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QCcheckpoint, v80

Runs standard QC metrics on log2 normalized or fold change data.

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Algorithm Version:

Introduction

[Why use this module? What does it do? If this is one of a set of modules, how does this module fit in the set?]

Algorithm

[if applicable: a short overview of the algorithm in normal prose, followed by any details; write overview as if you are explaining to a novice]

References

[appropriate papers cited]

Parameters

Name	Description
gctFiles *	Between 1 and up to 7 .gct files of log2 normalized data.
extension *	String to add to output file names.
log2 *	Is this log2 normalized data or after fold change calculation?
zmed_threshold *	Lines with zmed below this value will be marked as potential failures.
ZnegStd_threshold *	Lines with ZnegStd above this value will be marked as potential failures.

* - required

Input Files

1. [parameter name]
   [Description. For example: The segmentation file contains the segmented data for all the samples identified by GLAD, CBS, or some other segmentation algorithm. (See GLAD file format in the GenePattern file formats documentation.) It is a six column, tab-delimited file with an optional first line identifying the columns. Positions are in base pair units.

Output Files

1. [File name]
   [Description of the content, file format, and how to interpret the results.]

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:

CPU Type:
any

Operating System:
any

Language:
any

Version Comments

Version	Release Date	Description
80		