Package ‘syntenet’

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**Title**  Inference And Analysis Of Synteny Networks

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**Description**  syntenet can be used to infer synteny networks from whole-genome protein sequences and analyze them. Anchor pairs are detected with the MCScanX algorithm, which was ported to this package with the Rcpp framework for R and C++ integration. Anchor pairs from synteny analyses are treated as an undirected unweighted graph (i.e., a synteny network), and users can perform: i. network clustering; ii. phylogenomic profiling (by identifying which species contain which clusters) and; iii. microsynteny-based phylogeny reconstruction with maximum likelihood.

**License**  GPL-3

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**BugReports**  https://support.bioconductor.org/t/syntenet

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Description

syntenet can be used to infer syntenic networks from whole-genome protein sequences and analyze them. Anchor pairs are detected with the MCScanX algorithm, which was ported to this package with the Rcpp framework for R and C++ integration. Anchor pairs from syntenic analyses are treated as an undirected unweighted graph (i.e., a syntenic network), and users can perform: i. network clustering; ii. phylogenomic profiling (by identifying which species contain which clusters) and; iii. microsynteny-based phylogeny reconstruction with maximum likelihood.

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See Also

Useful links:

• https://github.com/almeidasilvaf/syntenet
• Report bugs at https://support.bioconductor.org/t/syntenet
Microsynteny-based angiosperm phylogeny.

Description

Original tree file obtained from Zhao et al., 2021. The tree is an object of class 'phylo', which can be created by reading the tree file with `treeio::read.tree()`.

Usage

data(angiosperm_phylogeny)

Format

An object of class 'phylo'.

References


Examples

data(angiosperm_phylogeny)

Filtered genome annotation for Ostreococcus sp. species

Description

Data obtained from Pico-PLAZA 3.0. Only annotation data for primary transcripts were included, and only genes for chromosomes 1, 2, and 3.

Usage

data(annotation)

Format

A CompressedGRangesList containing the elements Olucimarinus, 0sp_RCC809, and Otauri.

References

binarize_and_transpose

**Examples**

```r
data(annot)
```

**Description**

Binarize and transpose the phylogenomic profile matrix

**Usage**

```r
binarize_and_transpose(profile_matrix = NULL)
```

**Arguments**

- `profile_matrix` A matrix with phylogenomic profiles obtained with `phylogenomic_profile`.

**Value**

A binary and transposed version of the profiles matrix.

**Examples**

```r
data(clusters)
profile_matrix <- phylogenomic_profile(clusters)
tmat <- binarize_and_transpose(profile_matrix)
```

---

**blast_list**  
*List of data frames containing BLAST-like tabular output*

**Description**

The object was created by running `run_diamond` on the protein sequences for the Ostreococcus algae available in the `proteomes` example data. Hits with <50% identity were filtered out. Code to recreate this data is available at the `script/` subdirectory.

**Usage**

```r
data(blast_list)
```

**Format**

A list of data frames containing the pairwise comparisons between proteomes of Ostreococcus species.
check_input

Check if input objects are ready for further analyses

Description
Check if input objects are ready for further analyses

Usage

check_input(seq = NULL, annotation = NULL, gene_field = "gene_id")

Arguments

seq
A list of AAStringSet objects, each list element containing protein sequences for a given species. This list must have names (not NULL), and names of each list element must match the names of list elements in annotation.

annotation
A GRangesList, CompressedGRangesList, or list of GRanges with the annotation for the sequences in seq. This list must have names (not NULL), and names of each list element must match the names of list elements in seq.

gene_field
Character, name of the column in the GRanges objects that contains gene IDs. Default: "gene_id".

Details
This function checks the input data for 3 required conditions:

1. Names of seq list (i.e., names(seq)) match the names of annotation GRangesList/CompressedGRangesList (i.e., names(annotation))

2. For each species (list elements), the number of sequences in seq is not greater than the number of genes in annotation. This is a way to ensure users do not input the translated sequences for multiple isoforms of the same gene (generated by alternative splicing). Ideally, the number of sequences in seq should be equal to the number of genes in annotation, but this may not always stand true because of non-protein-coding genes.

3. For each species, sequence names (i.e., names(seq[[x]]), equivalent to FASTA headers) match gene names in annotation.

Value
TRUE if the objects pass the check.

