GenePattern

SOMClusterViewer Documentation

Module name: SOMClusterViewer
Description: Used to view SOM clustering results
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Date: 10/23/03
Release: 1.0

Summary: Once a data set has been clustered with the SOMClustering algorithm, the results can be viewed with the SOMClusterViewer. This view will have a **View Type** format of Data Means, SOM Centers, or Both where the type is chosen from the pull down menu before clicking the **Show** button. The left half of the panel shows plots of the clusters while the right half of the panel shows the elements contained in the selected cluster and distances to the centroid. A particular cluster can be selected for viewing by clicking on one of the plots on the left side of the panel (which will then be highlighted by a yellow box around it). The right side of the panel will then display the samples contained in the cluster and their distance from the cluster centroid. Clicking on the **Save Current…** button will save the clustering results will produce an output file with a summary of objects and their clusters.

References:

- None.

Parameters:

Name	Description	Choices
filename:	SOM Properties ODF file	
display:	The display method	0=Data Means;1=SOM Centers;2=Both

Return Value:
        Stdout.txt: the "stdout" text output from running the program.

Platform dependencies:

Task type:	Visualizer
CPU type:	any
OS:	any
Java JVM level:	1.3
Language:	Java