Performing hierarchical clustering

The gene list in spreadsheet Down_Syndrome_vs_Normal (A) can be used for hierarchical clustering to visualize patterns in the data.

• Under the Visualization section in the Gene Expression workflow, select Cluster Based on Significant Genes

The Cluster Significant Genes dialog asks you to specify the type of clustering you want to perform.

- Choose Hierarchical Clustering and select OK
- Choose the Down_Syndrome_vs_Normal (A) spreadsheet under the Spreadsheet with differentially expressed genes
- Choose the Standardize shift genes to mean of zero and scale to standard deviation of one under the *Expression normalization* panel (Figure 1)

This option will adjust all the gene intensities such that the mean is zero and the standard deviation is 1.

Ø Cluster the significant genes	×
Cluster genes using hierarchical dustering on the expression values using only the genes present in the selected spreadsheet.	
Spreadsheet with list of significant differentially expressed genes.	0
1/Down_Syndrome_vs_Normal (A)	~
 Expression normalization Standardize - shift genes to mean of zero and scale to standard deviation of one Shift - shift genes to mean of zero None - do not adjust the values 	Cancel

Figure 1. Configuring Hierarchical Clustering

• Select **OK** to generate a *Hierarchical Clustering* tab (Figure 2)



Figure 2. Hierarchical Clustering of Down_Syndrome_vs_Normal (A)

The graph (Figure 2) illustrates the standardized gene expression level of each gene in each sample. Each gene is represented in one column, and each sample is represented in one row. Genes with no difference in expression have a value of zero and are colored black. Genes with increased expression in Down syndrome samples have positive values and are colored red. Genes with reduced expression in Down syndrome samples have negative values and are colored green. Down syndrome samples are colored red and normal samples are colored orange. On the left-hand side of the graph, we can see that the Down syndrome samples cluster together.

For more information on the methods used for clustering, you can refer to **Chapter 8: Hierarchical & Partitioning Clustering** in **Help > User's Manual**. For a tutorial on configuring the clustering plot, please refer to Hierarchical Clustering Analysis.

« Creating gene lists from ANOVA results Adding gene annotations »

Additional Assistance

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

