

Package ‘RUtil’

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

Title Raivos util functions

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Depends R (>= 2.10)

Imports plyr, reshape, stringr, ggplot2, RCurl

Collate 'gprofiler.r' 'make_unique_comb.r' 'RUtil-package.r'

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RUtil-package	<i>A set of useful functions by Raivo...</i>
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Description

A set of useful functions by Raivo

gconvert

Convert gene ID-s.

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")
```

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>

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
```

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>, 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

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

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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