Sort Rows by Prototype

Sort Rows by Prototype is a function that can identify genes with similar expression patterns. For example, if a gene with an interesting expression pattern has been detected, using *Sort Rows by Prototype* makes it possible to find other genes that have a similar pattern of intensity values. Although this is most commonly used for changes in gene expression over a time course, it can be applied to other experimental designs as well.

To invoke *Sort Rows by Prototype,* probe(sets)/genes must be on rows. If you want to use this tool to analyze the main intensity values spreadsheet, the spreadsheet must be transposed prior to analysis. A common way to view and analyze gene expression in a time-series experiment is to include means or LS means in the ANOVA spreadsheet.

- Configure the ANOVA dialog to include the factor or interaction of interest
- Select **Advanced...** from the ANOVA dialog
- Select **LS-Mean** or **Mean**
- Use the drop down menus to select the factors or interaction you want the LS mean / mean of
- Select **Add** for each
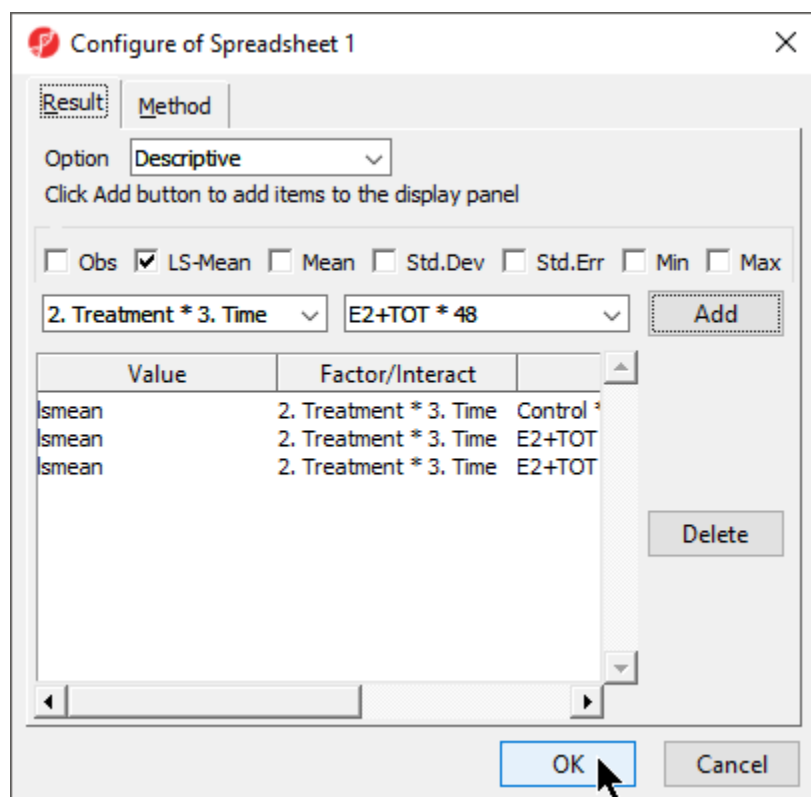- Select **OK** (Figure 1)

Figure 6. Using Advanced ANOVA setup to include group means in the ANOVA output

- Select **OK** to close the ANOVA configuration dialog and open the ANOVA spreadsheet

The *Sort Rows by Prototype* function uses every non-text column in a spreadsheet to build and compare patterns; any columns you do not want to include in the pattern similarity analysis need to be removed before running the function.

If you want to preserve the ANOVA spreadsheet contents, clone the ANOVA spreadsheet prior to deleting columns.

- Select columns you want to remove
- Right-click on a selected column headers
- Select **Delete** from the pop-up menu

- Select (⊞) from the main command bar to save the modified spreadsheet

We can now invoke *Sort Rows by Prototype* on the modified spreadsheet.

