



## J-Express Pro

This document contains screenshots of the J-Express pro version 2.7. All images may be copied and used freely without molmines permission.

This document contains just a selection of the available features in the J-Express package.

### The J-Express desktop

Just as the windows desktop, windows may be moved, maximized, resized and iconified within the main J-Express desktop. This makes methods comparison and data mining easy as multiple analyses may be performed simultaneously. For instance, as shown in figure 1, Significance Analysis of Microarrays (SAM) is applied to a sample dataset (Colon cancer dataset. Alon et al., 1999). The genes are sorted in regards to the SAM d-score. From this list the top genes are selected and the selection is automatically picked up by a line chart component and viewed simultaneously. Selecting subsets is a frequent task in microarray data analysis. In J-Express subsets can be stored as groups and labeled with a color, or extracted from the dataset to form a subset and added to the *project tree*.

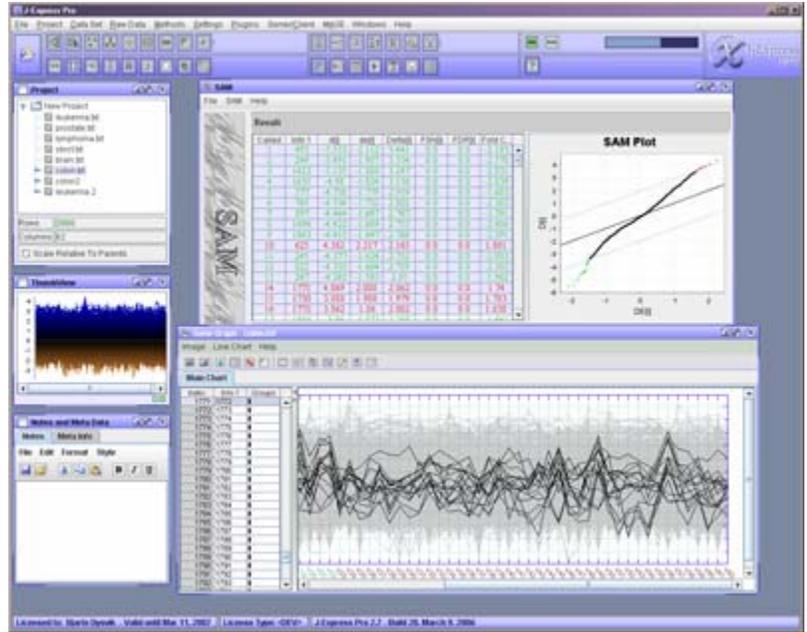
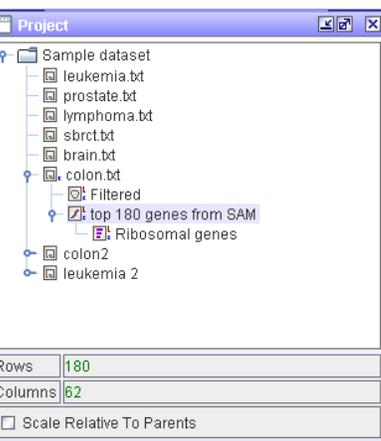


Figure 1 – The J-Express main desktop



The Project tree helps you keep track of the data analysis. Methods applied to a dataset, such as filtering and normalization creates sub-nodes in the tree and lets you go back and apply other methods to the source dataset. All analysis steps are automatically logged and can be viewed from the *meta info window* (figure 5). This window also contains a text-editor for manual logging and keeping notes of the analysis. By selecting a dataset in the project tree, analysis can be performed on subsets created from other analyses. The dataset thumbnail (Figure 3) shows the layout and scale of the selected dataset.

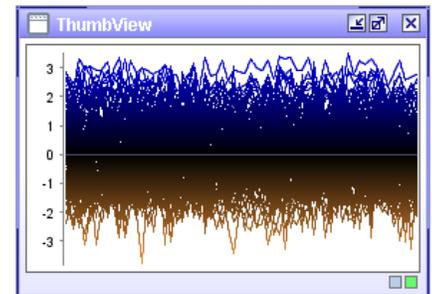


Figure 2 – The dataset thumbnail

Figure 3 – The project tree



Whenever a subset of genes is selected, these genes shows in the selection window (figure 6). The selection can also be viewed in the selection chart component and exported as an image. All charts and figures in J-Express can be exported to various image formats, including bitmap image formats such as jpg and png, and various vector image formats for superior image quality.

Index	ID	Name	Replicates	Used replic...	Gene Product
3	J222_2	PFJ0218	1	1,0,1,1,1,1,...	J222_2::PF...
4	Kn3690_3	PFK0370	1	1,1,1,1,1,1,...	Kn3690_3::PFL
5	M5894_7	PFM0820	1	1,1,1,1,1,1,...	M5894_7::MAI
6	B174	PFB0038	1	1,1,1,1,1,1,...	B174::PFB...

Selected 4

Figure 5 – The selection container

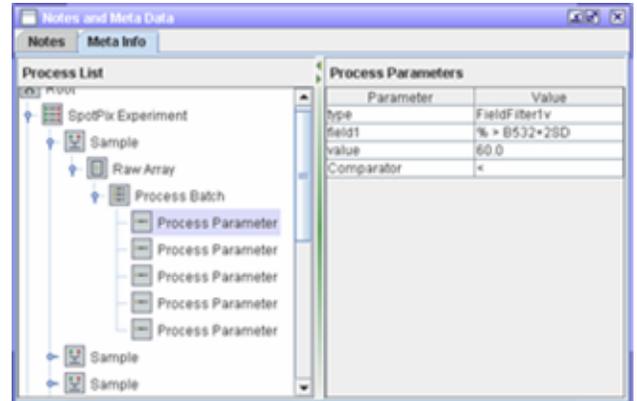


Figure 4 – The meta info window for analysis logging

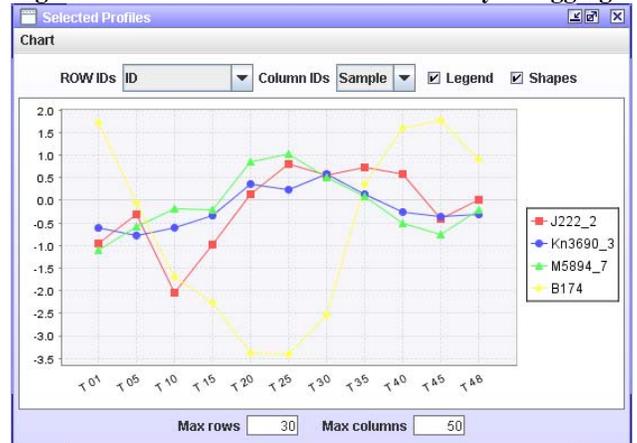


Figure 6 – The Selection chart

## Low level data analysis and preparation

Data from most image analysis systems can be imported and preprocessed in the J-Express low level analysis and preparation tool (Figure 7).

The raw data files can be dropped in the window and associated with image files for quality control and spot mapping (for two channel arrays).

The Low-level data import and processing window can also be used for data quality control and replicate combination/variance control.

Two-channel dye-swaps can easily be tagged and will automatically be handled by the framework.

Any data field column in the image output file can be selected as the data source. Other fields can be used for filtering and quality control.