Examples

data(translation)
data(proteomes)
check_input(proteomes, annotation)
clusters

Description

Data obtained from Zhao & Schranz, 2019.

Usage

data(clusters)

Format

A 2-column data frame containing the following variables:

- **Gene**  Gene ID
- **Cluster**  Cluster ID

References


Examples

data(clusters)

cluster_network

Cluster the synteny network using the Infomap algorithm

Description

Cluster the synteny network using the Infomap algorithm

Usage

cluster_network(
  network = NULL,
  clust_function = igraph::cluster_infomap,
  clust_params = NULL
)

collapse_protein_ids

Arguments

- **network**: A network represented as an edge list, which is a 2-column data frame with node 1 in the first column and node 2 in the second column. In a synteny network, node 1 and node are the anchor pairs.

- **clust_function**: Function to be used to cluster the network. It must be one the functions from the `cluster_*` family in the `igraph` package (e.g., `cluster_infomap`, `cluster_leiden`, etc). Default: `igraph::cluster_infomap`.

- **clust_params**: A list with additional parameters (if any) to be passed to the igraph clustering function. Default: `NULL` (no additional parameters).

Value

A 2-column data frame with the following variables:

- **Gene**: Gene ID.
- **Cluster**: Cluster ID as identified by infomap.

Examples

```r
data(network)
clusters <- cluster_network(network[1:500, ])
```

collapse_protein_ids

**Collapse protein IDs into gene IDs in sequence names of AAStringSet objects**

Description

This function can be used if the sequence names of the AAStringSet objects contain protein IDs instead of gene IDs (what syntenet requires)

Usage

```r
collapse_protein_ids(seq, protein2gene = NULL)
```

Arguments

- **seq**: A list of AAStringSet objects, each list element containing protein sequences for a given species. This list must have names (not NULL), and names of each list element must match the names of list elements in `protein2gene`.

- **protein2gene**: A list of 2-column data frames containing protein-to-gene ID correspondences, where the first column contains protein IDs, and the second column contains gene IDs. Names of list elements must match names of `seq`.
create_species_id_table

Details
For each species, this function will replace the protein IDs in sequence names with gene IDs using the protein-to-gene correspondence table in `protein2gene`. After replacing protein IDs with gene IDs, if there are multiple sequences with the same gene ID (indicating different isoforms of the same gene), only the longest sequence is kept, so that the number of sequences is not greater than the number of genes.

Value
A list of AAStringSet objects as in `seq`, but with protein IDs replaced with gene IDs.

Examples
# Load data
seq_path <- system.file(  
  "extdata", "RefSeq_parsing_example", package = "syntenet"  
)
seq <- fasta2AAStringSetlist(seq_path)
annot <- gff2GRangesList(seq_path)

# Clean sequence names
names(seq$Aalosa) <- gsub(" .*", 
"", names(seq$Aalosa))

# Create a correspondence data frame
cor_df <- as.data.frame(annot$Aalosa[annot$Aalosa$type == "CDS", ])
cor_df <- cor_df[, c("Name", "gene")]

# Create a list of correspondence data frames
protein2gene <- list(Aalosa = cor_df)

# Collapse IDs
new_seqs <- collapse_protein_ids(seq, protein2gene)


create_species_id_table
Create a data frame of species IDs (3-5-character abbreviations)

Description
Create a data frame of species IDs (3-5-character abbreviations)

Usage
create_species_id_table(species_names)

Arguments

species_names  A character vector of names extracted from the `seq` or `annotation` lists, which can be extracted with `names(seq)` or `names(annotation)`. 
Value

A 2-column data frame with the following variables:

- **species_id**  Character, species ID consisting of 3-5 characters.
- **species_name**  Character, original names passed as input.

Examples

```r
# Load 'seq' list (list of AAStringSet objects)
data(proteomes)

# Create ID table
create_species_id_table(names(proteomes))
```

---

**diamond_is_installed**  Check if DIAMOND is installed

Description

Check if DIAMOND is installed

Usage

```r
diamond_is_installed()
```

Value

Logical indicating whether DIAMOND is installed or not.

Examples

```r
diamond_is_installed()
```

---

**edges**  Synteny network of Ostreococcus genomes represented as an edge list

Description

The object was created by running `infer_syntenet` on the `blast_list` example data. Code to recreate this data set is available at the script/ subdirectory.

