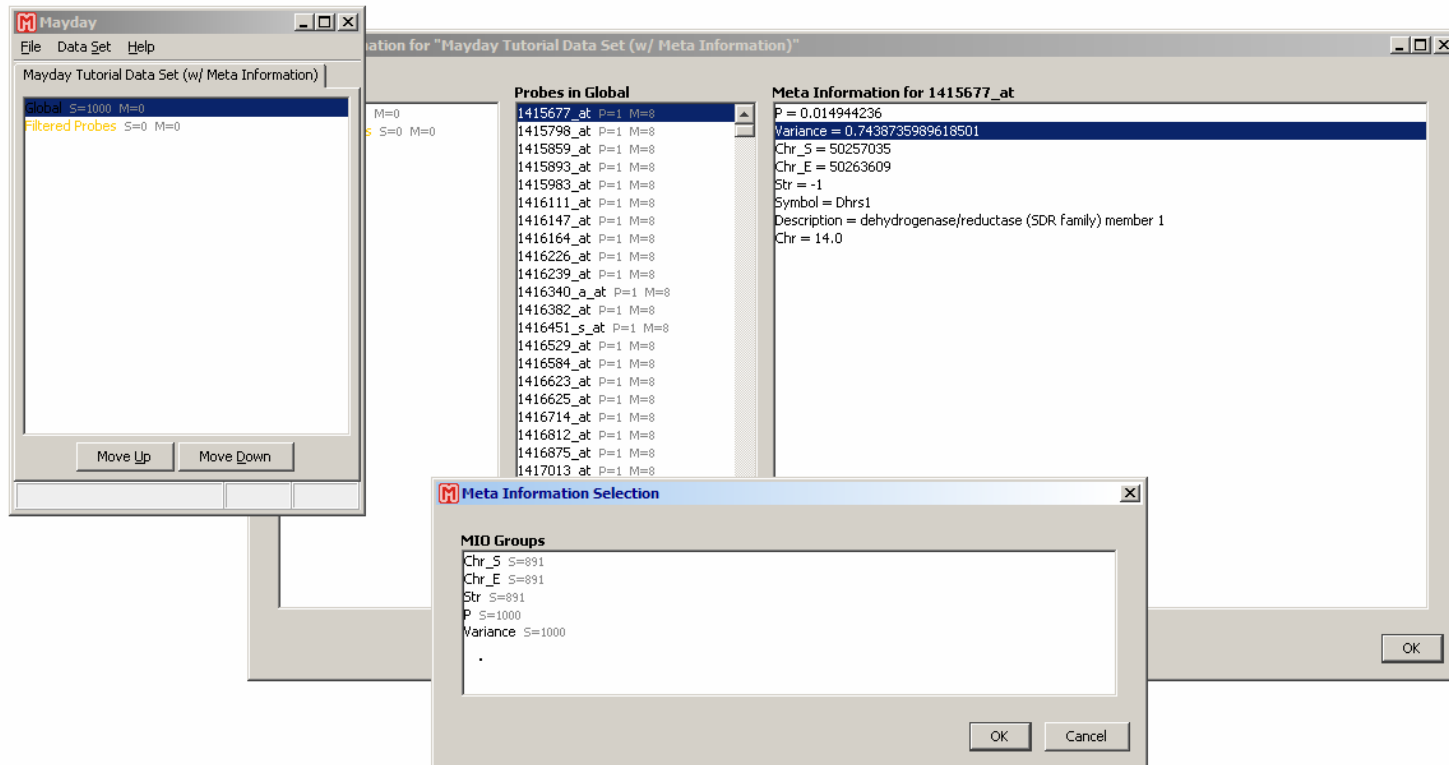
Select the global probe list in the probe list manager.



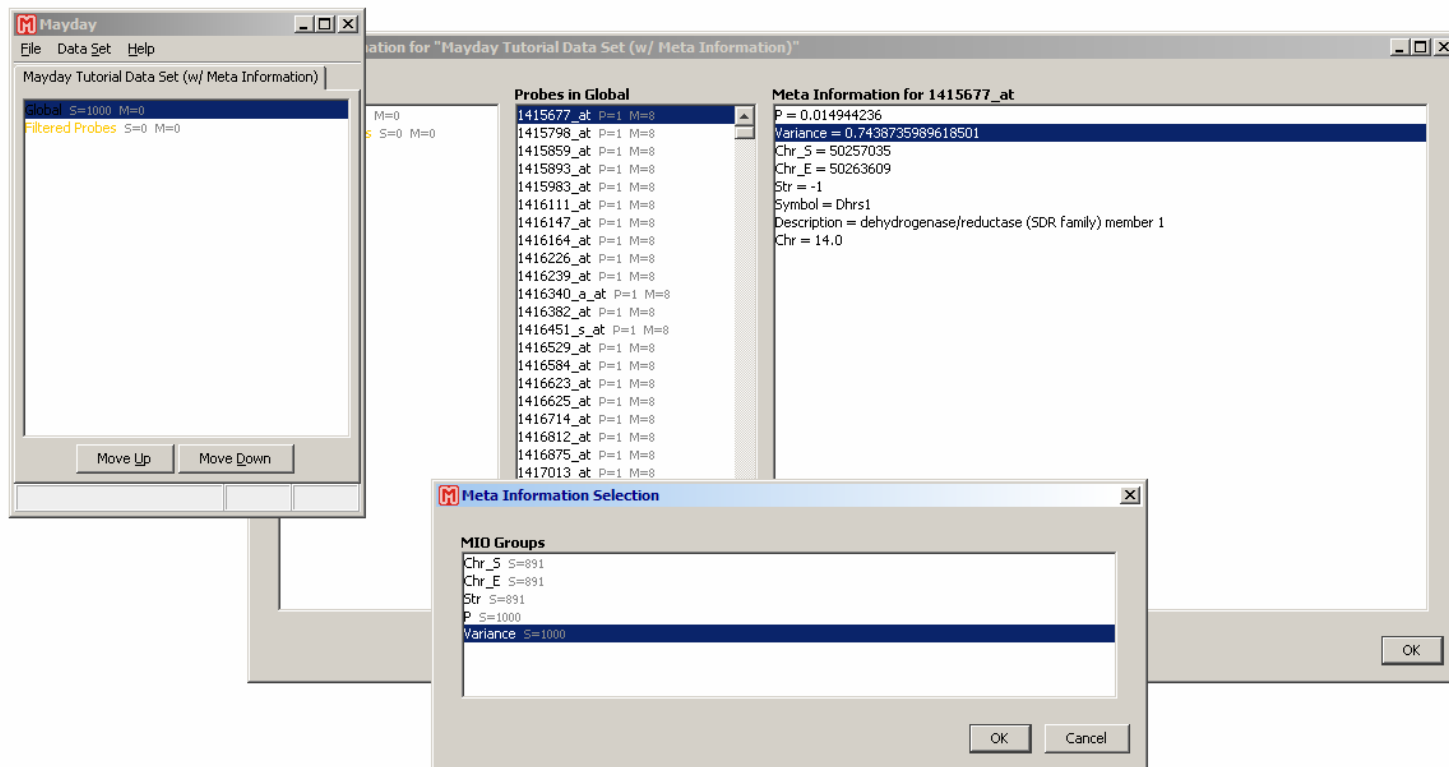
Open the probe list manager's context menu and go to submenu "Scoring functions".



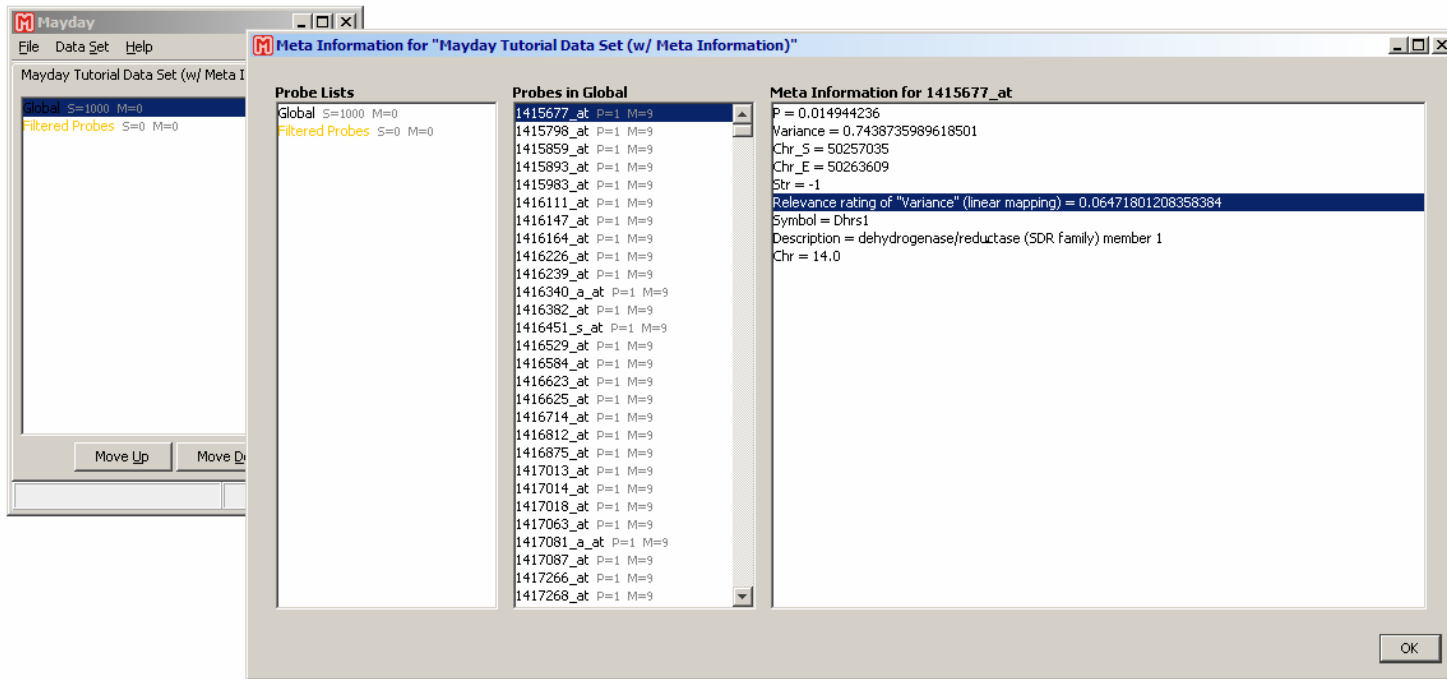
Select "Linear Mapping".



Select "Variance"
from the list of MIO
groups.



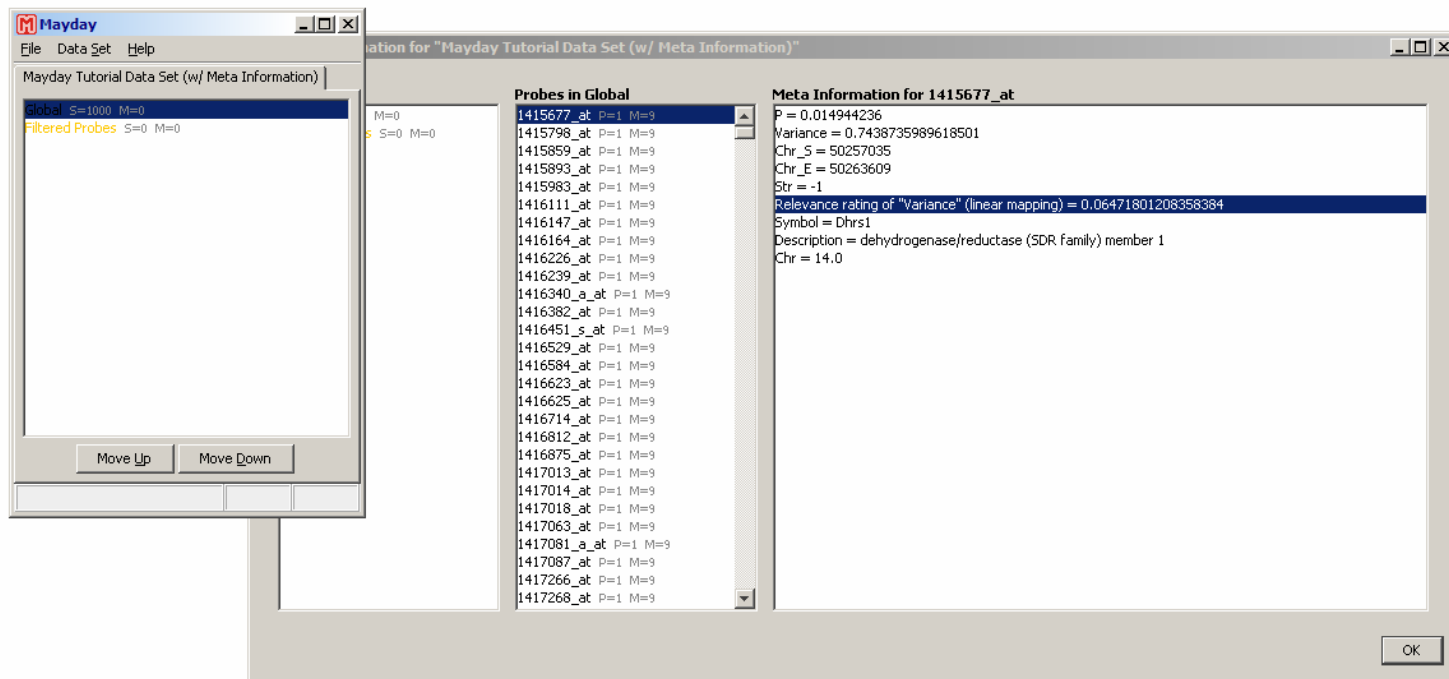
Click "OK" to run.



You have now created a score (between 0 = irrelevant and 1 = most relevant) for the variance.

More about this in the paper on the enhanced heatmap (see Resources section at the beginning of this document) and in the Meta Information How-To on the Mayday website.

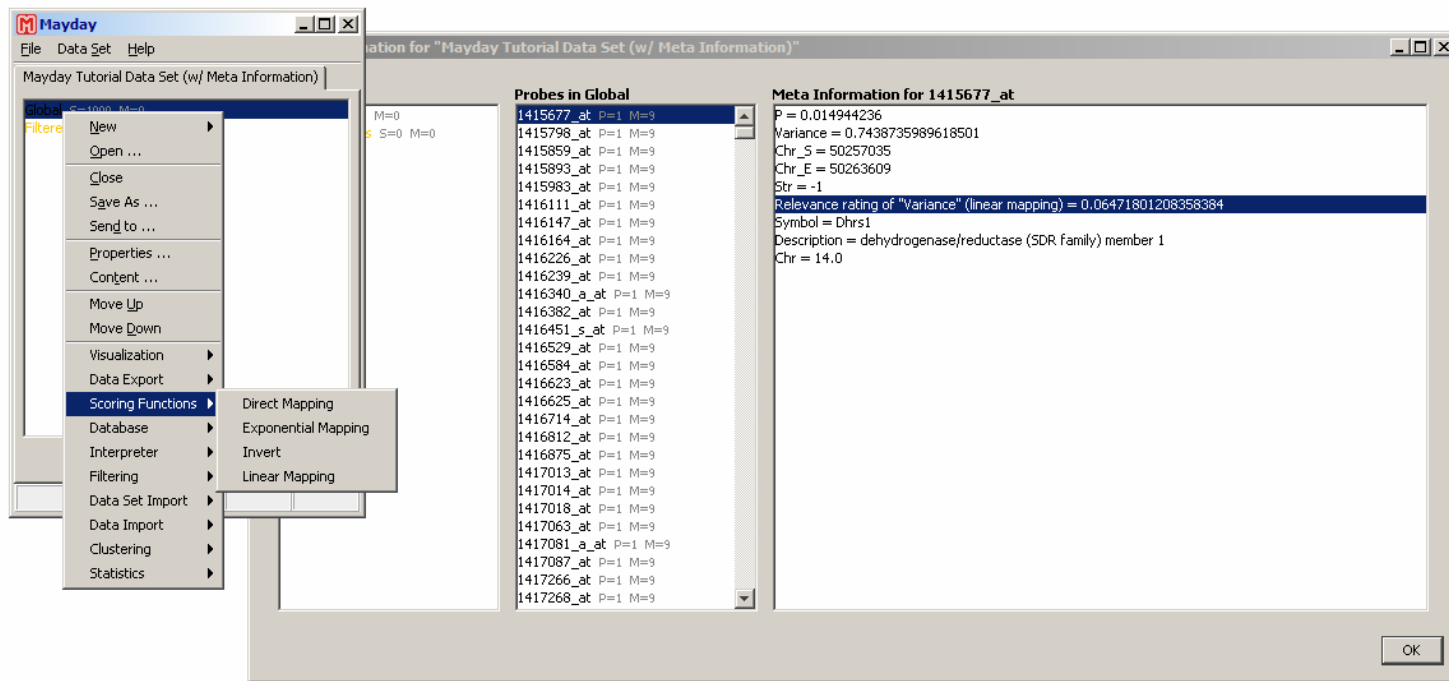
Bring the main window to the front.



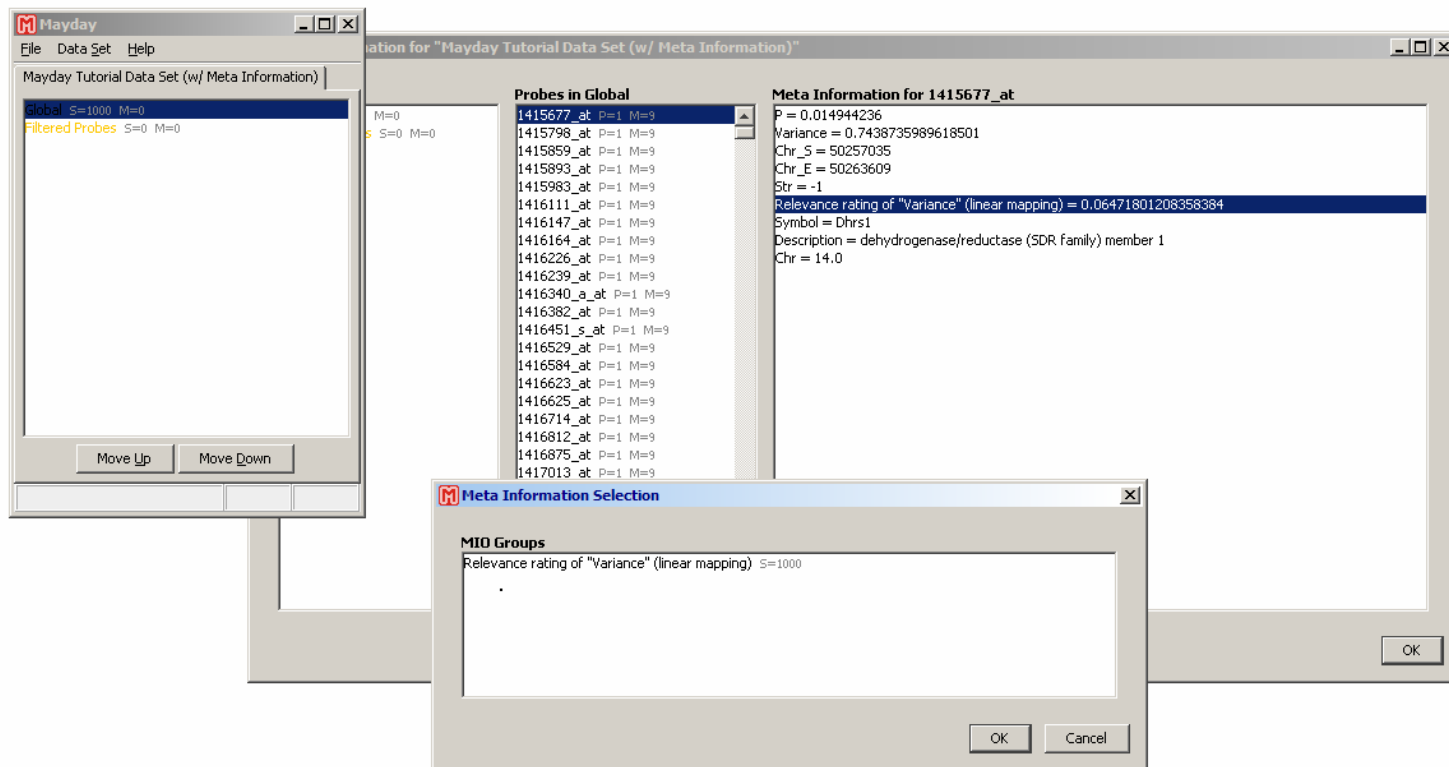
Open the probe list manager's context menu and go to submenu "Scoring functions".

Inverting relevance scores

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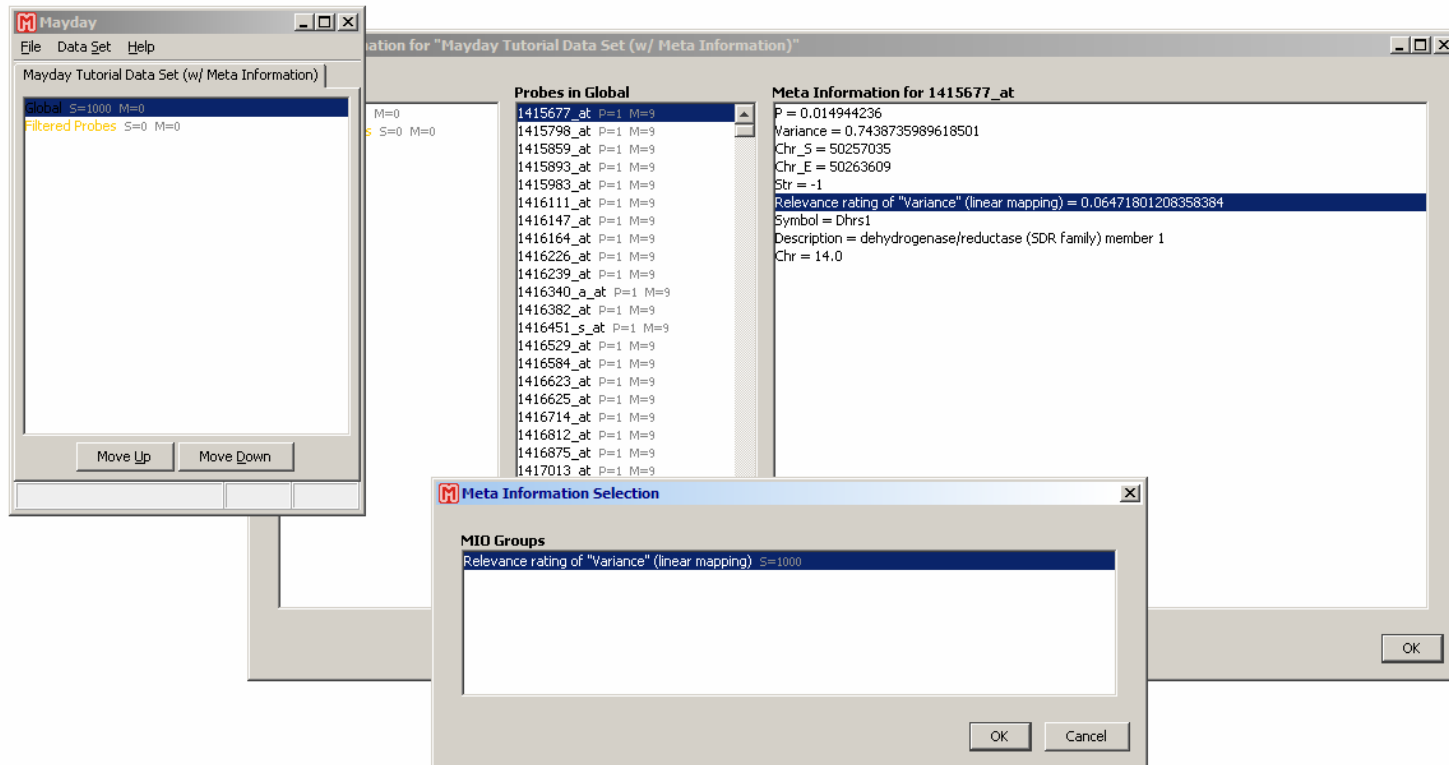
Select "Invert".



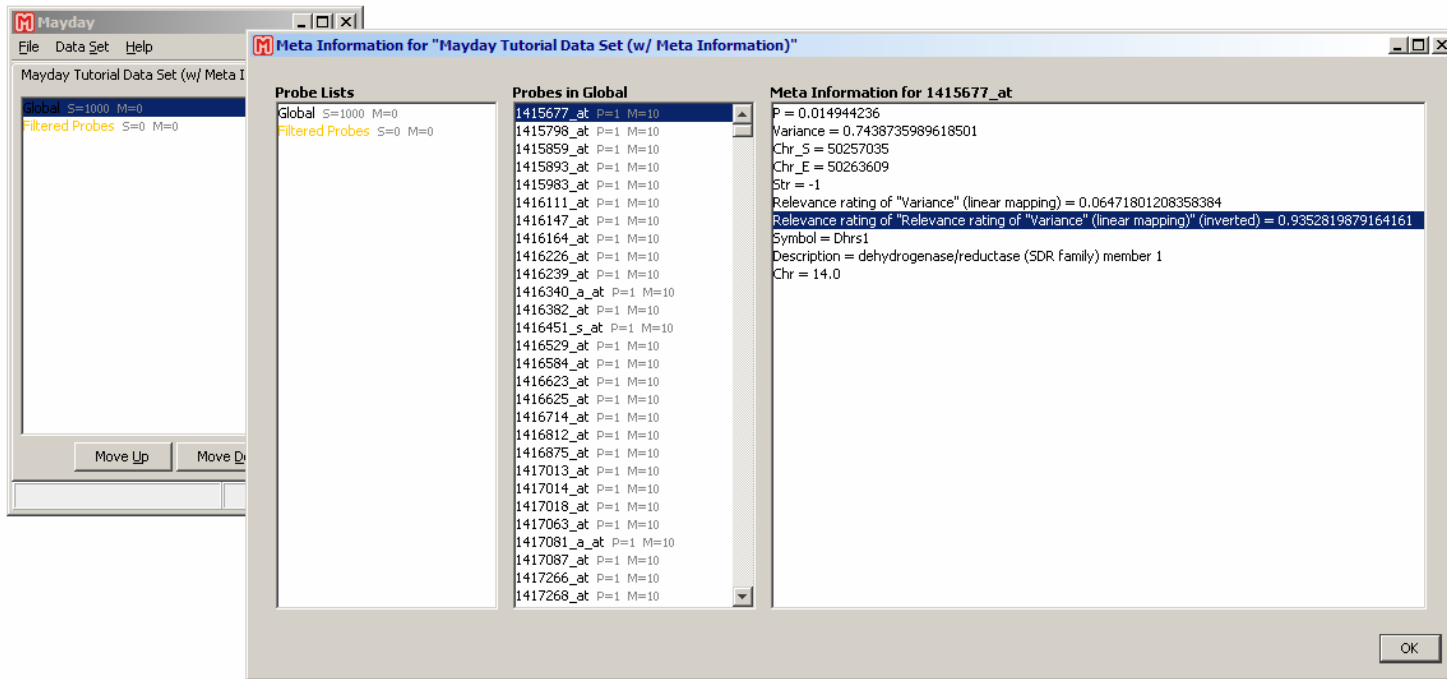
Select "Relevance rating of 'Variance' (linear mapping)".

