

# Package: aPEAR (via r-universe)

August 30, 2024

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

**Roxygen** list(markdown = TRUE)

**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)

**Config/testthat/edition** 3

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

**VignetteBuilder** knitr

**Repository** <https://kerseviciute.r-universe.dev>

**RemoteUrl** <https://gitlab.com/vugene/appear>

**RemoteRef** HEAD

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aPEAR.methods

*Default method configuration for aPEAR*

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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'

cluster: method for detecting pathway clusters. Available methods: 'markov', 'hier' and 'spectral'. Using 'spectral' method requires that you have the Spectrum package installed

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*

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## 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)

`repelLabels`: whether the cluster label positions should be corrected (default: FALSE)

**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
```

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enrichmentNetwork	<i>aPEAR enrichment network</i>
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**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 <code>aPEAR.methods.config</code>
theme	object of class <code>aPEAR.theme.config</code>
verbose	enable / disable log messages
...	additional parameters (see <code>?aPEAR.methods</code> and <code>?aPEAR.theme</code> )

**Value**

a `ggplot2` object

**See Also**

`?findPathClusters`, `?plotPathClusters`

## 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')

# 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)
```

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findPathClusters	<i>Find pathway clusters</i>
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## Description

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

## Usage

```
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  
a list of clusters and similarity matrix

**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

```

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plotPathClusters      *aPEAR enrichment network*

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**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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