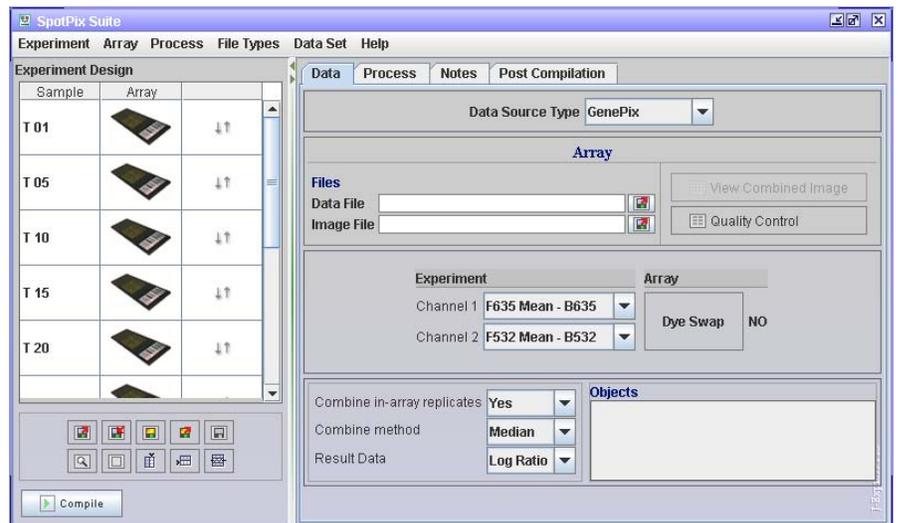
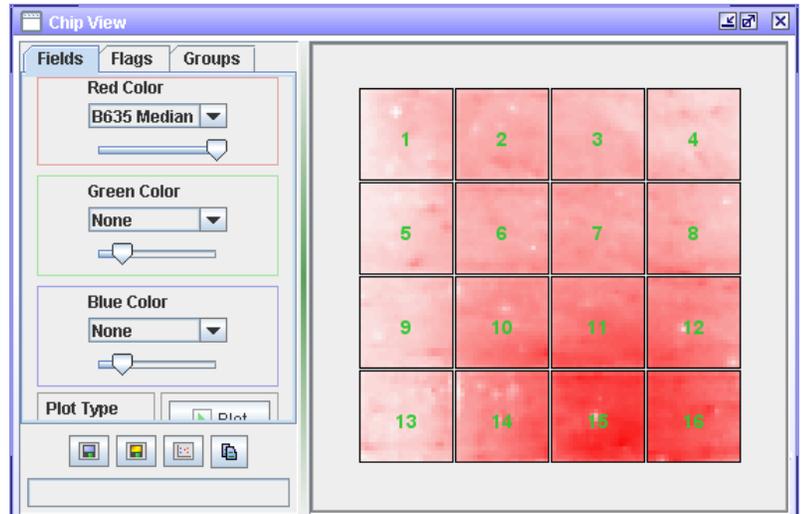
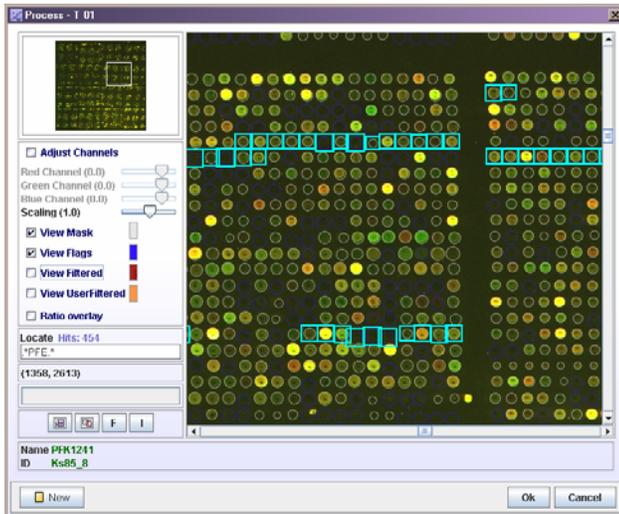


Figure 7 – The low level data import and preparation framework

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Some of the methods available for data quality control. The image view for two-channel images can be used to see filtered and flagged spots. The chip view can be used to view data layout and explore features such as spatial effects.

The processing widow lets you select from a wide range of different filters, normalization methods and viewers such as plots and fold change viewers to explore the effects of processes.

The process list can be loaded, saved and copied between arrays.

The compile button applies the process list to each array data file and compiles a gene expression matrix. It also combine in-array replicates and merges array replicates.

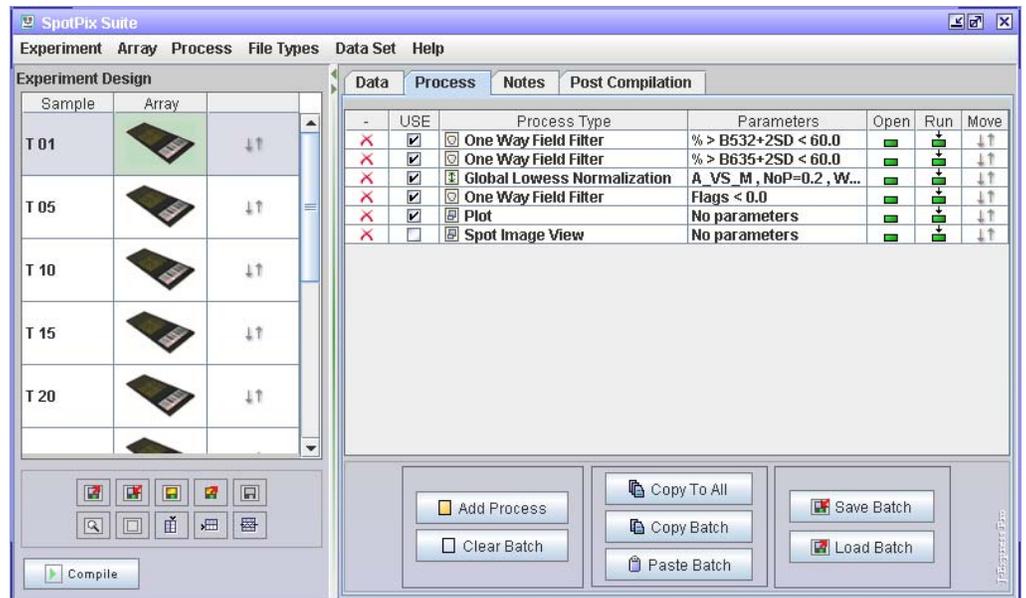


Figure 8 – The low level data import and pre-processing component



## Low-level processes

From the process selector you can select between several processing and viewing components. These are added to the process list

Below are examples of processes. A lowess process, MA plot (from the scripting interface) and a log plot.

