

GO Browser

Provides access to Gene Ontology database.

Inputs

- Cluster Data: Data on clustered genes.
- Reference Data: Data with genes for the reference set (optional).

Outputs

- Data on Selected Genes: Data on genes from the selected GO node.
- Enrichment Report: Data on GO enrichment analysis.

GO Browser widget provides access to [Gene Ontology database](#). Gene Ontology (GO) classifies genes and gene products to terms organized in a graph structure called an ontology. The widget takes any data on genes as an input (it is best to input statistically significant genes, for example from the output of the **Differential Expression** widget) and shows a ranked list of GO terms with p-values. This is a great tool for finding biological processes that are over- or under-represented in a particular gene set. The user can filter input data by selecting terms in a list.

GO Browser

Input Filter Select

Info

588 unique genes on input
583 (99.1%) genes with known annotations

Ontology/Annotation Info

Reference

Entire genome
Reference set (input)

Aspect

Biological process
Cellular component
Molecular function

GO term	Cluster	Reference	p-value	FDR	Genes	Enrichment
carbohydrate transmembrane transport	14 (2.38%)	27 (0.43%)	4.2e-07	9.3e-04	856496, 851...	
▼ carbohydrate transport	16 (2.72%)	46 (0.73%)	1.0e-05	0.00561	856496, 851...	
▼ carbohydrate transmembrane transport	14 (2.38%)	27 (0.43%)	4.2e-07	9.3e-04	856496, 851...	
▼ monosaccharide transmembrane transport	13 (2.21%)	25 (0.40%)	1.0e-06	9.3e-04	856496, 851...	
▼ hexose transmembrane transport	13 (2.21%)	25 (0.40%)	1.0e-06	9.3e-04	856496, 851...	
fructose transmembrane transport	10 (1.70%)	18 (0.29%)	1.0e-05	0.00561	856496, 851...	
mannose transmembrane transport	9 (1.53%)	16 (0.25%)	2.6e-05	0.01157	856496, 851...	
glucose transmembrane transport	6 (1.02%)	13 (0.21%)	0.00156	0.15603	856496, 851...	
▼ small molecule metabolic process	106 (18.03%)	783 (12.43%)	6.0e-05	0.02311	854874, 85...	
organic acid metabolic process	61 (10.37%)	430 (6.83%)	8.7e-04	0.11922	854874, 85...	
one-carbon metabolic process	7 (1.19%)	17 (0.27%)	0.00125	0.14644	855227, 852...	
sulfur amino acid biosynthetic process	11 (1.87%)	39 (0.62%)	0.00133	0.14740	852378, 851...	
small molecule catabolic process	24 (4.08%)	129 (2.05%)	0.00137	0.14740	852721, 856...	
cation transmembrane transport	33 (5.61%)	180 (2.86%)	2.5e-04	0.06212	851944, 850...	
▼ cellular amino acid metabolic process	41 (6.97%)	244 (3.87%)	2.8e-04	0.06212	854874, 85...	
▼ alpha-amino acid metabolic process	34 (5.78%)	178 (2.83%)	9.3e-05	0.03146	854874, 85...	
alpha-amino acid catabolic process	11 (1.87%)	40 (0.64%)	0.00162	0.15603	855227, 852...	

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alpha-amino acid metabolic process	34 (5.78%)	178 (2.83%)	9.3e-05	0.03146	854874, 85...	
methionine metabolic process	13 (2.21%)	42 (0.67%)	2.1e-04	0.06212	856766, 852...	
cation transmembrane transport	33 (5.61%)	180 (2.86%)	2.5e-04	0.06212	851944, 850...	
sulfur amino acid metabolic process	14 (2.38%)	49 (0.78%)	2.8e-04	0.06212	856766, 852...	
cellular amino acid metabolic process	41 (6.97%)	244 (3.87%)	2.8e-04	0.06212	854874, 85...	
monovalent inorganic cation transport	22 (3.74%)	103 (1.64%)	3.7e-04	0.07215	851944, 850...	
drug metabolic process	43 (7.31%)	264 (4.19%)	3.8e-04	0.07215	854850, 85...	
carboxylic acid metabolic process	60 (10.20%)	411 (6.53%)	4.8e-04	0.08613	854874, 85...	
cellular amino acid catabolic process	14 (2.38%)	54 (0.86%)	7.1e-04	0.11922	855227, 852...	

INPUT tab

1. Information on the input data set. *Ontology/Annotation Info* reports the current status of the GO database.
2. Select the reference. You can either have the *entire genome* as reference or a *reference set* from the input.
3. Select the ontology where you want to calculate the enrichment. There are three *Aspect* options:

- Biological process
- Cellular component)
- Molecular function

4. A ranked tree (upper pane) and list (lower pane) of GO terms for the selected aspect:

- **GO term**
- **Cluster**: number of genes from the input that are also annotated to a particular GO term (and its proportion in all the genes from that term).
- **Reference**: number of genes that are annotated to a particular GO term (and its proportion in the entire genome).
- **P-value**: probability of seeing as many or more genes at random. The closer the p-value is to zero, the more significant a particular GO term is. Value is written in **e notation**).
- **FDR**: **false discovery rate** - a multiple testing correction that means a proportion of false discoveries among all discoveries up to that FDR value.
- **Genes**: genes in a biological process.
- **Enrichment** level