Inverting relevance scores

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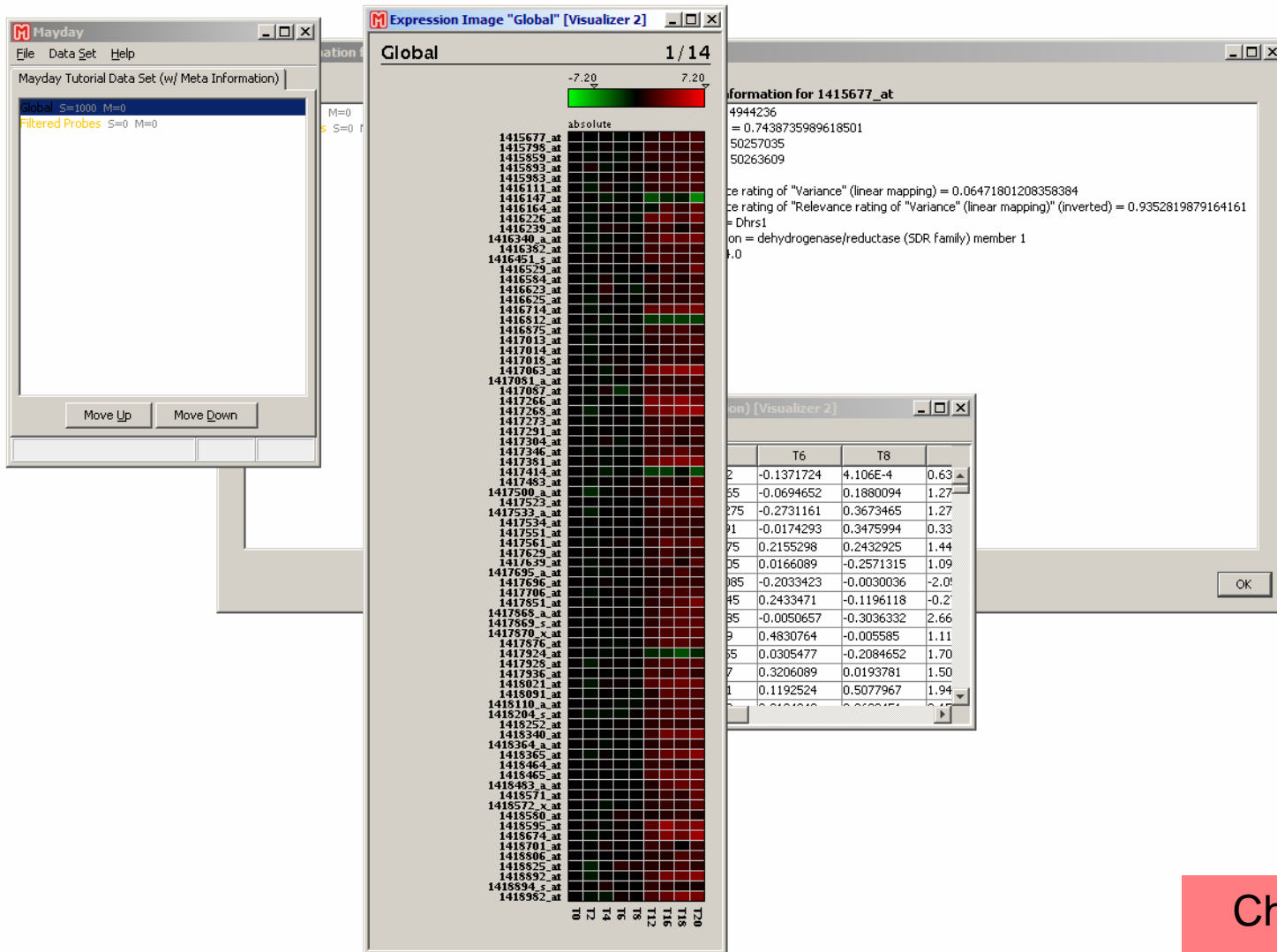


Click "OK" to perform the conversion.

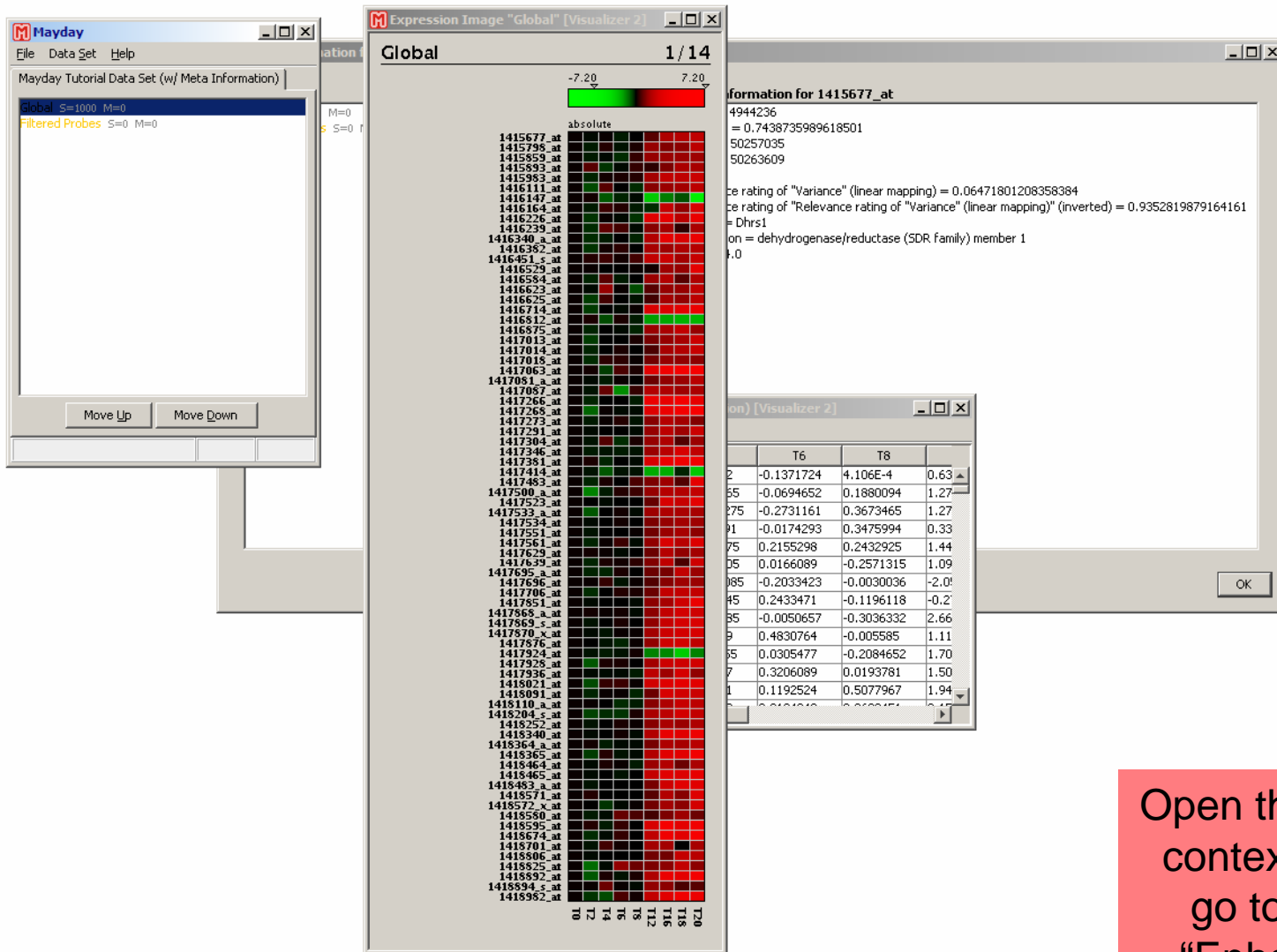


You have inverted the score and created a new MIO for all probes that were associated with the original score. This is useful for instance if you want to use a p-value as a relevance score. Interesting p-values are close to 0, while scores are defined to be interesting when they are close to 1.

Open a new enhanced heatmap view for the global probe list using the probe list manager's context menu.



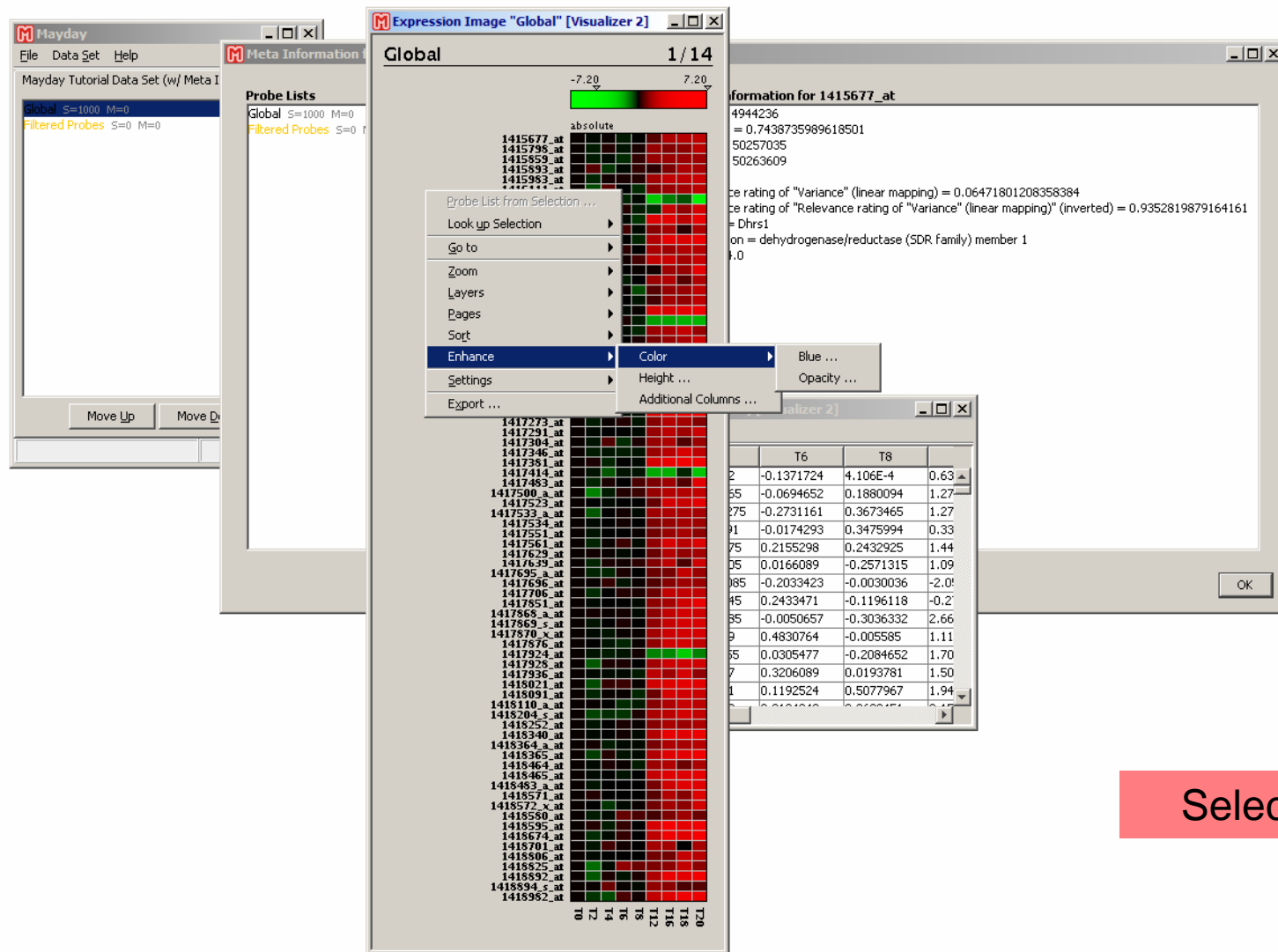
Change the color gradient to sigmoid with steepness 20.



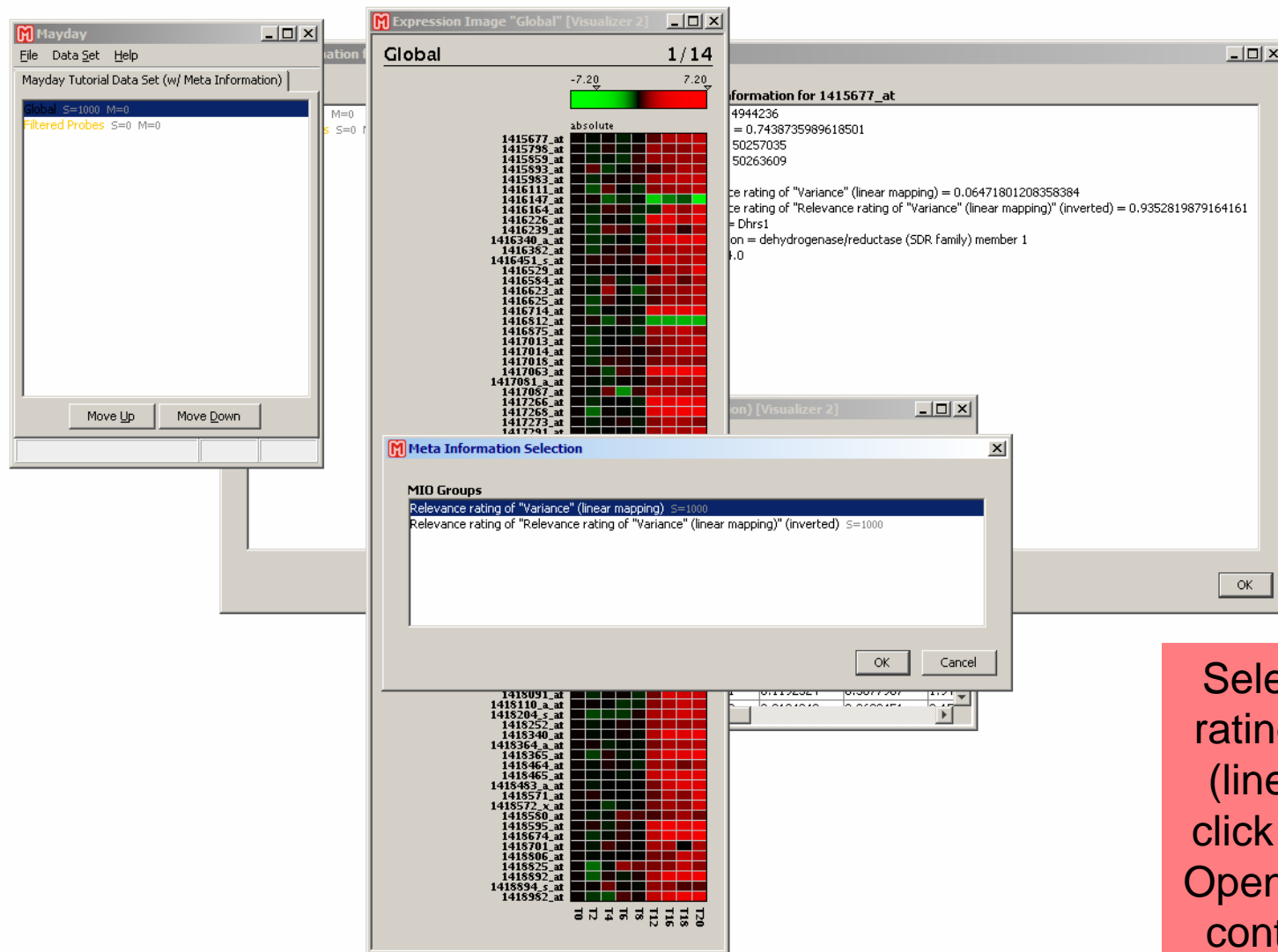
Open the heatmap's context menu and go to submenu "Enhance", then "Color".

