

# Package ‘RUtil’

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**Version** 0.01

**License** GPL (>= 2)

**Description** A package collecting useful R code snippets from different projects made by Raivo Kolde.

**Title** Raivos util functions

**Author** Raivo Kolde <rkolde@gmail.com>

**Maintainer** Raivo Kolde <rkolde@gmail.com>

**Depends** R (>= 2.10)

**Imports** plyr, reshape, stringr, ggplot2, RCurl

**Collate** 'gprofiler.r' 'make\_unique\_comb.r' 'RUtil-package.r'

## R topics documented:

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## Description

A set of useful functions by Raivo

gconvert

*Convert gene ID-s.*

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**Description**

Convert gene ID-s.

**Usage**

```
gconvert(ids, organism="hsapiens", target="ENSG", df=T)
```

**Arguments**

ids	gene list.
organism	gene list origin.
target	target ID.
df	logical showing if the output will be a data.frame or list.

**Details**

Wrapper for g:Convert web toolkit.

**Value**

The output can be either list or data.frame. List has an entry for every input gene. Data frame is just a two column table with inputs and corresponding outputs. The input names may be duplicated.

**Author(s)**

Juri Reimand <jyri.reimand@ut.ee>, Raivo Kolde <rkolde@gmail.com>

**References**

J. Reimand, M. Kull, H. Peterson, J. Hansen, J. Vilo: g:Profiler - a web-based toolset for functional profiling of gene lists from large-scale experiments (2007) NAR 35 W193-W200

**Examples**

```
gconvert(c("Klf4", "Pax5", "Sox2", "Nanog"), organism = "mmusculus")
```

---

```
generate_gcocoa_query
```

*Generate query for g:Cocoa web tool...*

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### Description

Generate query for g:Cocoa web tool

### Usage

```
generate_gcocoa_query(glist)
```

### Arguments

`glist`                      a list of vectors of gene names

### Details

Function that prints out a g:Gogoa query string given a list of gene name vectors.

### Value

Prints out the query string

### Author(s)

Raivo Kolde <rkolde@gmail.com>

### Examples

```
glist = list(a = c("pax6", "klf9"), b = c("nanog", "Pou5f1"))
```

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```
gorth
```

*Find orthologs.*

---

### Description

Find orthologs.

### Usage

```
gorth(genelist, source_organism="mmusculus", target_organism="hsapiens", mthresh
```

### Arguments

`genelist`                      list of gene names to be translated.

`source_organism`

organism of the input genes.

`target_organism`

name for the target organism.

`mthreshold`                      how many ortholog names per gene to show

`df`                                      logical showing if the output will be a data.frame or list.

## Details

Wrapper for g:Orth web toolkit. The organism names are constructed, by combining the first letter of the name and family name. For example human - 'hsapiens' and mouse- 'mmusculus'

To alleviate the problem of having many orthologs per gene (most of them uninformative) one can set a threshold of how many results to show. The programs tries to find the most informative by selecting the most popular ones.

## Value

The output can be either list or data.frame. List has an entry for every input gene. Data frame is just a two column table with inputs and corresponding outputs. The input names may be duplicated.

## Author(s)

Raivo Kolde <rkolde@gmail.com>, Juri Reimand <jyri.reimand@ut.ee>

## References

J. Reimand, M. Kull, H. Peterson, J. Hansen, J. Vilo: g:Profiler – a web-based toolset for functional profiling of gene lists from large-scale experiments (2007) NAR 35 W193-W200

## Examples

```
gorth(c("Klf4", "Pax5", "Sox2", "Nanog"), source_organism = "mmusculus", target_organism
```

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gprofiler	<i>Annotate gene list functionally.</i>
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## Description

Annotate gene list functionally.

## Usage

```
gprofiler(organism="scerevisiae", query, ordered_query=0, significant=1)
```

## Arguments

organism	gene list origin
query	vector of gene names or list of such vectors
ordered_query	when output gene lists are ranked one can use this option to get GSEA style p-values.
significant	logical indicating if all or only statistically significant results should be returned.

## Details

Wrapper for g:Profiler web toolkit for finding enrichments in gene lists.

**Value**

Data frame with the Enricment analysis results. If input consisted of several lists the corresponding list is indicated with a variable 'query number'

**Author(s)**

Juri Reimand <jyri.reimand@ut.ee>

**References**

J. Reimand, M. Kull, H. Peterson, J. Hansen, J. Vilo: g:Profiler - a web-based toolset for functional profiling of gene lists from large-scale experiments (2007) NAR 35 W193-W200

**Examples**

```
gprofiler(c("Klf4", "Pax5", "Sox2", "Nanog"), organism = "mmusculus")
```

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make_unique_comb	<i>Function for producing all unique combinations of elements from one vector.</i>
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**Description**

Function for producing all unique combinations of elements from one vector.

**Usage**

```
make_unique_comb(l)
```

**Arguments**

l                      vector of some values

**Details**

The function creates all unique combinations of different values in vector l.

**Value**

A matrix with two columns. Rownames are the element names pasted together and separated by "\_". The rows are ordered alphabetically according to rownames. The two values in each row are also ordered alphabetically.

**Author(s)**

Raivo Kolde <rkolde@gmail.com>

**Examples**

```
make_unique_comb(letters[1:3])
```

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