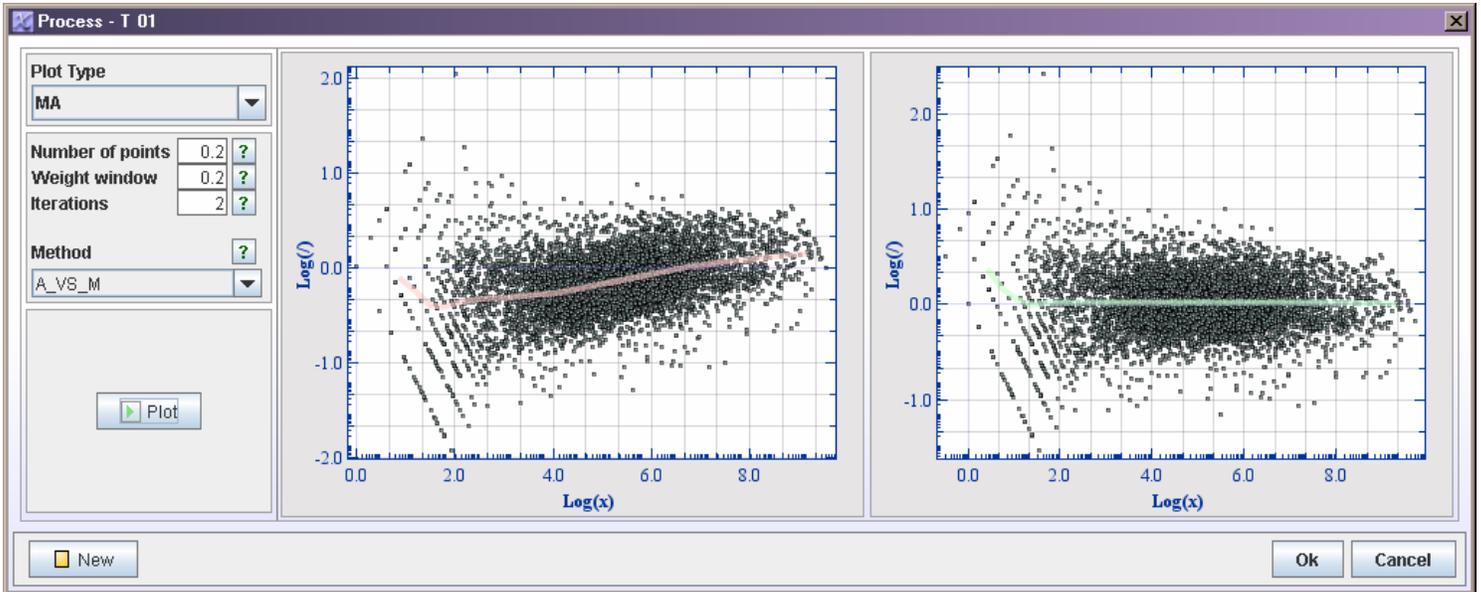
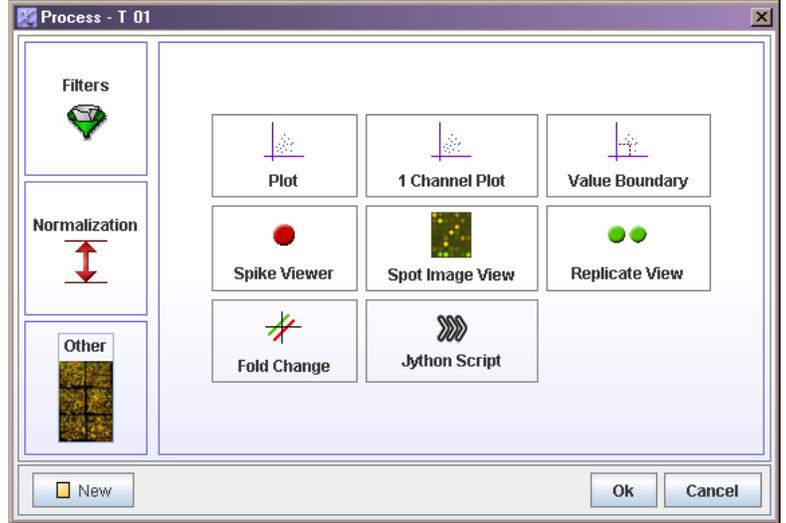
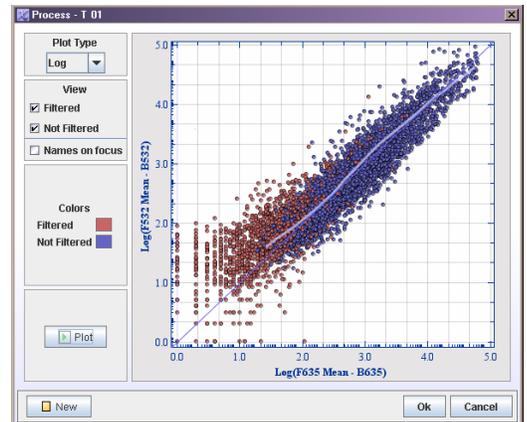
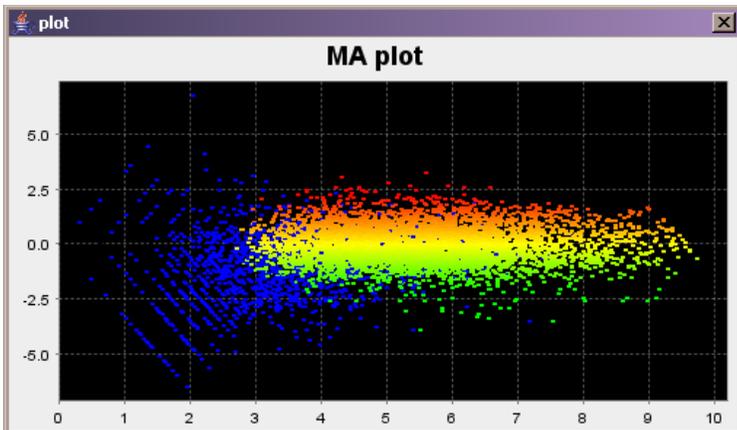


Figure 9 – A lowess normalization process



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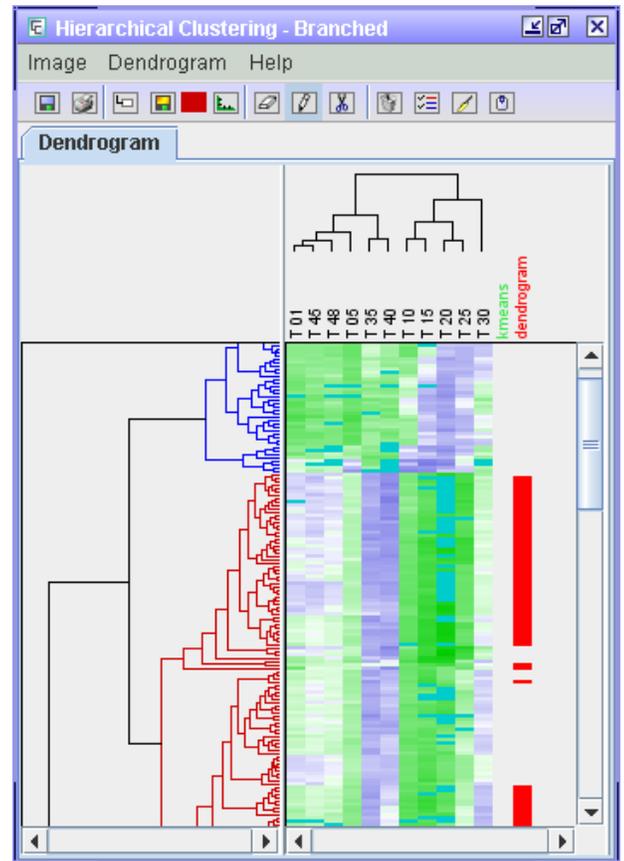
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## Clustering and projections

Hierarchical two-way clustering

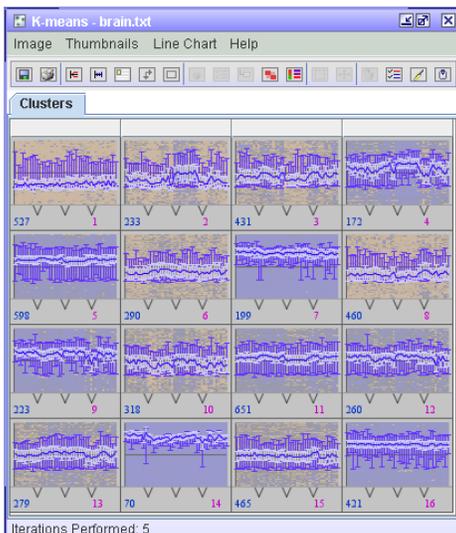
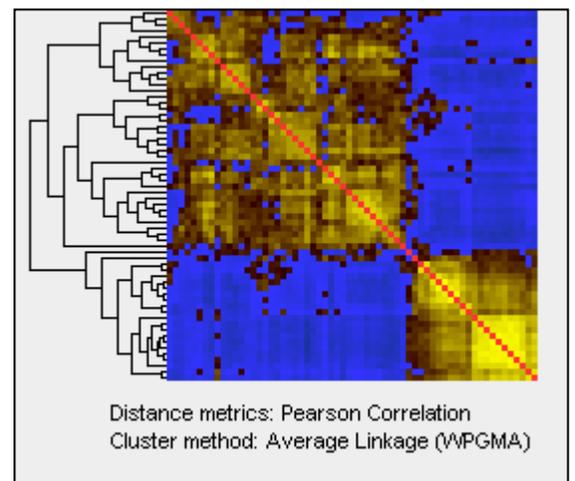
Clustering performed on both rows (genes) and columns (samples). One way clustering is also available for both genes and samples.