Visualizing relevance scores

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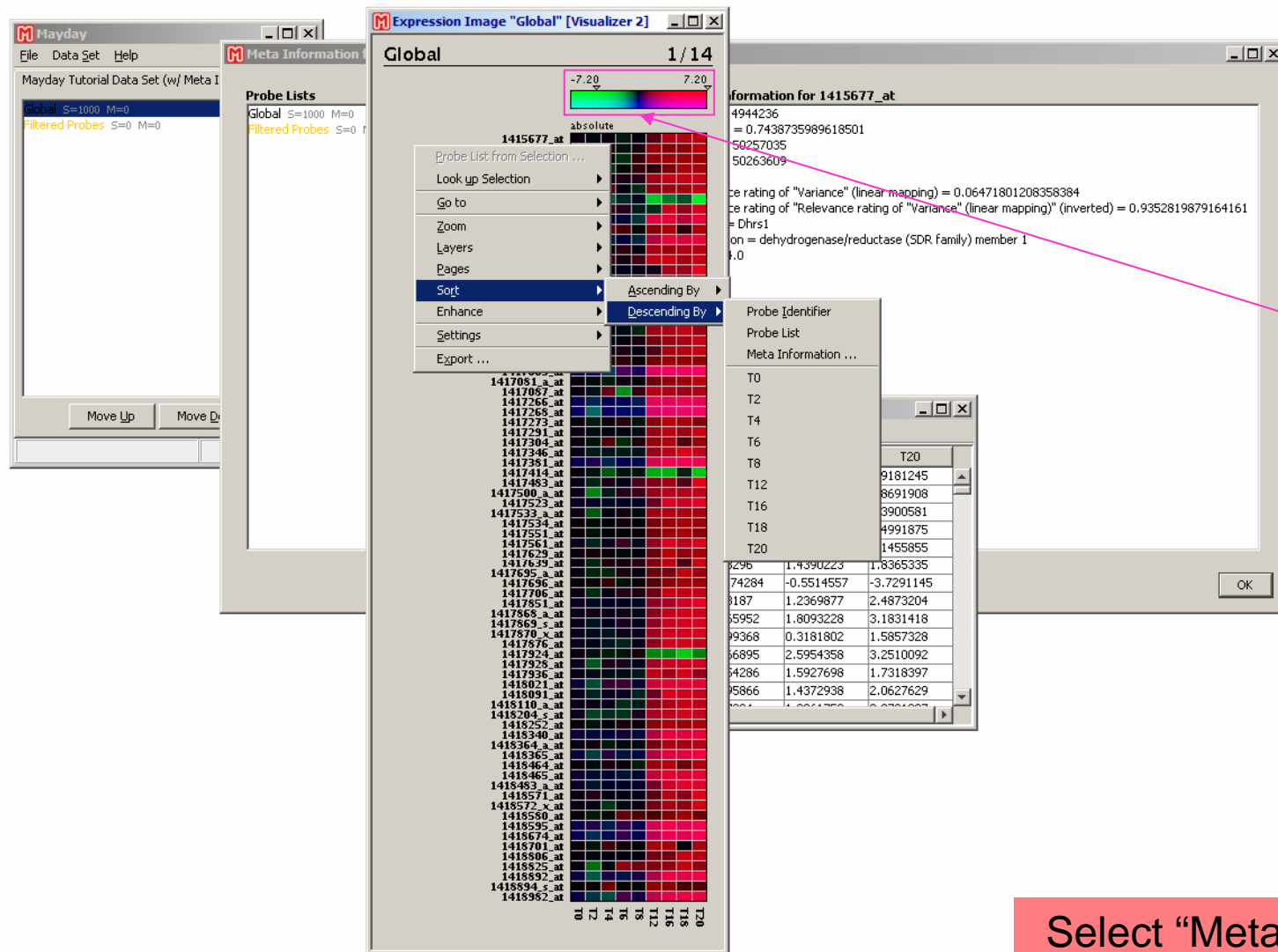
Select "Blue ...".



Select "Relevance rating of "Variance" (linear mapping)", click OK to confirm. Open the heatmap's context menu and go to "Sort", then "Descending by".

Using meta information as sort key

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Using meta information as sort key

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The image shows a screenshot of the Mayday software interface, which is used for analyzing gene expression data. The main window displays a heatmap of gene expression data, with a color scale ranging from -7.20 (blue) to 7.20 (red). The heatmap is titled "Global" and shows data for 14 genes (1415677_at to 1417791_at). A color scale bar is visible above the heatmap, labeled "absolute".

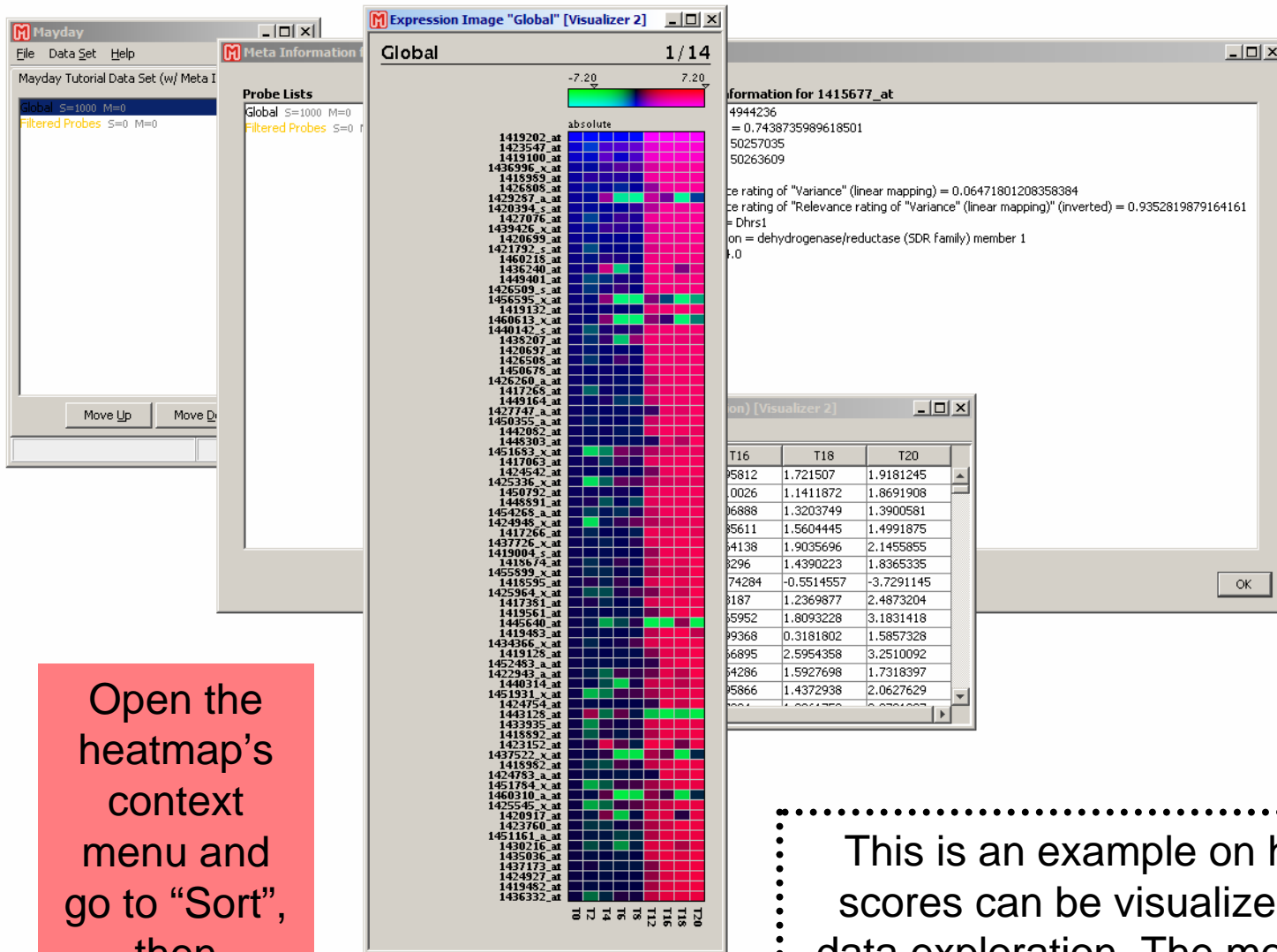
Overlaid on the main window is a "Meta Information Selection" dialog box. This dialog box allows users to select a meta-information key for sorting the data. The "MIO Groups" list includes:

- Chr S=891
- Chr_S S=891
- Chr_E S=891
- Str S=891
- P S=1000
- Variance S=1000** (selected)
- Relevance rating of "Variance" (linear mapping) S=1000
- Relevance rating of "Relevance rating of "Variance" (linear mapping)" (inverted) S=1000

The "OK" button is highlighted, indicating that the user has selected "Variance" as the sort key.

In the background, another window titled "Expression Image 'Global' [Visualizer 2]" is visible, showing a heatmap of gene expression data for the same set of genes. A detailed view of the meta-information for gene 1415677_at is also shown, including its accession number (4944236), gene symbol (Dhrs1), and description (dehydrogenase/reductase (SDR family) member 1).

Select "Variance".



Open the heatmap's context menu and go to "Sort", then "Ascending By".

This is an example on how relevance scores can be visualized and used for data exploration. The more blue a probe appears, the higher it's relevance score (the higher it's variance in this case).

Using meta information as sort key

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The screenshot shows the Mayday software interface. The main window is 'Expression Image Global [Visualizer 2]' with a color scale from -7.20 to 7.20. A menu is open over the heatmap, showing options like 'Sort', 'Enhance', and 'Settings'. The 'Sort' menu is expanded, showing 'Ascending By' and 'Descending By' options. The 'Meta Information ...' option is selected, opening a sub-menu with 'Probe Identifier', 'Probe List', and 'Meta Information ...'. The 'Meta Information ...' option is also selected, opening a window displaying detailed information for probe 1415677_at.

Meta Information for 1415677_at

4944236
= 0.7438735989618501
50257035
50263609

ce rating of "Variance" (linear mapping) = 0.06471801208358384
ce rating of "Relevance rating of "Variance" (linear mapping)" (inverted) = 0.9352819879164161
= Dhrrs1
on = dehydrogenase/reductase (SDR family) member 1
1.0

T0	T2	T4	T6	T8	T12	T16	T18	T20
181245	591908	900581	991875	455855	365335	7291145		
187	1.2369877	2.4873204						
5952	1.8093228	3.1831418						
99368	0.3181802	1.5857328						
6895	2.5954358	3.2510092						
4286	1.5927698	1.7318397						
5866	1.4372938	2.0627629						

Select "Meta Information ...".

Using meta information as sort key

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The screenshot displays the Mayday software interface with several windows open. The 'Mayday' window shows a list of probes with 'Global' selected. The 'Expression Image "Global" [Visualizer 2]' window displays a heatmap of gene expression data for 14 probes, with a color scale from -7.20 to 7.20. The 'Meta Information Selection' window is open, showing a list of 'MIO Groups' with 'P' selected. The 'Meta Information for 1415677_at' window shows detailed information for a specific probe, including its symbol, description, and various ratings.

Mayday
File Data Set Help
Mayday Tutorial Data Set (w/ Meta Information)
Global S=1000 M=0
Filtered Probes S=0 M=0
Move Up Move Down

Expression Image "Global" [Visualizer 2]
Global 1 / 14
-7.20 7.20
absolute
1419202_at
1423547_at
1419100_at
1436996_x_at
1418989_at
1426805_at
1429287_a_at
1420394_s_at
1427076_at
1439426_x_at
1420659_at
1421792_s_at
1460218_at
1436240_at
1449401_at
1426509_s_at
1456595_x_at
1419132_at
1460613_x_at
1440142_s_at
1435207_at
1420697_at
1426508_at
1450675_at
1426260_a_at
1417268_at
1449164_at
1427747_a_at
1450355_x_at
1447087_x_at

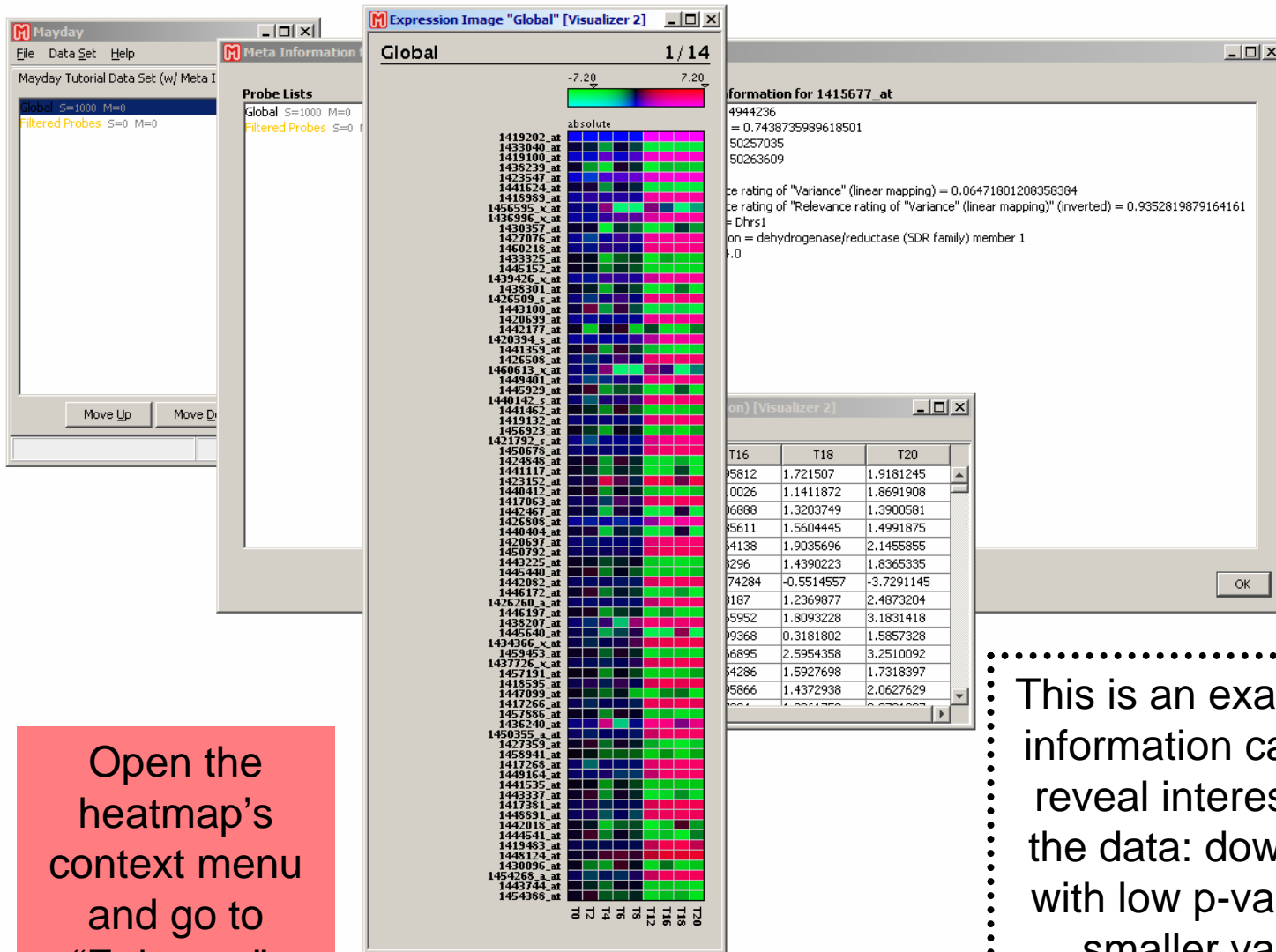
Meta Information Selection
MIO Groups
Symbol S=792
Description S=724
Chr S=891
Chr_S S=891
Chr_E S=891
Str S=891
P S=1000
Variance S=1000
OK Cancel

