

EVERY

ALL PROTEIN. NO ANIMAL.

*Since The EVERY Company is a start up, the R Shiny script for the application cannot be distributed. The following screenshots illustrate just a sample of what the application can do! All information regarding the sample of interest has been redacted to respect the privacy of the company.

- Heatmaps For GO Terms Using DAVID Tool
- Heatmaps For log2FC
- Volcano Plots log2FC
- Fisher's Exact Test
- Gene Search in DESeq Matrix
- Fisher's Test (↑ Regulated Genes)
- Fisher's Test (↓ Regulated Genes)
- Heatmaps for GO Terms

NUMBER OF GENES IN CURRENT DATABASE:

Usage Instructions

To garner the p-value table, please utilize the Browse buttons in order to input the corresponding files. Further, please select which annotation category you would like by utilizing the radio buttons below.

File Instructions

In order to utilize this tab, please make sure that all of your files are in a .csv format. The two input files should be the DESeq Matrix as well as the complete DAVID Database that contains all of the species' genes and their corresponding annotation terms.

p-value Table Interpretation

The p-value table is generated utilizing the DE matrix as well as the DAVID Database. The p-values are calculated by performing the Fisher's Exact test on every annotation term. Please make sure to click on the p-value dropdown arrow on the produced table so that the pvalue terms are arranged from lowest pvalue, at the top, to the highest pvalue on the bottom.

Please load the DESeq Matrix of Your Choice

Browse...

Upload complete

Please load the DAVID Database

Browse...

Upload complete

Which Annotation Category Would You Like?

☐ GOTERM_BP_DIRECT

☐ GOTERM_CC_DIRECT

☐ GOTERM_MF_DIRECT

☐ INTERPRO

☐ KEGG_PATHWAY

☐ UP_KW_BIOLOGICAL_PROCESS

☐ UP_KW_CELLULAR_COMPONENT

☐ UP_KW_DOMAIN

☐ UP_KW_LIGAND

☐ UP_KW_MOLECULAR_FUNCTION

☐ UP_KW_PTM

☐ UP_SEQ_FEATURE

p-values for Terms:

*All p-values are generated via the Fisher's Exact Test

*All p-values are generated via a one-tailed test

*If you would like to utilize the Heatmaps for GO Terms Tab, then please download this file.

Download

Show 5 entries

Search:

Term	pvalue
46	0.00287301173708815
47	0.00287301173708815
45	0.00493983019998138
21	0.0199592668024439
22	0.0199592668024439

Showing 1 to 5 of 47 entries

Previous12345...10Next

Heatmaps For GO Terms Using DAVID Tool

Heatmaps For log2FC

Volcano Plots log2FC

Fisher's Exact Test

Gene Search in DESeq Matrix

Fisher's Test (↑ Regulated Genes)

Fisher's Test (↓ Regulated Genes)

Heatmaps for GO Terms

Usage Instructions

To garner the p-value table, please utilize the Browse buttons in order to input the corresponding files. These files should be garnered from either one of the Fisher's Exact Test Calculation subtabs.

File Instructions

In order to utilize this tab, please make sure that all of your files are in a .csv format. Once again, these files should be garnered from the Fisher's Exact Test Calculation subtab. These files will contain 2 columns: one of GO Term and another for its corresponding p-value. These p-values are calculated via the statistical procedure: Fisher's Exact Test.

Heatmap Interpretation

The heatmap generated has multiple aspects to it. The more yellow an individual cell is, the closer the p-value is to 1. The darker the blue color is, the closer the p-value is to 0. You can hover over an individual cell in order to see the term it corresponds to as well as its exact p-value.

Please load the T1 File for GO Term Information

Browse...

Upload complete

Please load the T2 File for GO Term Information

Browse...

Upload complete

Please load the T3 File for GO Term Information

Browse...

Upload complete

Please load the T4 File for GO Term Information

Browse...

Upload complete

Please load the T5 File for GO Term Information

Browse...

Upload complete

Please load the T6 File for GO Term Information

Browse...

Upload complete

Please load the T7 File for GO Term Information

Browse...

Upload complete

This is the Heatmap for Timepoints Vs. GO Term of Choice:

*If a Timepoint is not on the resulting heatmap, then it means that there were 0 genes after filtering for $\log_2\text{FoldChange} > 2$ and $\text{padj} < 0.05$ at that Timepoint. Thus, this means that there would be no GO Terms.

Timepoints Vs. GO Terms

