

Pathway Analysis

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2023-05-09

Call libraries

```
library(clusterProfiler)
```

```
## Warning: replacing previous import 'utils::findMatches' by  
## 'S4Vectors::findMatches' when loading 'AnnotationDbi'
```

```
##
```

```
## Registered S3 method overwritten by 'ggtree':  
##   method      from  
##   identify.gg ggfun
```

```
## clusterProfiler v4.8.1 For help: https://yulab-smu.top/biomedical-knowledge-mining-book/  
##
```

```
## If you use clusterProfiler in published research, please cite:
```

```
## T Wu, E Hu, S Xu, M Chen, P Guo, Z Dai, T Feng, L Zhou, W Tang, L Zhan, X Fu, S Liu, X Bo, and G Yu.
```

```
##
```

```
## Attaching package: 'clusterProfiler'
```

```
## The following object is masked from 'package:stats':
```

```
##
```

```
##      filter
```

```
library(DOSE)
```

```
## DOSE v3.26.1 For help: https://yulab-smu.top/biomedical-knowledge-mining-book/  
##
```

```
## If you use DOSE in published research, please cite:
```

```
## Guangchuang Yu, Li-Gen Wang, Guang-Rong Yan, Qing-Yu He. DOSE: an R/Bioconductor package for Disease
```

```
library(R.utils)
```

```
## Loading required package: R.oo
```

```
## Loading required package: R.methodsS3
```

```
## R.methodsS3 v1.8.2 (2022-06-13 22:00:14 UTC) successfully loaded. See ?R.methodsS3 for help.
```

```
## R.oo v1.25.0 (2022-06-12 02:20:02 UTC) successfully loaded. See ?R.oo for help.
```

```
##
```

```
## Attaching package: 'R.oo'
```

```
## The following object is masked from 'package:R.methodsS3':
```

```
##
```

```
##      throw
```

```
## The following objects are masked from 'package:methods':
```

```
##
```

```
##      getClasses, getMethods
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      attach, detach, load, save
```

```
## R.utils v2.12.2 (2022-11-11 22:00:03 UTC) successfully loaded. See ?R.utils for help.
```

```
##
```

```
## Attaching package: 'R.utils'
```

```
## The following object is masked from 'package:utils':
```

```
##
```

```
##      timestamp
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      cat, commandArgs, getOption, isOpen, nullfile, parse, warnings
```

```
library(gtools)
```

```
##
```

```
## Attaching package: 'gtools'
```

```
## The following object is masked from 'package:R.utils':
```

```
##
```

```
##      capture
```

```
library(org.Hs.eg.db)
```

```
## Loading required package: AnnotationDbi
```

```
## Loading required package: stats4
```

```
## Loading required package: BiocGenerics
```

```

##
## Attaching package: 'BiocGenerics'

## The following objects are masked from 'package:stats':
##
##     IQR, mad, sd, var, xtabs

## The following objects are masked from 'package:base':
##
##     anyDuplicated, append, as.data.frame, basename, cbind, colnames,
##     dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##     grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,
##     order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
##     rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,
##     union, unique, unsplit, which.max, which.min

## Loading required package: Biobase

## Welcome to Bioconductor
##
##     Vignettes contain introductory material; view with
##     'browseVignettes()'. To cite Bioconductor, see
##     'citation("Biobase")', and for packages 'citation("pkgname)".

## Loading required package: IRanges

## Loading required package: S4Vectors

##
## Attaching package: 'S4Vectors'

## The following object is masked from 'package:clusterProfiler':
##
##     rename

## The following object is masked from 'package:utils':
##
##     findMatches

## The following objects are masked from 'package:base':
##
##     expand.grid, I, unname

##
## Attaching package: 'IRanges'

## The following object is masked from 'package:R.oo':
##
##     trim

```

```
## The following object is masked from 'package:clusterProfiler':
##
## slice
```

```
## The following object is masked from 'package:grDevices':
##
## windows
```

```
##
## Attaching package: 'AnnotationDbi'
```

```
## The following object is masked from 'package:clusterProfiler':
##
## select
```

```
##
```

```
library(enrichplot)
library(ggplot2)
library(stringr)
library(tibble)
library(ggupset)
library(DOSE)
library(AnnotationDbi)
library(pathview)
```

```
## #####
## Pathview is an open source software package distributed under GNU General
## Public License version 3 (GPLv3). Details of GPLv3 is available at
## http://www.gnu.org/licenses/gpl-3.0.html. Particullary, users are required to
## formally cite the original Pathview paper (not just mention it) in publications
## or products. For details, do citation("pathview") within R.
##
## The pathview downloads and uses KEGG data. Non-academic uses may require a KEGG
## license agreement (details at http://www.kegg.jp/kegg/legal.html).
## #####
```

Set wd and read data

```
setwd('E:/R-Programming-Practices/Functional Enrichment/Pathway Analysis')
data= data.frame(read.csv('GBM.csv'))
```