Meta Information for 1415677_at
4944236
= 0.7438735989618501
50257035
50263609
ce rating of "Variance" (linear mapping) = 0.06471801208358384
ce rating of "Relevance rating of "Variance" (linear mapping)" (inverted) = 0.9352819879164161
= Dhrl1
on = dehydrogenase/reductase (SDR family) member 1
.0

Meta Information for 1415677_at
OK

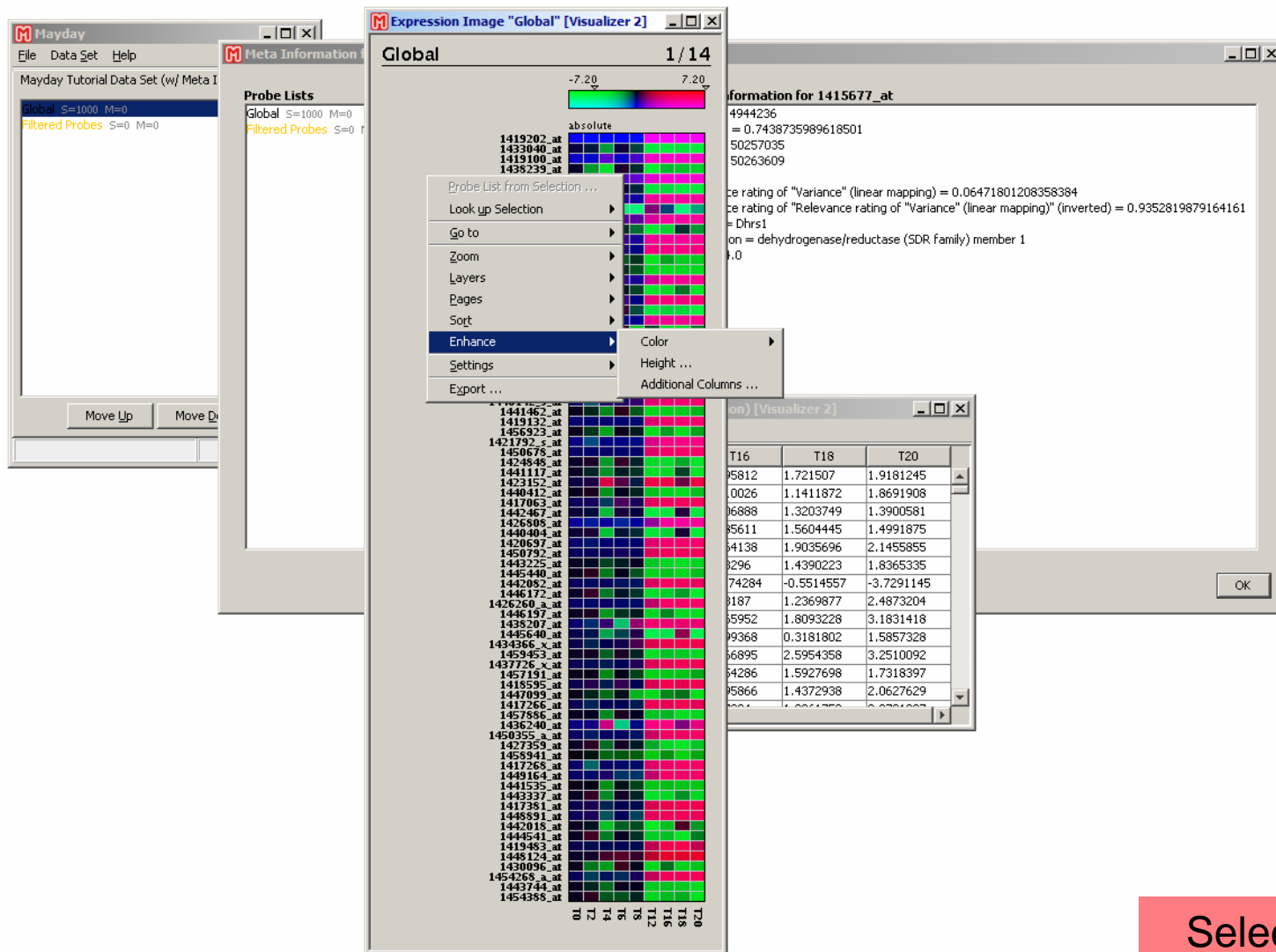
1451931_x_at
1424754_at
1443128_at
1433935_at
1418892_at
1423152_at
1437522_x_at
1418982_at
1424753_a_at
1451784_x_at
1460310_a_at
1425545_x_at
1420917_at
1423760_at
1451161_a_at
1430216_at
1435036_at
1437173_at
1424927_at
1419482_at
1436332_at
T20
T18
T16
T14
T8
T12
T10

Select "P" and click
"OK" to confirm.

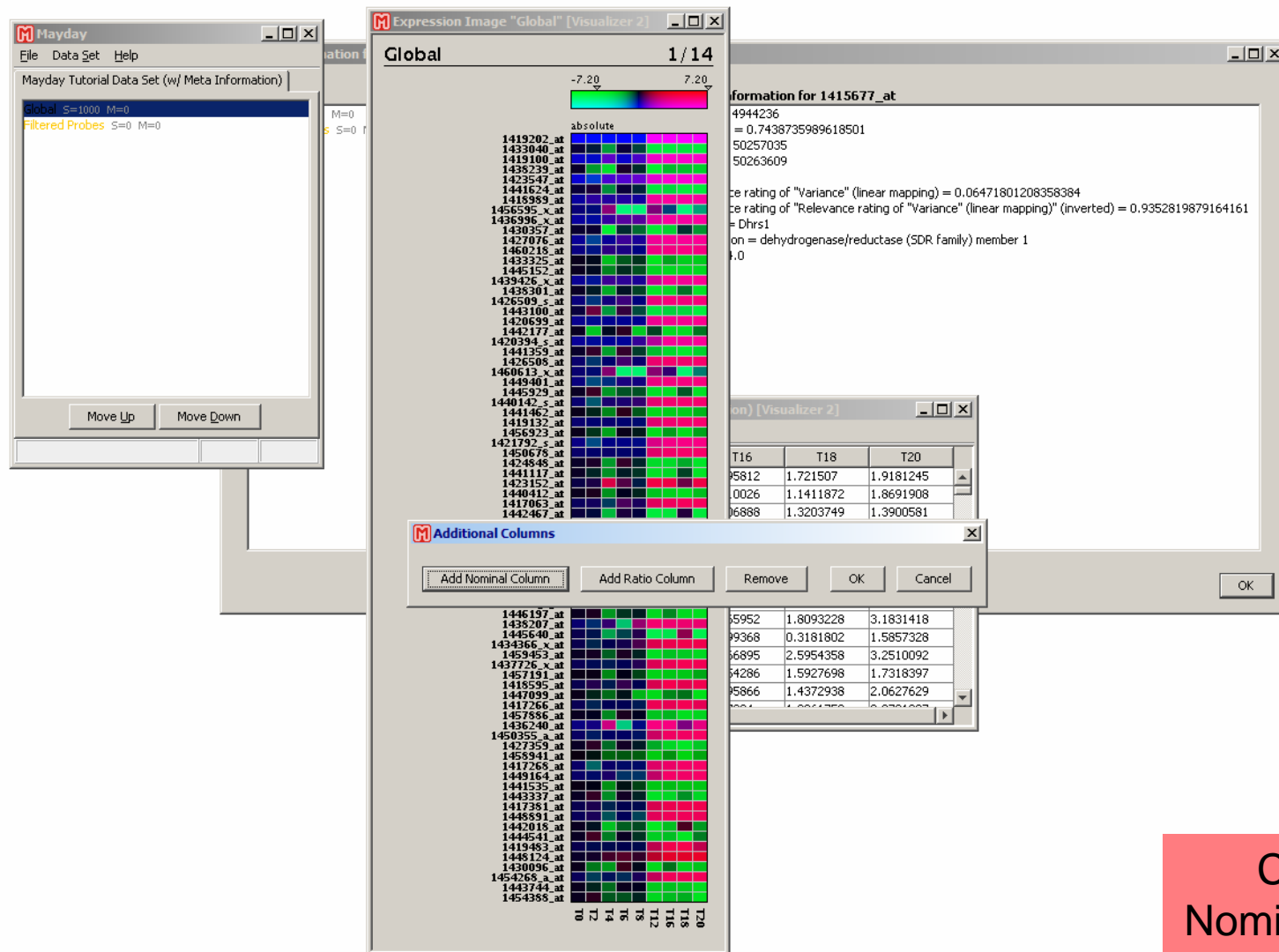


Open the heatmap's context menu and go to "Enhance".

This is an example on how meta information can be combined to reveal interesting properties of the data: downregulated genes with low p-values have a much smaller variance than the upregulated genes with similarly low p-values.

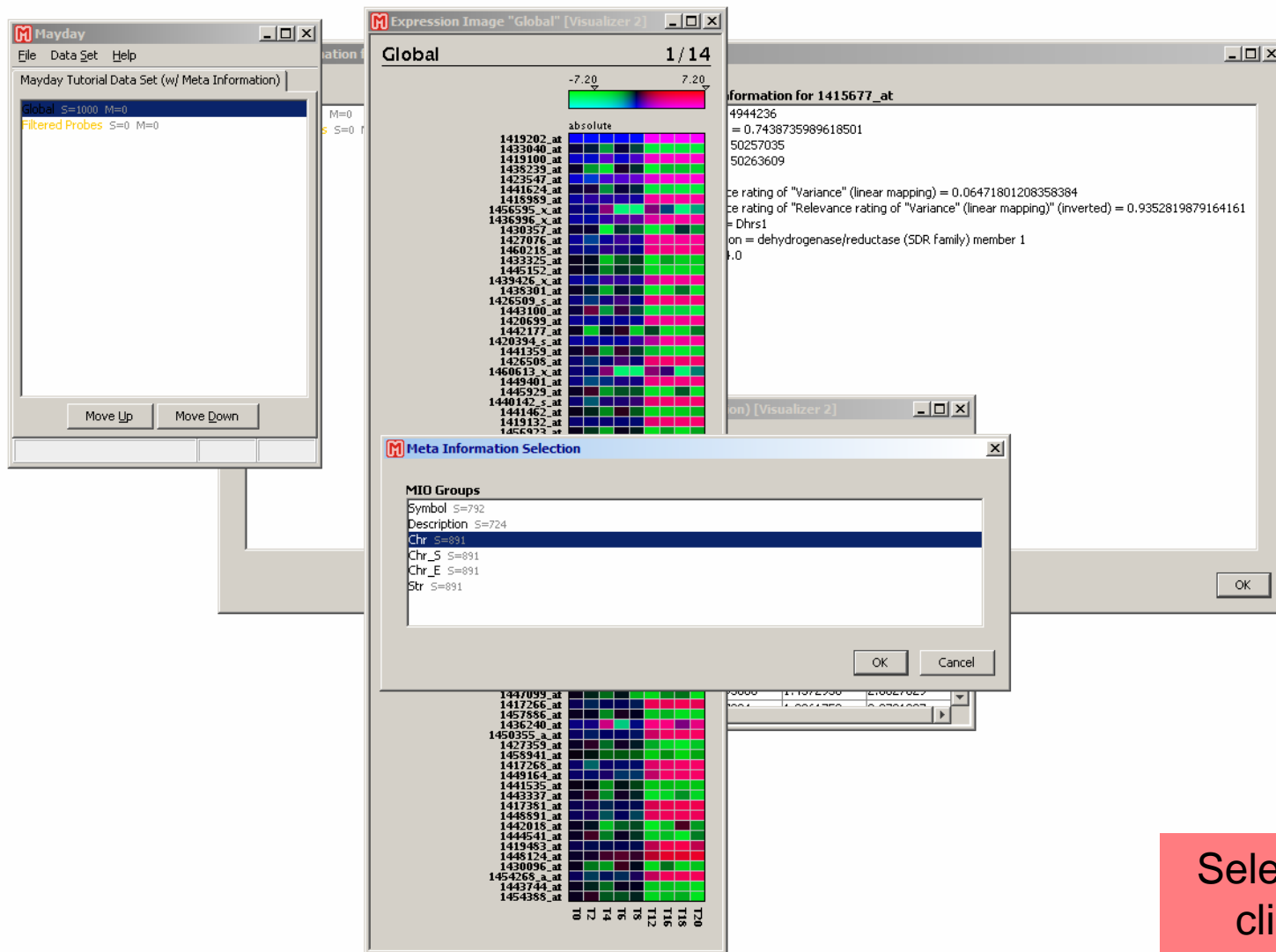


Select "Additional Columns ...".



Visualizing categorical meta information

264



Select "Chr" and click "OK" to confirm.

Mayday

File Data Set Help

Mayday Tutorial Data Set (w/ Meta Information)

Global S=1000 M=0

Filtered Probes S=0 M=0

Move Up Move Down

Expression Image "Global" [Visualizer 2]

Global 1 / 14

-7.20 7.20

absolute

Information for 1415677_at

4944236

= 0.7438735989618501

Additional Columns

nominal_column_0

Name

nominal_column_0

Edit ...

Color Encoding

Category	Color
1.0	Blue
10.0	Blue
11.0	Blue
12.0	Blue
13.0	Blue
14.0	Blue
15.0	Blue
16.0	Blue
17.0	Blue
18.0	Blue
19.0	Blue
2.0	Blue
3.0	Blue
4.0	Blue
5.0	Blue
6.0	Blue
7.0	Blue
8.0	Blue
9.0	Blue
X	Blue

MIO Groups

Chr S=891

Add Nominal Column Add Ratio Column Remove OK Cancel

Click "Edit ..."
below "Name".

