Senior Design Project

TÜBİTAK 2247-C: Developing Web Application for Comparative Transcriptome Analysis of Host Response to Coronaviruses

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About Project

- Comparative Transcriptome Analysis of Host Response to Coronaviruses

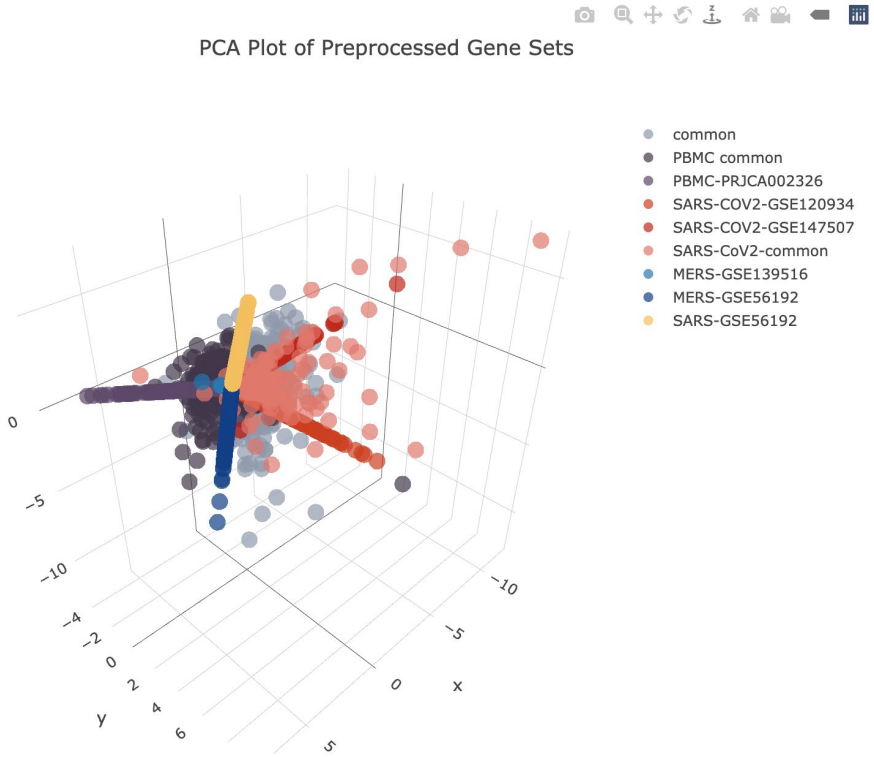
- Candidate drugs

What is Transcriptome Analysis?

- Study about the transcriptome of the complete set of RNA transcripts that are produced by the genome in a specific cell

- Used throughout diverse areas of biomedical research, including disease diagnosis, risk assessment of new drugs or environmental chemicals etc.

PCA Plot


PCA Plot of Preprocessed Gene Sets
common
PBMC common
PBMC-PRJCA002326
SARS-COV2-GSE120934
SARS-COV2-GSE147507
SARS-CoV2-common
MERS-GSE139516
MERS-GSE56192
SARS-GSE56192
0
−5
−10
−4
−2
0
2
4
6
y
0
−5
−10
x
5

Filtering

- Two different parameter can be used for filtering:

  1) p-value

  2) fold-change

- Filtering is applied according to the below formula:

