

## Tutorial 1.3: Run Enrichment Analysis

Run an enrichment analysis to test which biological processes are enriched among genes significantly up-regulated in different types of cancer

File Edit Data Help

New ▶ Analysis ▶ Enrichment analysis ...  
Open ▶ OncoDriver analysis ...  
Save Combination analysis ...  
Save As ... Correlation analysis ...

Close

Import ▶

Export ▶

Exit

gitools

Import data

Data formats

BioMart

intOgen

DATA MATRICES

MODULES

ANNOTATIONS

Start an analysis

ENRICHMENT ANALYSIS

DIVER ALTERATIONS

RESULTS COMBINATION

CORRELATIONS

**STEP 1**

Click Enrichment  
Analysis Button or  
select New>Analysis>  
Enrichment analysis...

## New enrichment analysis

## Select destination file

Name Folder Generated file **STEP 2**

Give a name to the analysis and indicate a Folder where to place it. Click Next.

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Next &gt;

Cancel

Finish

Help

New enrichment analysis

### Select data source

**STEP 3**

Select the format of the data matrix that you will load. In this case is a Continuous data matrix. And select the file that contains the data matrix.

Data contents: Continuous data matrix (cdm)

Data file: /Users/nlopez/GITTOOLS/datamatrices/intogen.combinations.all.tumortypes.cdm.gz Browse...

Population file: Browse...

☐ Filter rows by label from the file Browse...

☒ Include only rows which labels are in the file

☐ Exclude rows which labels are in the file

☒ Transform to 1.0 cells with value less than 0.05

☐ Filter out rows without module annotations

**STEP 4**

Transform the continuous data matrix to a binary matrix by choosing a transformation criteria. In this case, since the data matrix contains p-values, we want that values lower than 0.05 are converted to 1 (significantly up-regulated)

< Back Next > Cancel Finish Help



## Select modules

The extension of the data file doesn't match the select

File format Two columns mappings (tcm)

File /Users/nlopez/GITTOOLS/modulefiles/gene2GOprocess.tsv

Browse...

Modules filtering options:

☒ Omit modules having less annotated rows than 20

☐ Omit modules having more annotated rows than 20

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Next >

Cancel

Finish

Help

### STEP 5

Select the format of the modules file that you will load. In this case is a two columns mappings. And select the file that contains the data matrix and click Next



## Select statistical test

ENRICHMENT ANALYSIS



Binomial (Bernoulli)

**STEP 6**

Select the type of enrichment analysis that you want to run. In this case we will run a binomial test. Click Next

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Cancel

Finish

Help

## New enrichment analysis

## Analysis details



Title

EA for GO process in IntOGen cancer types upreg

Notes

Enrichment of GO process among genes significantly upregulated in different cancer types

Attributes

Name

Value

Add

Edit

Remove

**STEP 7**

Optionally type a Title and Notes for the analysis that you are running. Click Finish

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Cancel

Finish

Help



Welcome x Demo x IntOGen\_upreg\_tumortypes\_GOprocess.enrichment x

**Details****Name** EA for GO process in IntOGen cancer types upreg**Notes** Enrichment of GO process in IntOGen cancer types upreg calculated in different c**Attributes****Created** Sat Mar 27 08:23:22 CET 2010**Elapsed time** 1815 ns**Data****Filter** Binary cutoff filter for values less than 0.05**Modules****Minimum number of items** 20  
limit**Test configuration****Multiple test correction** Benjamini Hochberg FDR

Once the calculations are completed you will have a new tab with the details of the analysis.

This button will open a new tab for a browsable heatmap with the Results of your Analysis

This button will open a new tab for a browsable heatmap depicting your Data

**STEP 8**

Click the Results heatmap button



Details

Properties

Name

Links

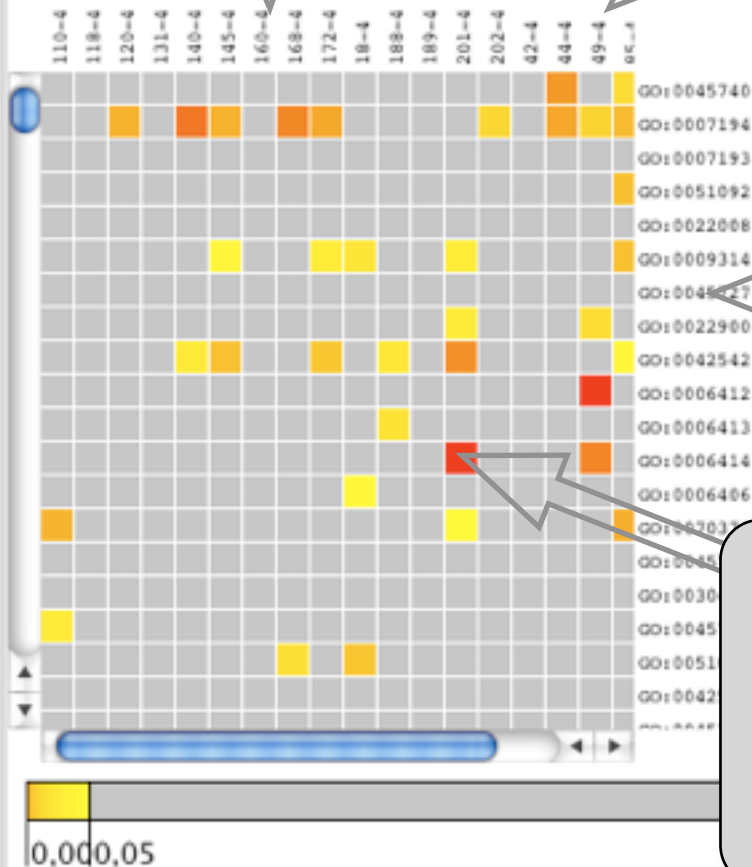
[\\$linkName](#)

IntOGen\_upreg\_tumortypes\_GOprocess-results-0.heatmap



Every column corresponds to a column in the data matrix. In this case each column is a tumor type

This heatmap contains the results of your enrichment analysis



Every row corresponds to a module. In this case a GO term

Every cell is the result of one enrichment analysis. The color of each cell indicates if the genes annotated with the GO term are enriched among gene up-regulated in this cancer type.



THANKS FOR USING GITTOOLS

<http://www.gittools.org>