Visualizing categorical meta information

266

The screenshot displays the Mayday software interface with several windows open. The 'Mayday' window shows a list of data sets: 'Global S=1000 M=0' and 'Filtered Probes S=0 M=0'. The 'Expression Image "Global" [Visualizer 2]' window shows a color scale from -7.20 to 7.20, labeled 'absolute'. The 'Additional Columns' dialog box is open, showing a table for 'nominal_column_0' with categories and corresponding colors. An 'Information' dialog box is also open, prompting the user to enter a new name for the column 'nominal_column_0', with 'nominal_column_0' entered in the text field. The 'MIO Groups' section at the bottom shows 'Chr S=891'.

Mayday
File Data Set Help
Mayday Tutorial Data Set (w/ Meta Information)
Global S=1000 M=0
Filtered Probes S=0 M=0
Move Up Move Down

Expression Image "Global" [Visualizer 2]
Global 1 / 14
-7.20 7.20
absolute
information for 1415677_at
4944236
= 0.7438735989618501

Additional Columns
nominal_column_0
Name
nominal_column_0
Edit ...
Color Encoding

Category	Color
1.0	
10.0	
11.0	
12.0	
13.0	
14.0	
15.0	
16.0	
17.0	
18.0	
19.0	
2.0	
3.0	
4.0	
5.0	
6.0	
7.0	
8.0	
9.0	
X	

MIO Groups
Chr S=891
Add Nominal Column Add Ratio Column Remove OK Cancel

Information
Enter a new name for column "nominal_column_0".
nominal_column_0
OK Cancel

71801206358384
ar mapping)" (inverted) = 0.9352819879164161
ember 1
OK

Change the name
to "chr".

Visualizing categorical meta information

267

The screenshot displays the Mayday software interface with several windows open:

- Mayday**: The main application window showing the 'Mayday Tutorial Data Set (w/ Meta Information)'. It lists 'Global S=1000 M=0' and 'Filtered Probes S=0 M=0'.
- Expression Image "Global" [Visualizer 2]**: A window showing a color scale from -7.20 to 7.20, labeled 'absolute'.
- Additional Columns**: A dialog box for adding a new column. It shows the column name 'nominal_column_0' and an 'Edit ...' button. Below is a 'Color Encoding' table with categories and corresponding colors.
- Information**: A small pop-up window asking for a new name for the column 'nominal_column_0'. The input field contains 'chr'.

The 'Color Encoding' table in the 'Additional Columns' dialog is as follows:

Category	Color
1.0	Light Blue
10.0	Light Green
11.0	Green
12.0	Dark Green
13.0	Light Green
14.0	Yellow-Green
15.0	Yellow
16.0	Orange
17.0	Red-Orange
18.0	Red
19.0	Dark Red
2.0	Light Blue
3.0	Light Green
4.0	Green
5.0	Dark Green
6.0	Light Green
7.0	Yellow-Green
8.0	Yellow
9.0	Orange
X	Dark Blue

The 'Information' dialog box contains the following text:

Enter a new name for column "nominal_column_0".
chr

Buttons: OK, Cancel

At the bottom of the 'Additional Columns' dialog, there are buttons for 'Add Nominal Column', 'Add Ratio Column', 'Remove', 'OK', and 'Cancel'.

Click "OK" to confirm.

Mayday

File Data Set Help

Mayday Tutorial Data Set (w/ Meta Information)

Global S=1000 M=0

Filtered Probes S=0 M=0

Move Up Move Down

Expression Image "Global" [Visualizer 2]

Global 1 / 14

-7.20 7.20

absolute

Additional Columns

nominal_column_0

Name

chr

Edit ...

Color Encoding

Category	Color
1.0	
10.0	
11.0	
12.0	
13.0	
14.0	
15.0	
16.0	
17.0	
18.0	
19.0	
2.0	
3.0	
4.0	
5.0	
6.0	
7.0	
8.0	
9.0	
X	

MIO Groups

Chr S=891

Add Nominal Column Add Ratio Column Remove OK Cancel

Information for 1415677_at

4944236

= 0.7438735989618501

71801208358384

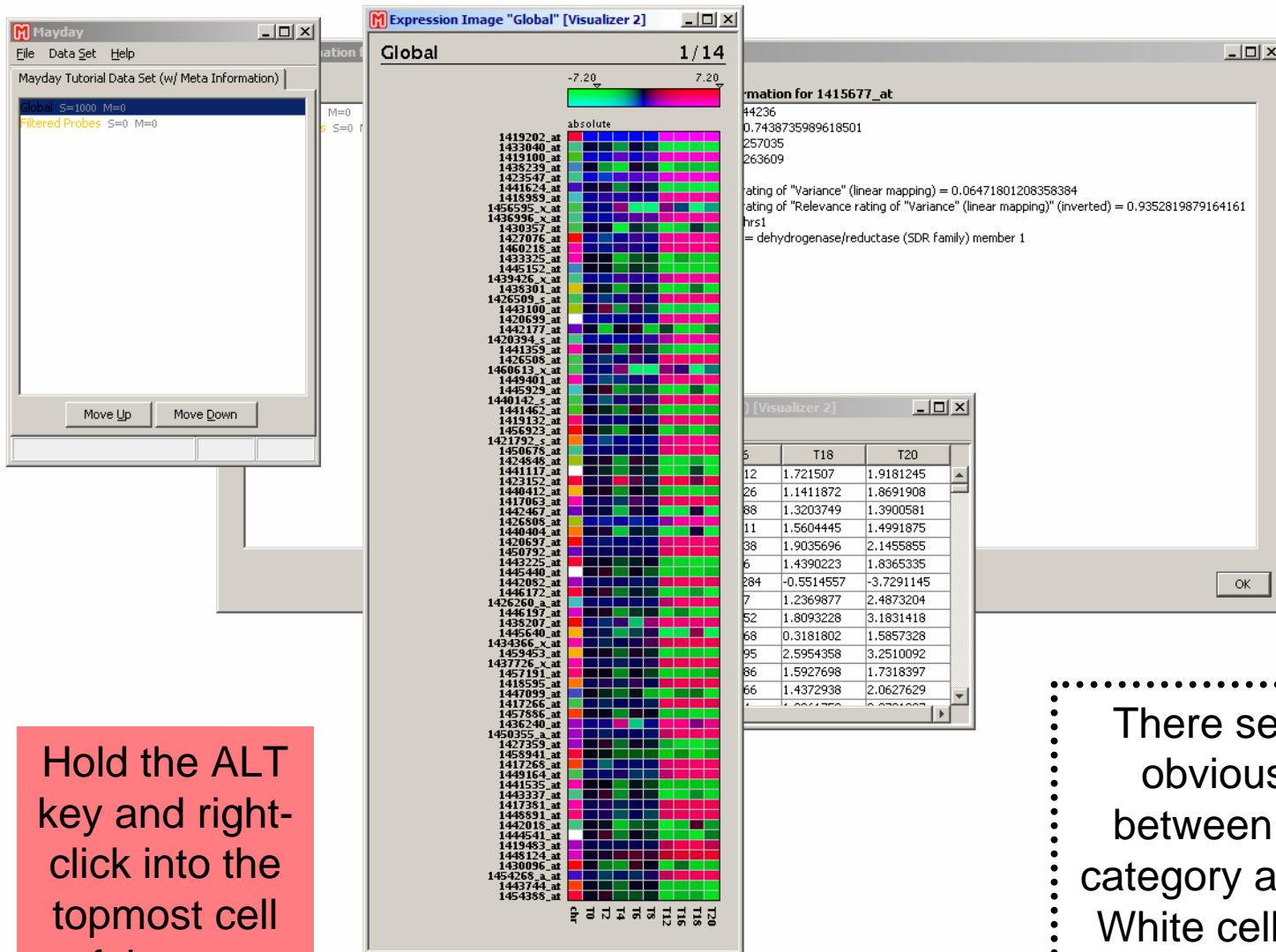
ar mapping)" (inverted) = 0.9352819879164161

ember 1

OK

Click "OK" to confirm.

You can also change the color of a category by clicking into the cell displaying the corresponding color.

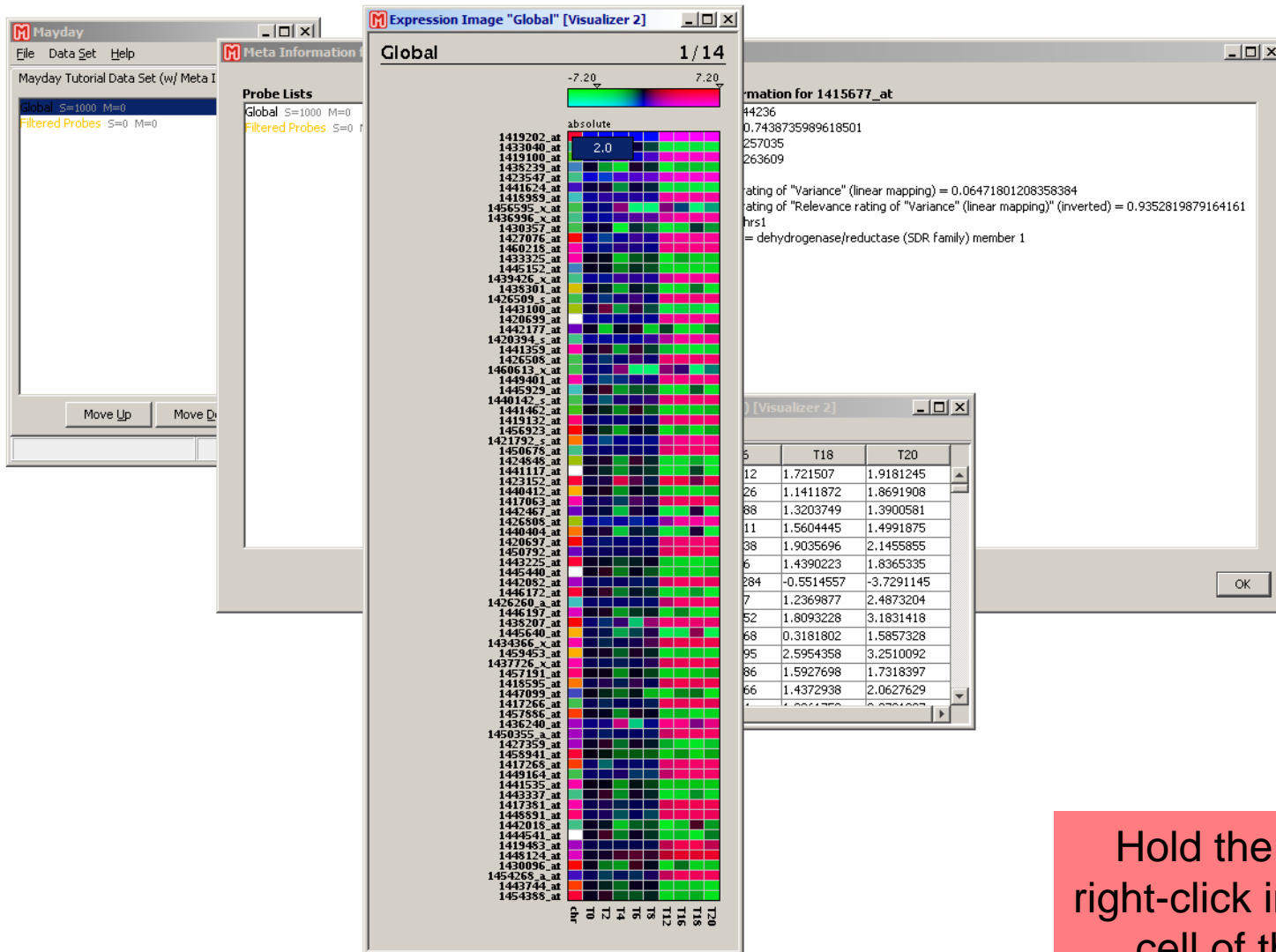


Hold the ALT key and right-click into the topmost cell of the new column.

There seems to be no obvious correlation between the assigned category and the p-value. White cells indicate that there was no meta information for that probe.

Checking meta information values

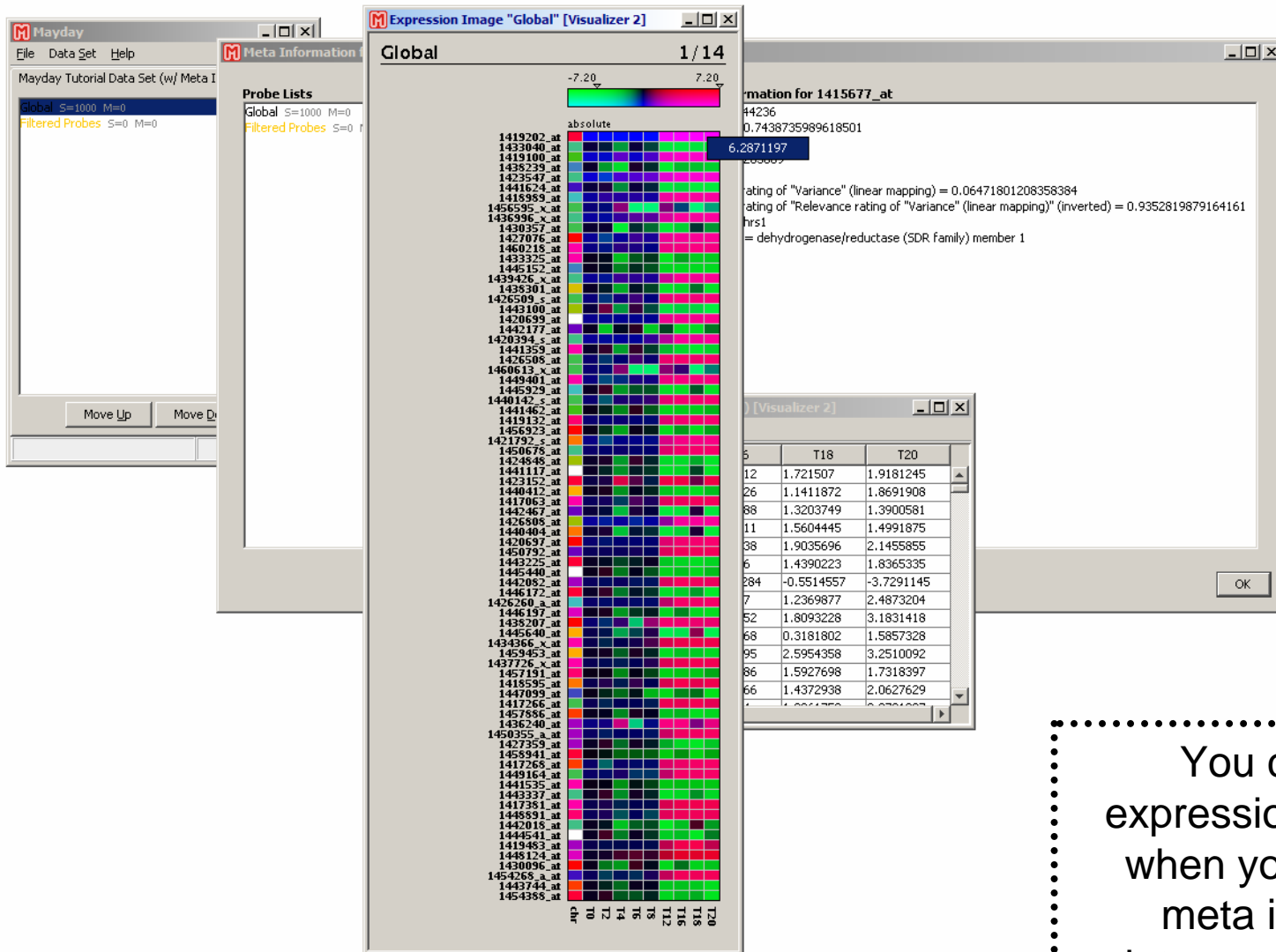
270



Hold the ALT key and right-click into the topmost cell of the rightmost column of the matrix.

