

Tutorial 1.3: Run Enrichment Analysis

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

GiTools 1.5.7

File Edit Data Analysis Help

Welcome x

The image shows the GiTools 1.5.7 web application interface. It features a top menu bar with 'File', 'Edit', 'Data', 'Analysis', and 'Help'. Below the menu is a 'Welcome' tab. The main content area is divided into three sections: 'Import data', 'Start an analysis', and 'More actions'. The 'Import data' section contains logos for intOgen, GO (the Gene Ontology), KEGG, and bioMart. The 'Start an analysis' section contains five buttons: 'Enrichment Analysis', 'Oncodrive', 'Correlations', 'Overlaps', and 'Results combination'. The 'More actions' section contains two links: 'Open an analysis' and 'Open data in a heatmap'. A 'Help' section on the right lists 'User guide', 'Tutorials', and 'Examples'. A grey callout box labeled 'STEP 1' contains the instruction: 'Click Enrichment Analysis Button or select File>New>Analysis>Enrichment analysis...'. Two arrows point from this box to the 'Enrichment Analysis' button and the 'File' menu item.

gitools

Import data

intOgen GO the Gene Ontology KEGG bioMart

Start an analysis

Enrichment Analysis Oncodrive Correlations Overlaps Results combination

More actions

Open an analysis
Open data in a heatmap

Help

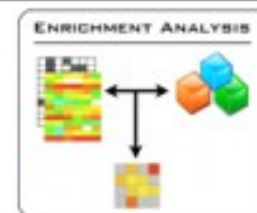
- User guide
- Tutorials
- Examples

STEP 1

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

Enrichment analysis

Enrichment analysis



You are about to perform an enrichment analysis.

This wizard will help you through simple steps on configuring the parameters of the analysis.

This wizard can be configured with the parameters of an example analysis so you won't need to fill any parameter to evaluate it. Select the option below that says "Fill this wizard with an example" and press the "Next" button.

You will find much more information on the user's guide at www.gitools.org

You have the option of fill automatically any analysis wizard in Gitools with an example to learn to perform the analysis

STEP 2

Click Next

☐ Fill this wizard with an example

☐ Don't show this page next time

< Back

Next >

Cancel

Finish

Help

Enrichment analysis

Select data source



Format Continuous data matrix (cdm, cdm.gz)

File /Users/nurialopez/GITTOOLS/datamatrices/intogen_combinations_all_tumortypes.cdm

Browse...

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. Click Next.

< Back

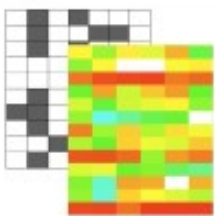
Next >

Cancel

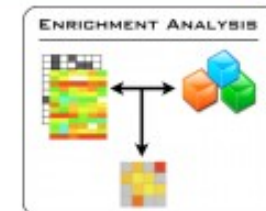
Finish

Help

Enrichment analysis



Select data filtering options



Optionally, a list of genes (elements) can be loaded to be excluded from the data matrix for the analysis.

☐ Population / Background elements:

Browse...

This should be a file containing one row id per line.

Default value to use when a row doesn't exist in the data

0

☒ Transform to 1 (0 otherwise) cells with value

less than

0.05

☐ Filter out rows for which no information appears in the modules

STEP 4

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

< Ba...

Next >

Cancel

Finish

Help

Select modules



File format Two columns mappings (tcm, tcm.gz)

File /Users/nurialopez/GITTOOLS/modulefiles/homo_sapiens__kegg_pathways__ensembl_genes.tcm

Browse...

Filtering options:

☒ Omit modules having less annotated rows than 20☐ Omit modules having more annotated rows than 20

< Back

Next >

Cancel

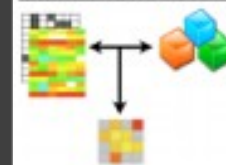
Finish

Help

STEP 5

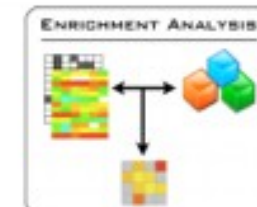
Select the format of the modules file that you will load. In this case is a two columns mappings. And select the file that contains the data matrix and click Next

ENRICHMENT ANALYSIS



Enrichment analysis

Select statistical test

☒ Binomial (Bernoulli)☐ Fisher Exact☐ Z Score**STEP 6**

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

Multiple test correction Benjamin Hochberg FDR

< Back

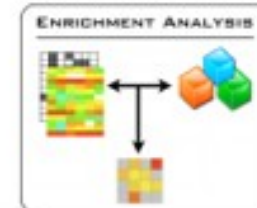
Next >

Cancel

Finish

Help

Select destination file



Name IntOGen_upreg_tumortype_KEGGpathways

Browse...

Folder /Users/nurialopez/GITTOOLS/results

Browse...

