Package ‘gProfileR’

April 27, 2016

Version 0.6.1
License GPL (>= 2)
Description Functional enrichment analysis, gene identifier conversion and mapping homologous genes across related organisms via the 'g:Profiler' toolkit (http://biit.cs.ut.ee/gprofiler/).

Title Interface to the 'g:Profiler' Toolkit
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Depends R (>= 2.10)
Imports RCurl, plyr, utils
Collate 'gProfileR.R'

RoxygenNote 5.0.1
NeedsCompilation no
Repository CRAN
Date/Publication 2016-04-27 18:56:49

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gconvert

Convert gene IDs.

Description

Interface to the g:Convert tool. Organism names are constructed by concatenating the first letter of the name and the family name. Example: human - 'hsapiens', mouse - 'mmusculus'.

Usage

```r
gconvert(query, organism = "hsapiens", target = "ENSG", region_query = F, numeric_ns = ",", mthreshold = Inf, filter_na = T, df = T)
```

Arguments

- `query` list of gene IDs.
- `organism` organism name.
- `target` target namespace.
- `region_query` interpret query as chromosomal ranges.
- `numeric_ns` namespace to use for fully numeric IDs.
- `mthreshold` maximum number of results per initial alias to show.
- `filter_na` logical indicating whether to filter out results without a corresponding target.
- `df` logical indicating whether the output will be a data.frame or list.

Value

The output can be either a list or a data.frame. The list has an entry for every input gene. The data frame is a table closely corresponding to the web interface output.

Author(s)

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References


Examples

```r
gconvert(c("POU5F1", "SOX2", "NANOG"), organism = "hsapiens", target="AFFY_HG_U133PLUS2")
```
get_base_url

Get the base URL.

Description
Get the base URL.

Usage
get_base_url()

get_user_agent

Get current user agent string.

Description
Get the HTTP User-Agent string.

Usage
get_user_agent()

gorth

Find orthologs.

Description
Interface to the g:Orth tool. Organism names are constructed by concatenating the first letter of the name and the family name. Example: human - 'hsapiens', mouse - 'mmusculus'.

Usage
gorth(query, source_organism = "hsapiens", target_organism = "mmusculus", region_query = F, numeric_ns = "", mthreshold = Inf, filter_na = T, df = T)
Arguments

query list of gene IDs to be translated.
source_organism name of the source organism.
target_organism name of the target organism.
region_query interpret query as chromosomal ranges.
numeric_ns namespace to use for fully numeric IDs.
mthreshold maximum number of ortholog names per gene to show.
filter_na logical indicating whether to filter out results without a corresponding target name.
df logical indicating whether the output will be a data.frame or list.

Details

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

Value

The output can be either a list or a data.frame. The list has an entry for every input gene. The data frame is a table closely corresponding to the web interface output.

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References


Examples

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


**Description**

Interface to the g:Profiler tool for finding enrichments in gene lists. Organism names are constructed by concatenating the first letter of the name and the family name. Example: human - 'hsapiens', mouse - 'mmusculus'. If requesting PNG output, the request is directed to the g:GOSt tool in case 'query' is a vector and the g:Cocoa (compact view of multiple queries) tool in case 'query' is a list. PNG output can fail (return FALSE) in case the input query is too large. In such case, it is advisable to fall back to a non-image request.

**Usage**

```r
gprofiler(query, organism = "hsapiens", ordered_query = F,
        significant = T, exclude_iae = F, underrep = F, evcodes = F,
        region_query = F, max_p_value = 1, min_set_size = 0, max_set_size = 0,
        min_isect_size = 0, correction_method = "analytical",
        hier_filtering = "none", domain_size = "annotated", custom_bg = "",
        numeric_ns = "", png_fn = NULL, include_graph = F, src_filter = NULL)
```

**Arguments**

- **query**
  - vector of gene IDs or a list of such vectors.
- **organism**
  - organism name.
- **ordered_query**
  - in case output gene lists are ranked this option may be used to get GSEA style p-values.
- **significant**
  - whether all or only statistically significant results should be returned.
- **exclude_iae**
  - exclude electronic annotations (IEA).
- **underrep**
  - measure underrepresentation.
- **evcodes**
  - include GO evidence codes as the final column of output. Note that this can decrease performance and make the query slower.
- **region_query**
  - interpret query as chromosomal ranges.
- **max_p_value**
  - custom p-value threshold, results with a larger p-value are excluded.
- **min_set_size**
  - minimum size of functional category, smaller categories are excluded.
- **max_set_size**
  - maximum size of functional category, larger categories are excluded.
- **min_isect_size**
  - minimum size of the overlap (intersection) between query and functional category, smaller intersections are excluded.
- **correction_method**
  - the algorithm used for determining the significance threshold, one of "gSCS", "fdr", "bonferroni".
- **hier_filtering**
  - hierarchical filtering strength, one of "none", "moderate", "strong".
- **domain_size**
  - statistical domain size, one of "annotated", "known".
custom_bg vector of gene names to use as a statistical background.
numeric_ns namespace to use for fully numeric IDs.
png_fn request the result as PNG image and write it to png_fn.
include_graph request inclusion of network data with the result.
src_filter a vector of data sources to use. Currently, these include GO (GO:BP, GO:MF, GO:CC to select a particular GO branch), KEGG, REAC, TF, MI, CORUM, HP, HPA, OMIM. Please see the g:GOST web tool for the comprehensive list and details on incorporated data sources.

Value
A data frame with the enrichment analysis results. If the input consisted of several lists the corresponding list is indicated with a variable 'query number'. When requesting a PNG image, either TRUE or FALSE, depending on whether a non-empty result was received and a file written or not, respectively. If 'include_graph' is set, the return value may include the attribute 'networks', containing a list of all network sources, each in turn containing a list of graph edges. The edge structure is a list containing the two interacting symbols and two boolean values (in that order), indicating whether the first or second interactor is part of the input query (core nodes).

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References

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

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set_base_url
Set the base URL.

Description
Set the base URL. Useful for overriding the default URL (http://biit.cs.ut.ee/gprofiler) with the bleeding-edge beta or an archived version.

Usage
set_base_url(url)

Arguments
url the base URL.
set_user_agent

set_user_agent  Set custom user agent string.

Description
Set the HTTP User-Agent string. Useful for overriding the default user agent for packages that depend on gProfileR functionality.

Usage
set_user_agent(ua, append = F)

Arguments

ua  the user agent string.
append  logical indicating whether to append the passed string to the default user agent string.
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