Many different similarity measures exist including correlation measures, Euclidean distance, Manhattan distance and Spearman rank correlation.



## Clustering samples with correlation matrix

A hierarchical clustering applied to samples to discover correlation in gene expression between samples.



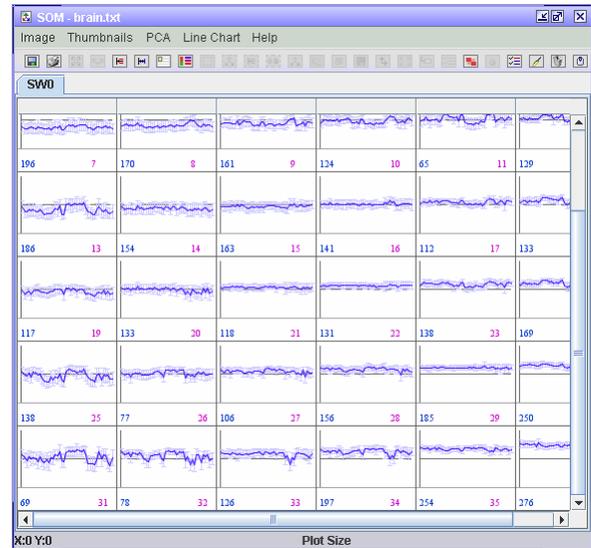
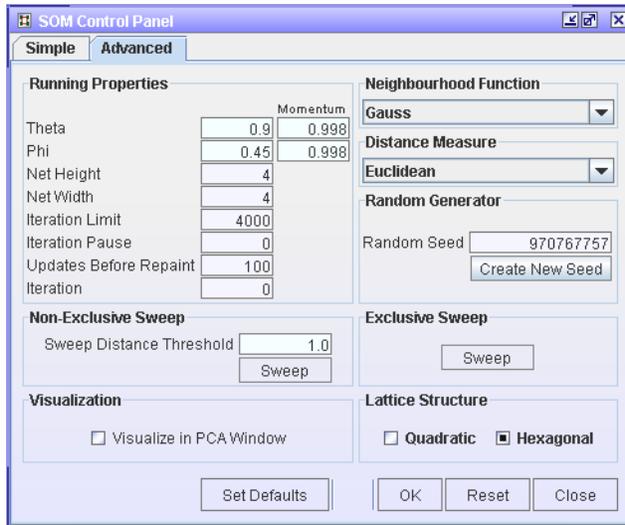
## k-means clustering

One of the simplest divisive clustering algorithms. This is a very good method to divide the data into subgroups which can be branched to subsets and analyzed individually to reduce complexity and increase effectivity.

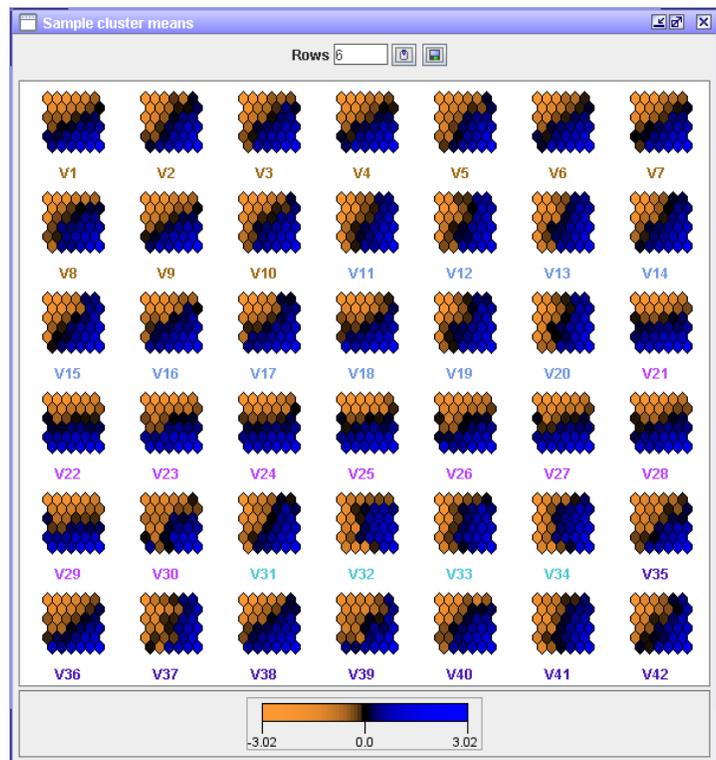
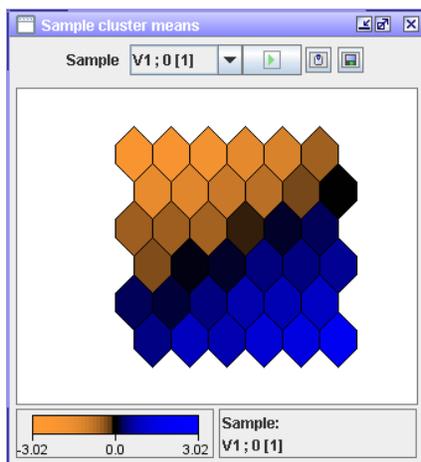
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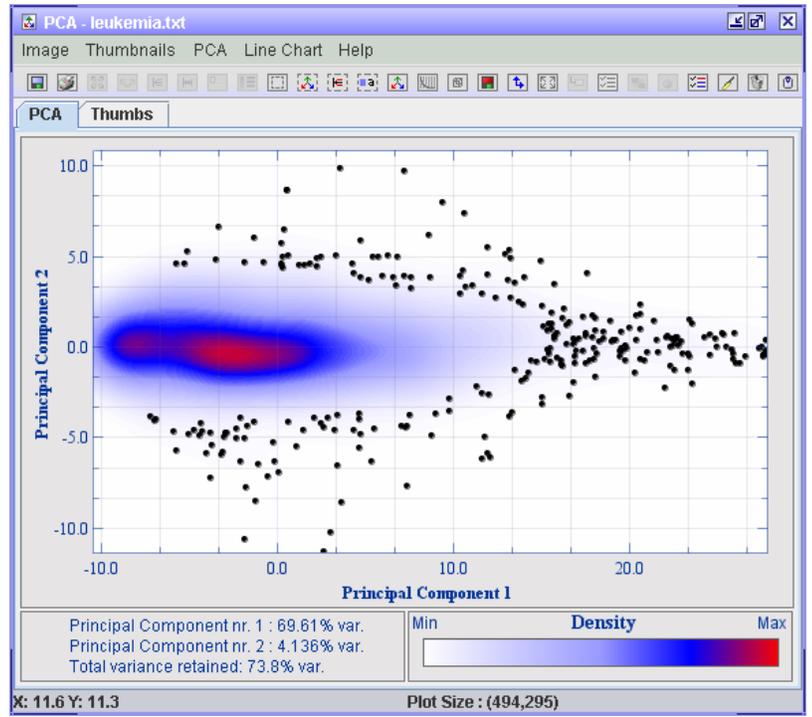
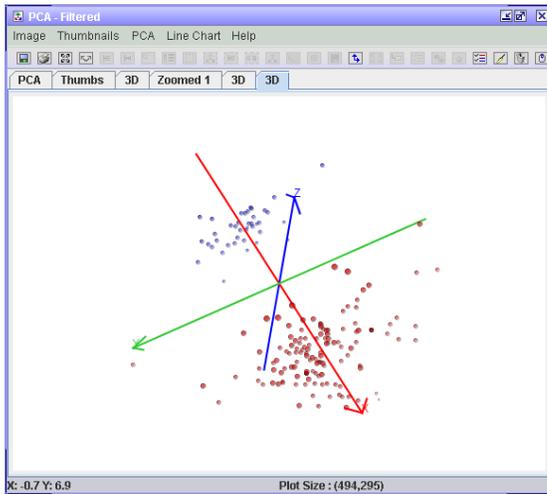
## Self organizing map



