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PTM_SEA, v2

PTM-SEA for use with PTMsigDB

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Algorithm Version:

Introduction

Module for PTM site-specific gene set analysis.

Algorithm

Modification of GSEA to handle PTM sites and direction of change

References

Krug, et. al. Under Review. MCP.

Parameters

Name	Description
input data *	Input data file (gct format)
output prefix *	Prefix for output file names
pathway db *	Pathway database (gmt format)
normalization *	Sample normalization method
weight *	When weight==0, all genes have the same weight; if weight>0 actual values matter and can change the resulting score
correlation *	Correlation type

Name	Description
test type *	Test statistic
score type *	Enrichment score type
n permutations *	Number of permutations
min overlap *	Minimum overlap between signature and data set
extended output *	If TRUE additional stats on signature coverage etc. will be included as row annotations in the GCT results files
export *	For each signature export expression GCT files
global FDR *	If TRUE global FDR across all data columns is calculated
light speed *	If TRUE processing will be parallized across gene sets

* - 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:

Proteomics

CPU Type:

any

Operating System:

any

Language:

R

Version Comments

Version	Release Date	Description
2		Initial Version to accompany PTM-SEA manuscript



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