

# Package ‘EnrichIntersect’

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**Type** Package

**Title** Enrichment Analysis and Intersecting Sankey Diagram

**Version** 0.2

**Date** 2022-08-10

**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](https://doi.org/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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**Repository** CRAN

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cancers\_drug\_groups    *Data set 'cancers\_drug\_groups'*

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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

Zhao Z, Wang S, Zucknick M and Aittokallio T (2019). *Tissue-specific identification of multi-omics features for pan-cancer drug response prediction*. *iScience*, doi:10.1016/j.isci.2022.104767.

### Examples

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

---

cancers\_genes\_drugs      *Data set 'cancers\_genes\_drugs'*

---

**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**

Zhao Z, Wang S, Zucknick M and Aittokallio T (2019). *Tissue-specific identification of multi-omics features for pan-cancer drug response prediction*. iScience, doi:10.1016/j.isci.2022.104767.

**Examples**

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

---

enrichment      *Plot enrichment map*

---

**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)

**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-axis 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**

Reimand J, Isserlin R, Voisin V, et al (2019). *Pathway enrichment analysis and visualization of omics data using g:profiler, gsea, cytoscape and enrichmentmap*. Nature protocols, 14:482–517.

**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
```

```

custom.set <- cancers_drug_groups$custom.set
set.seed(123)
enrich <- enrichment(x, custom.set, permute.n=5)

```

---

intersectSankey      *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)
...	graphics parameters to be passed to sankeyNetwork() from R package networkD3

## 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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