

Step by step instructions for methylGSA shiny app

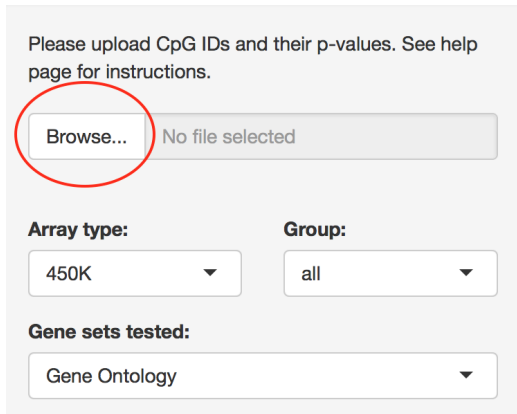
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This app is a web interface for gene set testing using the outcome of differential methylation.

Step 1

Click on “Browse” to upload differential methylation result.



Please upload CpG IDs and their p-values. See help page for instructions.

Browse... No file selected

Array type: 450K

Group: all

Gene sets tested: Gene Ontology

Users are expected to upload a txt file with 1st column CpG IDs, and 2nd column p-values correspond to the CpGs. For example:

```
cg13869341 0.307766
cg14008030 0.257672
cg12045430 0.552322
cg20826792 0.056383
cg00381604 0.468549
cg20253340 0.483770
cg21870274 0.812402
...
...
...
cg21106100 0.079276
cg08265308 0.748265
cg14273923 0.553923
```

Files should be no more than 100MB. Please check **[cpg_file_example.txt](https://github.com/reese3928/methylGO-RShiny-app/raw/master/cpy_file_example.txt)** (https://github.com/reese3928/methylGO-RShiny-app/raw/master/cpy_file_example.txt) for a toy dataset on Illumina 450 K Beadchip.

Step 2

Choose array type and group.

Please upload CpG IDs and their p-values. See help page for instructions.

Browse... No file selected

Array type:
450K ▲
450K
EPIC ▼

Group:
all ▼

Please upload CpG IDs and their p-values. See help page for instructions.

Browse... No file selected

Array type:
450K ▼

Gene sets tested:
Gene Ontology

Minimum gene set size:
0 100 1,000

Group:
all ▲
all
body
promoter1
promoter2

Array type:

450K : Illumina 450 K Beadchip

EPIC : Illumina EPIC Beadchip

Group:

Group is the type of CpG to be considered in methylRRA or methylglm. By default, group is `all`, which means all CpGs are considered regardless of their gene group. If group is `body`, only CpGs on gene body will be considered. If group is `promoter1` or `promoter2`, only CpGs on promoters will be considered. Based on the annotation in `IlluminaHumanMethylation450kanno.ilmn12.hg19` and

`IlluminaHumanMethylationEPICanno.ilm10b4.hg19`, `body`, `promoter1` and `promoter2` are defined as:

`body` : CpGs whose gene group correspond to “Body” or “1stExon”

`promoter1` : CpGs whose gene group correspond to “TSS1500” or “TSS200”

`promoter2` : CpGs whose gene group correspond to “TSS1500”, “TSS200”, “1stExon”, or “5’UTR”

Step 3

Select gene sets to test.

Array type:
450K ▼

Group:
all ▼

Gene sets tested:
Gene Ontology ▲
Gene Ontology
KEGG
Reactome

Gene ontology : <http://www.geneontology.org> (<http://www.geneontology.org>)

KEGG (Kyoto Encyclopedia of Genes and Genomes): <https://www.genome.jp/kegg/>
(<https://www.genome.jp/kegg/>)

Reactome : <https://reactome.org> (<https://reactome.org>)

Step 4

Select gene set sizes.

Minimum gene set size:

0 100 1,000

0 100 200 300 400 500 600 700 800 900 1,000

Maximum gene set size:

0 500 1,000

0 100 200 300 400 500 600 700 800 900 1,000

Test method:

methylglm

GO!

Gene sets outside this range will not be tested.

Step 5

Select gene set testing method.

Maximum gene set size:

0 500 1,000

0 100 200 300 400 500 600 700 800 900 1,000

Test method:

methylglm

methylglm

gometh

RRA(ORA)

RRA(GSEA)

Check this page (<https://bioconductor.org/packages/devel/bioc/vignettes/methylGSA/inst/doc/methylGSA-vignette.html>) for a description of methods.

Step 6

Hit "GO!".

Test method:

methylglm

GO!

Gene set testing is running in the background. Depending on the number of gene sets tested, it may take several seconds to several minutes. Once it is done, the result is going to show up on the right hand panel.

Interpreting the results

The result of gene set testing is presented in two formats, namely table and box plot.

Hit "Download as csv" or "Download as txt" to save the results table to a csv or txt file:

Table Plot

Show 10 entries Search:

ID	Description	Count	size	pvalue	padj	
GO:0043547	GO:0043547	positive regulation of GTPase activity	15	439	0.028062003	0.99940649
GO:0019932	GO:0019932	second-messenger-mediated signaling	15	445	0.031225148	0.99940649
GO:0051222	GO:0051222	positive regulation of protein transport	15	474	0.050297925	0.99940649
GO:0031047	GO:0031047	gene silencing by RNA	15	476	0.051861024	0.99940649
GO:0050769	GO:0050769	positive regulation of neurogenesis	14	468	0.080177675	0.99940649
GO:0001558	GO:0001558	regulation of cell growth	13	433	0.084120203	0.99940649
GO:0035194	GO:0035194	posttranscriptional gene silencing by RNA	13	444	0.097907926	0.99940649
GO:0060589	GO:0060589	nucleoside-triphosphatase regulator activity	14	485	0.10043212	0.99940649
GO:0016441	GO:0016441	posttranscriptional gene silencing	13	446	0.10055617	0.99940649
GO:0007389	GO:0007389	pattern specification process	14	500	0.12071003	0.99940649

Showing 1 to 10 of 126 entries Previous 1 2 3 4 5 ... 13 Next

Download as csv Download as txt

Various options are provided for users to customize the box plot:

Table Plot

Number of gene sets to display: 9 x-axis: Number of significant genes Color by: Raw p-value

Number of gene sets to display : The number of genes sets to display on the plot.

x-axis : Either the number of significant genes in each gene set or the total number of genes. The number of significant genes is not available for methylglm and methylRRA(GSEA) because they are FCS methods.

color by : Color the barplot by either raw p-value or adjusted p-value.

Hit "Download as pdf" or "Download as png" to save the boxplot to a pdf or png file:

