Package 'RUtil'

January 9, 2011

Version 0.02

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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, grid

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

R topics documented:

RUtil-package   *A set of useful functions by Raivo...*

Description

A set of useful functions by Raivo

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bubbleplot	*Function to draw the bubbleplots - an alternative to Venn diagram...*

Description

Function to draw the bubbleplots - an alternative to Venn diagram

Usage

```
bubbleplot(lists, percentage=TRUE)
```

Arguments

lists	input element lists
percentage	logical showing if percentages or raw numbers are displayed

Details

Function to draw the bubbleplots - an alternative to Venn diagram

Value

Returns nothing only draws the picture

Author(s)

Raivo Kolde <rkolde@gmail.com>

Examples

```
bubbleplot(list(Asadsa = sample(letters, 14), Gadsa = sample(letters, 9)))
bubbleplot(list(Badsad = sample(letters, 16), Asadsa = sample(letters, 14), Gadsa = sampl
```

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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 corrsponding 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")
```

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generate_gcocoa_query

Generate query for g:Cocoa web tool...

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"))
generate_gcocoa_query(glist)
```

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gorth   *Find orthologs.*

Description

Find orthologs.

Usage

```
gorth(genelist, source_organism="mmusculus", target_organism="hsapiens",
    mthreshold=3, df=T)
```

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 corrsponding 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
```

---

gprofiler *Annotate gene list functionally.*

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")
```

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

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 togeteher 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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