Package ‘aPEAR’

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**Title**  Advanced Pathway Enrichment Analysis Representation

**Version**  1.0.0

**Description**  Simplify pathway enrichment analysis results by detecting clusters of similar pathways and visualizing it as an enrichment network, where nodes and edges describe the pathways and similarity between them, respectively. This reduces the redundancy of the overlapping pathways and helps to notice the most important biological themes in the data (Kerseviciute and Gordevicius (2023) <doi:10.1101/2023.03.28.534514>).

**URL**  https://gitlab.com/vugene/aPEAR

**BugReports**  https://gitlab.com/vugene/aPEAR/-/issues

**License**  MIT + file LICENSE

**Encoding**  UTF-8

**RoxygenNote**  7.2.3

**Suggests**  Spectrum, clusterProfiler, gprofiler2, DOSE, org.Hs.eg.db, testthat (>= 3.0.0), knitr, rmarkdown, stringr

**Depends**  R (>= 3.5.0)

**Imports**  arules, bayesbio, data.table, dplyr, igraph, lsa, MCL, reshape2, tibble, utils, methods, ggplot2, ggrepel, ggforce

**VignetteBuilder**  knitr

**NeedsCompilation**  no

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**Description**

A list with parameters for customizing how the clusters within the enrichment data are calculated.

**Usage**

aPEAR.methods

**Format**

An object of class aPEAR.methods.config of length 5.

**Details**

- similarity: method for calculating similarity matrix between the pathways. Available methods: 'jaccard', 'cosine' and 'correlation'
- clusterName: method for selecting cluster names. Available methods: 'pagerank', 'hits', 'nes' and 'pval'. The 'pagerank' and 'hits' algorithms analyse the connectivity within the cluster to detect the most important node. The 'nes' and 'pval' methods use enrichment results to determine the most important node within the cluster: the 'nes' method will choose the node with the maximum absolute enrichment score value and the 'pval' method will choose the node with the lowest p-value. When using the 'nes' and 'pval' methods, please specify which column in the data to use with the clusterNameColumn parameter
- clusterNameColumn: which column in the dataset should be used to select the cluster title. Required when clusterName = 'nes' and clusterName = 'pval'
- minClusterSize: minimum cluster size (default: 2). Clusters with less elements than specified will be dropped

**Value**

an object of class aPEAR.methods.config
Examples

# Display all default methods used by aPEAR
aPEAR.methods

# Update methods to use different similarity metric
settings <- aPEAR.methods
settings$similarity <- 'cosine'
settings

aPEAR.theme  

Default theme configuration for aPEAR

Description

A list with parameters for customizing the theme of the enrichment network plot.

Usage

aPEAR.theme

Format

An object of class aPEAR.theme.config of length 9.

Details

colorBy: which column in the data should be used to color the nodes in the enrichment network plot (default: ‘NES’)
nodeSize: which column in the data should be used to get the node size for the enrichment network plot (default: ‘setSize’)
innerCutoff: similarity cutoff for within-cluster nodes (default: 0.1). Decreasing this value results in greater connectivity within the nodes in the same cluster. For example, innerCutoff = 0 would display all connections within the same cluster.
outerCutoff: similarity cutoff for between-cluster nodes (default: 0.5). Decreasing this value results in greater connectivity between the nodes in different clusters. For example, outerCutoff = 0 would display all connections between different clusters.
colorType: how to colour the nodes: ‘nes’ - will center around 0 with blue min and red max, ‘pval’ - will use log transform on the colorBy column and adjust color range (default: ‘nes’)
pCutoff: adjust p-value colouring cutoff when using colorType = ‘pval’ (default: -10)
drawEllipses: enable / disable ellipse drawing (default: FALSE)
fontSize: adjust cluster label font size (default: 3)
repellLabels: whether the cluster label positions should be corrected (default: FALSE)
enrichmentNetwork

Value

an object of class aPEAR.theme.config

Examples

# Display the default theme configuration used by aPEAR
aPEAR.theme

# Update the theme to draw ellipses
settings <- aPEAR.theme
settings$drawEllipses <- TRUE
settings

enrichmentNetwork  aPEAR enrichment network

Description

Creates an enrichment network plot. This function internally calls findPathClusters to obtain pathway clusters and then plotPathClusters to create the enrichment network visualization.