Checking expression values

271

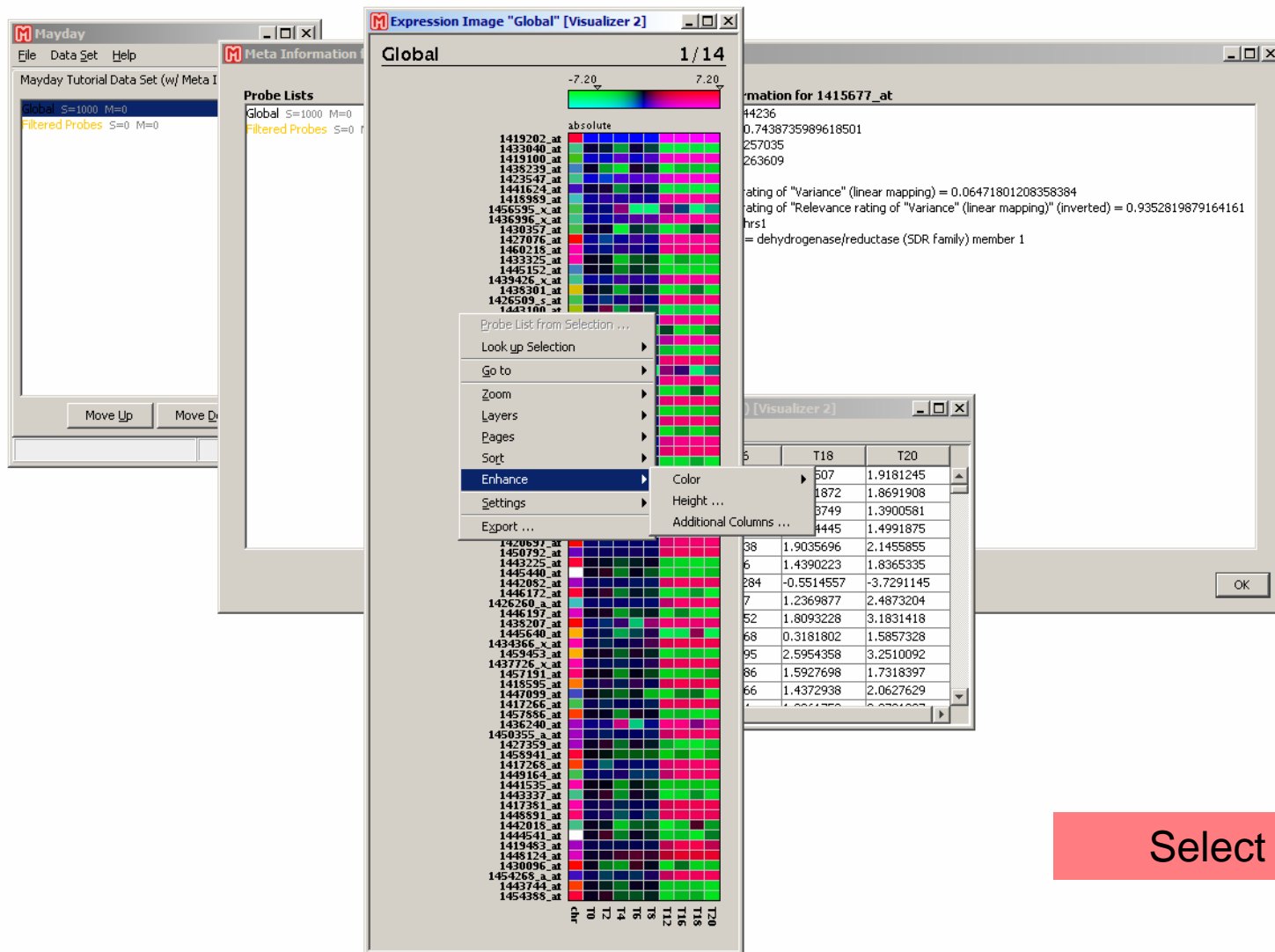


Open the heatmap's context menu and go to submenu "Enhance".

You can check expression values also when you don't have meta information integrated or loaded.

Visualizing relevance scores by scaling

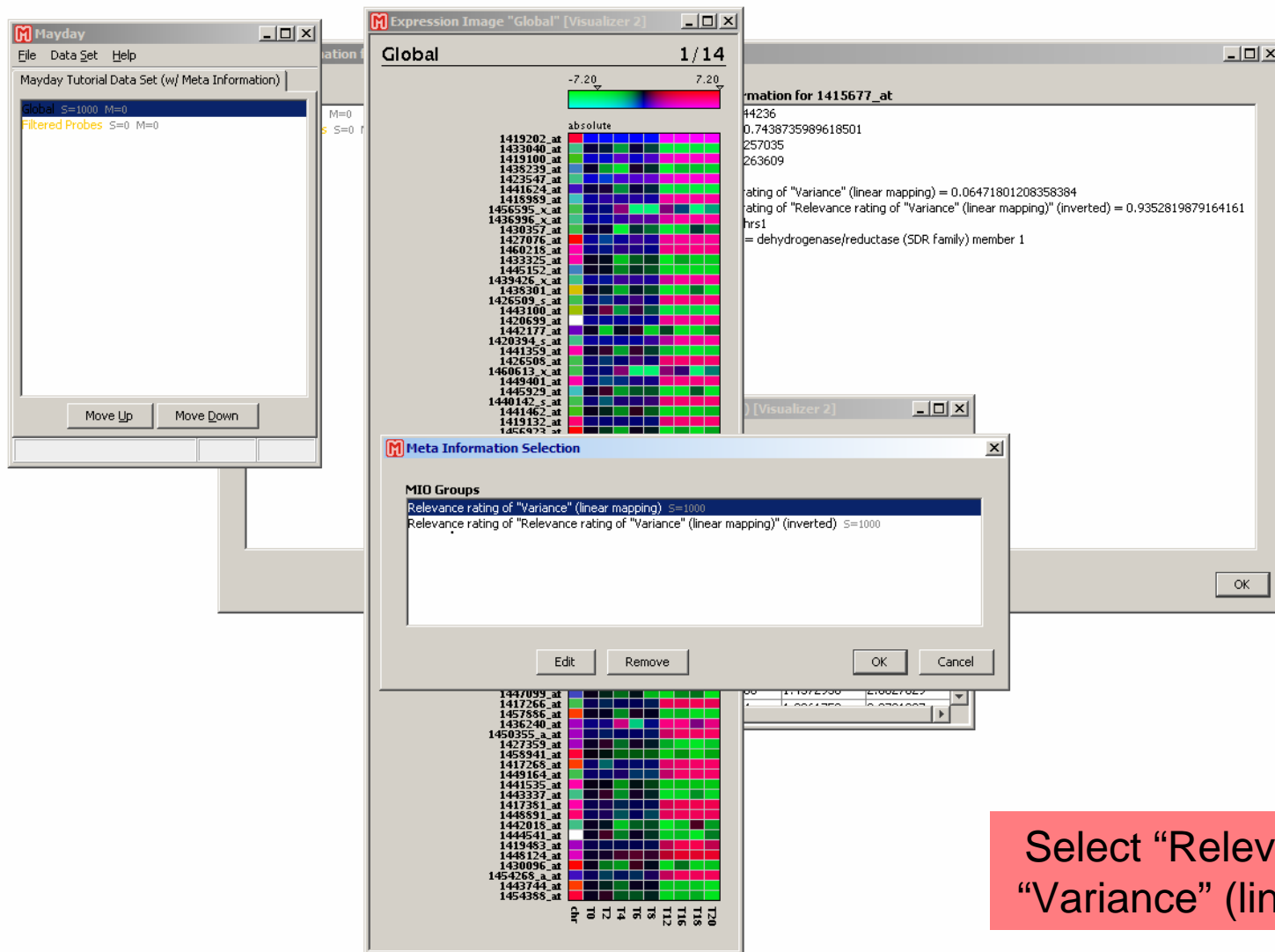
272



Select "Height ...".