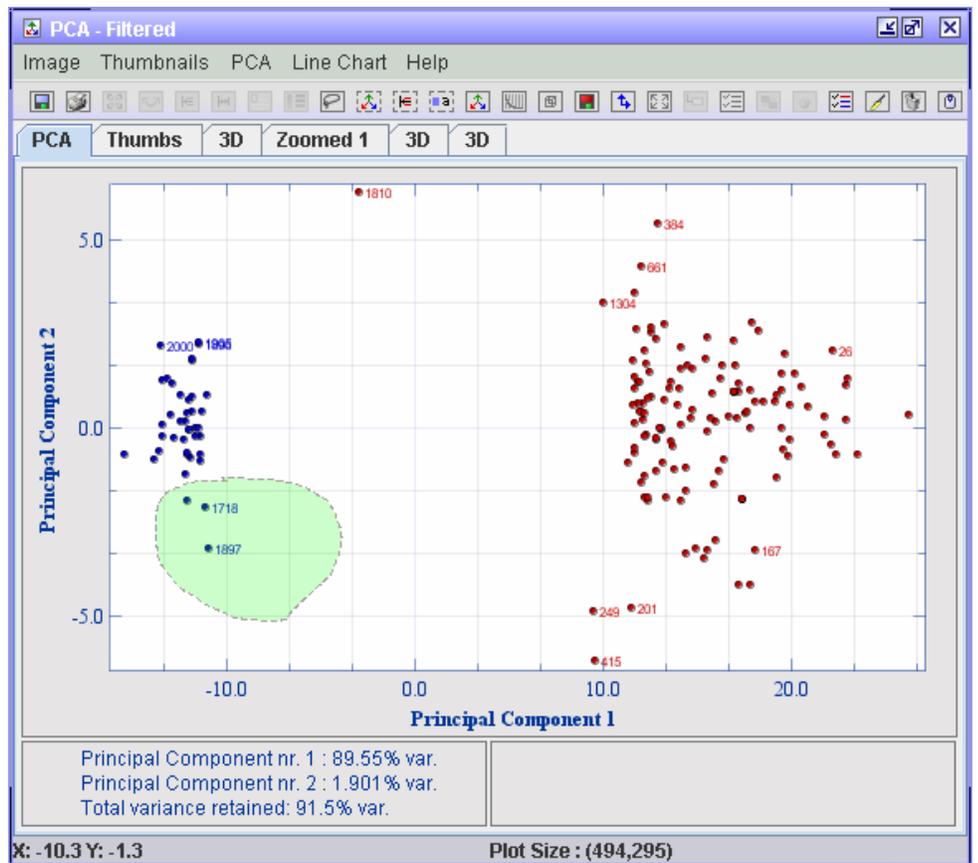
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## Principal component analysis

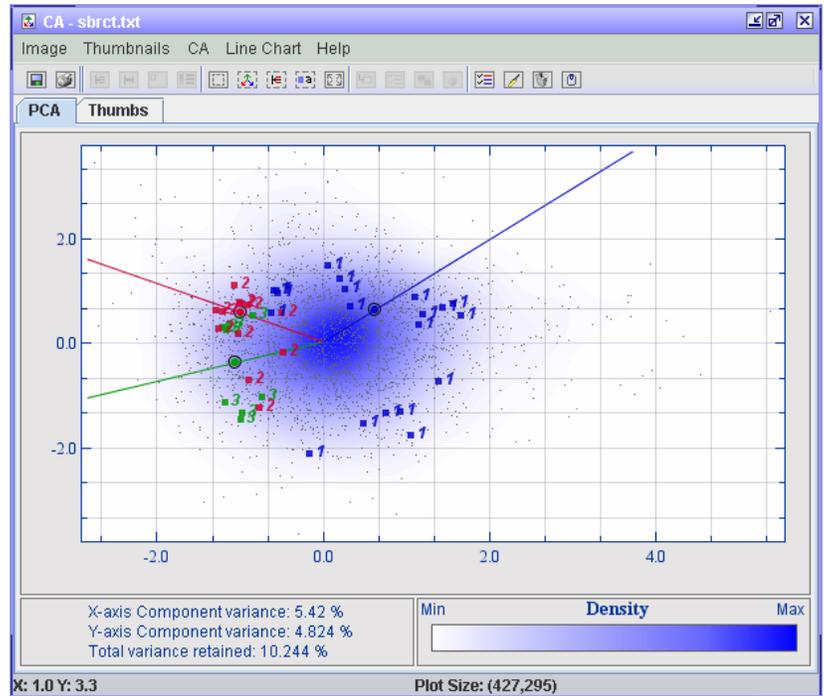
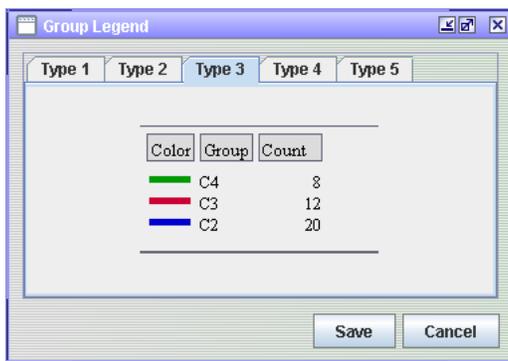


