

[← Go Back \(/\)](#)

NormToNegCtrls, v9

Normalizes screening data to a file of negative control identifiers

Author: Barbara Weir, Han Xu;The Broad Institute

Contact: bweir@broadinstitute.org

Algorithm Version:

Introduction

NormToNegCtrls is a GenePattern module that normalizes reagent data based on the supplied negative controls. The user inputs a GCT file of data to be normalized and a txt file with a list of negative control sequences. The module then subtracts the column medians of the negative control sequences from the data and returns a normalized GCT file.

Parameters

Name	Description
inGctFile *	Input GCT formatted file to normalize
outGctFile *	Name of output file
negCtrlFile *	one column text file of negative controls (list of barcode sequences)

* - required

Input Files

1. inGctFile

The inGctFile should be data in a GCT file format containing at least 20 reagents (row names) that match those in the negCtrlFile.

2. negCtrlFile

The negCtrlFile is a one column text file with a list of sequences matching at least 20 sequences in the inGctFile.

Output Files

1. Normalized GCT file *[outGctFile].gct*

The normalized GCT file contains the normalized data from the inGctFile with respect to column medians.

Example Data

[provide example data, including input files and parameter settings]. (we'll put the input files on the ftp site and link to them from the doc)

Requirements

[any software requirements for running this, e.g., version of R, licensing]

Platform Dependencies

Task Type:

RNAi

CPU Type:

any

Operating System:

any

Language:

R

Version Comments

Version	Release Date	Description
9		Updated from NormtoNegControls



(<http://www.broadinstitute.org>)©2021
Broad Institute of MIT & Harvard (<http://www.broadinstitute.org>)