Package 'orthogene'

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Type Package

Title Interspecies gene mapping

Version 1.13.0

Description `orthogene` is an R package for easy mapping of orthologous genes across hundreds of species. It pulls up-to-date gene ortholog mappings across **700+ organisms**.
It also provides various utility functions to aggregate/expand common objects (e.g. data.frames, gene expression matrices, lists) using **1:1**, **many:1**, **1:many** or **many:many** gene mappings, both within- and between-species.

URL https://github.com/neurogenomics/orthogene

BugReports https://github.com/neurogenomics/orthogene/issues

License GPL-3

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`orthogene-package` **orthogene***: Interspecies gene mapping*

Description

orthogene is an R package for easy mapping of orthologous genes across hundreds of species.

Details

It pulls up-to-date interspecies gene ortholog mappings across 700+ organisms.
It also provides various utility functions to map common objects (e.g. data.frames, gene expression matrices, lists) onto 1:1 gene orthologs from any other species.

Author(s)

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Source

- GitHub : Source code and Issues submission.
- Author Site : `orthogene` was created by Brian M. Schilder.

See Also

Useful links:

- https://github.com/neurogenomics/orthogene
- Report bugs at https://github.com/neurogenomics/orthogene/issues

add_synonyms *Add gene synonyms*

Description

Add gene synonyms back into `gene_map` `data.frame`.

Usage

```
add_synonyms(gene_map, syn_map)
```

Details

`gene_map` is the output of convert_orthologs.

Value

`gene_map` `data.frame`

aggregate_mapped_genes *Aggregate/expand a gene matrix by gene mappings*

Description

Aggregate/expand a gene matrix (`gene_df`) using a gene mapping data.frame (`gene_map`). Importantly, mappings can be performed across a variety of scenarios that can occur during within-species and between-species gene mapping:

- 1 gene : 1 gene
- many genes : 1 gene
- 1 gene : many genes
- many genes : many genes

For more details on how aggregation/expansion is performed, please see: many2many_rows.

Usage

```
aggregate_mapped_genes(
  gene_df,
  gene_map = NULL,
  input_col = "input_gene",
  output_col = "ortholog_gene",
  input_species = "human",
  output_species = input_species,
```

```
  method = c("gprofiler", "homologene", "babelgene"),
  agg_fun = "sum",
  agg_method = c("monocle3", "stats"),
  aggregate_orthologs = TRUE,
  transpose = FALSE,
  mthreshold = 1,
  target = "ENSG",
  numeric_ns = "",
  as_integers = FALSE,
  as_sparse = TRUE,
  as_DelayedArray = FALSE,
  dropNA = TRUE,
  sort_rows = FALSE,
  verbose = TRUE
)
```

Arguments

gene_df	Input matrix where row names are genes.
gene_map	A data.frame that maps the current gene names to new gene names. This function's behaviour will adapt to different situations as follows: • gene_map=<data.frame> : When a data.frame containing the gene key:value columns (specified by input_col and output_col, respectively) is provided, this will be used to perform aggregation/expansion. • gene_map=NULL and input_species!=output_species : A gene_map is automatically generated by map_orthologs to perform inter-species gene aggregation/expansion. • gene_map=NULL and input_species==output_species : A gene_map is automatically generated by map_genes to perform within-species gene gene symbol standardization and aggregation/expansion.
input_col	Column name within gene_map with gene names matching the row names of X.
output_col	Column name within gene_map with gene names that you wish you map the row names of X onto.
input_species	Name of the input species (e.g., "mouse","fly"). Use map_species to return a full list of available species.
output_species	Name of the output species (e.g. "human","chicken"). Use map_species to return a full list of available species.
method	R package to use for gene mapping: • "gprofiler" : Slower but more species and genes. • "homologene" : Faster but fewer species and genes. • "babelgene" : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
agg_fun	Aggregation function.
agg_method	Aggregation method.

aggregate_orthologs
: [Optional] After performing an initial round of many:many aggregation/expansion with many2many_rows, ensure each orthologous gene only appears in one row by using the aggregate_rows function (default: TRUE).

transpose
: Transpose gene_df before mapping genes.

mthreshold
: maximum number of results per initial alias to show. Shows all by default.

target
: target namespace.

numeric_ns
: namespace to use for fully numeric IDs (list of available namespaces).

as_integers
: Force all values in the matrix to become integers, by applying floor (default: FALSE).

as_sparse
: Convert aggregated matrix to sparse matrix.

as_DelayedArray
: Convert aggregated matrix to DelayedArray.

dropNA
: Drop genes assigned to NA in groupings.

sort_rows
: Sort gene_df rows alphanumerically.

verbose
: Print messages.

Value

Aggregated matrix

Examples

```
#### Aggregate within species: gene synonyms ####
data("exp_mouse_enst")
X_agg <- aggregate_mapped_genes(gene_df = exp_mouse_enst,
                                input_species = "mouse")

#### Aggregate across species: gene orthologs ####
data("exp_mouse")
X_agg2 <- aggregate_mapped_genes(gene_df = exp_mouse,
                                 input_species = "mouse",
                                 output_species = "human",
                                 method="homologene")
```

---

aggregate_rows *Aggregate rows of matrix*

Description

Aggregate rows of a matrix for many:1 mappings, using a grouping vector.

Usage

```
aggregate_rows(
  X,
  groupings,
  agg_fun = "sum",
  agg_method = c("monocle3", "stats"),
  as_sparse = TRUE,
  as_DelayedArray = TRUE,
  dropNA = TRUE,
  verbose = TRUE
)
```

Arguments

X	Input matrix.
groupings	Gene groups of the same length as nrow(X).
agg_fun	Aggregation function.
agg_method	Aggregation method.
as_sparse	Convert aggregated matrix to sparse matrix.
as_DelayedArray	Convert aggregated matrix to DelayedArray.
dropNA	Drop genes assigned to NA in groupings.
verbose	Print messages.

Value

Aggregated matrix

Source

```
 data("exp_mouse_enst") X <- exp_mouse_enst gene_map <- map_genes(genes = rownames(X),species
= "mouse") X_agg <- orthogene:::aggregate_rows(X = X, groupings = gene_map$name) sum(duplicated(rownames
# 0 sum(duplicated(rownames(X))) # 1215 sum(duplicated(rownames(X_agg))) # 0
```

---

aggregate_rows_monocle3

Aggregate rows: monocle3

Description

Aggregate rows: monocle3

Usage

```
aggregate_rows_monocle3(
  x,
  groupings = NULL,
  form = NULL,
  fun = "sum",
  na.action = stats::na.omit
)
```

Arguments

x	Input matrix.
groupings	Gene groups of the same length as nrow(X).
form	Formula.
fun	Aggregation function.
na.action	Na action.

Value

Aggregated matrix.

Source

```
X <- Matrix::rsparsematrix(nrow = 1000, ncol = 2000, density = .10) groupings <- rep(c("A","B"),nrow(X)/2
X2 <- orthogene:::aggregate_rows_monocle3(x = X, groupings=groupings)
```

---

all_genes *Get all genes*

Description

Return all known genes from a given species.

Usage

```
all_genes(
  species,
  method = c("gprofiler", "homologene", "babelgene"),
  ensure_filter_nas = FALSE,
  run_map_species = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

species	Species to get all genes for. Will first be standardised with map_species.
method	R package to use for gene mapping: • "gprofiler" : Slower but more species and genes. • "homologene" : Faster but fewer species and genes. • "babelgene" : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
ensure_filter_nas	Perform an extra check to remove genes that are NAs of any kind.
run_map_species	Standardise species names with map_species first (Default: TRUE).
verbose	Print messages.
...	Additional arguments to be passed to gorth or homologene. *NOTE*: To return only the most "popular" interspecies ortholog mappings, supply mthreshold=1 here AND set method="gprofiler" above. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs. For more details, please see here.

Details

References homologeneData or gconvert.

Value

Table with all gene symbols from the given species.

Examples

```
genome_mouse <- all_genes(species = "mouse")
genome_human <- all_genes(species = "human")
```

---

all_genes_babelgene *Get all genes: babelgene*

Description

Get all genes for a given species using the method "babelgene".

Usage

```
all_genes_babelgene(
  species,
  run_map_species = TRUE,
  save_dir = tools::R_user_dir("orthogene", which = "cache"),
  use_old = FALSE,
  min_support = 1,
  verbose = TRUE
)
```

Arguments

species	Species to get all genes for. Will first be standardised with map_species.
run_map_species	Standardise species names with map_species first (Default: TRUE).
save_dir	Directory to save babelgene mapping files to.
use_old	Use an old version of babelgene::orthologs_df (stored on GitHub Releases) for consistency.
verbose	Print messages.

Value

All genes.

Source

babelgene::orthologs_df version differences

---

all_species *All species*

Description

List all species currently supported by **orthogene**. Wrapper function for map_species. When method=NULL, all species from all available methods will be returned.

Usage

```
all_species(method = NULL, verbose = TRUE)
```

Arguments

method	R package to use for gene mapping: • "gprofiler" : Slower but more species and genes. • "homologene" : Faster but fewer species and genes. • "babelgene" : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
verbose	Print messages.

Value

data.table of species names, provided in multiple formats.

Examples

```
species_dt <- all_species()
```

`check_gene_df_type` *Check gene_df*

Description

Handles gene_df regardless of whether it's a data.frame, matrix, list, or vector

Usage

```
check_gene_df_type(gene_df, gene_input, verbose = TRUE)
```

Arguments

`gene_df`	Data object containing the genes (see `gene_input` for options on how the genes can be stored within the object). Can be one of the following formats: • `matrix` : A sparse or dense matrix. • `data.frame` : A `data.frame`, `data.table`. or `tibble`. • codelist : A `list` or character `vector`. Genes, transcripts, proteins, SNPs, or genomic ranges can be provided in any format (HGNC, Ensembl, RefSeq, UniProt, etc.) and will be automatically converted to gene symbols unless specified otherwise with the `...` arguments. *Note*: If you set `method="homologene"`, you must either supply genes in gene symbol format (e.g. "Sox2") OR set `standardise_genes=TRUE`.
`gene_input`	Which aspect of `gene_df` to get gene names from: • `"rownames"` : From row names of data.frame/matrix. • `"colnames"` : From column names of data.frame/matrix. • `<column name>` : From a column in `gene_df`, e.g. `"gene_names"`.
`verbose`	Print messages.

Value

List of gene_df and gene_input

`convert_orthologs` *Map genes from one species to another*

Description

Currently supports ortholog mapping between any pair of 700+ species.
Use map_species to return a full list of available organisms.

Usage

```
convert_orthologs(
  gene_df,
  gene_input = "rownames",
  gene_output = "rownames",
  standardise_genes = FALSE,
  input_species,
  output_species = "human",
  method = c("gprofiler", "homologene", "babelgene"),
  drop_nonorths = TRUE,
  non121_strategy = "drop_both_species",
  agg_fun = NULL,
  mthreshold = Inf,
  as_sparse = FALSE,
  as_DelayedArray = FALSE,
  sort_rows = FALSE,
  gene_map = NULL,
  input_col = "input_gene",
  output_col = "ortholog_gene",
  verbose = TRUE,
  ...
)
```

Arguments

`gene_df` Data object containing the genes (see `gene_input` for options on how the genes can be stored within the object).
Can be one of the following formats:

- `matrix` :
  A sparse or dense matrix.
- `data.frame` :
  A `data.frame`, `data.table`. or `tibble`.

- codelist :
  A `list` or character `vector`.

Genes, transcripts, proteins, SNPs, or genomic ranges can be provided in any format (HGNC, Ensembl, RefSeq, UniProt, etc.) and will be automatically converted to gene symbols unless specified otherwise with the ... arguments.
Note: If you set `method="homologene"`, you must either supply genes in gene symbol format (e.g. "Sox2") OR set `standardise_genes=TRUE`.

`gene_input` Which aspect of `gene_df` to get gene names from:

- `"rownames"` :
  From row names of data.frame/matrix.
- `"colnames"` :
  From column names of data.frame/matrix.
- `<column name>` :
  From a column in `gene_df`, e.g. `"gene_names"`.

`gene_output` How to return genes. Options include:

- `"rownames"` :
  As row names of `gene_df`.
- `"colnames"` :
  As column names of `gene_df`.
- `"columns"` :
  As new columns "input_gene", "ortholog_gene" (and "input_gene_standard" if `standardise_genes=TRUE`) in `gene_df`.
- `"dict"` :
  As a dictionary (named list) where the names are input_gene and the values are ortholog_gene.
- `"dict_rev"` :
  As a reversed dictionary (named list) where the names are ortholog_gene and the values are input_gene.

`standardise_genes`
If `TRUE` AND `gene_output="columns"`, a new column "input_gene_standard" will be added to `gene_df` containing standardised HGNC symbols identified by gorth.

`input_species` Name of the input species (e.g., "mouse","fly"). Use map_species to return a full list of available species.

`output_species` Name of the output species (e.g. "human","chicken"). Use map_species to return a full list of available species.

`method` R package to use for gene mapping:

- `"gprofiler"` : Slower but more species and genes.
- `"homologene"` : Faster but fewer species and genes.
- `"babelgene"` : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.

`drop_nonorths` Drop genes that don't have an ortholog in the `output_species`.

non121_strategy

How to handle genes that don't have 1:1 mappings between input_species:output_species. Options include:

- "drop_both_species" or "dbs" or 1 :
  Drop genes that have duplicate mappings in either the input_species or output_species
  (*DEFAULT*).
- "drop_input_species" or "dis" or 2 :
  Only drop genes that have duplicate mappings in the input_species.
- "drop_output_species" or "dos" or 3 :
  Only drop genes that have duplicate mappings in the output_species.
- "keep_both_species" or "kbs" or 4 :
  Keep all genes regardless of whether they have duplicate mappings in either species.
- "keep_popular" or "kp" or 5 :
  Return only the most "popular" interspecies ortholog mappings. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.
- "sum","mean","median","min" or "max" :
  When gene_df is a matrix and gene_output="rownames", these options will aggregate many-to-one gene mappings (input_species-to-output_species) after dropping any duplicate genes in the output_species.

agg_fun — Aggregation function passed to aggregate_mapped_genes. Set to NULL to skip aggregation step (default).

mthreshold — Maximum number of ortholog names per gene to show. Passed to gorth. Only used when method="gprofiler" (*DEFAULT :* Inf).

as_sparse — Convert gene_df to a sparse matrix. Only works if gene_df is one of the following classes:

- matrix
- Matrix
- data.frame
- data.table
- tibble

If gene_df is a sparse matrix to begin with, it will be returned as a sparse matrix (so long as gene_output= "rownames" or "colnames").

as_DelayedArray

Convert aggregated matrix to DelayedArray.

sort_rows — Sort gene_df rows alphanumerically.

gene_map — A data.frame that maps the current gene names to new gene names. This function's behaviour will adapt to different situations as follows:

- gene_map=<data.frame> :
  When a data.frame containing the gene key:value columns (specified by input_col and output_col, respectively) is provided, this will be used to perform aggregation/expansion.

- gene_map=NULL and input_species!=output_species :
  A gene_map is automatically generated by map_orthologs to perform inter-species gene aggregation/expansion.
- gene_map=NULL and input_species==output_species :
  A gene_map is automatically generated by map_genes to perform within-species gene gene symbol standardization and aggregation/expansion.

input_col — Column name within gene_map with gene names matching the row names of X.

output_col — Column name within gene_map with gene names that you wish you map the row names of X onto.

verbose — Print messages.

... — Additional arguments to be passed to gorth or homologene.

NOTE: To return only the most "popular" interspecies ortholog mappings, supply mthreshold=1 here AND set method="gprofiler" above. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.

For more details, please see here.

Value

gene_df with orthologs converted to the output_species.
Instead returned as a dictionary (named list) if gene_output="dict" or "dict_rev".

Examples

```
data("exp_mouse")
gene_df <- convert_orthologs(
    gene_df = exp_mouse,
    input_species = "mouse"
)
```

---

create_background *Create gene background*

Description

Create a gene background as the union/intersect of all orthologs between input species (species1 and species2), and the output_species. This can be useful when generating random lists of background genes to test against in analyses with data from multiple species (e.g. enrichment of mouse cell-type markers gene sets in human GWAS-derived gene sets).

Usage

```
create_background(
  species1,
  species2,
  output_species = "human",
  as_output_species = TRUE,
  use_intersect = TRUE,
  bg = NULL,
  gene_map = NULL,
  method = "homologene",
  non121_strategy = "drop_both_species",
  verbose = TRUE
)
```

Arguments

species1	First species.
species2	Second species.
output_species	Species to convert all genes from species1 and species2 to first. Default="human", but can be to either any species supported by **orthogene**, including species1 or species2.
as_output_species	Return background gene list as output_species orthologs, instead of the gene names of the original input species.
use_intersect	When species1 and species2 are both different from output_species, this argument will determine whether to use the intersect (TRUE) or union (FALSE) of all genes from species1 and species2.
bg	User supplied background list that will be returned to the user after removing duplicate genes.
gene_map	User-supplied gene_map data table from map_orthologs or map_genes.
method	R package to use for gene mapping: • "gprofiler" : Slower but more species and genes. • "homologene" : Faster but fewer species and genes. • "babelgene" : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
non121_strategy	How to handle genes that don't have 1:1 mappings between input_species:output_species. Options include: • "drop_both_species" or "dbs" or 1 : Drop genes that have duplicate mappings in either the input_species or output_species (*DEFAULT*). • "drop_input_species" or "dis" or 2 : Only drop genes that have duplicate mappings in the input_species.

- "drop_output_species" or "dos" or 3 :
  Only drop genes that have duplicate mappings in the output_species.
- "keep_both_species" or "kbs" or 4 :
  Keep all genes regardless of whether they have duplicate mappings in either species.
- "keep_popular" or "kp" or 5 :
  Return only the most "popular" interspecies ortholog mappings. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.
- "sum","mean","median","min" or "max" :
  When gene_df is a matrix and gene_output="rownames", these options will aggregate many-to-one gene mappings (input_species-to-output_species) after dropping any duplicate genes in the output_species.

verbose Print messages.

Value

Background gene list.

Examples

```
bg <- orthogene::create_background(species1 = "mouse",
                                   species2 = "rat",
                                   output_species = "human")
```

---

dMcast *dMcast*

Description

Reimplementation of function that originally part of the R package Matrix.utils before the package was deprecated. The only difference is that this version of dMcast does not include an aggregation feature at the end.

Usage

```
dMcast(
  data,
  formula,
  value.var = NULL,
  as.factors = FALSE,
  na.action = stats::na.pass,
  factor.nas = TRUE,
  drop.unused.levels = TRUE
)
```

Arguments

data	A data.frame.
formula	Casting formula, see details for specifics.
value.var	Name of column that stores values to be aggregated numerics.
as.factors	If TRUE, treat all columns as factors, including
factor.nas	If TRUE, treat factors with NAs as new levels. Otherwise, rows with NAs will receive zeroes in all columns for that factor.
drop.unused.levels	Should factors have unused levels dropped? Defaults to TRUE, in contrast to model.matrix

Value

matrix

Source

```
groupings <- data.frame(A = as.factor(sample(1e4,1e6,TRUE))) formula <- stats::as.formula("~0+.")
dm <- orthogene:::dMcast(data = groupings, formula = formula)
```

---

earthworm2human_map *Earthworm to human map*

Description

Orthologous gene mapping between earthworm (Eisenia andrei) and human (Homo sapiens) genes.

Usage

```
earthworm2human_map(
  evalue_threshold = NULL,
  save_dir = tools::R_user_dir("orthogene", which = "cache")
)
```

Arguments

evalue_threshold	Only include mappings with an E-value below a set threshold. See here for further guidance.
save_dir	Directory to save mapping file to.

Details

These mappings were generated using BLAST (a protein sequence tool) implemented within SAMap. This mapping data was provided upon request by the authors of Wang et al. 2022. Column names were collected from Metagenomics Wiki.

Value

data.table containing earthworm-to-human gene orthologs.

---

exp_mouse *Gene expression data: mouse*

Description

Mean pseudobulk single-cell RNA-seq gene expression matrix.

Data originally comes from Zeisel et al., 2018 (Cell).

Usage

```
data("exp_mouse")
```

Format

sparse matrix

Source

Publication `ctd <- ewceData::ctd() exp_mouse <- as(ctd[[1]]$mean_exp, "sparseMatrix") usethis::use_data(exp_mouse, overwrite = TRUE)`

---

exp_mouse_enst *Transcript expression data: mouse*

Description

Mean pseudobulk single-cell RNA-seq Transcript expression matrix.

Data originally comes from Zeisel et al., 2018 (Cell).

Usage

```
data("exp_mouse_enst")
```

Format

sparse matrix

Source

Publication `data("exp_mouse") mapped_genes <- map_genes(genes = rownames(exp_mouse)[seq(1,100)], target = "ENST", species = "mouse", drop_na = FALSE) exp_mouse_enst <- exp_mouse[mapped_genes$input,] rownames(exp_mouse_enst) <- mapped_genes$target all_nas <- orthogene:::find_all_nas(rownames(exp_mouse exp_mouse_enst <- exp_mouse_enst[!all_nas,] exp_mouse_enst <- phenomix::add_noise(exp_mouse_enst) usethis::use_data(exp_mouse_enst, overwrite = TRUE)`

format_species *Format species names*

Description

Format scientific species names into a standardised manner.

Usage

```
format_species(
  species,
  remove_parentheses = TRUE,
  abbrev = FALSE,
  remove_subspecies = FALSE,
  remove_subspecies_exceptions = c("Canis lupus familiaris"),
  split_char = " ",
  collapse = " ",
  remove_chars = c(" ", ".", "(", ")", "[", "]"),
  replace_char = "",
  lowercase = FALSE,
  trim = "'",
  standardise_scientific = FALSE
)
```

Arguments

species	Species query (e.g. "human", "homo sapiens", "hsapiens", or 9606). If given a list, will iterate queries for each item. Set to NULL to return all species.
remove_parentheses	Remove substring within parentheses: e.g. "Xenopus (Silurana) tropicalis" –> "Xenopus tropicalis"
abbrev	Abbreviate all taxonomic levels except the last one: e.g. "Canis lupus familiaris" ==> "C l familiaris"
remove_subspecies	Only keep the first two taxonomic levels: e.g. "Canis lupus familiaris" –> "Canis lupus"
remove_subspecies_exceptions	Selected species to ignore when remove_subspecies=TRUE. e.g. "Canis lupus familiaris" –> "Canis lupus familiaris"
split_char	Character to split species names by.
collapse	Character to re-collapse species names with after splitting with split_char.
remove_chars	Characters to remove.
replace_char	Character to replace remove_chars with.
lowercase	Make species names all lowercase.

`trim` Characters to trim from the beginning/end of each species name.

`standardise_scientific`
Automatically sets multiple arguments at once to create standardised scientific names for each species. Assumes that `species` is provided in some version of scientific species names: e.g. "Xenopus (Silurana) tropicalis" –> "Xenopus tropicalis"

Value

A named vector where the values are the standardised species names and the names are the original input species names.

Examples