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## Correspondence analysis



## Similarity and profile search

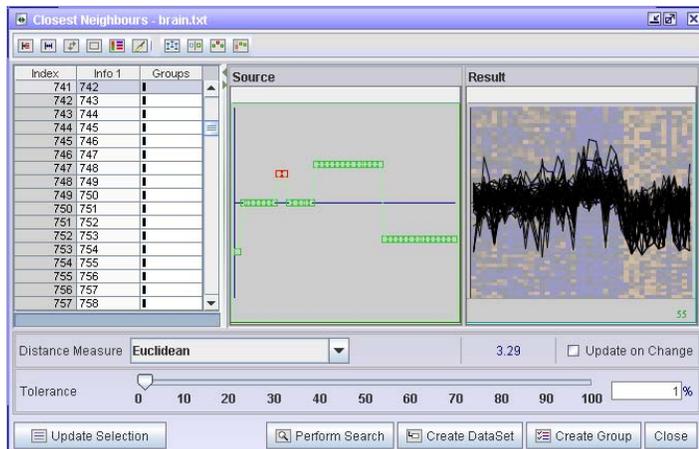


Figure 11 – Searching for specific profiles

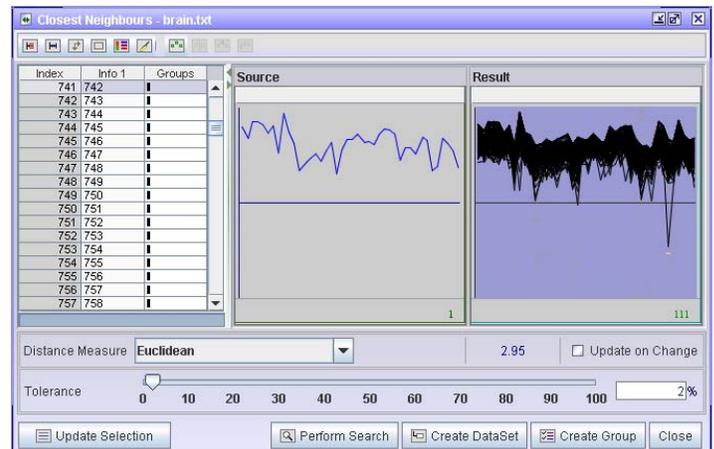


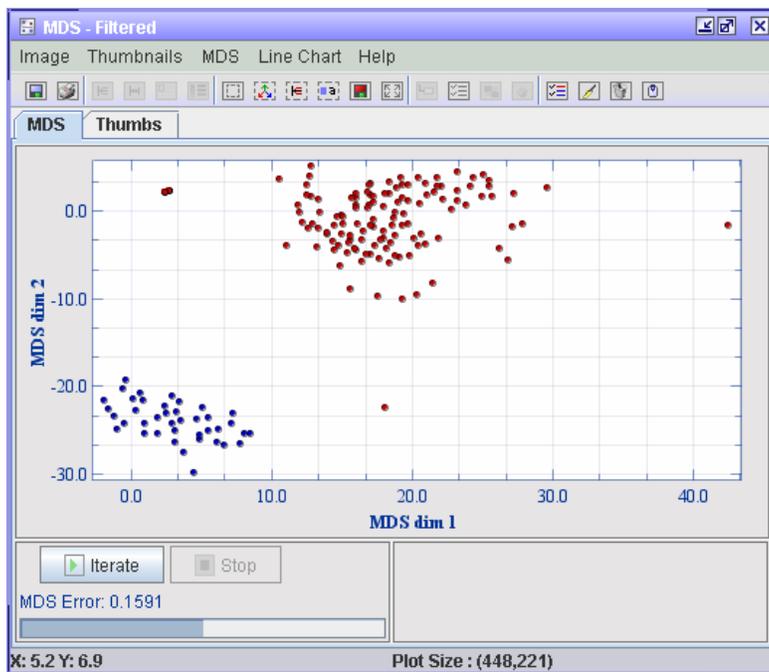
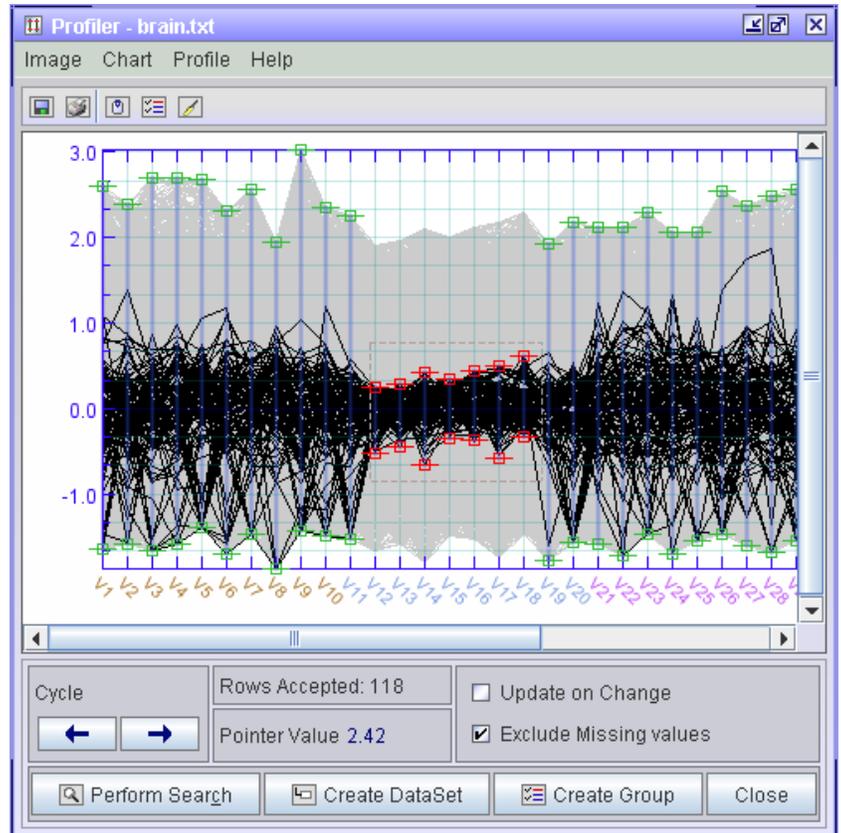
Figure 10 – Searching for expression similarity

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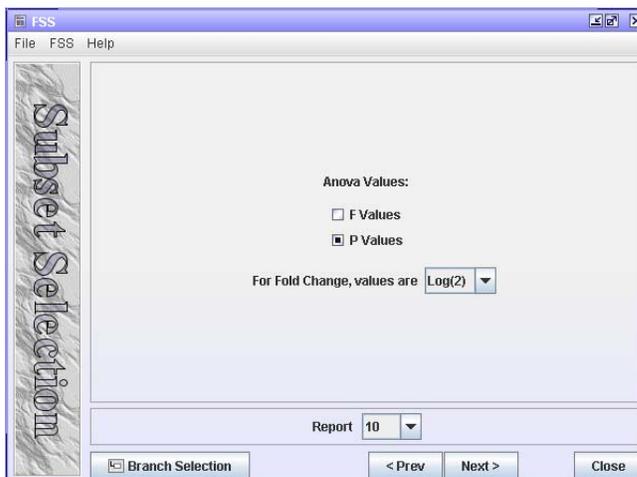
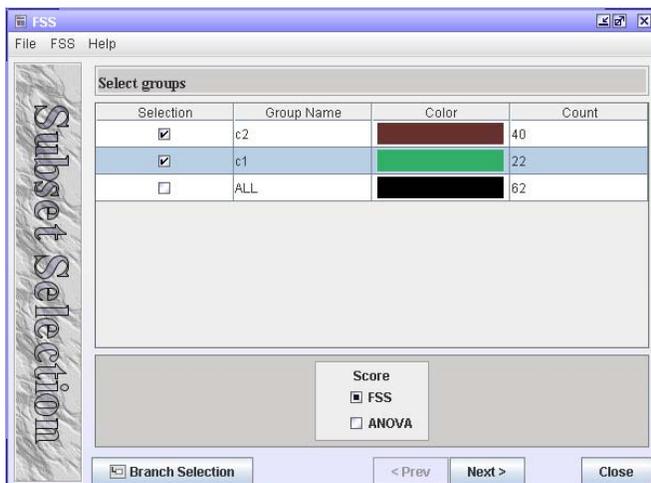
## Profile search



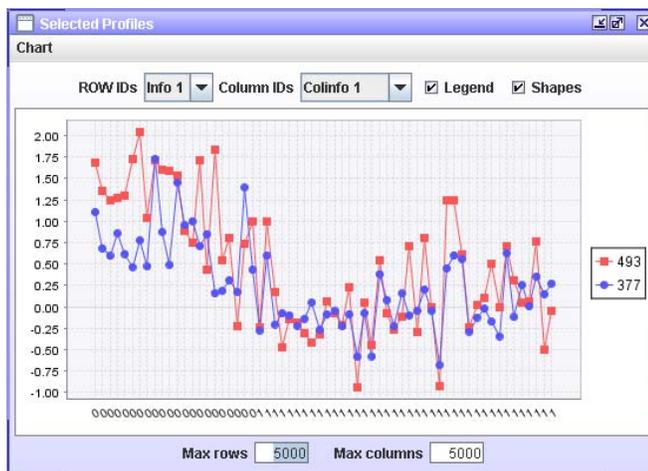
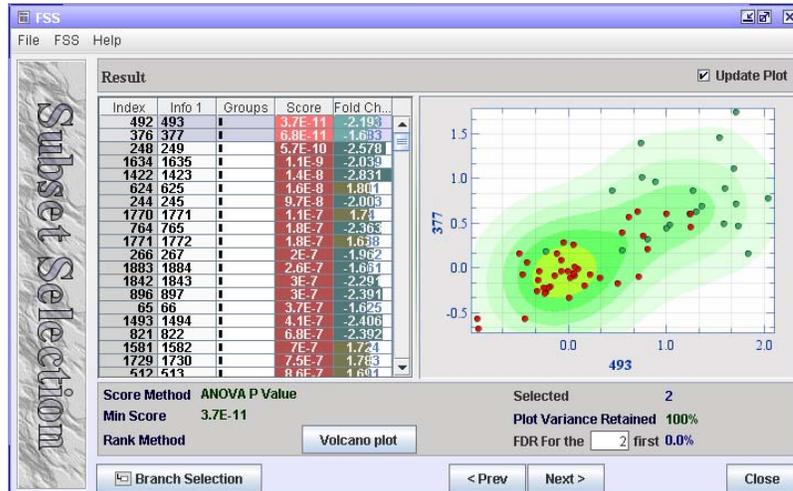
## Multidimensional scaling (MDS)



