Package ‘EnrichIntersect’

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Type Package

Title Enrichment Analysis and Intersecting Sankey Diagram

Version 0.2

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URL https://github.com/zhizuio/EnrichIntersect

BugReports https://github.com/zhizuio/EnrichIntersect/issues

Description A flexible tool for enrichment analysis based on user-defined sets. It allows users to perform over-representation analysis of the custom sets among any specified ranked feature list, hence making enrichment analysis applicable to various types of data from different scientific fields. ‘EnrichIntersect’ also enables an interactive means to visualize identified associations based on, for example, the mix-lasso model (Zhao et al. (2022) <doi:10.1016/j.isci.2022.104767>) or similar methods.

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Depends R (>= 4.0)

Encoding UTF-8

RoxygenNote 7.2.1

Imports ggplot2, dplyr, networkD3, jsonlite, htmlwidgets, webshot2, grDevices, methods

Suggests knitr

LazyData true

VignetteBuilder knitr

NeedsCompilation no

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**Description**

Data set 'cancers_drug_groups' is a list including a score dataframe with 147 drugs as rows and 19 cancer types as columns, and a dataframe with 9 self-defined drug groups (1st column) of the 147 drugs (2nd column). More details of the data can be found in the results of paper 'Tissue-specific identification of multi-omics features for pan-cancer drug response prediction' by Zhao Z., Wang S. Zucknick M. and Aittokallio T. (2022).

**Usage**

cancers_drug_groups

**Format**

An object of class list of length 2.

**Value**

No return value.

**References**


**Examples**

```r
# Load data
data(cancers_drug_groups, package = "EnrichIntersect")
```
Description

Data set 'cancers_genes_drugs' is an array with association scores between 56 genes (1st dimension), three cancer types (2nd dimension) and two drugs (3rd dimension). More details of the data can be found in the results of paper 'Tissue-specific identification of multi-omics features for pan-cancer drug response prediction' by Zhao Z., Wang S. Zucknick M. and Aittokallio T. (2022).

Usage

cancers_genes_drugs

Format

An object of class array of dimension 56 x 3 x 2.

Value

No return value.

References


Examples

```r
# Load data
data(cancers_genes_drugs, package = "EnrichIntersect")
```

Description

Plot enrichment map through a vector (matrix) of scores and a self-defined set that summarizes a few groups of the names (rownames) of the vector (matrix)
enrichment

Usage

enrichment(
  x,
  custom.set,
  alpha = 0,
  normalize = TRUE,
  permute.n = 100,
  pvalue.cutoff = 0.05,
  angle = 45,
  ...
)

Arguments

  x       a vector (matrix) of scores to be enriched
  custom.set   a self-defined set that summarizes a few groups of the names (rownames) of x
  alpha    exponent weight of the score of ordered features. Default is 0 for calculating enrichment score via classic Kolmogorov-Smirnov statistic
  normalize logic value to determine if normalizing enrichment scores, accounting for custom set size. Default is TRUE
  permute.n number of custom-set permutations for significance testing. Default is 100
  pvalue.cutoff a cutoff of p-value to mark significantly enriched classes. Default is 0.05
  angle     angle of rotating x-axix labels. Default is 45
  ...      other arguments

Value

Return a list including a matrix of (normalized) enrichment score, a matrix of corresponding p-value and ggplot object:

  • S - a matrix of calculated enrichment scores.
  • pvalue - a matrix of p-values using permutation test for the calculated enrichment scores.
  • g - a ggplot object for visualising the results of an enrichment analysis.

References


Examples

# Data set 'cancers_drug_groups' is a list including a score dataframe with 147 drugs as rows # and 19 cancer types as columns, and a dataframe with 9 self-defined drug groups (1st column) # of the 147 drugs (2nd column).
data(cancers_drug_groups, package = "EnrichIntersect")
x <- cancers_drug_groups$score
intersectSankey <- cancers_drug_groups$custom.set
set.seed(123)
enrich <- enrichment(x, custom.set, permute.n=5)

interactSankey

Plot Sankey diagram for intersecting sets

Description
Plot Sankey diagram for intersecting set through an array

Usage
intersectSankey(
  x,
  out.fig = NULL,
  color = NULL,
  step.names = c("Levels", "Variables", "Tasks"),
  fontSize = c(20, 13, 20),
  ...
)

Arguments

x an array for constructing intersecting set
out.fig print the figure into "html", "pdf" or "png" file. Default is NULL with R graphics device
color a vector of colors corresponding to individual tasks
step.names names of the three dimensions of the array x, i.e. names of multiple levels, intermediate variables and tasks. Default is c("Levels","Variables","Tasks"). If step.names=NULL, it will not show the names
fontSize a value or vector of three values. If it is one value, it is the font size for all labels. But a vector of three values specifies the font size of the labels in the left, middle and right, respectively. Default is c(20, 10, 20)
...

Value
An object of a D3 JavaScript intersecting Sankey diagram for visualising associations based on the input array.
Examples

# Data set 'cancers_genes_drugs' is an array with association scores between 56 genes (1st
# dimension), three cancer types (2nd dimension) and two drugs (3rd dimension)
data(cancers_genes_drugs, package = "EnrichIntersect")

intersectSankey(cancers_genes_drugs, step.names=c("Cancers","Genes","Drugs"))
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