Usage

```r
data(edges)
```
export_sequences

Format

A data frame containing anchor pairs between two Ostreococcus proteomes.

Examples

data(edges)

Description

Export processed sequences as FASTA files

Usage

export_sequences(seq = NULL, outdir = tempdir())

Arguments

seq  A processed list of AAStringSet objects as returned by process_input().
outdir  Path to output directory where FASTA files will be stored.

Value

Path to exported FASTA files.

Examples

# Load data
data(proteomes)
data(annotation)

# Process data
pdata <- process_input(proteomes, annotation)

# Export data
outdir <- file.path(tempdir(), "example_test")
export_sequences(pdata$seq, outdir)
### fasta2AAStringSetlist

**Description**

Read FASTA files in a directory as a list of AAStringSet objects

**Usage**

```r
fasta2AAStringSetlist(fasta_dir)
```

**Arguments**

- **fasta_dir** Character indicating the path to the directory containing FASTA files.

**Value**

A list of AAStringSet objects, where each element represents a different FASTA file.

**Examples**

```r
fasta_dir <- system.file("extdata", "sequences", package = "syntenet")
aastringsetlist <- fasta2AAStringSetlist(fasta_dir)
```

### find_GS_clusters

**Description**

Find group-specific clusters based on user-defined species classification

**Usage**

```r
find_GS_clusters(
    profile_matrix = NULL,
    species_annotation = NULL,
    min_percentage = 50
)
```
Arguments

profile_matrix  A matrix of phylogenomic profiles obtained with phylogenomic_profile.

species_annotation  A 2-column data frame with species IDs in the first column (same as column names of profile matrix), and species annotation (e.g., higher-level taxonomic information) in the second column.

min_percentage  Numeric scalar with the minimum percentage of species in a group to consider group specificity. For instance, if a given cluster is present in only 1 group of species, but in less than min_percentage of the species for this group, it will not be considered a group-specific cluster. This filtering criterion is useful to differentiate group-specific clusters (e.g., family-specific) from subgroup-specific clusters (e.g., genus-specific). Default: 50.

Value

A data frame with the following variables:

Group  To which group of species the cluster is specific.

Percentage  Percentage of species from the group that are represented by the cluster.

Cluster  Cluster ID.

Examples

data(clusters)
profile_matrix <- phylogenomic_profile(clusters)

# Species annotation
      "Lang", "car", "pmu", "ppe", "pbr", "mdo", "roc", "fve", 
      "Mnot", "Zjuj", "hlu", "jcu", "mes", "rco", "lus", "ptr")

species_annotation <- data.frame(
  Species = species_order,
  Family = c(rep("Fabaceae", 11), rep("Rosaceae", 6),
             "Moraceae", "Rhamnaceae", "Cannabaceae",
             rep("Euphorbiaceae", 3), "Linaceae", "Salicaceae")
)
gs_clusters <- find_GS_clusters(profile_matrix, species_annotation)
Usage

```r
infer_microsynteny_phylogeny()
```

Arguments

- `transposed_profiles`: A binary and transposed profile matrix. The profile matrix can be obtained with `phylogenomic_profile()`.
- `bootr`: Numeric scalar with the number of bootstrap replicates. Default: 1000.
- `alrtboot`: Numeric scalar with the number of replicates for the SH-like approximate likelihood ratio test. Default: 1000.

Value

- `infer_microsynteny_phylogeny()`: Infers microsynteny-based phylogeny with IQTREE.

Examples

```r
transposed_profiles <- NULL
bootr <- 1000
alrtboot <- 1000
threads <- "AUTO"
model <- "MK+FO+R"
outdir <- tempdir()
outgroup <- NULL
verbose <- FALSE

infer_microsynteny_phylogeny(transposed_profiles = transposed_profiles,
                               bootr = bootr,
                               alrtboot = alrtboot,
                               threads = threads,
                               model = model,
                               outdir = outdir,
                               outgroup = outgroup,
                               verbose = verbose)
```
threads Numeric scalar indicating the number of threads to use or "AUTO", which allows IQTREE to automatically choose the best number of threads to use. Default: "AUTO".

data model Substitution model to use. If you are unsure, pick the default. Default: "MK+FO+R".

data outdir Path to output directory. By default, files are saved in a temporary directory, so they will be deleted when the R session closes. If you want to keep the files, specify a custom output directory.

data outgroup Name of outgroup clade to group the phylogeny. Default: NULL (unrooted phylogeny).

data verbose Logical indicating if progress messages should be prompted. Default: FALSE.

data Value A character vector of paths to output files.