## Supervised analysis

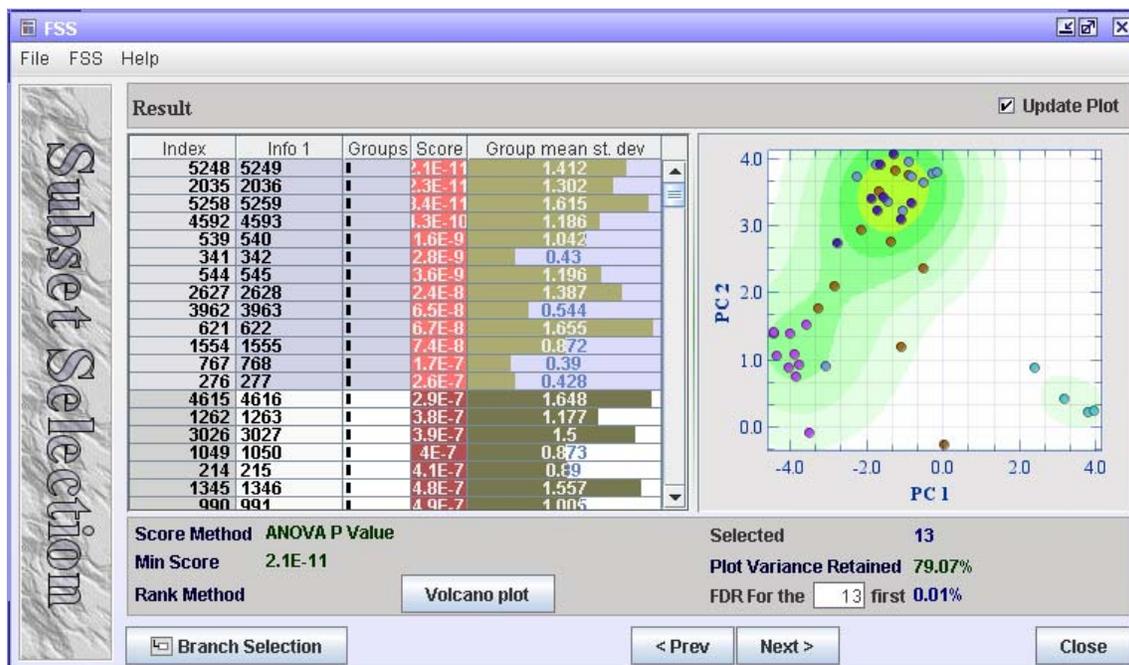


## Feature selection

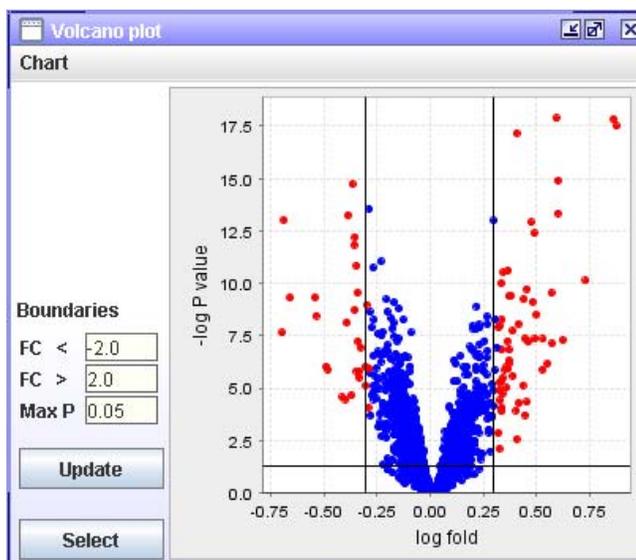




## Feature selection for three groups using ANOVA

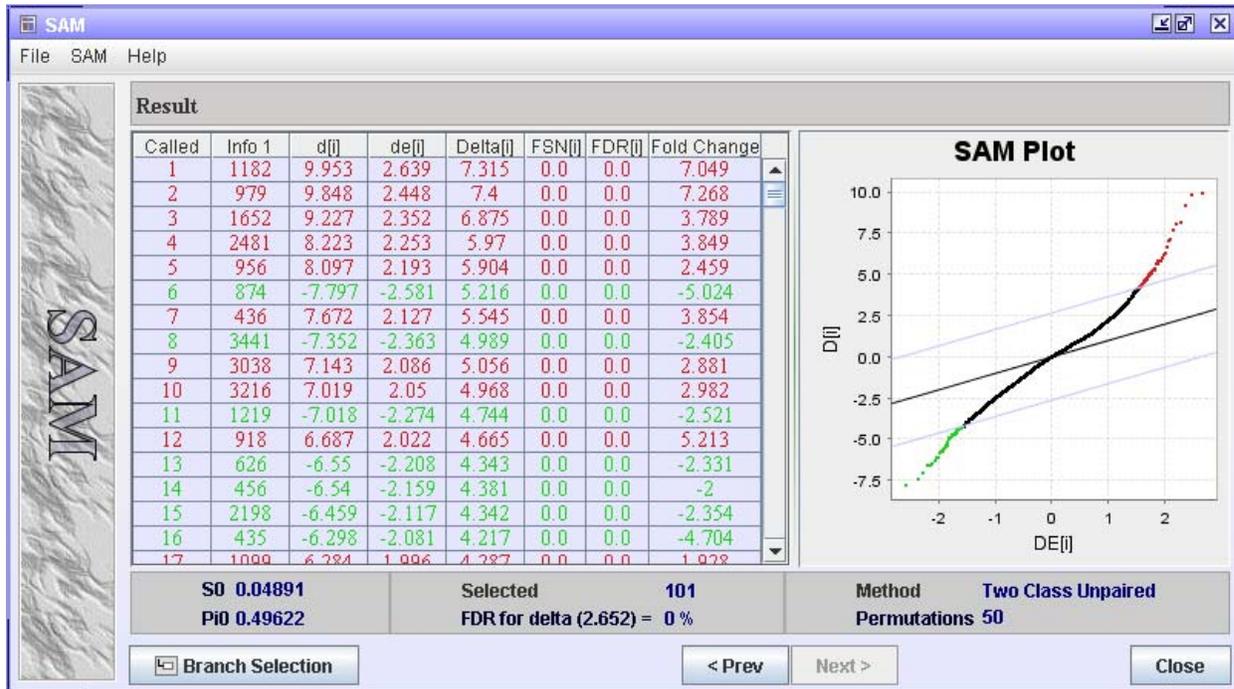


## Interactive feature selection volcano plot



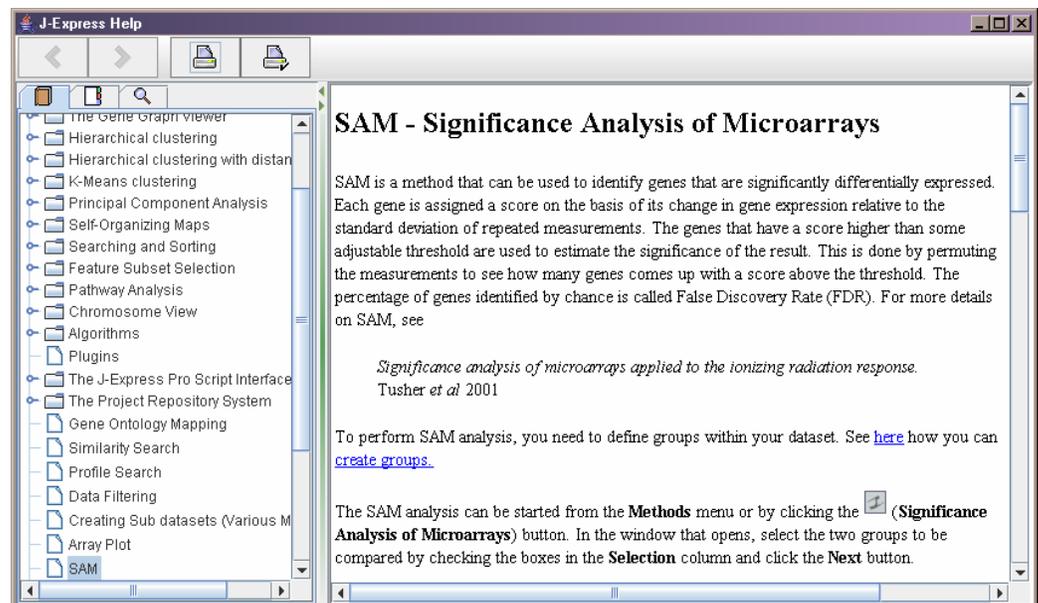


## Significance analysis of microarrays



## Interactive help

By pressing the F1 key in any active window, context sensitive help is available describing all parameters and result charts





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## Annotation mapping

The annotation manager component can be used to modify, add or delete annotation on genes and samples. You may double-click any cell to change its value. Right-click the table to add annotation columns or delete existing columns. The Current annotation tab shows the annotation currently in the selected data set. The add annotation tab lets you map tabular annotation files to the selected dataset.

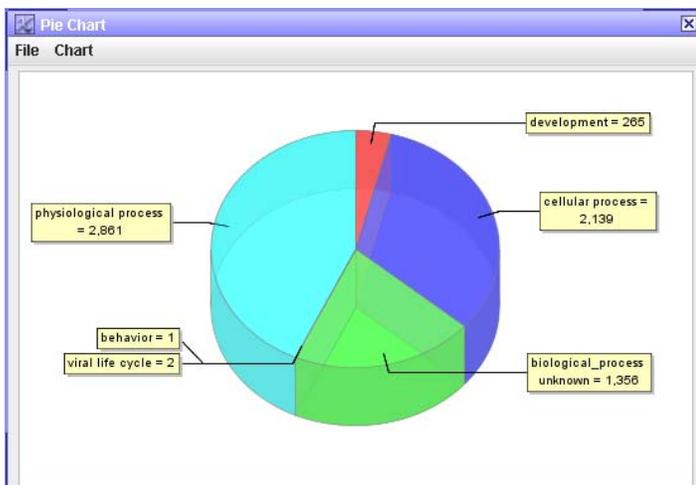
**Source File:** C:\data\Sri lankalhuman\_V3.0.3\_genelist\_s.txt

**Annotation mapping:** DataSet Key Column: Info 1, File Key Column: 3

**Selected annotation:** Annotation columns to import (comma separated): 5,6

Sample	1	2	3	4	5	6	7
PROPRIE...	384_number	384_positi...	oligo_id	oligo_seq...	gene_id	transcript_id	oligo_exo...
1	A01	-	-	-	-	-	-
1	A03	H200012278	GGGTCT...	ENSG000...	ENST000...	E	-
1	A05	H200013059	ATGAAC...	ENSG000...	ENST000...	E	-
1	A07	H200000993	GGAAGT...	ENSG000...	ENST000...	E	-
1	A09	H200003382	TGGGAC...	ENSG000...	ENST000...	E	-
1	A11	H300016831	TCCAGA...	-	-	-	-

## Gene Ontology analysis



**Name:** conjugation with cellular fusion  
**GO:** GO:000747

**Selection:**  Automatic Selection Update,  Recursive Selection, Maximum Members: 100,  Use Synonyms

**Mapping File:** gene\_association.sgd, **Data Identifier Column:** Info 0

Parameter	Value