Usage

enrichmentNetwork(
  enrichment,
  methods = aPEAR.methods,
  theme = aPEAR.theme,
  verbose = FALSE,
  ...
)

Arguments

  enrichment a data.frame containing enrichment results
  methods   object of class aPEAR.methods.config
  theme     object of class aPEAR.theme.config
  verbose   enable / disable log messages
  ...       additional parameters (see ?aPEAR.methods and ?aPEAR.theme)

Value

  a ggplot2 object

See Also

  ?findPathClusters, ?plotPathClusters
Examples

```r
# Load libraries
library(clusterProfiler)
library(DOSE)
library(org.Hs.eg.db)
data(geneList)

# Perform enrichment using clusterProfiler
enrich <- gseGO(geneList, OrgDb = org.Hs.eg.db, ont = 'CC')

# Create enrichment network visualization with default parameters
enrichmentNetwork(enrich@result)

# Create enrichment network visualization with repelled labels and ellipses
enrichmentNetwork(enrich@result, repelLabels = TRUE, drawEllipses = TRUE)
```

findPathClusters  Find pathway clusters

Description

Calculates the clusters within the enrichment data based on pathway similarity.

Usage

```r
findPathClusters(enrichment, methods = aPEAR.methods, verbose = FALSE, ...)
```

Arguments

- **enrichment**: a data.frame containing enrichment results
- **methods**: methods for calculating the pathway clusters within the enrichment result (object of class aPEAR.methods; default: aPEAR.methods)
- **verbose**: enable / disable log messages (default: FALSE)
- **...**: additional parameters (see ?aPEAR.methods)

Value

A list of two objects: sim - pathway similarity matrix; and clusters - pathway clusters.
Examples

# Load libraries
library(clusterProfiler)
library(DOSE)
library(org.Hs.eg.db)
data(geneList)

# Perform enrichment using clusterProfiler
enrich <- gseGO(geneList, OrgDb = org.Hs.eg.db, ont = 'CC')

# Obtain clusters within the enriched pathways using default parameters
data <- findPathClusters(enrich@result)
data$clusters

# Obtain clusters within the enriched pathways using hierarchical clustering
# and minClusterSize = 1
data <- findPathClusters(enrich@result, cluster = 'hier', minClusterSize = 1)
data$clusters

plotPathClusters

Description

Creates enrichment network plot.

Usage

plotPathClusters(
  enrichment,
  sim,
  clusters,
  theme = aPEAR.theme,
  verbose = FALSE,
  ...
)

Arguments

enrichment a data.frame containing enrichment results
sim similarity matrix of the enriched pathways
clusters clusters of the enriched pathways
theme object of class aPEAR.theme.config
verbose enable / disable log messages
... additional parameters (see ?aPEAR.theme)
Value

a ggplot2 object

Examples

# Load libraries
library(clusterProfiler)
library(DOSE)
library(org.Hs.eg.db)
data(geneList)

# Perform enrichment using clusterProfiler
enrich <- gseGO(geneList, OrgDb = org.Hs.eg.db, ont = 'CC')

# Obtain clusters within the enriched pathways using default parameters
data <- findPathClusters(enrich@result)

# Create the enrichment network visualization using default parameters
plotPathClusters(enrich@result, data$sim, data$clusters)

# Create the enrichment network visualization with repelled labels and ellipses
plotPathClusters(enrich@result, data$sim, data$clusters, repelLabels = TRUE, drawEllipses = TRUE)
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