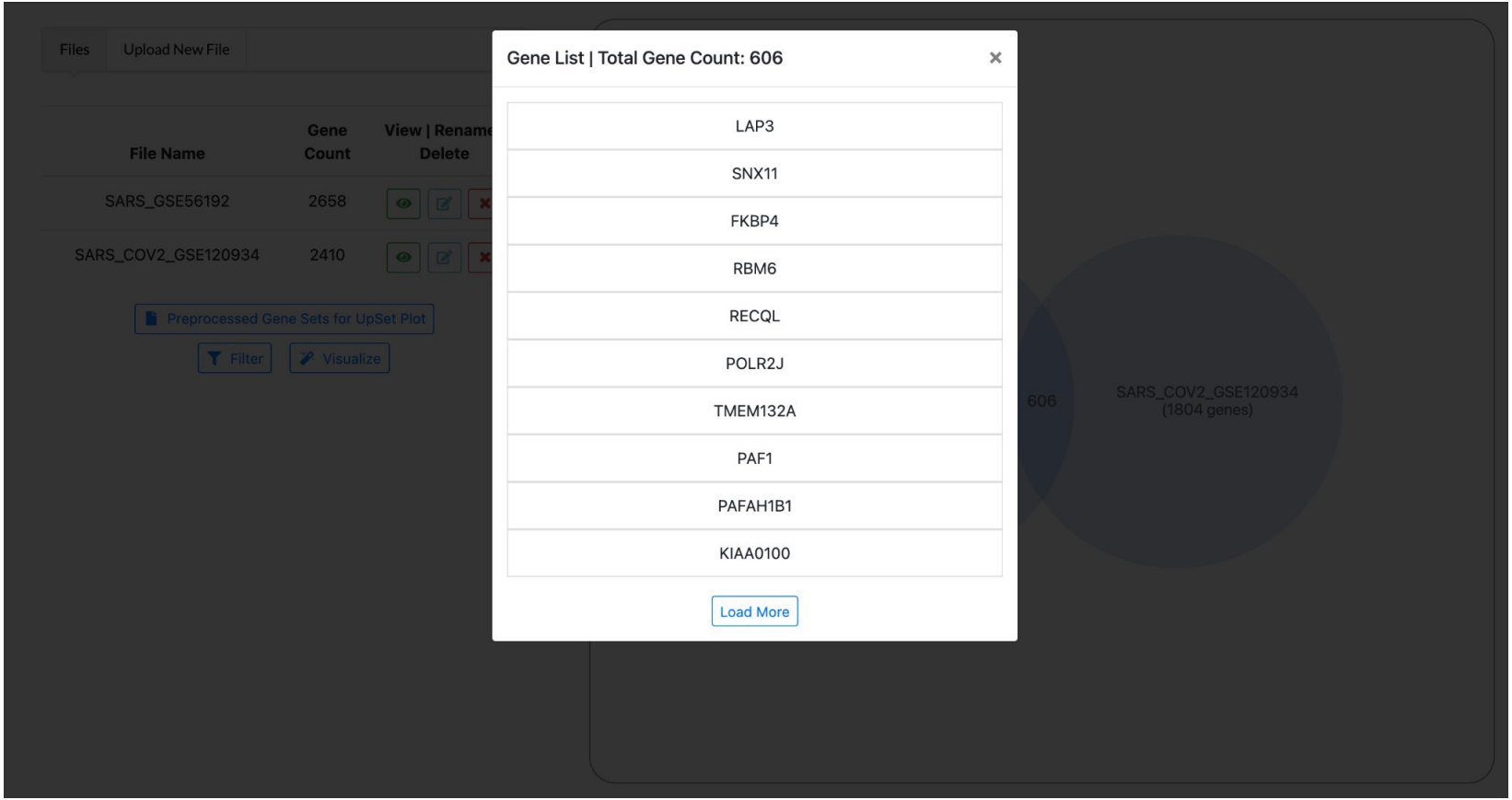
  gene.pval < *selected-value* and $|\log_2(\text{gene.fc})| >$ *selected-value*

Files | Upload New File

File Name	Gene Count	View | Rename | Delete
SARS_COV2_GSE120934	2410	
SARS_GSE56192	2658	

Preprocessed Gene Sets for UpSet Plot

Filter | Visualize


Files
Upload New File
File Name
Gene Count
View | Rename | Delete
SARS_GSE56192
2658
SARS_COV2_GSE120934
2410
Preprocessed Gene Sets for UpSet Plot
Filter
Visualize
Gene List | Total Gene Count: 606
LAP3
SNX11
FKBP4
RBM6
RECQL
POLR2J
TMEM132A
PAF1
PAFAH1B1
KIAA0100
Load More
606
SARS_COV2_GSE120934
(1804 genes)

Deployment

- The application is deployed on the following address:

  http://compcorona.mu.edu.tr

Thank You