

# Package ‘FunJaccR’

March 25, 2025

**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) + file LICENSE

**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*

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### 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")
```

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```
funjacc
```

*Run FunJacc*

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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)
```

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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>

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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

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