Examples

data(clusters)
profile_matrix <- phylogenomic_profile(clusters)
tmat <- binarize_and_transpose(profile_matrix)

# Leave only some legumes and P. mume as an outgroup for testing purposes
included <- c("gma", "pvu", "vra", "van", "cca", "pmu")
tmat <- tmat[rownames(tmat) %in% included, ]

# Remove non-variable sites
tmat <- tmat[, colSums(tmat) != length(included)]

if(iqtree_is_installed()) {
phylo <- infer_microsynteny_phylogeny(tmat, outgroup = "pmu",
threads = 1)
}

Infer synteny network

Description

Infer synteny network

Usage

infer_syntenet(
    blast_list = NULL,
    annotation = NULL,
    outdir = tempdir(),
    threads = "AUTO",
anchors = 5,
max_gaps = 25,
is_pairwise = TRUE,
verbose = FALSE,
bp_param = BiocParallel::SerialParam(),
...
)

Arguments

- **blast_list**
  A list of data frames, each data frame having the tabular output of BLASTp or similar programs, such as DIAMOND. This is the output of the function run_diamond(). If you performed pairwise comparisons on the command line, you can read the tabular output as data frames and combine them in a list. List names must be have species names separated by underscore. For instance, if the first list element is a data frame containing the comparison of speciesA (query) against speciesB (database), its name must be "speciesA_speciesB".

- **annotation**
  A processed GRangesList, CompressedGRangesList, or list of GRanges as returned by process_input().

- **outdir**
  Path to the output directory. Default: tempdir().

- **anchors**
  Numeric indicating the minimum required number of genes to call a syntenic block. Default: 5.

- **max_gaps**
  Numeric indicating the number of upstream and downstream genes to search for anchors. Default: 25.

- **is_pairwise**
  Specify if only pairwise blocks should be reported. Default: TRUE

- **verbose**
  Logical indicating if log messages should be printed on screen. Default: FALSE.

- **bp_param**
  BiocParallel back-end to be used. Default: BiocParallel::SerialParam().

- **...**
  Any additional arguments to the MCScanX algorithm. For a complete list of all available options, see the man page of rcpp_mcsanx_file().

Value

A network represented as an edge list.

Examples

```r
# Load data
data(proteomes)
data(annotation)
data(blast_list)

# Create processed annotation list
annotation <- process_input(proteomes, annotation)$annotation

# Infer the synteny network
net <- infer_syntenet(blast_list, annotation)
```
interspecies_synteny

Detect interspecies synteny

**Description**

Detect interspecies synteny

**Usage**

```r
interspecies_synteny(
  blast_inter = NULL,
  annotation = NULL,
  inter_dir = file.path(tempdir(), "inter"),
  anchors = 5,
  max_gaps = 25,
  is_pairwise = TRUE,
  verbose = FALSE,
  bp_param = BiocParallel::SerialParam(),
  ...
)
```

**Arguments**

- `blast_inter`: A list of BLAST/DIAMOND data frames for interspecies comparisons as returned by `run_diamond()`.
- `annotation`: A processed GRangesList or CompressedGRangesList object as returned by `process_input()`.
- `inter_dir`: Path to output directory where .collinearity files will be stored.
- `anchors`: Numeric indicating the minimum required number of genes to call a syntenic block. Default: 5.
- `max_gaps`: Numeric indicating the number of upstream and downstream genes to search for anchors. Default: 25.
- `is_pairwise`: specify if only pairwise blocks should be reported. Default: TRUE.
- `verbose`: Logical indicating if log messages should be printed on screen. Default: FALSE.
- `bp_param`: BiocParallel back-end to be used. Default: BiocParallel::SerialParam().
- `...`: Any additional arguments to the MCScanX algorithm. For a complete list of all available options, see the man page of `rcpp_mcscanx_file()`.

