Package ‘GOpro’

May 12, 2024

Type     Package
Title    Find the most characteristic gene ontology terms for groups of human genes
Version  1.30.0
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Description Find the most characteristic gene ontology terms for groups of human genes.
This package was created as a part of the thesis which was developed under the auspices of MI^2 Group (http://mi2.mini.pw.edu.pl/, https://github.com/geneticsMiNIng).
License  GPL-3
Depends  R (>= 3.4)
Imports  AnnotationDbi, dendextend, doParallel, foreach, parallel, org.Hs.eg.db, GO.db, Rcpp, stats, graphics, MultiAssayExperiment, IRanges, S4Vectors
LinkingTo Rcpp, BH
RoxygenNote 6.0.1
Suggests knitr, rmarkdown, RTCGA.PANCAN12, BiocStyle, testthat
VignetteBuilder knitr
LazyData true
biocViews Annotation, Clustering, GO, GeneExpression, GeneSetEnrichment, MultipleComparison
URL     https://github.com/mi2-warsaw/GOpro
BugReports https://github.com/mi2-warsaw/GOpro/issues
git_url  https://git.bioconductor.org/packages/GOpro
git_branch RELEASE_3_19
git_last_commit d8d04af
git_last_commit_date 2024-04-30
Repository Bioconductor 3.19
Date/Publication 2024-05-12
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exrtcga  

Expressions of human genes.

Description

A dataset containing gene expressions of 300 human genes randomly chosen from a list returned by function `prepareData(RTCGA = TRUE, cohorts = c('leukemia', 'colon', 'bladder'))`.

Usage

exrtcga

Format


Value

data

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findGO  

Find top Gene Ontology terms for given genes.

Description

Find top Gene Ontology terms for given genes.

Usage

findGO(groups, topAOV = 50, sig.levelAOV = 0.05, parallel = FALSE, grouped = "tukey", sig.levelGO = 0.05, minGO = 5, maxGO = 500, clust.metric = NULL, clust.method = NULL, dist.matrix = NULL, topGO = 3, sig.levelTUK = 0.05, onto = c("MF", "BP", "CC"), extend = FALSE, over.rep = FALSE)
**findGO**

**Arguments**

- **groups**: a MultiAssayExperiment object containing an ExperimentList class object representing gene expressions for at least 3 cohorts. Rows must be named with genes’ aliases. The order of samples and genes has to be the same for each ExperimentList class object.

- **topAOV**: A numeric value, a number of most significantly differentiated genes to be returned.

- **sig.levelAOV**: a numeric value, a significance level used in BH correction for multiple testing (aovTopTest).

- **parallel**: A logical value indicating if a task should be run on more than one core.

- **grouped**: A method of grouping genes, one of 'tukey' and 'clustering'.

- **sig.levelGO**: A numeric value, a significance level used in BH correction for multiple testing (findTopGOs).

- **minGO**: A minimum number of functions that a gene needs to represent to be considered as frequent.

- **maxGO**: A maximum number of functions that a gene needs to represent to be considered as frequent.

- **clust.metric**: The method to calculate a distance measure used in hierarchical clustering, possible names: "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski".

- **clust.method**: The agglomeration method used to cluster genes. This should be one of "ward.D", "ward.D2", "single", "complete", "average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC).

- **dist.matrix**: A matrix with calculated distances to be used as a metric by hclust function.

- **topGO**: A number of the most characteristic functions of groups of genes to be returned.

- **sig.levelTUK**: A numeric value, a significance level used in Tukey’s all pairwise comparison (groupByTukey).

- **onto**: An ontology or ontologies to be searched for significant GO terms, at least one of 'MF' (molecular function), 'BP' (biological process), and 'CC' (cellular component).

- **extend**: A logical value indicating if an extended version of the output should be presented.

- **over.rep**: A logical value indicating if an over represented GO terms should be presented in the plot.

**Value**

A data frame containing the top gene ontology terms for each group of genes and the gene aliases.

**Examples**

```r
findGO(exrtcga, grouped = 'clustering', topGO = 10, onto = 'MF')
findGO(exrtcga, grouped = 'tukey', topGO = 2, extend = TRUE)
```
Description

Based on the gene expressions find the structure somewhat comparable to gene signature. From all given genes, determine which are significantly different between sets. These sets may relate to different health conditions of patients, i.e. different types of cancer. Then divide interesting genes into subsets. Genes belong to a particular subset if they share the same feature. There are two implemented methods that can be used to create genes’ subsets. The first method is so-called all pairwise comparisons by Tukey’s procedure. Genes that have the same profile (a result of all comparisons) are assigned to one subset. The second way of determining subsets is a method of hierarchical clustering. When all genes are divided into subsets, then for each subset all relevant GO terms are searched for in org.Hs.eg.db database. Each found GO terms is tested using Fisher’s test to find out which of them are the most characteristic for the given subset of genes.

See Also

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