Generated file /Users/nurialopez/GITTOOLS/results/IntOGen_upreg_tumortype_KEGGpathways.enrichment

STEP 7

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

< Back

Next >

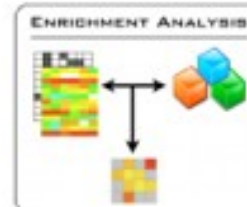
Cancel

Finish

Help

Enrichment analysis

Analysis details



Title

EA of KEGG pathways in genes significantly upregulated in different tumour types

Notes

Attributes

Name

Value

Add

Edit

Remove

STEP 8

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

< Back

Next >

Cancel

Finish

Help



Details Properties

Welcome x IntOGen_upreg_tumortype_KEGGpathways.enrichment x

Details

Title EA of KEGG pathways in genes upregulated in different tumour types

Notes

Created Thu Oct 28 10:07:56 CEST

Elapsed time 886 ns

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

Data

File IntOGen_upreg_tumortype_KEGGpathways-data.cdm.gz

Filter Binary cutoff filter for values less than 0.05

[Heatmap](#)**Modules**

File IntOGen_upreg_tumortype_KEGGpathways-modules.ixm.gz

Minimum size 20

Maximum size No limit

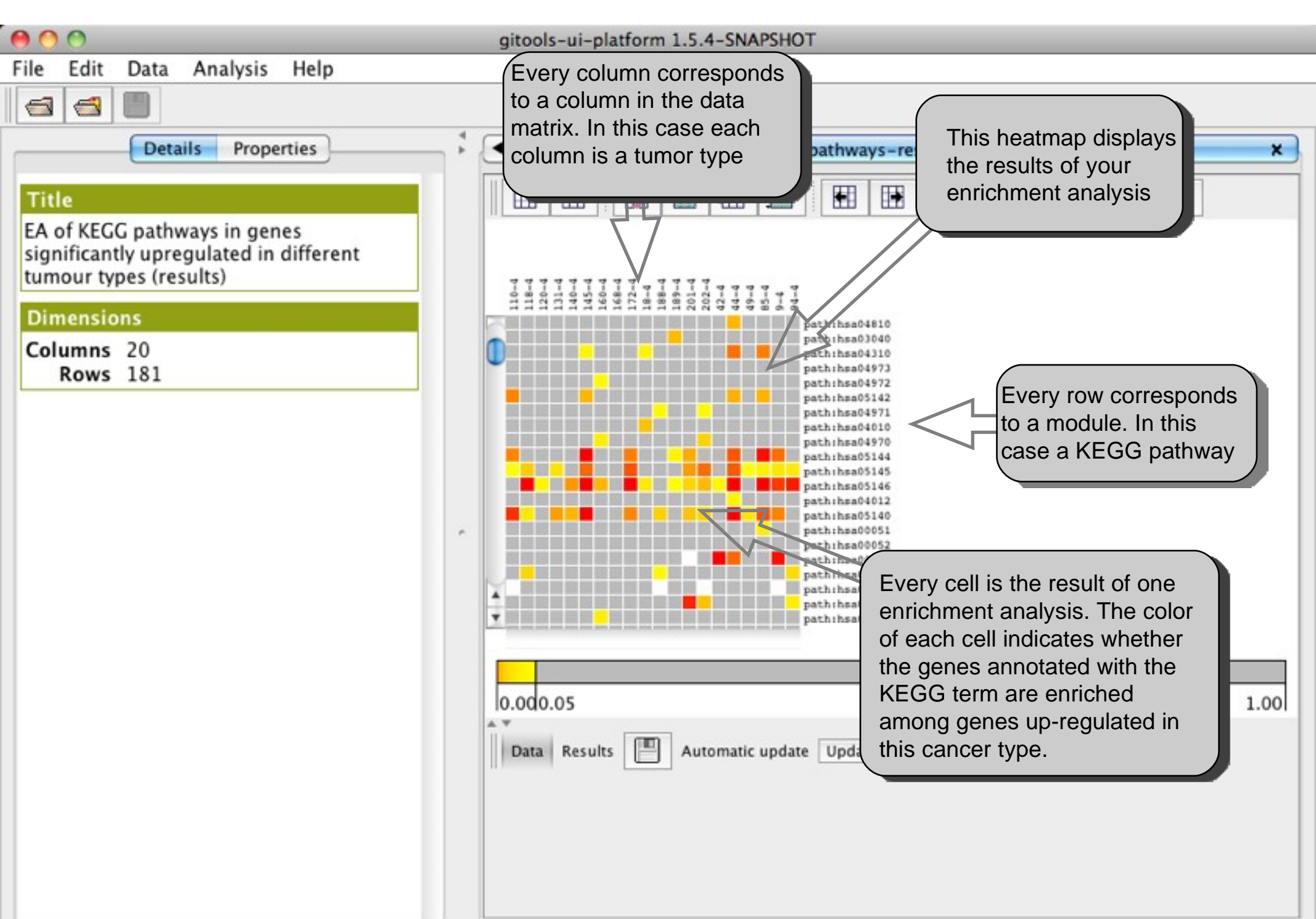
[View](#)**Results**

Multiple test correction

Benjamini Hochberg FDR

[Heatmap](#)**STEP 8**

Click the Results heatmap button





THANKS FOR USING GITTOOLS

<http://www.gittools.org>