**Value**

Paths to .collinearity files.
Examples

```r
# Load data
data(proteomes)
data(blast_list)
data(annotation)

# Get DIAMOND and processed annotation lists
blast_inter <- blast_list[2]
annotation <- process_input(proteomes, annotation)$annotation

# Detect interspecies synteny
intersyn <- interspecies_synteny(blast_inter, annotation)
```

---

**intraspecies_synteny**  
*Detect intraspecies synteny*

Description

Detect intraspecies synteny

Usage

```r
intraspecies_synteny(
  blast_intra = NULL,
  annotation = NULL,
  intra_dir = file.path(tempdir(), "intra"),
  anchors = 5,
  max_gaps = 25,
  is_pairwise = TRUE,
  verbose = FALSE,
  bp_param = BiocParallel::SerialParam(),
  ...
)
```

Arguments

- `blast_intra`: A list of BLAST/DIAMOND data frames for intraspecies comparisons as returned by `run_diamond()`.
- `annotation`: A processed GRangesList or CompressedGRangesList object as returned by `process_input()`.
- `intra_dir`: Path to output directory where .collinearity files will be stored.
- `anchors`: Numeric indicating the minimum required number of genes to call a syntenic block. Default: 5.
- `max_gaps`: Numeric indicating the number of upstream and downstream genes to search for anchors. Default: 25.
- `is_pairwise`: Logical indicating if only pairwise blocks should be reported. Default: TRUE.
Description

Check if IQTREE is installed

Usage

iqtree_is_installed()

Value

Logical indicating whether IQTREE is installed or not.

Examples

iqtree_is_installed()
**iqtree_version**

*Get IQ-TREE version*

**Description**

Get IQ-TREE version

**Usage**

iqtree_version()

**Value**

Numeric indicating IQ-TREE version, with either 1 or 2.

**Examples**

iqtree_version()

---

**last_is_installed**

*Check if last is installed*

**Description**

Check if last is installed

**Usage**

last_is_installed()

**Value**

Logical indicating whether last is installed or not.

**Examples**

last_is_installed()
network

Description

Data obtained from Zhao & Schranz, 2019.

Usage

data(network)

Format

An edgelist (i.e., a 2-column data frame with node 1 in column 1 and node 2 in column 2).

References


Examples

data(network)

parse_collinearity

Parse .collinearity files obtained with MCScan

Description

The .collinearity files can be obtained with intraspecies_synteny and interspecies_synteny, which execute a native version of the MCScan algorithm.

Usage

parse_collinearity(collinearity_paths = NULL, as = "anchors")

Arguments

collinearity_paths
  Character vector of paths to .collinearity files.

as
  Character specifying what to extract. One of "anchors" (default), "blocks", or "all".
### phylogenomic_profile

**Value**

If `as` is "anchors", a data frame with variables "Anchor1", and "Anchor2". If `as` is "blocks", a data frame with variables "Block", "Block_score", "Chr", and "Orientation". If `as` is "all", a data frame with all aforementioned variables, which indicate:

- **Block** Numeric, synteny block ID
- **Block_score** Numeric, score of synteny block.
- **Chr** Character, query and target chromosome of the synteny block formatted as ".&."
- **Orientation** Character, the orientation of genes within blocks, with "plus" indicating that genes are in the same direction, and "minus" indicating that genes are in opposite directions.
- **Anchor1** Character, gene ID of anchor 1.
- **Anchor2** Character, gene ID of anchor 2.

**Examples**

```r
collinearity_paths <- system.file(
  "extdata", "Scerevisiae.collinearity", package = "syntenet"
)
net <- parse_collinearity(collinearity_paths)

phylogenomic_profile <- phylogenomic_profile(clusters)
```

---

### phylogenomic_profile

**Perform phylogenomic profiling for synteny network clusters**

**Description**

Perform phylogenomic profiling for synteny network clusters

**Usage**

```r
phylogenomic_profile(clusters = NULL)
```

**Arguments**

- **clusters** A 2-column data frame with variables `Gene` and `Cluster` as returned by `cluster_network`.

**Value**

A matrix of i rows and j columns containing the number of genes in cluster i for each species j. The number of rows is equal to the number of clusters in `clusters`, and the number of columns is equal to the number of species in `clusters`.

