Package: Paralogs (via r-universe)

October 18, 2026

Type Package

Title Visualizing Differential Expression of Paralogs in KEGG Gene Pathways

Version 0.2.1

Description This package provides functions to visualize the differential expression of paralogs in KEGG gene pathways. The package includes functions to download KEGG gene pathways, extract paralogs from the pathways, and visualize the differential expression of the paralogs. The package also includes functions to visualize the expression of paralogs in the context of the KEGG gene pathways.

License MIT + file LICENSE

Encoding UTF-8

LazyData true

suggests org.Sc.sgd.db, clusterProfiler

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.3.2

Imports AnnotationDbi, ggplot2, ggkegg, dplyr, edgeR, KEGGREST, magrittr, stringr, tibble, tidyr, RColorBrewer

Depends R (>= 2.10)

Config/pak/sysreqs libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libglpk-dev make libmagick++-dev gsfonts libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev zlib1g-dev

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

Date/Publication 2025-03-13 14:51:24 UTC

RemoteUrl https://github.com/clstacy/Paralogs

RemoteRef HEAD

RemoteSha 7c1ba2bfc174fbd433511c07a1cb1387a9952827

Contents

create_ggkegg 2
createParalogPlots 3
example_enrich_results 3
fetchKeggReactions 4
getPathwayNumber 4
loadEnrichResults 5
loadGeneData 5
lrt_yeast 6
plotParalogs 6
process_ggkegg 7

Index **9**

`create_ggkegg` *Create ggkegg Object for KEGG Pathway Visualization*

Description

Creates a ggkegg object from KEGG results using specified parameters.

Usage

```
create_ggkegg(kegg_results, pathway_id, pathway_number, organism_code = "sce")
```

Arguments

`kegg_results`	An enrichKEGG output from clusterProfiler (provided by user).
`pathway_id`	A string specifying the pathway ID (provided by user).
`pathway_number`	The number representing the pathway in KEGG.
`organism_code`	A string representing the organism code in KEGG (e.g., "sce").

Value

A ggkegg object.

createParalogPlots *Create KEGG Pathway Graphs*

Description

Creates comparative graphs for gene expression data on KEGG pathways.

Usage

```
createParalogPlots(graph_data, pathway_id, fc_column, juke = 20, title)
```

Arguments

graph_data	A dataframe with KEGG pathway data processed for visualization.
pathway_id	A string indicating the pathway ID for overlay.
fc_column	A string naming the first fold change column.
juke	A number for amount of space to separate names. Default is 20.
title	A title for the plot.

Value

A ggplot object displaying the pathway graphs side by side.

---

example_enrich_results

An example output of enrichKEGG is provided in the 'example_enrich_results' dataset. The results are the top enrichments for the genes in the lrt_yeast example. This data is used in vignette examples.

Description

An example output of enrichKEGG is provided in the 'example_enrich_results' dataset. The results are the top enrichments for the genes in the lrt_yeast example. This data is used in vignette examples.

Usage

```
example_enrich_results
```

Format

An object of class `enrichResult` with 37 rows and 11 columns.

`fetchKeggReactions` *Fetch KEGG Reactions*

Description

Retrieves KEGG reaction mappings and formats them for use.

Usage

```
fetchKeggReactions()
```

Value

A dataframe containing KEGG reactions with their descriptions.

`getPathwayNumber` *Get Pathway Number to match row of enrichKEGG to KEGG pathway of interest*

Description

Retrieves the pathway number based on a pathway ID from KEGG data.

Usage

```
getPathwayNumber(kegg_results, pathway_id)
```

Arguments

`kegg_results`	An enrichKEGG output from clusterProfiler (provided by user).
`pathway_id`	A string specifying the pathway ID (provided by user).

Value

An integer representing the pathway number.

loadEnrichResults *load Input data (enrichKEGG object)*

Description

Processes outputs from enrichKEGG.

Usage

```
loadEnrichResults(enrich_results)
```

Arguments

enrich_results	enrichResult Object from enrichKEGG.

Value

A dataframe with results for subsequent analysis.

loadGeneData *load Input data (enrichKEGG object)*

Description

Processes outputs from enrichKEGG.

Usage

```
loadGeneData(DE_results, FC_col_name)
```

Arguments

DE_results	gene results object, either edgeR, DESeq2, limma, or data frame.
FC_col_name	A string specifying the column name for log fold change.

Value

A dataframe with results for subsequent analysis.

`lrt_yeast` *An example DGELRT object is provided in the 'lrt_yeast' dataset. This object contains the results of a differential gene expression analysis using the edgeR package. logFC values correspond to the effect of a gene knockout on response to ethanol stress in yeast.*

Description

An example DGELRT object is provided in the 'lrt_yeast' dataset. This object contains the results of a differential gene expression analysis using the edgeR package. logFC values correspond to the effect of a gene knockout on response to ethanol stress in yeast.

Usage

```
lrt_yeast
```

Format

An object of class `DGELRT` with 5615 rows and 4 columns.

`plotParalogs` *Full Workflow for KEGG Pathway Visualization*

Description

Executes a complete workflow from raw DE results to visualizing them on a KEGG pathway.

Usage

```
plotParalogs(
  enrich_results,
  DE_results,
  organism_code = "sce",
  annotation_package = org.Sc.sgd.db,
  keytype = "ORF",
  pathway_code,
  fc_column = "logFC",
  juke = 20,
  title = NULL
)
```

Arguments

enrich_results	The enrichKEGG results (from clusterProfiler).
DE_results	The DE results (e.g. from edgeR).
organism_code	The organism code for KEGG pathways (e.g., 'sce').
annotation_package	The Bioconductor package for annotations relevant to the organism.
keytype	The type of key used in the gene IDs (e.g., "SYMBOL", "ENTREZID", "ENSEMBL").
pathway_code	The KEGG pathway code to visualize (e.g. 'sce00020')
fc_column	The first fold change column name for visualization.
juke	A number for amount of space to separate names. Default is 20.
title	A title for the plot.

Value

A ggplot object displaying the pathway graphs.

---

process_ggkegg *Process ggkegg Data for Visualization*

Description

Processes ggkegg object data to prepare it for visualization, enhancing gene data with KEGG reactions and annotations.

Usage

```
process_ggkegg(
  KEGG_data,
  topTags_results,
  KEGG_reactions_df,
  annotation_db,
  organism_code = "sce"
)
```

Arguments

KEGG_data	A ggkegg object containing KEGG pathway data.
topTags_results	A dataframe containing gene results.
KEGG_reactions_df	A dataframe containing KEGG reaction descriptions.
annotation_db	An AnnotationDbi object for gene annotations.
organism_code	A string representing the organism code in KEGG (e.g., "sce").

Value

A dataframe ready for plotting.

Index

∗ **datasets**
example_enrich_results, 3
lrt_yeast, 6

create_ggkegg, 2
createParalogPlots, 3

example_enrich_results, 3

fetchKeggReactions, 4

getPathwayNumber, 4

loadEnrichResults, 5
loadGeneData, 5
lrt_yeast, 6

plotParalogs, 6
process_ggkegg, 7