```
species <- c("Xenopus (Silurana) tropicalis","Canis lupus familiaris")
species2 <- format_species(species = species, abbrev=TRUE)
species3 <- format_species(species = species,
                           standardise_scientific=TRUE,
                           remove_subspecies_exceptions=NULL)
```

---

get_orgdb_genomeinfodbdata

Import organism database: GenomeInfoDbData

Description

Import and format organism ID table from **GenomeInfoDbData** to be comparable to `get_orgdb_gprofiler`.

Usage

```
get_orgdb_genomeinfodbdata(verbose = TRUE)
```

Value

Organisms `data.table`

Source

GenomeInfoDbData GitHub

`get_silhouettes` *Get silhouettes*

Description

Get silhouette images of each species from phylopic.

Usage

```
get_silhouettes(
  species,
  which = rep(1, length(species)),
  run_format_species = TRUE,
  include_image_data = FALSE,
  mc.cores = 1,
  add_png = FALSE,
  remove_bg = FALSE,
  verbose = TRUE
)
```

Arguments

`species`	A character vector of species names to query phylopic for.
`which`	An integer vector of the same length as `species`. Lets you choose which image you want to use for each species (1st, 2nd 3rd, etc.).
`run_format_species`	Standardise species names with format_species before querying phylopic (default: `TRUE`).
`include_image_data`	Include the image data itself (not just the image UID) in the results.
`mc.cores`	Accelerate multiple species queries by parallelising across multiple cores.
`add_png`	Return URLs for both the SVG and PNG versions of the image.
`remove_bg`	Remove image background.
`verbose`	Print messages.

Value

data.frame with:

- input_species : Species name (input).
- species : Species name (standardised).
- uid : Species UID.
- url : Image URL.

Source

Related function: `ggimage::geom_phylopic`

phylopic/rphylopic API changes

ggimage: Issue with finding valid PNGs

Examples

```
species <- c("Mus_musculus","Pan_troglodytes","Homo_sapiens")
uids <- get_silhouettes(species = species)
```

---

ggtree_plot *Plot a phylogenetic tree*

Description

Plot a phylogenetic tree with ggtree and metadata from report_orthologs.

Usage

```
ggtree_plot(
  tr,
  d,
  scaling_factor = 1,
  clades = NULL,
  clades_palette = NULL,
  reference_species = NULL,
  verbose = TRUE
)
```

Arguments

`tr`	Tree.
`d`	Metadata
`scaling_factor`	How much to scale y-axis parameters (e.g. offset) by.
`clades`	Clades metadata.
`clades_palette`	Palette to color highlighted `clades` with.
`verbose`	Print messages.

Value

ggplot object.

---

gprofiler_namespace *gconvert namespaces*

Description

Available namespaces used by link[gprofiler2]gconvert.

Format

data.frame

Source

gProfiler site

Manually-prepared CSV #### path <- "inst/extdata/gprofiler_namespace.csv.gz" gprofiler_namespace <- data.table::fread(path)

---

gprofiler_orgs *Reference organisms*

Description

Organism for which gene references are available via gProfiler API. Used as a backup if API is not available.

Format

data.frame

Source

gProfiler site

NOTE!: Must run usethis::use_data for all internal data at once. # otherwise, the prior internal data will be overwritten. #### Internal data 1: gprofiler_namespace #### #### Manually-prepared CSV #### path <- "inst/extdata/gprofiler_namespace.csv.gz" gprofiler_namespace <- data.table::fread(path) #### Internal data 2: gprofiler_orgs gprofiler_orgs <- orthogene:::get_orgdb_ #### Save #### usethis::use_data(gprofiler_orgs,gprofiler_namespace, overwrite = TRUE, internal=TRUE)

infer_species *Infer species from gene names*

Description

Infers which species the genes within gene_df is from. Iteratively test the percentage of gene_df genes that match with the genes from each test_species.

Usage

```
infer_species(
  gene_df,
  gene_input = "rownames",
  test_species = c("human", "monkey", "rat", "mouse", "zebrafish", "fly"),
  method = c("homologene", "gprofiler", "babelgene"),
  make_plot = TRUE,
  show_plot = TRUE,
  verbose = TRUE
)
```

Arguments

gene_df — Data object containing the genes (see gene_input for options on how the genes can be stored within the object).
Can be one of the following formats:

- matrix :
  A sparse or dense matrix.
- data.frame :
  A data.frame, data.table. or tibble.
- codelist :
  A list or character vector.

Genes, transcripts, proteins, SNPs, or genomic ranges can be provided in any format (HGNC, Ensembl, RefSeq, UniProt, etc.) and will be automatically converted to gene symbols unless specified otherwise with the ... arguments.
Note: If you set method="homologene", you must either supply genes in gene symbol format (e.g. "Sox2") OR set standardise_genes=TRUE.

gene_input — Which aspect of gene_df to get gene names from:

- "rownames" :
  From row names of data.frame/matrix.
- "colnames" :
  From column names of data.frame/matrix.
- <column name> :
  From a column in gene_df, e.g. "gene_names".

test_species	Which species to test for matches with. If set to NULL, will default to a list of humans and 5 common model organisms. If test_species is set to one of the following options, it will automatically pull all species from that respective package and test against each of them: • "homologene" : 20+ species (default) • "gprofiler" : 700+ species • "babelgene" : 19 species
method	R package to use for gene mapping: • "gprofiler" : Slower but more species and genes. • "homologene" : Faster but fewer species and genes. • "babelgene" : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
make_plot	Make a plot of the results.
show_plot	Print the plot of the results.
verbose	Print messages.

Value

An ordered dataframe of test_species from best to worst matches.

Examples

```
data("exp_mouse")
matches <- orthogene::infer_species(gene_df = exp_mouse[1:200,])
```

---

infer_species_plot *infer_species_plot*

Description

Plot results from infer_species.

Usage

```
infer_species_plot(matches, show_plot = TRUE)
```

Value

ggplot object.

invert_dictionary *Invert dictionary*

Description

Switch the names/items in a named list.

Usage