**Examples**

```r
data(clusters)
profiles <- phylogenomic_profile(clusters)
```
Description
Plot network

Usage
plot_network(
  network = NULL,
  clusters = NULL,
  cluster_id = NULL,
  color_by = "cluster",
  interactive = FALSE,
  dim_interactive = c(600, 600)
)

Arguments

  network The synteny network represented as an edge list, which is a 2-column data frame with each member of the anchor pair in a column.
  clusters A 2-column data frame with the variables Gene and Cluster representing gene ID and cluster ID, respectively, exactly as returned by cluster_network.
  cluster_id Character scalar or vector with cluster ID. If more than one cluster is passed as input, clusters are colored differently.
  color_by Either "cluster" or a 2-column data frame with gene IDs in the first column and variable to be used for coloring (e.g., taxonomic information) in the second column.
  interactive Logical scalar indicating whether to display an interactive network or not. Default: FALSE.
  dim_interactive Numeric vector of length 2 with the window dimensions of the interactive plot. If interactive is set to FALSE, this parameter is ignored.

Value
A ggplot object with the network.

Examples

data(network)
data(clusters)
# Option 1: 1 cluster
cluster_id <- 25
plot_network(network, clusters, cluster_id)
# Option 2: 2 clusters
cluster_id <- c(25, 1089)
plot_network(network, clusters, cluster_id)

# Option 3: custom annotation for coloring
species_order <- c(
  "Lang", "car", "pmu", "ppe", "pbr", "mdo", "roc", "fve",
  "Mnot", "Zjuj", "jcu", "mes", "rco", "lus", "ptr"
)
species_annotation <- data.frame(
  Species = species_order,
  Family = c(rep("Fabaceae", 11), rep("Rosaceae", 6),
             "Moraceae", "Ramuaceae", rep("Euphorbiaceae", 3),
             "Linaceae", "Salicaceae")
)
genes <- unique(c(network$node1, network$node2))
gene_df <- data.frame(
  Gene = genes,
  Species = unlist(lapply(strsplit(genes, "_"), head, 1))
)
gene_df <- merge(gene_df, species_annotation)[, c("Gene", "Family")]
plot_network(network, clusters, cluster_id = 25, color_by = gene_df)

---

**plot_profiles**

*Plot a heatmap of phylogenomic profiles*

**Description**

Plot a heatmap of phylogenomic profiles

**Usage**

```r
plot_profiles(
  profile_matrix = NULL,
  species_annotation = NULL,
  palette = "Greens",
  dist_function = stats::dist,
  dist_params = list(method = "euclidean"),
  clust_function = stats::hclust,
  clust_params = list(method = "ward.D"),
  cluster_species = FALSE,
  show_colnames = FALSE,
  discretize = TRUE,
  ...
)
```
Arguments

profile_matrix  A matrix of phylogenomic profiles obtained with phylogenomic_profile.

species_annotation  A 2-column data frame with species IDs in the first column (same as column names of profile matrix), and species annotation (e.g., higher-level taxonomic information) in the second column.

palette  A character vector of colors or a character scalar with the name of an RColorBrewer palette. Default: "RdYlBu".

dist_function  Function to use to calculate a distance matrix for synteny clusters. Popular examples include stats::dist, labdsv::dsvdis, and vegan::vegdist. Default: stats::dist.

dist_params  A list with parameters to be passed to the function specified in parameter dist_function. Default: list(method = "euclidean").

clust_function  Function to use to cluster the distance matrix returned by the function specified in dist_function. Examples include stats::hclust and Rclusterpp::Rclusterpp.hclust. Default: stats::hclust.

clust_params  A list with additional parameters (if any) to be passed to the function specified in parameter clust_function. Default: list(method = "ward.D").

cluster_species  Either a logical scalar (TRUE or FALSE) or a character vector with the order in which species should be arranged. TRUE or FALSE indicate whether hierarchical clustering should be applied to rows (species). Ideally, the character vector should contain the order of species in a phylogenetically meaningful way. If users pass a named vector, vector names will be used to rename species. If users have a species tree, they can read it with treeio::read.tree(), plot it with ggtree::ggtree(), and get the species order from the ggtree object with ggtree::get_taxa_name(). Default: FALSE.

show_colnames  Logical indicating whether to show column names (i.e., cluster IDs) or not. Showing cluster IDs can be useful when visualizing a small subset of them. When visualizing all clusters, cluster IDs are impossible to read. Default: FALSE.

discretize  Logical indicating whether to discretize clusters in 4 categories: 0, 1, 2, and 3+. If FALSE, counts will be log2 transformed. Default: TRUE.

...  Additional parameters to pheatmap::pheatmap().

Value

A pheatmap object.

