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MatchToReference, v79

Matches the genotypes of the input cell lines to all previously run cell lines.

Author: Ann Sizemore;The Broad Institute

Contact: AchillesTeamArchive@gmail.com

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
plate name *	Prefix for files. Example: Plate_20
input_file *	.csv file of cell line genotypes from FPmatching module.
threshold	Fraction of genotypes that must match exactly for the pair to be considered a match.
master file *	File containing all lines to match against.
concatenate *	Indication of whether new cell lines should be added to the master file.
reps *	Has this plate been included in the master file before or is this a brand new plate?

* - 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
79		



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