

shRNAscores Documentation

Description: Collapses replicate array measurements and compare each cell line to a reference array. Returns a .gct file of shRNA scores per cell line.

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Summary

Collapses replicate arrays and compares each cell line to a reference array. Outputs three different scoring schemes, including fold change, signal to noise, and adjusted fold change. Fold change = [sum of cell line replicates]-[sum of reference replicates]. Signal to noise = fold change/ ([standard deviation of cell line replicates]+[standard deviation of reference replicates]). Adjusted fold change = fold change/[standard deviation of reference replicates mean centered at 1 and floored at 1].

References

Cheung et al.

Input Parameters

Name	Description
gct	Input file of pre-processed array data from dCHIP. Must be in .gct file format, use 'RNAigctconverter' module.
array info	Array annotation from the 'makeArrayInfo' module. One array per row, annotations in columns.
reference	Reference to compare each line to. Allowed values= {partial or total match to anything in 'Array_timepoint' column of the array info file above}. (Default=DNA)
annotation	shRNA annotation file (.chip file). Use TRChuV2.chip file for 55K pool.
output prefix	Prefix for output file names. (Default=test)

Input files

1. Input .gct data file **REQUIRED**

Input pre-processed data file of replicate arrays (columns) and shRNAs (rows) in .gct file format.

2. Array annotation file **REQUIRED**

Array annotation from the 'makeArrayInfo' module. One array per row, annotations in columns.

3. shRNA annotation file **REQUIRED**

shRNA annotation file (.chip file). Use TRChuV2.chip file for 55K pool.

Output Files

1. Signal to noise data file (<extension>_S2N.gct)

A data file of cell lines (columns) and shRNAs (rows) in .gct file format.

2. Fold change data file (<extension>_FC.gct)

A data file of cell lines (columns) and shRNAs (rows) in .gct file format.

3. Adjusted fold change data file (<extension>_adjustedFC.gct)

A data file of cell lines (columns) and shRNAs (rows) in .gct file format.

4. Sample annotation file (<extension>_SampleInfo.txt)

Annotation file for only the cell lines found in the output data files.

Platform Dependencies

Module Type:	RNAi
CPU type:	any
OS:	any
Language:	R