

Package ‘FunJaccR’

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Type Package

Title Interpretation of Gene Lists Using Clustering of Functionally Enriched Terms

Version 0.1.0

Description Given a gene list, functionally enriched terms are determined using gProfiler. MCL is used to cluster these terms based on the Jaccard similarity of the lists of genes associated with them. This can be visualised in Cytoscape using the RCy3 package.

License GPL (>=3)

Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

Imports MCL, RCy3, gprofiler2, gRbase, stringr

NeedsCompilation no

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Depends R (>= 3.5.0)

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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