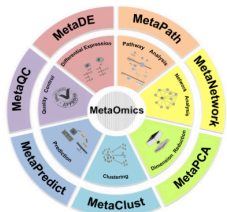


Welcome to MetaOmics



MetaOmics is a browser-based software suite for transcriptomic meta-analysis with R shiny-based graphical user interface (GUI). Many state-of-the-art meta analysis tools are available in this software, including MetaQC for quality control, MetaDE for differential expression analysis, MetaPath for pathway enrichment analysis, MetaNetwork for differential co-expression network analysis, MetaPredict for classification analysis, MetaClust for sparse clustering analysis and MetaPCA for principal component analysis.

Our software is available for download on github: [MetaOmics](#). For detailed implementation of each tool, please refer to our [Tutorials](#).

MetaOmics is developed and maintained by [Dr. George Tseng's group](#) from the Department of Biostatistics, University of Pittsburgh.

We recommend users to use R 3.3 to implement our tool. If you are using R 3.4, you may encounter errors in installing dependencies of the modules. You can manually install the dependencies by running the following commands in R:

```
install.packages(c("GSA", "combinat", "samr", "survival", "cluster", "gplots", "ggplot2", "irr", "shape", "snow", "snowfall", "igraph", "doMC", "PMA"));
source("https://bioconductor.org/biocLite.R"); biocLite(c("multtest", "Biobase", "edgeR", "DESeq2", "impute", "lmma", "AnnotationDbi", "ConsensusClusterPlus", "genefilter", "GSEABase", "Rgraphviz"))
```

For Windows, users need to run the following command in R to install the package 'doMC':

```
install.packages("doMC", repos='http://R-Forge.R-project.org')
```

Session Information

```
protocol: http:
hostname: 127.0.0.1
port: 9987
server type: local
```

Directory for Saving Output Files: ?

select a directory

(4)

...

Toolsets

Package	Status
MetaQC	MetaQC is not installed: Install
MetaDE	✓ installed
MetaPath	✓ installed
MetaNetwork	✓ installed
MetaPredict	✓ installed
MetaClust	✓ installed
MetaPCA	✓ installed