- Select **Tools** from the main toolbar
- Select **Discovery**
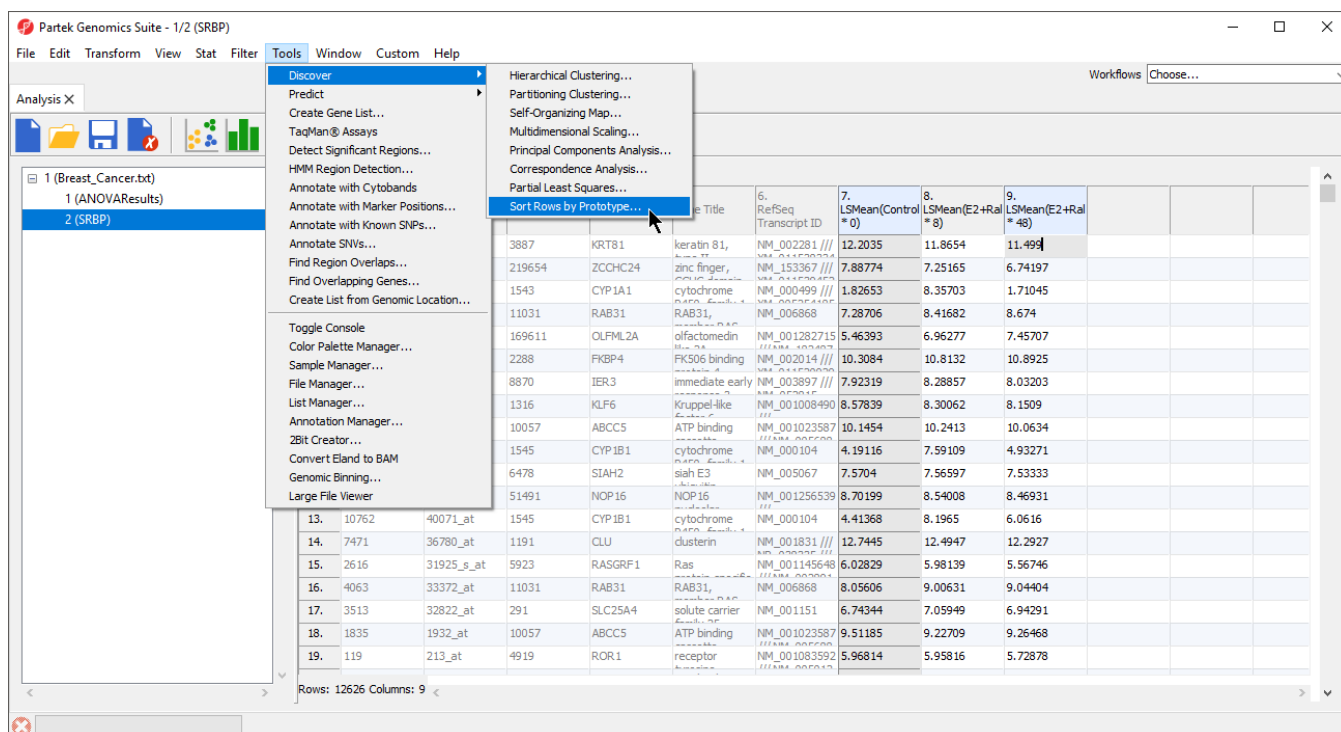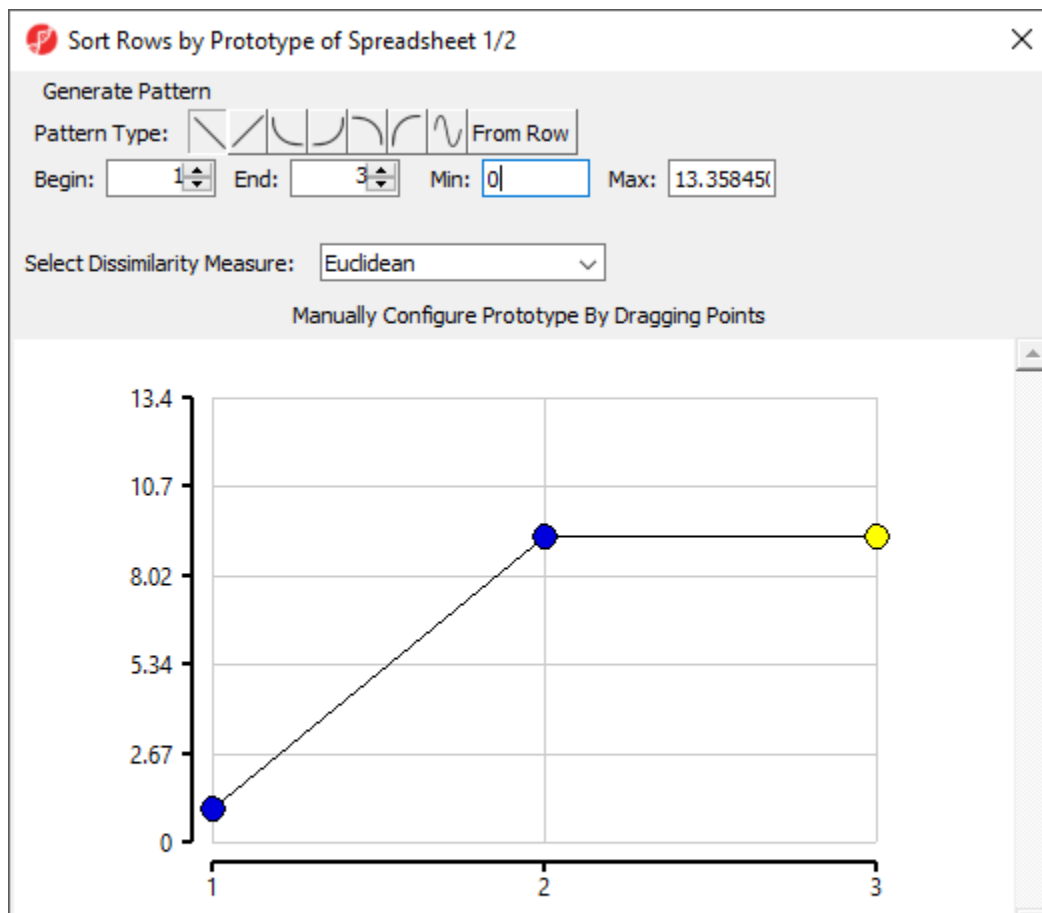- Select **Sort Rows by Prototype...** (Figure 2)

Figure 7. Invoking Sort Rows by Prototype on spreadsheet with LS mean values for conditions/time points

The *Sort Rows by Prototype* dialog will launch (Figure 3).

Sort Rows by Prototype of Spreadsheet 1/2   ✕

Generate Pattern

Pattern Type: [⟍] [⟋] [⌴] [⌣] [⌐] [⌢] [ᴧ] [From Row]

Begin: [1 ⬍] End: [3 ⬍] Min: [0|] Max: [13.35845(]

Select Dissimilarity Measure: [Euclidean ⌄]

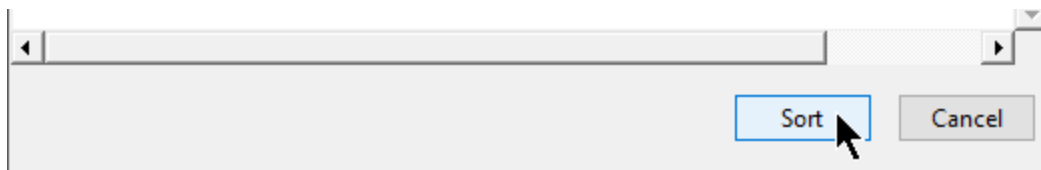Manually Configure Prototype By Dragging Points

Figure 8. Sort Rows by Prototype dialog

This dialog allows you to configure the pattern, or prototype, that all probe(sets)/genes will be compared to by *Sort Rows by Prototype.*

The *Pattern Type* options ( ) allow preset shapes to be applied to the prototype within the range specified by the *Begin, End, Min,* and *Max* parameters. The final option *From Row* allows you to select any row number in the spreadsheet to serve as the prototype. This is a useful option if you have a particular gene of interest and want to find other genes with similar expression profiles in your data set. You can also manually configure the prototype by dragging the points.

