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PertFoldChange, v9

Calculate the fold change of each sample in a gct file, based on the appropriate DNA reference value (present in a gct file of the same dimension).

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Algorithm Version:

Introduction

PertFoldChange is a GenePattern module that calculates the fold change values of all reagents for each sample in a GCT file. The fold change is calculated by subtracting the starting DNA reference matrix in the user-uploaded DNA reference file from the reagent value matrix in the user-uploaded DNA reference file from the reagent value matrix in the user-uploaded DNA reference file from the reagent value matrix in the user-uploaded GCT file (both matrices should have the same dimensions). The module outputs a GCT file containing the fold change of each sample, for each reagent in the dataset.

Parameters

Name	Description
gct file *	Data file (.gct) containing reagent data.
DNA reference file *	A GCT file containing the values of the DNA pool reference per sample/reagent (same dimensions as input GCT file).
prefix *	User defined prefix of output file names.

* - required

Input Files

1. gct file
   Data file containing reagent data, with cell lines as columns and reagents as rows.

2. DNA reference file
   A GCT file containing the values of the DNA pool reference per sample/reagent (same dimensions as input GCT file).

Output Files

1. Data file with fold change values   *[prefix]_*FC.gct
   A GCT file containing the fold change values of each sample in the user-inputted dataset.

Platform Dependencies

Task Type:
RNAi

CPU Type:
any

Operating System:
any

Language:
R

Version Comments

Version	Release Date	Description
9	2013-03-20	

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