Examples

data(clusters)
profile_matrix <- phylogenomic_profile(clusters)
)  

```r
species_names <- c(
  "V. radiata", "V. angularis", "P. vulgaris", "G. max", "C. cajan",
  "T. pratense", "M. truncatula", "A. duranensis", "L. japonicus",
  "L. angustifolius", "C. arietinum", "P. mume", "P. persica",
  "P. bretschneideri", "M. domestica", "R. occidentalis",
  "F. vesca", "M. notabilis", "Z. jujuba", "J. curcas",
  "M. esculenta", "R. communis", "L. usitatissimum", "P. trichocarpa"
)

names(species_order) <- species_names

species_annotation <- data.frame(
  Species = species_order,
  Family = c(rep("Fabaceae", 11), rep("Rosaceae", 6),
            "Moraceae", "Ramnaceae", rep("Euphorbiaceae", 3),
            "Linaceae", "Salicaceae")
)

p <- plot_profiles(profile_matrix, species_annotation,
                    cluster_species = species_order)

p <- plot_profiles(profile_matrix, species_annotation,
                    cluster_species = species_order,
                    discretize = FALSE)
```

---

**process_input**  
**Process sequence data**

**Description**

Process sequence data

**Usage**

```r
process_input(
  seq = NULL,
  annotation = NULL,
  gene_field = "gene_id",
  filter_annotation = FALSE
)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>seq</td>
<td>A list of AAStringSet objects, each list element containing protein sequences for a given species. This list must have names (not NULL), and names of each list element must match the names of list elements in <code>annotation</code>.</td>
</tr>
<tr>
<td>annotation</td>
<td>A GRangesList, CompressedGRangesList, or list of GRanges with the annotation for the sequences in <code>seq</code>. This list must have names (not NULL), and names of each list element must match the names of list elements in <code>seq</code>.</td>
</tr>
<tr>
<td>gene_field</td>
<td>Character, name of the column in the GRanges objects that contains gene IDs. Default: &quot;gene_id&quot;.</td>
</tr>
</tbody>
</table>
Logical indicating whether `annotation` should be filtered to keep only genes that are also in `seq`. This is particularly useful if users want to remove information on non-protein coding genes from `annotation`, since such genes are typically not present in sets of whole-genome protein sequences. Default: FALSE.

### Details

This function processes the input sequences and annotation to:

1. Remove whitespace and anything after it in sequence names (i.e., `names(seq[[x]])`, which is equivalent to FASTA headers), if there is any.
2. Add a unique species identifier to sequence names. The species identifier consists of the first 3-5 strings of the element name. For instance, if the first element of the `seq` list is named "Athaliana", each sequence in it will have an identifier "Atha_" added to the beginning of each gene name (e.g., Atha_AT1G01010).
3. If sequences have an asterisk (*) representing stop codon, remove it.
4. Add a unique species identifier (same as above) to gene and chromosome names of each element of the `annotation` GRangesList/CompressedGRangesList.
5. Filter each element of the `annotation` GRangesList/CompressedGRangesList to keep only seqnames, ranges, and gene ID.

### Value

A list of 2 elements:

- `seq` The processed list of AAStringSet objects from `seq`.
- `annotation` The processed GRangesList or CompressedGRangesList object from `annotation`.

### Examples

```r
data(annotation)
data(proteomes)
seq <- proteomes
clean_data <- process_input(seq, annotation)
```

---

**Description**

Save the transposed binary profiles matrix to a file in PHYLIP format

**Usage**

```r
profiles2phylip(transposed_profiles = NULL, outdir = tempdir())
```
Arguments

transposed_profiles
   A binary and transposed profile matrix. The profile matrix can be obtained with phylogenomic_profile().
outdir
   Path to output directory. By default, files are saved in a temporary directory, so they will be deleted when the R session closes. If you want to keep the files, specify a custom output directory.

Value

Character specifying the path to the PHYLIP file.

Examples

```r
data(clusters)
profile_matrix <- phylogenomic_profile(clusters)
tmat <- binarize_and_transpose(profile_matrix)
profiles2phylip(tmat)
```

proteomes

Filtered proteomes of Ostreococcus sp. species

Description

Data obtained from Pico-PLAZA 3.0. Only the translated sequences of primary transcripts were included, and only genes from chromosomes 1, 2, and 3.

Usage

