

Package ‘FunJacc’

March 13, 2025

Type Package
Title What the Package Does (Title Case)
Version 0.1.0
Author Who wrote it
Maintainer The package maintainer <yourself@somewhere.net>
Description More about what it does (maybe more than one line)
Use four spaces when indenting paragraphs within the Description.
License What license is it under?
Encoding UTF-8
LazyData true
RoxygenNote 7.3.2
Imports MCL, RCy3, gprofiler2, gRbase, stringr

Contents

create_cytoscape_network	1
funjacc	2
funjacc_res	3
gene_list	3
run_gprofiler	4

create_cytoscape_network
Create a FunJacc network in Cytoscape

Description

Draw the FunJacc results as a network in an open instance of Cytoscape running on the same machine

Usage

```
create_cytoscape_network(  
  funjacc_results,  
  title = "my first network",  
  collection = "Funjacc Networks"  
)
```

Arguments

funjacc_results	Funjacc results
title	Network title
collection	Network collection

Value

Sets up a network in your Cytoscape application

Examples

```
create_cytoscape_network(funjacc_res, title="Test network")
```

funjacc	<i>Run FunJacc</i>
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Description

Determine enriched functional term clusters with FunJacc

Usage

```
funjacc(
  gene_list,
  p_cut = 0.01,
  jaccard_cut = 0.5,
  data_types = c("GO:BP"),
  inflation = 2,
  species = "hsapiens",
  default_node_label_size = 10,
  cluster_label_size = 20
)
```

Arguments

gene_list	List of genes in which to look for enriched terms
p_cut	P-value cutoff for gProfiler results
jaccard_cut	Jaccard index cutoff for identifying high scoring links between terms
data_types	List of functional terms to include e.g.c('GO:BP', 'GO:MF', 'GO:CC', 'KEGG', 'REAC', 'TF', 'MIRNA', 'CORUM', 'HP', 'HPA', 'WP'). Supplying 'all' will include all these terms
inflation	Inflation parameter for MCL clustering ~0.5-2
species	Organism to use for gProfiler to interpret gene list e.g. 'hsapiens', 'mmusculus'
default_node_label_size	Node size to use for Cytoscape plotting
cluster_label_size	Node size for cluster labels in Cytoscape plotting

Value

list of results elements 'annotation' = clusters and their annotation, 'network' = network of clusters

Examples

```
funjacc(gene_list, data_types='all', species='hsapiens', inflation=2)
```

funjacc_res	<i>Data file of output from run_funjacc function for testing create_cytoscape_network function</i>
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Description

Data file of output from run_funjacc function for testing create_cytoscape_network function

Usage

```
funjacc_res
```

Format

An object of class `list` of length 2.

Author(s)

Adam Reid <ajr236@cam.ac.uk>

gene_list	<i>Data file of gene lists for testing</i>
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Description

Data file of gene lists for testing

Usage

```
gene_list
```

Format

An object of class `character` of length 79.

Author(s)

Adam Reid <ajr236@cam.ac.uk>

run_gprofiler	<i>Run gProfiler</i>
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Description

Get gProfiler results for further processing

Usage

```
run_gprofiler(gene_list, organism)
```

Arguments

gene_list	List of genes in which to look for enriched terms
organism	Name of species relating to gene list