```
invert_dictionary(dict)
```

Value

Named list

many2many_rows *Expand/aggregate rows of matrix for many:many mappings*

Description

Expand/aggregate rows of a matrix with any combination of many:many mappings. This method ensures that total counts per gene remain the same regardless of how many genes it has split/condensed into. This allows for many:many mappings that are otherwise not possible using standard aggregation functions, since they all require many:1 scenarios.
Internally, this is done as follows:

1. Identify genes that appear more than once in `gene_map[[input_col]]`.
2. For each gene identified, split its row into multiple rows, where the number of new rows is equal to the number of times that gene appears within `gene_map[[input_col]]`. In the new expanded matrix, each row will be equal to the column sums divided by the number of new rows. This means that averaged counts will be split equally amongst the new rows, in a column-specific manner.
   Thus, the column sums of the output matrix will be equal to the column sums in the input matrix. In the case of gene expression count matrices, this means that the total counts will remain equal between matrices, while avoiding being forced to drop genes with many:many mappings (as is the case with most other aggregation methods).
3. Map rownames of the expanded matrix onto the orthologous gene names from `gene_map$ortholog_gene`.
4. [Optional] : When `aggregate_orthologs=TRUE`, aggregate rows of the expanded/mapped matrix such that there will only be 1 row per ortholog gene, using aggregate_rows. The arguments `FUN`, `method`, `as_sparse`, `as_DelayedArray`, and `dropNA` will all be passed to aggregate_rows if this step is selected.

Usage

```
many2many_rows(
  X,
  gene_map,
  input_col = "input_gene",
  output_col = "ortholog_gene",
  agg_fun = "sum",
  agg_method = c("monocle3", "stats"),
  as_sparse = TRUE,
  as_DelayedArray = FALSE,
  dropNA = TRUE,
  aggregate_orthologs = TRUE,
  verbose = TRUE
)
```

Arguments

X	Input matrix.
gene_map	A data.frame generated by map_orthologs, with columns mapping input_col to output_col.
input_col	Column name within gene_map with gene names matching the row names of X.
output_col	Column name within gene_map with gene names that you wish you map the row names of X onto.
agg_fun	Aggregation function.
agg_method	Aggregation method.
as_sparse	Convert aggregated matrix to sparse matrix.
as_DelayedArray	Convert aggregated matrix to DelayedArray.
dropNA	Drop genes assigned to NA in groupings.
aggregate_orthologs	[Optional] After performing an initial round of many:many aggregation/expansion with many2many_rows, ensure each orthologous gene only appears in one row by using the aggregate_rows function (default: TRUE).
verbose	Print messages.

Value

Expanded/aggregated matrix.

Source

```
data("exp_mouse") X <- exp_mouse gene_map <- orthogene:::map_orthologs(genes = rownames(exp_mouse),
input_species = "mouse", method="homologene") X_agg <- orthogene:::many2many_rows(X
= X, gene_map = gene_map) sum(duplicated(rownames(exp_mouse))) # 0 sum(duplicated(gene_map$input_gene))
# 46 sum(duplicated(gene_map$ortholog_gene)) # 56 sum(duplicated(rownames(X_agg)))
# 56
```

`map_genes` *Map genes*

Description

Input a list of genes, transcripts, proteins, SNPs, or genomic ranges in any format (HGNC, Ensembl, RefSeq, UniProt, etc.) and return a table with standardised gene symbols (the "names" column).

Usage

```
map_genes(
  genes,
  species = "hsapiens",
  target = "ENSG",
  mthreshold = Inf,
  drop_na = FALSE,
  numeric_ns = "",
  run_map_species = TRUE,
  verbose = TRUE
)
```

Arguments

`genes`	Gene list.
`species`	Species to map against.
`target`	target namespace.
`mthreshold`	maximum number of results per initial alias to show. Shows all by default.
`drop_na`	Drop all genes without mappings. Sets `gprofiler2::gconvert(filter_na=)` as well an additional round of more comprehensive `NA` filtering by **orthogene**.
`numeric_ns`	namespace to use for fully numeric IDs (list of available namespaces).
`run_map_species`	Standardise `species` names with map_species first (Default: `TRUE`).
`verbose`	Print messages.

Details

Uses gconvert. The exact contents of the output table will depend on `target` parameter. See `?gprofiler2::gconvert` for more details.

Value

Table with standardised genes.

Examples

```
genes <- c(
    "Klf4", "Sox2", "TSPAN12", "NM_173007", "Q8BKT6",
    "ENSMUSG00000012396", "ENSMUSG00000074637"
)
mapped_genes <- map_genes(
    genes = genes,
    species = "mouse"
)
```

`map_genes_planosphere` *Map genes: SMED*

Description

Map planarian (Schmmidt mediterrani) genes to/from the SMED format using data from the planosphere database.

Usage

```
map_genes_planosphere(
  genes,
  output_format = "SMESG_dd_Smes_v2",
  drop_duplicates = TRUE,
  save_dir = tools::R_user_dir("orthogene", which = "cache"),
  verbose = TRUE
)
```

Arguments

`genes`	Gene list.
`drop_duplicates`	Only output one row per input gene.
`verbose`	Print messages.

Value

data.table

Source

`genes <- c("dd_Smed_v6_10690_0","dd_Smed_v6_10691_0","dd_Smed_v6_10693_0") gene_map <- map_genes_planosphere(genes=genes)`

map_orthologs *Map orthologs*

Description

Map orthologs from one species to another.

Usage

```
map_orthologs(
  genes,
  standardise_genes = FALSE,
  input_species,
  output_species = "human",
  method = c("gprofiler", "homologene", "babelgene"),
  mthreshold = Inf,
  gene_map = NULL,
  input_col = "input_gene",
  output_col = "ortholog_gene",
  verbose = TRUE,
  ...
)
```

Arguments

genes	can be a mixture of any format (HGNC, Ensembl, RefSeq, UniProt, etc.) and will be automatically converted to standardised HGNC symbol format.
standardise_genes	If TRUE AND gene_output="columns", a new column "input_gene_standard" will be added to gene_df containing standardised HGNC symbols identified by gorth.
input_species	Name of the input species (e.g., "mouse","fly"). Use map_species to return a full list of available species.
output_species	Name of the output species (e.g. "human","chicken"). Use map_species to return a full list of available species.
method	R package to use for gene mapping: • "gprofiler" : Slower but more species and genes. • "homologene" : Faster but fewer species and genes. • "babelgene" : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
mthreshold	Maximum number of ortholog names per gene to show. Passed to gorth. Only used when method="gprofiler" (*DEFAULT :* Inf).
gene_map	A data.frame that maps the current gene names to new gene names. This function's behaviour will adapt to different situations as follows:

- gene_map=<data.frame> :
  When a data.frame containing the gene key:value columns (specified by input_col and output_col, respectively) is provided, this will be used to perform aggregation/expansion.
- gene_map=NULL and input_species!=output_species :
  A gene_map is automatically generated by map_orthologs to perform inter-species gene aggregation/expansion.
- gene_map=NULL and input_species==output_species :
  A gene_map is automatically generated by map_genes to perform within-species gene gene symbol standardization and aggregation/expansion.

input_col — Column name within gene_map with gene names matching the row names of X.

output_col — Column name within gene_map with gene names that you wish you map the row names of X onto.

verbose — Print messages.

... — Additional arguments to be passed to gorth or homologene.

NOTE: To return only the most "popular" interspecies ortholog mappings, supply mthreshold=1 here AND set method="gprofiler" above. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.

For more details, please see here.

Details

map_orthologs() is a core function within convert_orthologs(), but does not have many of the extra checks, such as non121_strategy) and drop_nonorths.

Value

Ortholog map data.frame with at least the columns "input_gene" and "ortholog_gene".

Examples

```
data("exp_mouse")
gene_map <- map_orthologs(
    genes = rownames(exp_mouse),
    input_species = "mouse")
```

---

map_orthologs_babelgene

Map orthologs: babelgene

Description

Map orthologs from one species to another using orthologs.

Usage

```
map_orthologs_babelgene(
  genes,
  input_species,
  output_species = "human",
  min_support = 1,
  top = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

genes	Gene list.
input_species	Name of the input species (e.g., "mouse","fly"). Use map_species to return a full list of available species.
output_species	Name of the output species (e.g. "human","chicken"). Use map_species to return a full list of available species.
min_support	Minimum number of supporting source databases. Gene pairs available in this package are supported by 2 to 12 databases (the maximum varies depending on the species).
top	For each gene, output only the match with the highest support level if there are multiple hits.
verbose	Print messages.
...	Additional arguments to be passed to gorth or homologene. *NOTE*: To return only the most "popular" interspecies ortholog mappings, supply `mthreshold=1` here AND set `method="gprofiler"` above. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs. For more details, please see here.

