ComparativeMarkerSelectionViewer Documentation

Module name: ComparativeMarkerSelectionViewer
Description: Views the results from ComparativeMarkerSelection
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The ComparativeMarkerSelectionViewer provides tools for reviewing and working with ComparativeMarkerSelection results. These tools include plots, a data table, expression profiles and heatmaps, filters, annotations, and creating dataset and feature list files. (A feature list is a text file with one feature per line.)

ComparativeMarkerSelectionViewer is an interactive tool. For non-interactive access to annotations, heatmaps, and creation of datasets and features lists, see the GeneCruiser, HeatMapImage, and ExtractComparativeMarkerSelection modules.

Plots

Plots are displayed in the upper portion of the viewer. Use the *Window* menu to select the plot to display:

- **Upregulated Features** (initially displayed) plots the descending test statistic values versus features sorted by rank. This plot is useful for visualizing the number of features that have a positive and negative test statistic value in each class.
- **Comparison plots (such as FDR(BH) vs Q Value)** provide a pair-wise comparison of different significance measures. These plots are useful to assess the relative stringency of the selected hypothesis rejection criteria. To display the comparison plots, click *Window>FDR(BH) vs Q Value*. To compare different significance measures: use the drop-down lists below the plot to select the measures to display on the X and Y axes and click *Change Axes*. The viewer updates the plot and the *Window* menu to reflect the new comparison.
- **λ vs. π_0** plots the estimated π_0 versus the tuning parameter λ. Use this plot to see how well the spline fits the data; that is, the quality of the π_0 estimate (1).
- **Histograms** show the null distributions for each measure of significance.
- **General Information** lists the parameters used to generate the ComparativeMarkerSelection results.

Use the following menu items to work with any plot:

View>Zoom In View>Zoom Out	Zoom in and out on the plot. (Alternatively, use your mouse to click-and-drag over the area to zoom in on.)
View>Reset	Return to the default zoom level.
View>Display Options	Change the title, labels, and other visual attributes.

File>Save Image	Save the plot to an image file.
File>Print	Print the plot (formats the plot to fit the page).

Data Table

The table in the lower portion of the viewer lists the ComparativeMarkerSelection results. For a description of each column, see the ComparativeMarkerSelection documentation. By default, the features in the table are ordered by score. To reorder the features, click the title of the key column; for example, to order features by rank, click Rank.

To find a feature in the table, select *Edit>Find*.

Expression Profiles and Heatmaps

The expression profile for a feature plots expression value per sample. A heatmap shows the same information, but color codes the expression values from red for the highest expression values through blue for lowest expression values.

To display an expression profile or heatmap:

1. Select one or more features from the data table.
2. Click *View>Profile* or *View>Heatmap*. Alternatively, right-click the data table and select *Profile* or *Heatmap* from the context menu.

If no features are selected, all features are displayed. Ordering all features by score and displaying them in a heatmap can be very informative. Displaying all features in a profile can be time consuming and is less useful.

Note: If the *Profile* and *Heatmap* commands are unavailable, your dataset is not open. To open your dataset, specify the *dataset filename* parameter when you launch the ComparativeMarkerSelectionViewer or, from the viewer, select *File>Open Dataset*.

Filters

Use filters to display only features that you are interested in:

1. Select *Edit>Filter Features>Custom Filter*. The Filter Features window appears.
2. In the Filter Features window, set your filtering criteria and click OK. The viewer shows only those features that meet your criteria.
3. To redisplay all features, select *Edit>Filter Features>Show All.*

Creating Datasets/Feature Lists

You can use the viewer to create a new dataset or feature list from the ComparativeMarkerSelection results:

1. Select *File>Save Derived Dataset* or *File>Save Feature List*. A window appears.
2. Choose the features to include in the dataset/feature list:
   - **Use current features** – the features currently displayed in the viewer (use filters to display the features that you want in the new dataset/feature list).

- **Use all features** – all features (ignore any filters).
- **Use selected features** – the features currently selected in the data table.

3. Choose a location and name for the new dataset/feature list.
4. Click *Create* to save the new dataset/feature.

Note: If the *Save Derived Dataset* command is unavailable, your dataset is not open. To open your dataset, specify the *dataset filename* parameter when you launch the ComparativeMarkerSelectionViewer or, from the viewer, select *File>Open Dataset*.

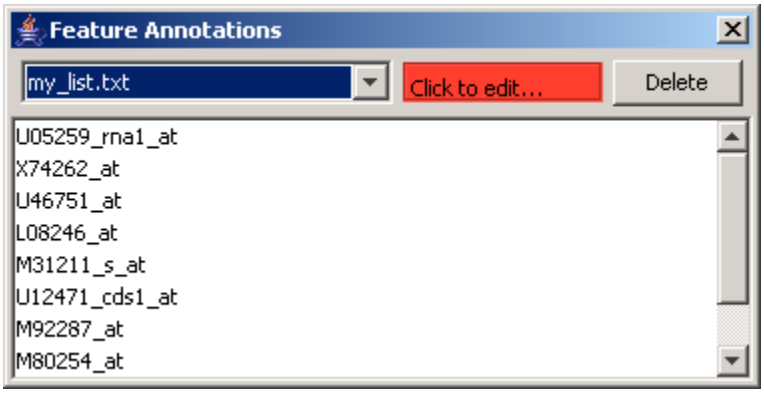
Annotations

The ComparativeMarkerSelectionViewer provides two annotation methods:

- Feature annotations use color to annotate features in the data table
- GeneCruiser annotations retrieve information about Affymetrix probe ids and add it to the data table

To use feature annotations:

1. Create a feature list file (one way of doing this is described above).
2. Select *File>Open Feature List(s)* to open your feature list file. In the Feature column of the data table, a color bar appears next to each feature in the feature list.
3. Select E*dit>Feature Annotations* to edit the color or close the feature list:



4. In the Feature Annotations window, select your feature list from the drop-down list. The color assigned to that feature list appears in the box to the right.
   - To change the color, click the box and select a new color.
   - To close the feature list and remove the color bars from the table, click *Delete*.

To use GeneCruiser annotations:

1. Select *GeneCruiser>Gene Information*.
2. Select the features that you want to retrieve annotations for in the table.
3. Choose which fields to retrieve from GeneCruiser in the GeneCruiser dialog.
4. The annotations appear in additional columns in the table.

Parameters:

Name	Description
comparative.marker.selection.filename	The output from ComparativeMarkerSelection
dataset.filename	The dataset file used as input to ComparativeMarkerSelection

References:

Gould et al. **Comparative Gene Marker Selection suite**. Bioinformatics Advance Access published on May 18, 2006, DOI 10.1093/bioinformatics/btl196.

Platform dependencies:

Task type: Visualizer
CPU type: any
OS: any
Language: Java
Java JVM level: 1.4