

GOGO Web Server file formats explanation

Calculate the semantic similarity between two or more GO terms

Functions:

Calculate the semantic similarity between two or more GO terms

Calculate semantic similarities of one or more pair(s) of genes

Calculate pairwise semantic similarities between a list of genes and then classify the genes based on their GO term similarities

When using this function, user can just input two GO terms from same ontology,

Input two GO terms: e.g. GO:0021727 GO:0044767

then click submit button, the result will be presented at the next page.

Or, user can fill in an email address, upload an input file and submit the job. The results will be sent by email after the job finished.

Email:

Note: Results will be sent to this email address if files are uploaded

Upload a file: No file chosen

Each line of the input file should contain two GO terms, which separated by space. In the result file, GOGO appends ontology and similarity of GO terms pair at the end of lines of the input file.

Input file:

GO:1903097 GO:0010847

GO:0045252 GO:0045240

GO:0031216 GO:0004553

...

<http://dna.cs.miami.edu/GOGO/>

Result file:

GO:1903097 GO:0010847 BPO 0.694

GO:0045252 GO:0045240 CCO 0.803

GO:0031216 GO:0004553 MFO 0.753

...

Calculate functional similarities of one or more pair(s) of genes

Functions:

Calculate the semantic similarity between two or more GO terms

Calculate semantic similarities of one or more pair(s) of genes

Calculate pairwise semantic similarities between a list of genes and then classify the genes based on their GO term similarities

Suppose user have some gene pairs to calculate, each line of the input file should contain two genes separated by “;”. The first field of each gene is gene name, then followed by its GO terms. Moreover, GOGO could identify the ontology of GO terms, and calculate similarities of genes based on BPO, CCO and MFO, respectively. In result file, GOGO appends ontology and similarity of gene pairs at the end of lines of the input file.

Input file:

ADH2 GO:0006067 GO:0004022 GO:0000947 GO:0006116 GO:0005737; PDC6

GO:0006067 GO:0004737 GO:0000949 GO:0006569 GO:0005737 GO:0006559

...

Result file:

ADH2 GO:0006067 GO:0004022 GO:0000947 GO:0006116 GO:0005737; PDC6

GO:0006067 GO:0004737 GO:0000949 GO:0006569 GO:0005737 GO:0006559 BPO 0.612

CCO 1.000 MFO 0.030

...

<http://dna.cs.miami.edu/GOGO/>

Calculate pairwise functional similarities between a list of genes and then classify the genes based on their GO term similarities

Functions:

Calculate the semantic similarity between two or more GO terms

Calculate semantic similarities of one or more pair(s) of genes

Calculate pairwise semantic similarities between a list of genes and then classify the genes based on their GO term similarities

Each line of the input file contains only one gene, and the first field of gene is gene name, then followed by its GO terms. In similarity result file, GOGO will present all the possible gene pairs of genes set uploaded by user. For each line, the first two fields are gene pairs, then followed by ontologies and similarities. In the cluster result file, we present the cluster of genes based on the ontologies. Note that GOGO couldn't get the cluster result for an ontology, if a gene isn't annotated with a GO term from the ontology. Each line is a cluster of genes, and the first field of a line is the exemplar of this cluster.

Input file:

ADH4 GO:0004022 GO:0000947 GO:0005739 GO:0006113

...

ARO9 GO:0009072 GO:0005634 GO:0008793 GO:0005737

...

ADH5 GO:0005634 GO:0043458 GO:0000947 GO:0006116 GO:0005737

...

Result file:

ADH4 PDC1 BPO 0.431 CCO 0.482 MFO 0.030

ADH4 ARO9 BPO 0.265 CCO 0.509 MFO 0.031

ADH4 PDC5 BPO 0.431 CCO 0.509 MFO 0.030

ADH4 SFA1 BPO 0.566 CCO 0.833 MFO 0.703

ADH4 ADH3 BPO 0.642 CCO 0.866 MFO 1.000

ADH4 ARO10 BPO 0.543 CCO 0.467 MFO 0.045

ADH4 ARO8 BPO 0.265 CCO 0.500 MFO 0.031

ADH4 ADH2 BPO 0.546 CCO 0.500 MFO 1.000

<http://dna.cs.miami.edu/GOGO/>

ADH4 PDC6 BPO 0.410 CCO 0.500 MFO 0.030

ADH4 ADH5 BPO 0.574 CCO 0.509 MFO NA

...

Cluster result file:

BPO:

ARO8 ARO9

PDC6 PDC1 PDC5 ARO10

ADH1 ADH4 SFA1 ADH3 ADH2 ADH5

CCO:

ADH3 ADH4

PDC6 SFA1 ARO10 ARO8 ADH2

ADH5 PDC1 ARO9 PDC5

ADH1