The *Select Dissimilarity Measure* drop-down menu allows to select from a wide variety of parametric and non-parametric measures of dissimilarity.

- After configuring the prototype and selecting a dissimilarity measure, select **Sort** to run the function
- Select **Cancel** to close the dialog

A new column 1 will be added to the spreadsheet and the rows will be reordered (Figure 4). The new column contains the dissimilarity score for each row; the lower the value, the more similar the row is to the prototype. The row with the highest similarity to the prototype is listed first, with the other rows listed in descending similarity to the prototype.
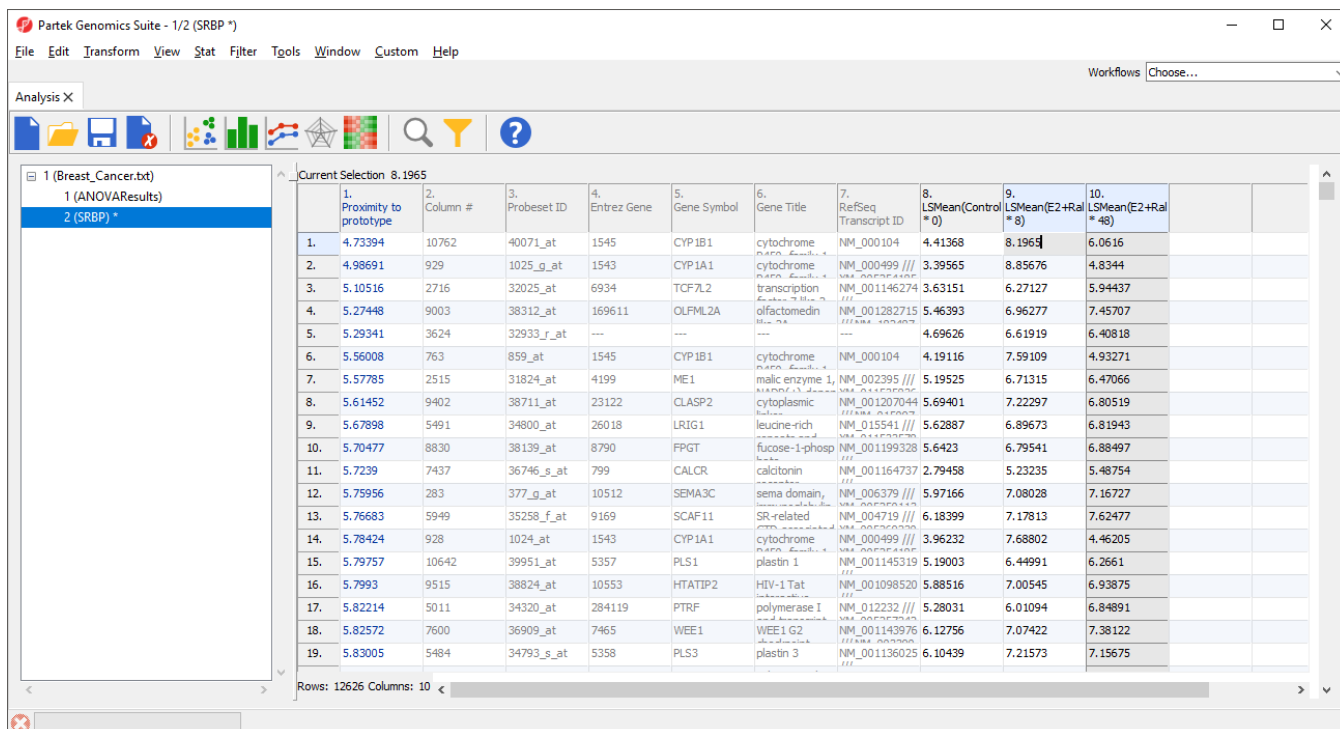

Figure 9. Result of sorting by prototype. The prototype gene is in the first row, while the other genes are listed based on their similarity to the prototype gene. Smaller proximity values imply more similarity to the selected shape

To view the results, we can generate a profile plot of several of the rows. For example, here we will show the top five most similar probe(sets)/genes.