Value

Ortholog map `data.frame`

Source

babelgene tutorial

`map_orthologs_custom` *Map orthologs: gprofiler*

Description

Map orthologs from one species to another using a custom `gene_map` table.

Usage

```
map_orthologs_custom(
  gene_map,
  input_species,
  output_species,
  input_col,
  output_col,
  verbose = TRUE
)
```

Arguments

`gene_map`	A data.frame that maps the current gene names to new gene names. This function's behaviour will adapt to different situations as follows: • `gene_map=<data.frame>` : When a data.frame containing the gene key:value columns (specified by `input_col` and `output_col`, respectively) is provided, this will be used to perform aggregation/expansion. • `gene_map=NULL` and `input_species!=output_species` : A `gene_map` is automatically generated by map_orthologs to perform inter-species gene aggregation/expansion. • `gene_map=NULL` and `input_species==output_species` : A `gene_map` is automatically generated by map_genes to perform within-species gene gene symbol standardization and aggregation/expansion.
`input_species`	Name of the input species (e.g., "mouse","fly"). Use map_species to return a full list of available species.
`output_species`	Name of the output species (e.g. "human","chicken"). Use map_species to return a full list of available species.
`input_col`	Column name within `gene_map` with gene names matching the row names of `X`.
`output_col`	Column name within `gene_map` with gene names that you wish you map the row names of `X` onto.
`verbose`	Print messages.

Value

Ortholog map `data.frame`

`map_orthologs_gprofiler` *Map orthologs: gprofiler*

Description

Map orthologs from one species to another using gorth.

Usage

```
map_orthologs_gprofiler(
  genes,
  input_species,
  output_species = "human",
  filter_na = FALSE,
  mthreshold = Inf,
  verbose = TRUE,
  ...
)
```

Arguments

`genes`	Gene list.
`input_species`	Name of the input species (e.g., "mouse","fly"). Use map_species to return a full list of available species.
`output_species`	Name of the output species (e.g. "human","chicken"). Use map_species to return a full list of available species.
`filter_na`	Logical indicating whether to filter out results without a corresponding target name. (*DEFAULT* is `FALSE`, so that `NA`s can be handled by **orthogene**).
`mthreshold`	Maximum number of ortholog names per gene to show. Passed to gorth. Only used when `method="gprofiler"` (*DEFAULT :* `Inf`).
`verbose`	Print messages.
`...`	Additional arguments to be passed to gorth.

Details

"`mthreshold` is used to set the maximum number of ortholog names per gene to show. This is useful to handle the problem of having many orthologs per gene (most of them uninformative). The function tries to find the most informative by selecting the most popular ones."
~ From `gprofiler2` vignette

Available namespaces for the `numeric_ns` argument can be found here.

Value

Ortholog map `data.frame`

map_orthologs_homologene *Map orthologs: homologene*

Description

Map orthologs from one species to another using homologene.

Usage

```
map_orthologs_homologene(
  genes,
  input_species,
  output_species = "human",
  verbose = TRUE,
  ...
)
```

Arguments

genes	Gene list.
input_species	Name of the input species (e.g., "mouse","fly"). Use map_species to return a full list of available species.
output_species	Name of the output species (e.g. "human","chicken"). Use map_species to return a full list of available species.
verbose	Print messages.
...	Additional arguments to be passed to homologene.

Value

Ortholog map data.frame

map_species *Standardise species names*

Description

Search gprofiler database for species that match the input text string. Then translate to a standardised species ID.

Usage

```
map_species(
  species = NULL,
  search_cols = c("display_name", "id", "scientific_name", "taxonomy_id"),
 output_format = c("scientific_name", "id", "display_name", "taxonomy_id", "version",
    "scientific_name_formatted"),
  method = c("homologene", "gprofiler", "babelgene"),
  remove_subspecies = TRUE,
  remove_subspecies_exceptions = c("Canis lupus familiaris"),
  use_local = TRUE,
  verbose = TRUE
)
```

Arguments

species	Species query (e.g. "human", "homo sapiens", "hsapiens", or 9606). If given a list, will iterate queries for each item. Set to NULL to return all species.
search_cols	Which columns to search for species substring in metadata API.
output_format	Which column to return.
method	R package to use for gene mapping: • "gprofiler" : Slower but more species and genes. • "homologene" : Faster but fewer species and genes. • "babelgene" : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
remove_subspecies	Only keep the first two taxonomic levels: e.g. "Canis lupus familiaris" –> "Canis lupus"
remove_subspecies_exceptions	Selected species to ignore when remove_subspecies=TRUE. e.g. "Canis lupus familiaris" –> "Canis lupus familiaris"
use_local	If TRUE *default*, map_species uses a locally stored version of the species metadata table instead of pulling directly from the gprofiler API. Local version may not be fully up to date, but should suffice for most use cases.
verbose	Print messages.

Value

Species ID of type output_format

Examples

```
ids <- map_species(species = c(
    "human", 9606, "mus musculus",
    "fly", "C elegans"
))
```

message_parallel *Send messages to console even from within parallel processes*

Description

Send messages to console even from within parallel processes

Usage

```
message_parallel(...)
```

Value

A message

plot_benchmark_bar *Plot benchmark: bar*

Description

Plot run time and # genes returned across species and function tests.

Usage

```
plot_benchmark_bar(bench_res, remove_failed_times = FALSE, show_plot = TRUE)
```

Arguments

bench_res	Results from
remove_failed_times	In instances where no genes were returned, set time to NA.
show_plot	Print plot.

Value

ggplot object

plot_benchmark_scatter *Plot benchmark: scatter*

Description

Plot run time vs. # genes returned across species and function tests.

Usage

```
plot_benchmark_scatter(
  bench_res,
  remove_failed_times = FALSE,
  show_plot = TRUE
)
```

Arguments

bench_res	Results from
remove_failed_times	In instances where no genes were returned, set time to NA.
show_plot	Print plot.

Value

ggplot object

plot_orthotree *Create a phylogenetic tree of shared orthologs*

Description

Automatically creates a phylogenetic tree plot annotated with metadata describing how many orthologous genes each species shares with the `reference_species` ("human" by default).

