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NormLines, v11

Normalizes shRNA or CRISPR guide scores across cell lines using ZMAD, PMAD, rank, Z scores, global z-scores, lowess or quantile - ignores NaNs

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Algorithm Version:

Introduction

This module takes the data and puts the cell line data ranges on the same scale. For each cell line, the module either quantile normalizes to the mean distribution of all cell lines, or subtracts the median (ZMAD) or peak/mode (PMAD) and divides by the MAD.

Parameters

Name	Description
gct file *	Input gct file after reagent scoring
method *	Method of normalization. Options are ZMAD, PMAD, quantile, Zscore, globalZ, lowess
plotfile *	Output filename for plot showing before and after normalization

* - required

Input Files

1. Input reagent data file
Input data file of cell lines (columns) and reagents (rows) in GCT file format.

Output Files

1. Output data file *[method]_[Input data filename].gct*
A normalized (by *[method]*) data file of cell lines (columns) and reagents (rows) in a GCT file format.

2. plotfile *[plot filename].pdf*

A density plot showing the reagent distribution before and after normalization for each cell line.

Platform Dependencies

Task Type:

RNAi

CPU Type:

any

Operating System:

any

Language:

R

Version Comments

Version	Release Date	Description
11		



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