GenePattern

ssGSEA_ROC Documentation

Description: Generate ROC curves and calculate the AUC from ssGSEA results and a binary phenotype classification.

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Summary: ssGSEA_ROC module implements the R package ROCR to analyze the coherence between ssGSEA enrichment scores for gene sets of interest and assigned phenotypes for the samples (e.g. high or low expression of a specific marker gene). For each gene set, the Matthews correlation coefficient, the area under the curve (AUC), a two-sided wilcox test on the ssSGEA scores and a number of other metrics are calculated.

Basic Parameters:

Name	Description
PROJ gct	PROJ.gct result from ssGSEA
CLS	Two Phenotype CLS file for classifying the ssGSEA projections

Advanced Parameters:

Name	Description
Reverse	Reverse direction of the projections. By default (FALSE) ROCR will calculate AUCs for the first phenotype in the cls vs. the second phenotype. Setting this flag to "TRUE" will calculate the second phenotype vs. the first phenotype
Plot Top Results	Two Phenotype CLS file for classifying the ssGSEA projections

Output File(s): A PDF file containing plots for the top N (specified by plot top results) scoring gene sets for each phenotype. A tab delimited text file containing calculated statistics for every gene set contained in the input PROJ.gct.

Module Language: R
Source Repository: https://github.com/genepattern/ssGSEA_ROC/releases/tag/v1
Docker image: python:3.8.8-slim-buster
Citations:

Sing T, Sander O, Beerenwinkel N, Lengauer T. ROCR: visualizing classifier performance in R. Bioinformatics. 2005;21(20):3940-3941. https://doi.org/10.1093/bioinformatics/bti623.

Benitez JA, Finlay D, Castanza A, Parisian AD, Ma J, Longobardi C, Campos A, Vadla R, Izurieta A, Scerra G, Koga T, Long T, Chavez L, Mesirov JP, Vuori K, Furnari F. Pten Deficiency Leads To Proteasome Addiction, A Novel Vulnerability In Glioblastoma. Neuro Oncol. 2021 Jan 11:noab001. doi: https://doi.org/10.1093/neuonc/noab001. Epub ahead of print. PMID: 33428749.

Version	Comment
1	Initial release.