

Package ‘Grouphmap’

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Type Package

Title 'Grouphmap' is an Automated One-Step Common Analysis of Batch Expression Profile

Version 1.0.0

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Depends R (>= 4.2.0)

Description The 'Grouphmap' was implemented in R, an open-source programming environment, and was released under the provided website. The difference analysis is based on the 'limma' package, which can cover gene and protein expression profiles (Reference: Matthew E Ritchie , Belinda Phipson , Di Wu , Yifang Hu , Charity W Law , Wei Shi , Gordon K Smyth (2015) <[doi:10.1093/nar/gkv007](https://doi.org/10.1093/nar/gkv007)>). The GO enrichment analysis is based on the 'clusterProfiler' package and supports three common species: human, mouse, and yeast (Reference: Guangchuang Yu, Li-Gen Wang, Yanyan Han, Qing-Yu He (2012) <[doi:10.1089/omi.2011.0118](https://doi.org/10.1089/omi.2011.0118)>). The results of batch difference analysis and enrichment analysis are output in separate folders for easy viewing and further visualization of the results during the process. The results returned a heatmap in R and exported to 3 folders named DEG, go, and merge.

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Encoding UTF-8

Imports limma, clusterProfiler, dplyr, org.Mm.eg.db, pheatmap, stringr, stats, utils, grDevices

RoxygenNote 7.2.3

References Matthew E Ritchie , Belinda Phipson , Di Wu , Yifang Hu , Charity W Law , Wei Shi , Gordon K Smyth (2015) <[doi:10.1093/nar/gkv007](https://doi.org/10.1093/nar/gkv007)>; Guangchuang Yu, Li-Gen Wang, Yanyan Han, Qing-Yu He (2012) <[doi:10.1089/omi.2011.0118](https://doi.org/10.1089/omi.2011.0118)>

NeedsCompilation no

Repository CRAN

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Description

Grouphmap: Automated one-step common analysis of Batch expression profile

Usage

ghmap(Path, conRep, treRep, OrgDb, TYPE, UP = TRUE, cutree, TOP)

Arguments

Path	"File storage path." Two groups are one file, and the control group should before the treatment group.
conRep	Number of repetitions in control group.
treRep	Number of repetitions in treatment group.
OrgDb	org.Mm.eg.db, org.Hs.eg.db, and org.Sc.sgd.db. Please library().
TYPE	"SYMBOL","ENSEMBOL"...
UP	up is TRUE and down is FALSE
cutree	heatmap can be devided multiple modules that make the functional difference and similarity of those group to be obvious
TOP	the numeric.Such as 10 is the top 10 of GO analysis in each file.

Value

p1

Examples

```
library(org.Mm.eg.db)
Path<-system.file("extdata", package = "Grouphmap")
ghmap(Path,2,2,org.Mm.eg.db,"ENSEMBL",FALSE,2,10)
```

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