Usage

```
plot_orthotree(
  tree = NULL,
  orth_report = NULL,
  species = NULL,
  method = c("babelgene", "homologene", "gprofiler"),
  tree_source = "timetree",
  non121_strategy = "drop_both_species",
  reference_species = "human",
```

```
  clades = list(Primates = c("Homo sapiens", "Macaca mulatta"), Eutherians =
    c("Homo sapiens", "Mus musculus", "Bos taurus"), Mammals = c("Homo sapiens",
   "Mus musculus", "Bos taurus", "Ornithorhynchus anatinus", "Monodelphis domestica"),
   Tetrapods = c("Homo sapiens", "Mus musculus", "Gallus gallus", "Anolis carolinensis",
    "Xenopus tropicalis"), Vertebrates = c("Homo sapiens", "Mus musculus",
   "Gallus gallus", "Anolis carolinensis", "Xenopus tropicalis", "Danio rerio"),
    Invertebrates = c("Drosophila melanogaster",
     "Caenorhabditis elegans")),
  clades_rotate = list(),
  scaling_factor = NULL,
  show_plot = TRUE,
 save_paths = c(tempfile(fileext = ".ggtree.pdf"), tempfile(fileext = ".ggtree.png")),
  width = 15,
  height = width,
  mc.cores = 1,
  verbose = TRUE
)
```

Arguments

`tree`	A phylogenetic tree of class phylo. If no tree is provided (`NULL`) a 100-way multiz tree will be imported from UCSC Genome Browser.
`orth_report`	An ortholog report from one or more species generated by report_orthologs.
`species`	Species to include in the final plot. If `NULL`, then all species from the given database (`method`) will be included (via map_species), so long as they also exist in the `tree`.
`method`	R package to use for gene mapping: • `"gprofiler"` : Slower but more species and genes. • `"homologene"` : Faster but fewer species and genes. • `"babelgene"` : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.
`tree_source`	Can be one of the following: • "timetree2022": Import and prune the TimeTree >147k species phylogenetic tree. Can also simply type "timetree". • "timetree2015": Import and prune the TimeTree >50k species phylogenetic tree. • "OmaDB": Construct a tree from OMA (Orthologous Matrix browser) via the getTaxonomy function. *NOTE:* Does not contain branch lengths, and therefore may have limited utility. • "UCSC": Import and prune the UCSC 100-way alignment phylogenetic tree (hg38 version). • "<path>": Read a tree from a newick text file from a local or remote URL using read.tree.

non121_strategy
: How to handle genes that don't have 1:1 mappings between input_species:output_species. Options include:

  - "drop_both_species" or "dbs" or 1 :
    Drop genes that have duplicate mappings in either the input_species or output_species
    (*DEFAULT*).
  - "drop_input_species" or "dis" or 2 :
    Only drop genes that have duplicate mappings in the input_species.
  - "drop_output_species" or "dos" or 3 :
    Only drop genes that have duplicate mappings in the output_species.
  - "keep_both_species" or "kbs" or 4 :
    Keep all genes regardless of whether they have duplicate mappings in either species.
  - "keep_popular" or "kp" or 5 :
    Return only the most "popular" interspecies ortholog mappings. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.
  - "sum","mean","median","min" or "max" :
    When gene_df is a matrix and gene_output="rownames", these options will aggregate many-to-one gene mappings (input_species-to-output_species) after dropping any duplicate genes in the output_species.

reference_species
: Reference species.

clades
: A named list of clades each containing a character vector of species used to define the respective clade using MRCA.

clades_rotate
: A list of clades to rotate (via rotate), each containing a character vector of species used to define the respective clade using MRCA.

scaling_factor
: How much to scale y-axis parameters (e.g. offset) by.

show_plot
: Whether to print the final tree plot.

save_paths
: Paths to save plot to.

width
: Saved plot width.

height
: Saved plot height.

mc.cores
: Number of cores to parallelise different steps with.

verbose
: Print messages.

Value

A list containing:

- plot : Annotated ggtree object.
- tree : The pruned, standardised phylogenetic tree used in the plot.
- orth_report : Ortholog reports for each species against the reference_species.

- metadata : Metadata used in the plot, including silhouette PNG ids from phylopic.
- clades : Metadata used for highlighting clades.
- method : `method` used.
- reference_species : `reference_species` used.
- save_paths : `save_paths` to plot.

Source

ggtree tutorial

Examples

```
orthotree <- plot_orthotree(species = c("human","monkey","mouse"))
```

`prepare_tree` *Prepare a phylogenetic tree*

Description

Import a phylogenetic tree and then conduct a series of optional standardisation steps. Optionally, if `output_format` is not `NULL`, species names from both the tree and the `species` argument will first be standardised using map_species.

Usage

```
prepare_tree(
  tree_source = "timetree",
  species = NULL,
  output_format = "scientific_name_formatted",
  run_map_species = c(TRUE, TRUE),
  method = c("homologene", "gprofiler", "babelgene"),
  force_ultrametric = TRUE,
  age_max = NULL,
  show_plot = TRUE,
  save_dir = tools::R_user_dir("orthogene", which = "cache"),
  verbose = TRUE,
  ...
)
```

Arguments

`tree_source` Can be one of the following:

- "timetree2022":
  Import and prune the TimeTree >147k species phylogenetic tree. Can also simply type "timetree".

- "timetree2015":
  Import and prune the TimeTree >50k species phylogenetic tree.
- "OmaDB":
  Construct a tree from OMA (Orthologous Matrix browser) via the getTaxonomy function. *NOTE:* Does not contain branch lengths, and therefore may have limited utility.
- "UCSC":
  Import and prune the UCSC 100-way alignment phylogenetic tree (hg38 version).
- "<path>":
  Read a tree from a newick text file from a local or remote URL using read.tree.

`species` Species names to subset the tree by (after `standardise_species` step).

`output_format` Which column to return.

`run_map_species`
Whether to first standardise species names with map_species.

`method` R package to use for gene mapping:

- `"gprofiler"` : Slower but more species and genes.
- `"homologene"` : Faster but fewer species and genes.
- `"babelgene"` : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.

`force_ultrametric`
Whether to force the tree to be ultrametric (i.e. make all tips the same date) using force.ultrametric.

`age_max` Rescale the edges of the tree into units of millions of years (MY) instead than evolutionary rates (e.g. dN/dS ratios). Only used if `age_max`, the max number , is numeric. Times are computed using makeChronosCalib and chronos.

`show_plot` Show a basic plot of the resulting tree.

`save_dir` Directory to cache full tree in. Set to `NULL` to avoid using cache.

`verbose` Print messages.

`...` Additional arguments passed to makeChronosCalib.

Value

A filtered tree of class "phylo" (with standardised species names).

Source

TimeTree 5: An Expanded Resource for Species Divergence Times

Examples

```
species <- c("human","chimp","mouse")
tr <- orthogene::prepare_tree(species = species)
```

remove_image_bg *Remove image background*

Description

Import and image and remove the background using **magick**.

Usage

```
remove_image_bg(
  path,
  color = "white",
  fuzz = 0,
 save_path = file.path(tempdir(), "phylopic_processed", paste0(basename(dirname(path)),
    ".png"))
)
```

Arguments

path	a file, url, or raster object or bitmap array
color	a valid color string such as "navyblue" or "#000080". Use "none" for transparency.
fuzz	relative color distance (value between 0 and 100) to be considered similar in the filling algorithm

Value

Named list containing the modified image itself and the saved path of the modified image.

Source

```
 path <- paste0("https://images.phylopic.org/images/","2de1c95c-7e1f-429b-9c08-17f0a27d176f/vector.sv
img_res <- remove_image_bg(path=path)
```

report_orthologs *Report orthologs*

Description

Identify the number of orthologous genes between two species.

Usage

```
report_orthologs(
  target_species = "mouse",
  reference_species = "human",
  standardise_genes = FALSE,
  method_all_genes = c("homologene", "gprofiler", "babelgene"),
  method_convert_orthologs = method_all_genes,
  drop_nonorths = TRUE,
  non121_strategy = "drop_both_species",
  round_digits = 2,
  return_report = TRUE,
  ref_genes = NULL,
  mc.cores = 1,
  verbose = TRUE,
  ...
)
```

Arguments

`target_species` Target species.

`reference_species`
Reference species.

`standardise_genes`
If `TRUE` AND `gene_output="columns"`, a new column "input_gene_standard" will be added to `gene_df` containing standardised HGNC symbols identified by gorth.

