1. Introduction

pathway analysis was usually done for top genes, lacking the ability to capture the mechanisms for subtle changes

integration of drug-gene interaction improves the identification of potential therapeutic targets

1. Methods

Transcriptomic data processing: edgeR

GSEA pathway analysis: fgsea

Enrichr pathway analysis: enrichr

iLINCS perturbagens identification: iLINCS API

Heatmap and report generation: need info from Khaled and Ali

Independent RNAseq dataset: cancer vs neurosciences dataset?

1. Algorithm

inputs: raw counts or normalized counts?

outputs: pathway heatmaps, leadedge genes, cell type from kaleidoscope, disease signature, etc.

options:

GSEA step:

generate rank file automatedly from DEG step

user own rank file

Enrichr step:

gene filtering options are p-value and number of genes

integrate other pathway databases: GO, KEGG, disease, etc.

1. Implementation

dataset

altered pathways in GSEA

altered pathways in Enrichr

perturbagens corresponding to gene alterations

1. Discussion

Comparison with similar tool/pipeline: what tools can we use to compare with?