- Select the row headers of the top 5 rows by selecting each while holding the **Ctrl** key or selecting the first then fifth while holding the **Shift** key
- Select **View** from the main toolbar
- Select **Profiles**
- Select **Row Profiles**
- Select **Select** for both *Plots* and *X-Axis* in the *Configure Data Source* dialog

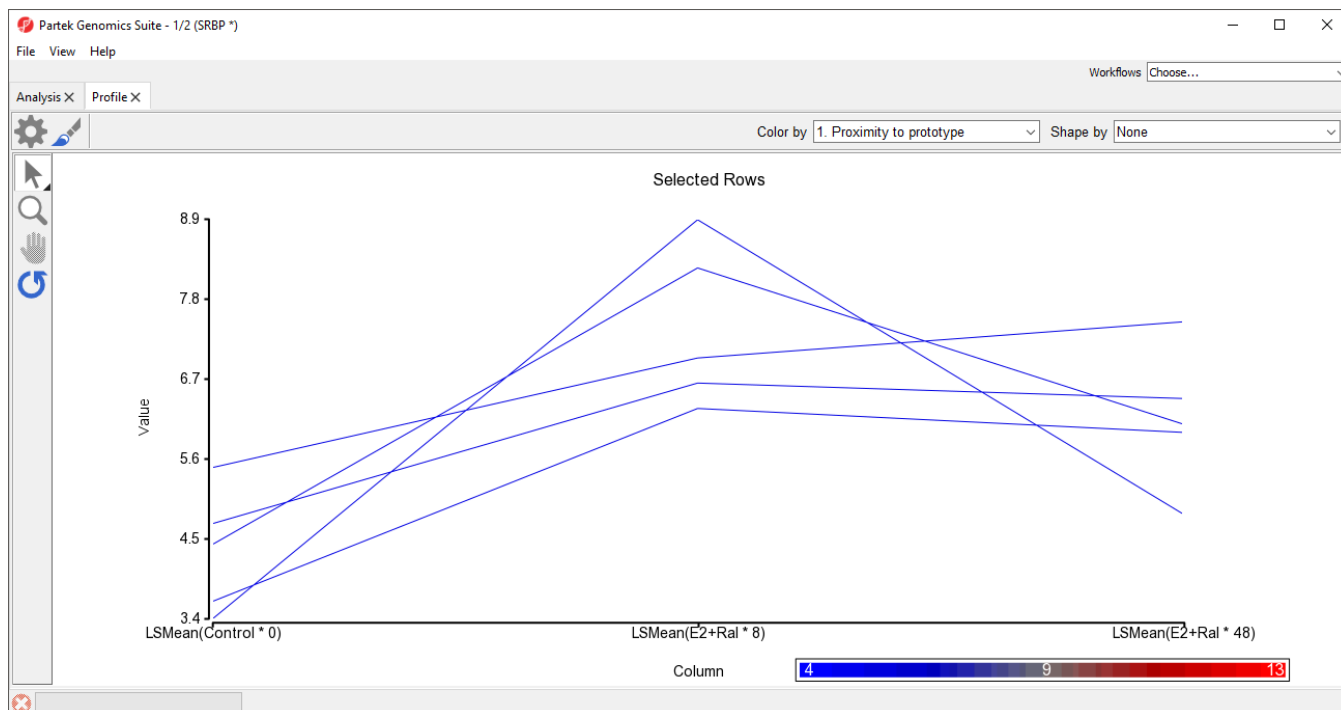The profile plot will open as a new tab (Figure 5).

Figure 10. Profile plot of 5 probe(sets)/genes most similar to the prototype used in Sort rows by prototype

« Scatter Plot and MA Plot   Manhattan Plot »

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.

Your Rating: ☆☆☆☆☆   Results: ★★★★⯪ 34 rates