





topographic merit analysis

- Purpose: performing enrichment analysis using R package topGO
- Input: a list of Ensembl Gene IDs



## Select your type of input file

The identifiers must be Ensembl gene IDs (e.g : ENSG00000139618). If it is not the case, please use the ID Mapping tool.

## Choose an input file

This file must imperatively have 1 column filled with IDs consistent with the database that will be used. Please use the MappingIDs component if this is not the case.

Please specify the column where you would like to apply the comparison (e.g : Enter c1)

Does your file have a header?

## Select a specie

## Ontology category

## Choose the topGO option for your analysis

Enter the p-value threshold level under the form 1e-level wanted (e.g : 1e-3)

## Choose a correction for multiple testing

23/01/18

11 shown, 10 [deleted](#), 3 [hidden](#)

816.51 KB

[15: GO Profile text output](#)

t

[14: GO Profile diagram outputs](#)

a list of datasets

[13: Venn diagram text output](#)[12: Venn diagram](#)[11: Mucilli.txt](#)[10: Bredberg.txt](#)[9: Expression levels by tissue \(from HPA\) on data 4](#)[4: ID Converter on data 2](#)[3: Filter lines by keywords or numerical value on Lacombe et al 2017 OK.txt - Remove](#)



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Yes

Select a specie

Human

Ontology category

Biological Process

Choose the topGO option for your analysis

Elim

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Benjamini and Hochberg

Rechercher des données

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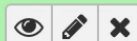
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# topGO enrichment analysis

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topGO enrichment analysis performs enrichment analysis using R package topGO (Galaxy Version 0.1.0) Options

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History

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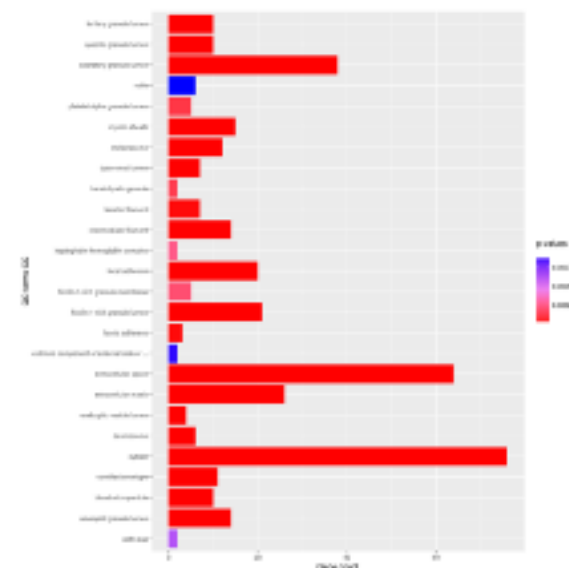
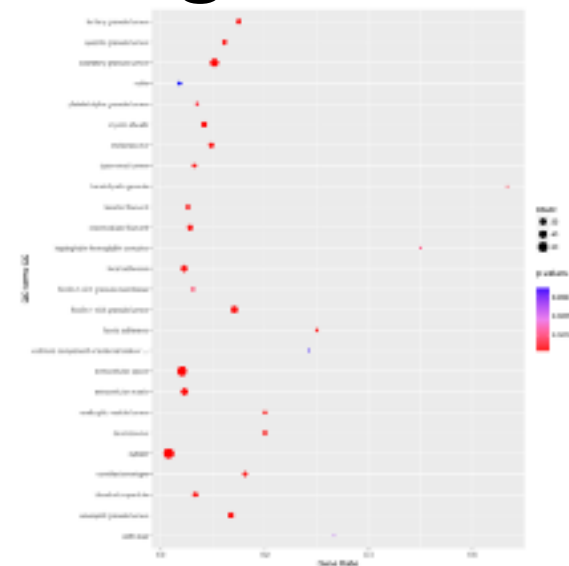
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# topGO enrichment analysis

- Results: bar plot, dot plot and textual output for each GO categories chosen



1	2	3	4	5	6
GO.ID	Term	Annotated	Significant	Expected	pvalues
GO:0045296	cadherin binding	328	21	2.29	3.9e-12
GO:0004869	cysteine-type endopeptidase inhibitor ac...	61	10	0.43	1.3e-11
GO:0004867	serine-type endopeptidase inhibitor acti...	103	10	0.72	2.7e-09
GO:0005200	structural constituent of cytoskeleton	120	10	0.84	1.2e-08
GO:0005198	structural molecule activity	778	27	5.44	4.9e-06
GO:0002020	protease binding	140	8	0.98	6.3e-06
GO:0001948	glycoprotein binding	108	7	0.76	1.1e-05
GO:0004197	cysteine-type endopeptidase activity	86	6	0.6	3.1e-05
GO:0004332	fructose-bisphosphate aldolase activity	3	2	0.02	0.00014
GO:0008426	protein kinase C inhibitor activity	3	2	0.02	0.00014
GO:0005509	calcium ion binding	751	15	5.25	0.00024
GO:0098641	cadherin binding involved in cell-cell a...	18	3	0.13	0.00025
GO:0019834	phospholipase A2 inhibitor activity	4	2	0.03	0.00029
GO:0004601	peroxidase activity	46	4	0.32	0.00030
GO:0016209	antioxidant activity	94	8	0.66	0.00031
GO:0051082	unfolded protein binding	132	6	0.92	0.00033
GO:0030492	hemoglobin binding	5	2	0.03	0.00048
GO:0003779	actin binding	433	13	3.03	0.00061
GO:0086083	cell adhesive protein binding involved i...	6	2	0.04	0.00071
GO:0042802	identical protein binding	1494	26	10.45	0.00076
GO:0003723	RNA binding	1776	28	12.42	0.00091
GO:0048306	calcium-dependent protein binding	62	4	0.43	0.00093

This tool uses R/Bioconductor package topGO - Alexa A and Rahnenfuhrer J (2016). topGO: Enrichment Analysis for Gene Ontology. R package version 2.30.0.