InputFilterSelect

Filter GO Term Nodes 1

☐ Genes
1

☐ p-value
p 0.01000000

☒ FDR
p 0.20000000

Significance test 2

☒ Binomial
☐ Hypergeometric

Evidence codes in annotation 3

☒ EXP: 0 annots(0 genes)
☒ IDA: 13907 annots(4459 genes)
☒ IPI: 2127 annots(1388 genes)
☒ IMP: 11240 annots(3902 genes)
☒ IGI: 3575 annots(1956 genes)
☒ IEP: 114 annots(94 genes)
☒ ISS: 1657 annots(980 genes)
☒ ISA: 168 annots(116 genes)
☒ ISO: 8 annots(6 genes)
☒ ISM: 1122 annots(1112 genes)
☒ IGC: 0 annots(0 genes)
☒ RCA: 0 annots(0 genes)
☒ TAS: 430 annots(229 genes)
☒ NAS: 94 annots(48 genes)
☒ IC: 1209 annots(764 genes)
☒ ND: 3592 annots(2095 genes)
☒ IEA: 34803 annots(5490 genes)
☒ NR: 0 annots(0 genes)

InputFilterSelect

Annotated genes 1

☒ Directly or Indirectly
☐ Directly

Output 2

☒ All selected genes
☐ Term-specific genes
☐ Common term genes

FILTER tab

1. Filter GO Term Nodes by:

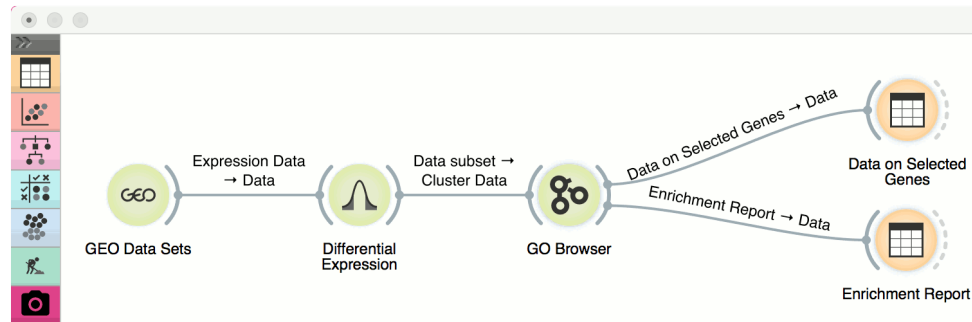
- **Genes** is a minimal number of genes mapped to a term
 - **P-value** is a max term p-value
 - **FDR**: is a max term **false discovery rate**
2. *Significance test* specifies distribution to use for null hypothesis:
- **Binomial**: use a binomial distribution
 - **Hypergeometric**: use a hypergeometric distribution
3. **Evidence codes in annotation** show how the annotation to a particular term is supported.

SELECT tab

4. *Annotated genes* outputs genes that are:
- **Directly or Indirectly** annotated (direct and inherited annotations)
 - **Directly** annotated (inherited annotations won't be in the output)
5. *Output*:
- **All selected genes**: outputs genes annotated to all selected GO terms
 - **Term-specific genes**: outputs genes that appear in only one of selected GO terms
 - **Common term genes**: outputs genes common to all selected GO terms
 - **Add GO Term as class**: adds GO terms as class attribute

Example

In the example below we have used **GEO Data Sets** widget, in which we have selected *Caffeine effects: time course and dose response* data set, and connected it to a **Differential Expression**. Differential analysis allows us to select genes with the highest statistical relevance (we used ANOVA scoring and agent label) and feed them to **GO Browser**. This widget lists four biological processes for our selected genes. Say we are interested in finding out more about *monosaccharide transmembrane transport* as this term has a high enrichment rate. To learn more about which genes are annotated to this GO term, select it in the view and observe the results in a **Data Table**, where we see all the genes participating in this process listed. The other output of **GO Browser** widget is enrichment report, which we observe in the second **Data Table**.



Data on Selected Genes

ANOVA Entrez ID	class	dose	time	agent	GAL2 15899571356728 850770	HXX1 55878540373034 850614	HXT11 30547477064218 854009
1	caffeine low ...	low	5 min	caffeine	0.174	-0.064	0.337
2	caffeine low ...	low	5 min	caffeine	0.281	0.590	0.134
3	calcofluor w...	low	5 min	calcofluor w...	0.141	-0.186	0.105
4	calcofluor w...	low	5 min	calcofluor w...	0.049	0.212	-0.115
5	congo red lo...	low	5 min	congo red	0.104	-0.607	0.233
6	congo red lo...	low	5 min	congo red	-0.033	-0.051	-0.027
7	caffeine low ...	low	15 min	caffeine	0.756	0.700	0.671
8	caffeine low ...	low	15 min	caffeine	0.576	0.854	0.472
9	calcofluor w...	low	15 min	calcofluor w...	0.113	-0.137	0.270
10	calcofluor w...	low	15 min	calcofluor w...	-0.262	-0.037	-0.213
11	congo red lo...	low	15 min	congo red	0.035	-0.259	0.110

GO Browser

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Enrichment Report

GO Term Id	GO Term Name	Cluster Frequency	Genes in Cluster	Reference Frequency
O:0034219	carbohydrate transmembrane t...	0.024	14	0.004
O:0008645	hexose transmembrane transp...	0.022	13	0.004
O:0015749	monosaccharide transmembra...	0.022	13	0.004
O:0015755	fructose transmembrane trans...	0.017	10	0.003
O:0008643	carbohydrate transport	0.027	16	0.007
O:0015761	mannose transmembrane trans...	0.015	9	0.003
O:0044281	small molecule metabolic proc...	0.180	106	0.124
O:1901605	alpha-amino acid metabolic pr...	0.058	34	0.028
O:0006555	methionine metabolic process	0.022	13	0.007
O:0098655	cation transmembrane transport	0.056	33	0.029
O:0000096	sulfur amino acid metabolic pro...	0.024	14	0.008
O:0006520	cellular amino acid metabolic p...	0.070	41	0.039