Package: PAVER (via r-universe)

September 3, 2024

Title PAVER: Pathway Analysis Visualization with Embedding
Representations

Version 0.0.0.9000

Description Summary visualization using embedding representations to
reveal underlying themes within sets of pathway terms.

License GPL (>= 3)

Imports circlize, ComplexHeatmap, dplyr, dynamicTreeCut, forcats,
ggplot2, ggplotify, ggprism, ggpubr, ggrepel, grid, magrittr,
purrr, randomcoloR, rlang, smacof, stringr, tibble, tidyr, umap

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Depends R (>= 2.10)

LazyData true

Config/testthat/edition 3

Repository https://cogdisreslab.r-universe.dev

RemoteUrl https://github.com/CogDisResLab/PAVER

RemoteRef HEAD

RemoteSha 9b74c6403f985e7a76e80354f7aaa4a0ee24e4d7

Contents

---

cosine_dissimilarity   *Compute Cosine Dissimilarity Matrix*

Description

This function computes the cosine dissimilarity matrix based on the input matrix. The cosine dissimilarity between two vectors is defined as 1 minus the cosine similarity.

Usage

```
cosine_dissimilarity(mat, root = FALSE)
```

Arguments

mat	A numeric matrix or data frame.
root	A logical value indicating whether to take the square root of the cosine dissimilarity matrix. Default is FALSE.

Value

A dissimilarity matrix of class "dist" containing the cosine dissimilarity between each pair of rows.

Examples

```
TRUE
```

---

generate_themes   *Cluster pathway embeddings and generate themes*

Description

This function clusters pathway embeddings using cosine similarity and generates themes for the clusters.

Usage

```
generate_themes(PAVER_result, hclust_method = "ward.D2", ...)
```

Arguments

`PAVER_result`	A list containing the result of running prepare_data
`hclust_method`	The agglomeration method to be used in hierarchical clustering. Default is "ward.D2".
`...`	Additional arguments to be passed to dynamicTreeCut

Value

A list containing the updated PAVER_result

Examples

```
TRUE
```

---

gsea_example *An example of GSEA results*

Description

A wide data frame with Normalized Enrichment Scores from Gene-Set Enrichment Analysis of three different comparisons.

Usage

```
gsea_example
```

Format

A data frame with 1080 rows and 4 columns:

GOID Gene Ontology Term IDs

SCZvsCtrl NES of GO terms

SCZvsCtrlD NES of GO terms

SCZvsCtrlS NES of GO terms

Source

https://doi.org/10.1038/s41380-021-01205-y

---

kegg_example   *An example of KEGG results*

Description

A wide data frame with enrichment scores (log10 FDR) from MetaboAnalyst of one comparison.

Usage

```
kegg_example
```

Format

A data frame with 183 rows and 2 columns:

MAP KEGG Pathway IDS

MA Enrichment Scores of KEGG pathways

Source

<https://doi.org/10.1101/2023.10.13.562226>

PAVER_combined_plot   *PAVER_combined_plot*

Description

This function takes a PAVER result object and generates a combined ggplot2 figure consisting of the PAVER_cluster_plot, PAVER_regulation_plot, PAVER_interpretation_plot, and PAVER_hunter_plot.

Usage

```
PAVER_combined_plot(PAVER_result, unit = NULL)
```

Arguments

PAVER_result	a list containing the output of PAVER analysis
unit	optionally, the unit of enrichment analysis for the figure legend title.

Value

A combined ggplot2 figure consisting of the PAVER_cluster_plot, PAVER_regulation_plot, PAVER_interpretation_plot, and PAVER_hunter_plot.

Examples

```
TRUE
```

PAVER_export   *Export PAVER results to a formatted data frame*

Description

This function takes a PAVER result object and prepares it for export as a wide format data frame. The resulting data frame will have GO Term IDs, Definitions, generated themes, and columns for each of the groups in the PAVER result, with values representing the original input value of each GO term for that group.

Usage

```
PAVER_export(PAVER_result)
```

Arguments

PAVER_result   A PAVER result object generated by the generate_themes function.

Value

A wide format data frame with GO Term IDs, Definitions, generated themes, and columns for each of the groups in the PAVER result, with values representing the original input value of each GO term for that group.

Examples

```
TRUE
```

PAVER_hunter_plot   *PAVER_hunter_plot*

Description

This function takes a PAVER result object and generates a heatmap of the enrichment analysis with clustering and color-coded values based on the direction of regulation.

Usage

```
PAVER_hunter_plot(PAVER_result, unit = NULL, show_row_titles = TRUE)
```

Arguments

PAVER_result   a list containing the output of PAVER analysis

unit   optionally, the unit of enrichment analysis for the figure legend title.

show_row_titles

                a logical indicating whether to show row titles in the heatmap.

Value

A heatmap of the expression data with clustering and color-coded values based on the direction of regulation.

Examples

```
TRUE
```

```
PAVER_interpretation_plot
```
PAVER_interpretation_plot

Description

This function takes a PAVER result object and generates a ggplot2 scatterplot of the MDS layout with labeled points colored by group.

Usage

```
PAVER_interpretation_plot(PAVER_result)
```

Arguments

PAVER_result   a list containing the output of PAVER analysis

Value

A ggplot2 scatterplot of the MDS layout with labeled points colored by group.

Examples

```
TRUE
```

PAVER_regulation_plot *PAVER_regulation_plot*

Description

This function takes a PAVER result object and generates a ggplot2 scatterplot of the UMAP layout colored by direction of regulation (up or down) for each group.

Usage

```
PAVER_regulation_plot(PAVER_result)
```

Arguments

PAVER_result   a list containing the output of PAVER analysis

Value

A ggplot2 scatterplot of the UMAP layout colored by direction of regulation (up or down) and faceted for each group.

Examples

```
TRUE
```

PAVER_theme_plot   *PAVER_theme_plot*

Description

This function takes a PAVER result object and generates a ggplot2 scatterplot of the UMAP layout colored by cluster assignments.

Usage

```
PAVER_theme_plot(PAVER_result, show_cluster_legend = TRUE)
```

Arguments

PAVER_result   a list containing the output of PAVER analysis

show_cluster_legend

               a logical indicating whether to show the cluster legend.

Value

A ggplot2 scatterplot of the UMAP layout colored by cluster assignments

Examples

```
TRUE
```

---

prepare_data	*Prepare pathway analysis results for downstream theme generation and summary visualization*

Description

This function prepares the results of pathway analysis for downstream theme generation and visualization using precomputed embeddings.

Usage

```
prepare_data(input, embeddings, term2name)
```

Arguments

input	A data frame in wide format containing the pathway analysis results. The first column is expected to be term IDs, e.g. GO:0000001, while the remaining columns are expected to be numeric values representing the enrichment of each term in each group.
embeddings	A matrix containing the precomputed embeddings of the input terms.
term2name	A data frame containing two columns that map pathway term IDs to pathway term names.

Value

A PAVER_result list with the prepared data ready for theme generation

Examples

```
TRUE
```

Index