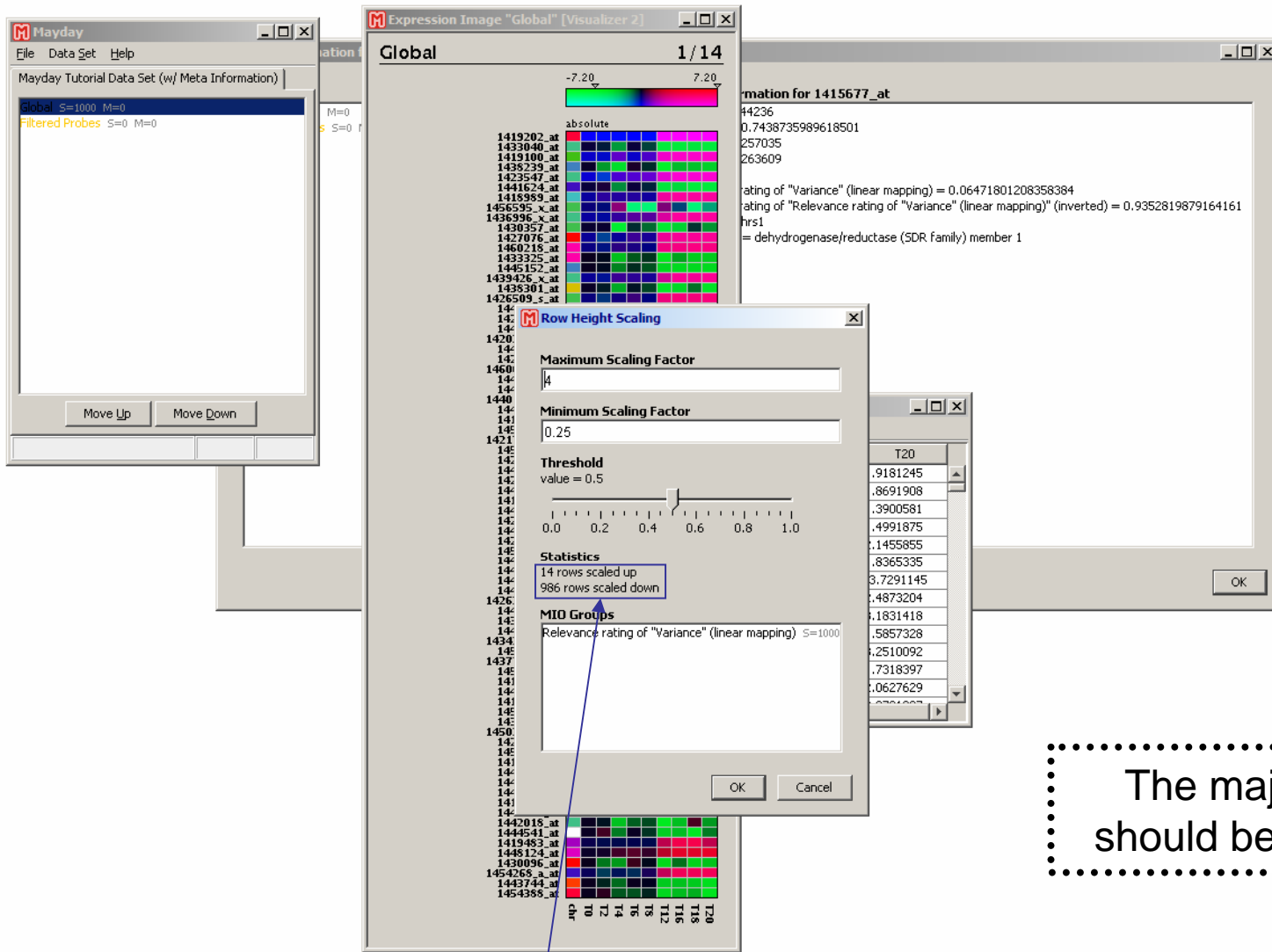
Visualizing relevance scores by scaling

273



Visualizing relevance scores by scaling

274



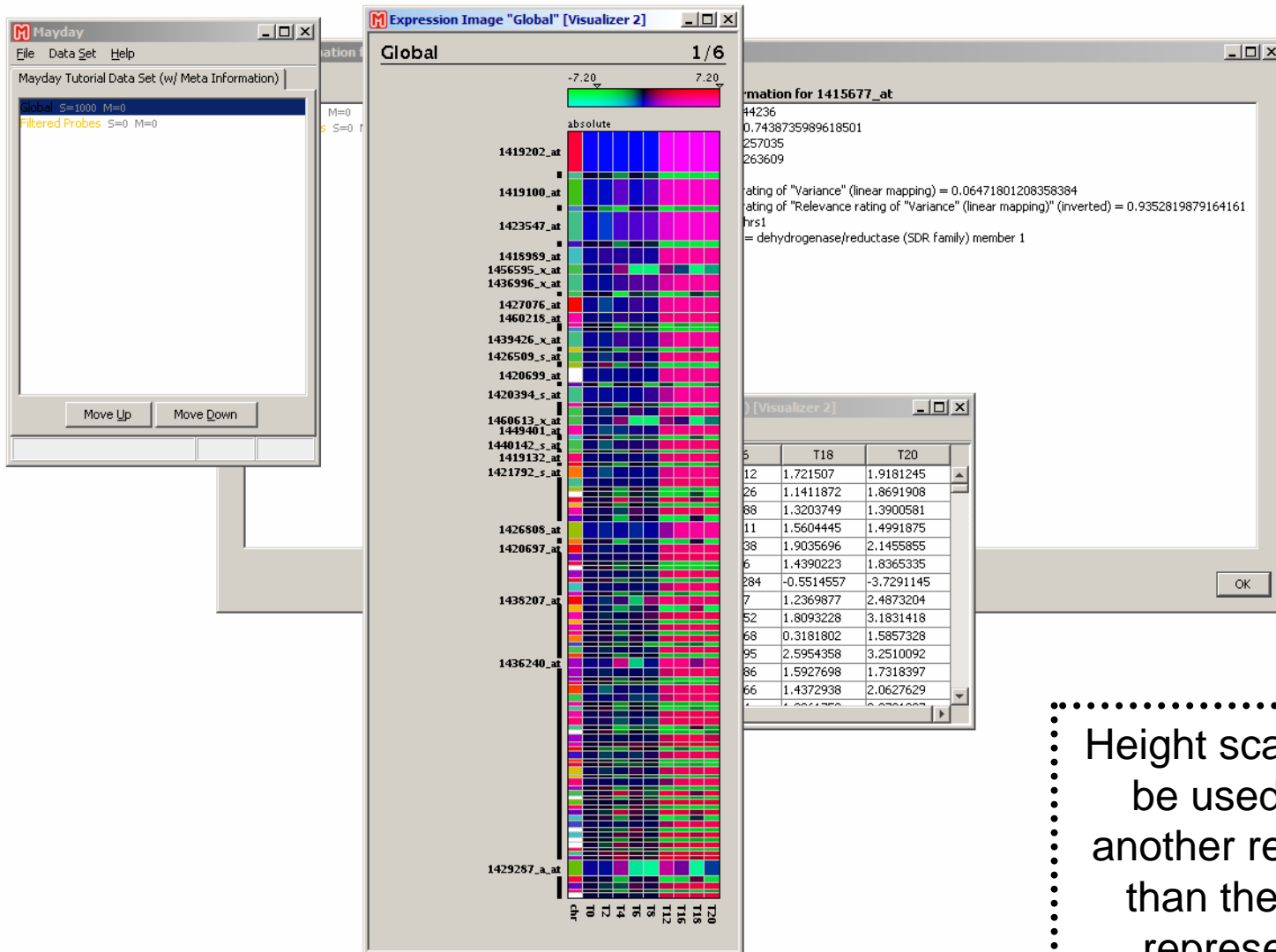
Review the settings and click "OK" to confirm.

The majority of rows should be scaled down.

information about how many rows will be scaled up and how many will be scaled down

Visualizing relevance scores by scaling

275



Open the heatmap's context menu and go to submenu "Enhance", then "Color".

Height scaling could also be used to integrate another relevance score than the one already represented by the additional blue gradient.

Removing relevance scores from viewer

276

The screenshot shows the Mayday software interface. The main window is titled 'Expression Image "Global" [Visualizer 2]'. It displays a heatmap with a color scale from -7.20 to 7.20. The heatmap is labeled 'Global' and '1/6'. A context menu is open over the heatmap, showing options like 'Probe List from Selection ...', 'Look up Selection', 'Go to', 'Zoom', 'Layers', 'Pages', 'Sort', 'Enhance', 'Settings', and 'Export ...'. The 'Enhance' option is selected, and a sub-menu is open showing 'Color', 'Height ...', and 'Additional Columns ...'. The 'Color' option is selected, and a 'Color' dialog box is open. The dialog box has a 'Blue ...' button selected. The dialog box also has a 'Height ...' button and an 'Additional Columns ...' button. The dialog box is showing a table of values for the selected probe, 1415677_at. The table has two columns: 'chr' and 'value'. The values are: 11872, 1.8691908, 1.3900581, 1.5604445, 1.4991875, 1.9035696, 2.1455855, 1.4390223, 1.8365335, -0.5514557, -3.7291145, 1.2369877, 2.4873204, 1.8093228, 3.1831418, 0.3181802, 1.5857328, 2.5954358, 3.2510092, 1.5927698, 1.7318397, 1.4372938, 2.0627629.

Mayday
File Data Set Help
Mayday Tutorial Data Set (w/ Meta I
Global S=1000 M=0
Filtered Probes S=0 M=0
Move Up Move D

Meta Information
Global S=1000 M=0
Filtered Probes S=0 M=0

Expression Image "Global" [Visualizer 2]
Global 1/6
-7.20 7.20
absolute
1419202_at
1419100_at
1423547_at
1418989_at
1456595_x_at
1436496_v_at
Probe List from Selection ...
Look up Selection
Go to
Zoom
Layers
Pages
Sort
Enhance
Settings
Export ...
Color
Height ...
Additional Columns ...
Blue ...
Opacity ... 45
11872 1.8691908
1.3900581
1.5604445 1.4991875
1.9035696 2.1455855
1.4390223 1.8365335
-0.5514557 -3.7291145
1.2369877 2.4873204
1.8093228 3.1831418
0.3181802 1.5857328
2.5954358 3.2510092
1.5927698 1.7318397
1.4372938 2.0627629
OK

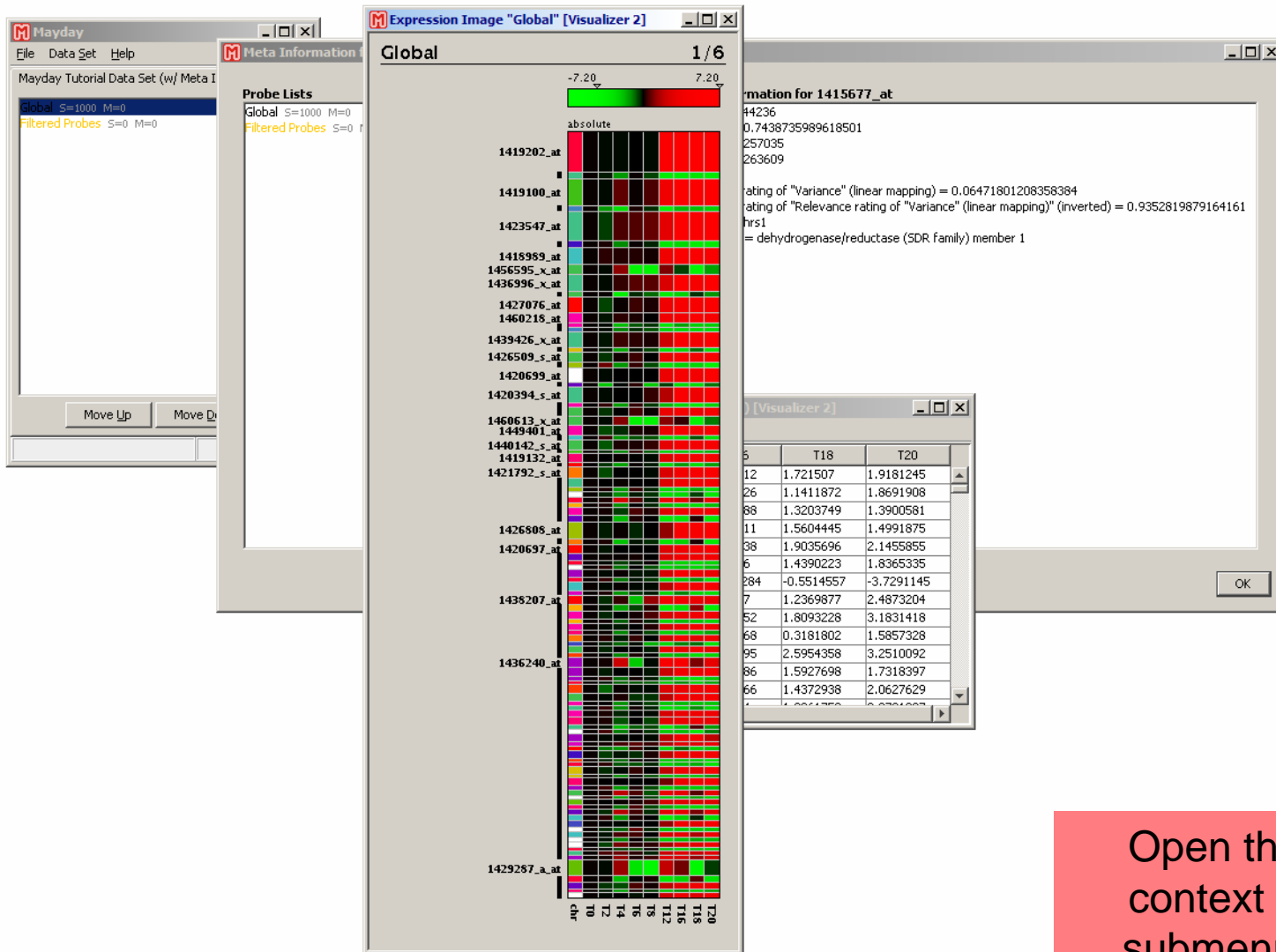
Information for 1415677_at
14236
0.7438735989618501
257035
263609
Rating of "Variance" (linear mapping) = 0.06471801208358384
Rating of "Relevance rating of "Variance" (linear mapping)" (inverted) = 0.9352819879164161
hrs1
= dehydrogenase/reductase (SDR family) member 1

1426508_at
1420697_at
1438207_at
1436240_at
1429287_a_at
chr
120
118
116
12
14
16
18
112

Select "Blue ...". In the MIO group selection dialog just hit "Cancel".

Removing relevance scores from viewer

277



Open the heatmap's context menu. Go to submenu "Enhance".

Adding relevance scores in a new column

278

The screenshot shows the Mayday software interface. The main window is 'Expression Image "Global" [Visualizer 2]' displaying a heatmap of gene expression data. A context menu is open over the heatmap, with 'Enhance' selected and 'Additional Columns ...' highlighted. To the right, the 'Meta Information for 1415677_at' window is open, showing details for a specific probe. Below the heatmap, a table of values is visible.

Meta Information for 1415677_at

14236
0.7438735989618501
257035
263609

Rating of "Variance" (linear mapping) = 0.06471801208358384
Rating of "Relevance rating of "Variance" (linear mapping)" (inverted) = 0.9352819879164161
hrs1
= dehydrogenase/reductase (SDR family) member 1

	T18	T20
12	1.721507	1.9181245
26	1.1411872	1.8691908
88	1.3203749	1.3900581
11	1.5604445	1.4991875
38	1.9035696	2.1455855
6	1.4390223	1.8365335
284	-0.5514557	-3.7291145
7	1.2369877	2.4873204
52	1.8093228	3.1831418
68	0.3181802	1.5857328
95	2.5954358	3.2510092
86	1.5927698	1.7318397
66	1.4372938	2.0627629

Select "Additional Columns ...".

Adding relevance scores in a new column

279

Mayday

File Data Set Help

Mayday Tutorial Data Set (w/ Meta Information)

Global S=1000 M=0

Filtered Probes S=0 M=0

Move Up Move Down

Expression Image "Global" [Visualizer 2]

Global 1/6

-7.20 7.20

absolute

Information for 1415677_at

44236

0.7438735989618501

Additional Columns

chr

Name

chr

Edit ...

Color Encoding

Category	Color
1.0	
10.0	
11.0	
12.0	
13.0	
14.0	
15.0	
16.0	
17.0	
18.0	
19.0	
2.0	
3.0	
4.0	
5.0	
6.0	
7.0	
8.0	
9.0	
X	

MIO Groups

Chr S=891

Add Nominal Column Add Ratio Column Remove OK Cancel

71801208358384

ar mapping)" (inverted) = 0.9352819879164161

ember 1

OK

Click "Add Ratio Column" at the bottom of the dialog.

Adding relevance scores in a new column

280

The screenshot displays the Mayday software interface with several windows open. The 'Mayday' window on the left shows a list of data sets: 'Global S=1000 M=0' and 'Filtered Probes S=0 M=0'. The 'Expression Image "Global" [Visualizer 2]' window in the center shows a color scale from -7.20 to 7.20, with a color bar labeled 'absolute'. The 'Additional Columns' window is open, showing a table with 'Category' and 'Color' columns. The 'Meta Information Selection' window is also open, showing a list of 'MIO Groups' with 'Relevance rating of "Variance" (linear mapping) S=1000' selected. The 'Meta Information Selection' window has 'OK' and 'Cancel' buttons. The 'Additional Columns' window has 'OK' and 'Cancel' buttons. The 'Expression Image' window has an 'OK' button.

Additional Columns Table:

Category	Color
1.0	Light Blue
10.0	Light Green
11.0	Green
12.0	Dark Green
13.0	Yellow-Green
14.0	Yellow
15.0	Orange

Meta Information Selection Table:

MIO Groups
Relevance rating of "Variance" (linear mapping) S=1000
Relevance rating of "Relevance rating of "Variance" (linear mapping)" (inverted) S=1000

Select "Relevance rating of "Variance" (linear mapping) and click "OK" to confirm.

Adding relevance scores in a new column

281

Mayday

File Data Set Help

Mayday Tutorial Data Set (w/ Meta Information)

Global S=1000 M=0

Filtered Probes S=0 M=0

Move Up Move Down

Expression Image "Global" [Visualizer 2]

Global 1 / 6

-7.20 7.20

absolute

Information for 1415677_at

44236

0.7438735989618501

Additional Columns

chr ratio_column_1

Name

ratio_column_1

Edit ...

Color Encoding

Category	Color
0	
1	

MIO Groups

Relevance rating of "Variance" (linear mapping) S=1000

Add Nominal Column Add Ratio Column Remove OK Cancel

71801208358384

ar mapping)" (inverted) = 0.9352819879164161

ember 1

OK

Change the name of the column to "var".

Adding relevance scores in a new column

282

The screenshot shows the Mayday software interface with the 'Additional Columns' dialog box open. The dialog is for adding a new ratio column named 'ratio_column_1'. It includes a color encoding table with categories 0 and 1, and a section for MIO Groups. The 'OK' button is highlighted in a red box.

Mayday
File Data Set Help
Mayday Tutorial Data Set (w/ Meta Information)
Global S=1000 M=0
Filtered Probes S=0 M=0
Move Up Move Down

Expression Image "Global" [Visualizer 2]
Global 1 / 6
-7.20 7.20
absolute
Information for 1415677_at
44236
0.7438735989618501

Additional Columns
chr ratio_column_1
Name
var
Edit ...
Color Encoding

Category	Color
0	
1	

MIO Groups
Relevance rating of "Variance" (linear mapping) S=1000
Add Nominal Column Add Ratio Column Remove OK Cancel

Click "OK" to confirm your changes.

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What to do next?

- load a data set that you are familiar with
- explore the data set using different viewers, clustering algorithms or statistical tools in R
- try to integrate your knowledge about the data set
 - as probe lists (sets of transcription factors, protein complexes, ...)
 - as meta information (p-values, GO annotation as categories, ...)
- gain new insights and write a paper
- quote Mayday
- get your paper published!