Package ‘Groupmap’

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Type Package

Title 'Groupmap' 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 'Groupmap' 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>). 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>). 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>; Guangchuang Yu, Li-Gen Wang, Yanyan Han, Qing-Yu He (2012) <doi:10.1089/omi.2011.0118>

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

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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