`method_all_genes`
R package to to use in all_genes step:

- `"gprofiler"` : Slower but more species and genes.
- `"homologene"` : Faster but fewer species and genes.
- `"babelgene"` : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.

`method_convert_orthologs`
R package to to use in convert_orthologs step:

- `"gprofiler"` : Slower but more species and genes.
- `"homologene"` : Faster but fewer species and genes.
- `"babelgene"` : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.

`drop_nonorths` Drop genes that don't have an ortholog in the `output_species`.

`non121_strategy`
How to handle genes that don't have 1:1 mappings between `input_species`:`output_species`. Options include:

- `"drop_both_species"` or `"dbs"` or `1` :
  Drop genes that have duplicate mappings in either the `input_species` or

output_species
(*DEFAULT*).

- "drop_input_species" or "dis" or 2 :
  Only drop genes that have duplicate mappings in the input_species.
- "drop_output_species" or "dos" or 3 :
  Only drop genes that have duplicate mappings in the output_species.
- "keep_both_species" or "kbs" or 4 :
  Keep all genes regardless of whether they have duplicate mappings in either species.
- "keep_popular" or "kp" or 5 :
  Return only the most "popular" interspecies ortholog mappings. This procedure tends to yield a greater number of returned genes but at the cost of many of them not being true biological 1:1 orthologs.
- "sum","mean","median","min" or "max" :
  When gene_df is a matrix and gene_output="rownames", these options will aggregate many-to-one gene mappings (input_species-to-output_species) after dropping any duplicate genes in the output_species.

round_digits
: Number of digits to round to when printing percentages.

return_report
: Return just the ortholog mapping between two species (FALSE) or return both the ortholog mapping as well a data.frame of the report statistics (TRUE).

ref_genes
: A table of all genes for the reference_species. If NULL (default), this will automatically be created using all_genes.

mc.cores
: Number of cores to parallelise each target_species with.

verbose
: Print messages.

...
: Arguments passed on to convert_orthologs

  gene_df Data object containing the genes (see gene_input for options on how the genes can be stored within the object).
  Can be one of the following formats:

  - matrix :
    A sparse or dense matrix.
  - data.frame :
    A data.frame, data.table. or tibble.
  - codelist :
    A list or character vector.

  Genes, transcripts, proteins, SNPs, or genomic ranges can be provided in any format (HGNC, Ensembl, RefSeq, UniProt, etc.) and will be automatically converted to gene symbols unless specified otherwise with the ... arguments.
  Note: If you set method="homologene", you must either supply genes in gene symbol format (e.g. "Sox2") OR set standardise_genes=TRUE.

  gene_input Which aspect of gene_df to get gene names from:

  - "rownames" :
    From row names of data.frame/matrix.

- `"colnames"` :
  From column names of data.frame/matrix.
- `<column name>` :
  From a column in `gene_df`, e.g. `"gene_names"`.

`gene_output` How to return genes. Options include:

- `"rownames"` :
  As row names of `gene_df`.
- `"colnames"` :
  As column names of `gene_df`.
- `"columns"` :
  As new columns "input_gene", "ortholog_gene" (and "input_gene_standard" if `standardise_genes=TRUE`) in `gene_df`.
- `"dict"` :
  As a dictionary (named list) where the names are input_gene and the values are ortholog_gene.
- `"dict_rev"` :
  As a reversed dictionary (named list) where the names are ortholog_gene and the values are input_gene.

`input_species` Name of the input species (e.g., "mouse","fly"). Use map_species to return a full list of available species.

`output_species` Name of the output species (e.g. "human","chicken"). Use map_species to return a full list of available species.

`agg_fun` Aggregation function passed to aggregate_mapped_genes. Set to `NULL` to skip aggregation step (default).

`mthreshold` Maximum number of ortholog names per gene to show. Passed to gorth. Only used when `method="gprofiler"` (*DEFAULT :* `Inf`).

`method` R package to use for gene mapping:

- `"gprofiler"` : Slower but more species and genes.
- `"homologene"` : Faster but fewer species and genes.
- `"babelgene"` : Faster but fewer species and genes. Also gives consensus scores for each gene mapping based on a several different data sources.

`as_sparse` Convert `gene_df` to a sparse matrix. Only works if `gene_df` is one of the following classes:

- `matrix`
- `Matrix`
- `data.frame`
- `data.table`
- `tibble`

If `gene_df` is a sparse matrix to begin with, it will be returned as a sparse matrix (so long as `gene_output= "rownames"` or `"colnames"`).

`sort_rows` Sort `gene_df` rows alphanumerically.

`gene_map` A data.frame that maps the current gene names to new gene names. This function's behaviour will adapt to different situations as follows:

- `gene_map=<data.frame>` :
  When a data.frame containing the gene key:value columns (specified by `input_col` and `output_col`, respectively) is provided, this will be used to perform aggregation/expansion.
- `gene_map=NULL` and `input_species!=output_species` :
  A `gene_map` is automatically generated by map_orthologs to perform inter-species gene aggregation/expansion.
- `gene_map=NULL` and `input_species==output_species` :
  A `gene_map` is automatically generated by map_genes to perform within-species gene gene symbol standardization and aggregation/expansion.

`as_DelayedArray` Convert aggregated matrix to DelayedArray.

`input_col` Column name within `gene_map` with gene names matching the row names of `X`.

`output_col` Column name within `gene_map` with gene names that you wish you map the row names of `X` onto.

Value

A list containing:

- map : A table of inter-species gene mappings.
- report : A list of aggregate orthology report statistics.

If >1 `target_species` are provided, then a table of aggregated `report` statistics concatenated across species will be returned instead.

Examples

```
orth_fly <- report_orthologs(
    target_species = "fly",
    reference_species = "human")
```

`run_benchmark` *Run benchmark tests*

Description

Runs benchmarks tests on all_genes and convert_orthologs across multiple species, using multiple methods ("homologene", and "gprofiler").

Usage

```
run_benchmark(
  species,
  method_list = c("homologene", "gprofiler", "babelgene"),
  run_convert_orthologs = TRUE,
  remove_failed_times = FALSE,
  save_path = tempfile(fileext = ".csv"),
  mc.cores = 1,
  verbose = TRUE
)
```

Arguments

species	Species names.
run_convert_orthologs	Benchmark convert_orthologs function.
remove_failed_times	In instances where no genes were returned, set time to NA.
save_path	Path to save results to.
mc.cores	Number of cores to parallelise species across.
verbose	Print messages.
benchmark_homologene	Benchmark method "homologene".
benchmark_gprofiler	Benchmark method "gprofiler".
benchmark_babelgene	Benchmark method "babelgene".

Value

data.table with benchmark results

---

set_gprofiler *Set gprofiler*

Description

Set the default URL for gprofiler API queries.

- default: http://biit.cs.ut.ee/gprofiler
- bea: http://biit.cs.ut.ee/gprofiler_beta

Usage

```
set_gprofiler(url = "http://biit.cs.ut.ee/gprofiler_beta")
```

Arguments

url	the base URL.

Value

Null

---

taxa_id_dict *Taxa ID dictionary*

Description

Dictionary of NCBI taxonomy IDs mapped to Latin and common names of 20+ organisms.

Usage

```
taxa_id_dict(
  species = c("human", "chimp", "monkey", "mouse", "rat", "dog", "cow", "chicken",
    "zebrafish", "frog", "fly", "worm", "rice"),
  include_common_names = TRUE
)
```

Arguments

species	Species to get dictionary for. Can supply either Latin names (e.g. "Homo sapiens") or common names (e.g, "human").

Value

Named list of taxa IDs to organism names.

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