alt_id	GO:0007322
alt_id	GO:0007333
alt_id	GO:0030461
alt_id	GO:0030477

**Data Set:**

Index	Info 0	Groups
5	YCL055W	
11	YDL039C	
18	YGL053W	
28	YBR040W	
33	YIR016W	
34	YIR145W	
40	YMR059C	



## Pathway analysis

**Kegg Pathways**

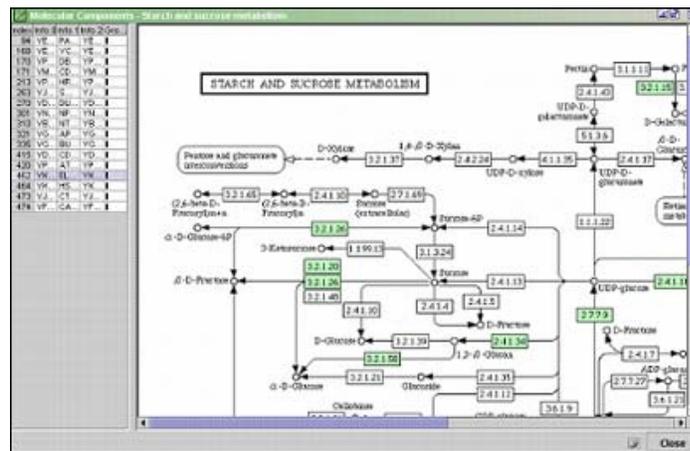
Pathway Set: *S.cerevisiae*

Filters:
 

- Minimum Number of Members: 1
- Maximum Standard Deviation Within Group: 0

Buttons: Download Set, Filter, Score Groups, Create Groups from Selected

Select	Name	Group	Open Pathway	
<input type="checkbox"/>	Starch and sucrose metabolism	6	3	Open Pathway
<input type="checkbox"/>	Inositol phosphate metabolism	4	4	Open Pathway



## Chromosome mapping

**Chromosomes**

Chromosome Help

- All Chromosomes
  - AE002566.pt
  - chromosomal\_feature.tab
  - Drosophila\_melanogaster
  - Plasmodium\_falciparum
  - Saccharomyces\_cerevisiae

Search: YPL\* Find Selected Genes in Selected Folder

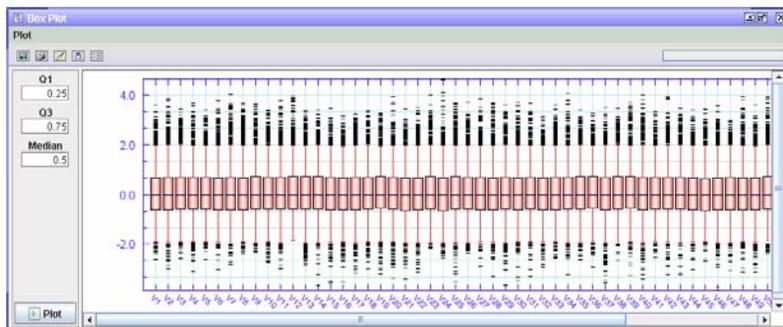
Use ID Column: 1 Clear results

File	Hit
Saccharomyces cerevisiae chromosome XIV, complete chromosome ...	YNL339C
Saccharomyces cerevisiae chromosome XVI, complete chromosome ...	YPL283C

Click to show selection Path, Double Click to open Chromosome View



## High level filtering and normalization



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## J-Express global repository

Load dataset from server

**Server**

**Disclaimer**

IMPORTANT: The Molmine server has a quota limit of 100MB per user, 1 user pr person. Note that Molmine is not responsible for the security or safety of the data you choose to save to the Molmine repository.

**Server and account settings**

Existing user  
 New user

User name:   
Password:   
Server url:   
Full name:

**Log in**  
Create new user  
Log out

**Group memberships**

Your are currently a member of: N/A  
Group name:   
Group password:   
Join group