```r
data(proteomes)
```

Format

A list of AAStringSet objects containing the elements Olucimarinus, Osp_RCC809, and Otauri.

References


Examples

```r
data(proteomes)
```
Description

MCSCanX provides a clustering module for viewing the relationship of collinear segments in multiple genomes (or heavily redundant genomes). It takes the predicted pairwise segments from dynamic programming (DAGchainer in particular) and then tries to build consensus segments from a set of related, overlapping segments.

Usage

```r
rcpp_mcscanx_file(
  blast_file,  
gff_file, 
  prefix = "out", 
  outdir = "", 
  match_score = 50L, 
  gap_penalty = -1L, 
  match_size = 5L, 
  e_value = 1e-05, 
  max_gaps = 25L, 
  overlap_window = 5L, 
  is_pairwise = FALSE, 
  in_synteny = 0L, 
  species_id_length = 3L, 
  verbose = FALSE
)
```

Arguments

- **blast_file**: Character indicating the path to the BLAST/DIAMOND output file.
- **gff_file**: Character indicating the path to the "gff" file, which is a tab-delimited file with 4 columns indicating the chromosome name, gene id, gene start position, and gene end position, respectively.
- **prefix**: Character indicating the prefix to output files. Default: "out".
- **outdir**: Character indicating the path to the output directory. Default: "".
- **match_score**: Numeric indicating the match score. Default: 50.
- **gap_penalty**: Numeric indicating the gap penalty. Default: -1.
- **match_size**: Numeric indicating the minimum number of genes required to call synteny. Default: 5.
- **e_value**: Numeric indicating the minimum e-value allowed. Default: 1e-5.
- **max_gaps**: Numeric indicating the maximum number of gaps between genes allowed. The unit measure of gaps is number of genes, so max_gaps = 20 indicates that a maximum of 20 genes can exist between two homologous genes for synteny to be called. Default: 25.
**read_diamond**

**Description**

Read DIAMOND/BLAST tables as a list of data frames

**Usage**

```r
read_diamond(diamond_dir = NULL)
```

**Arguments**

- `diamond_dir` Path to directory containing the tabular output of DIAMOND or similar programs (e.g., BLAST).

**Value**

A list of data frames with the tabular DIAMOND output.

**References**


run_diamond

Examples

# Path to output directory
diamond_dir <- system.file("extdata", package = "syntenet")

# Read output
l <- read_diamond(diamond_dir)

run_diamond

Wrapper to run DIAMOND from an R session

Description

Wrapper to run DIAMOND from an R session

Usage

run_diamond(
  seq = NULL,
  top_hits = 5,
  verbose = FALSE,
  outdir = tempdir(),
  threads = NULL,
  compare = "all",
  ...
)

Arguments

seq A processed list of AAStringSet objects as returned by process_input().
top_hits Number of top hits to keep in DIAMOND search. Default: 5.
verbose Logical indicating if progress messages should be printed. Default: FALSE.
outdir Output directory for DIAMOND results. By default, output files are saved to a
temporary directory.
threads Number of threads to use. Default: let DIAMOND auto-detect and use all avail-
able virtual cores on the machine.
compare Character scalar indicating which comparisons should be made when running
DIAMOND. Possible modes are "all" (all-vs-all comparisons), "intraspecies"
(intraspecies comparisons only), or "interspecies" (interspecies comparisons only).
Alternatively, users can pass a 2-column data frame as input with the names of
species to be compared.
...
Any additional arguments to diamond blastp.

Value

A list of data frames containing DIAMOND's tabular output for each pairwise combination of
species. For n species, the list length will be n^2.
Examples

```r
data(proteomes)
data(annotation)
seq <- process_input(proteomes, annotation)$seq[1:2]
if(diamond_is_installed()) {
  diamond_results <- run_diamond(seq)
}
```

run_last  
*Wrapper to run last from an R session*

Description

Wrapper to run last from an R session

Usage

```r
run_last(
  seq = NULL,
  verbose = FALSE,
  outdir = tempdir(),
  threads = 1,
  compare = "all",
  lastD = 1e6,
  ...
)
```

Arguments

- **seq**: A processed list of AStringSet objects as returned by `process_input()`.
- **verbose**: Logical indicating if progress messages should be printed. Default: FALSE.
- **outdir**: Output directory for last results. By default, output files are saved to a temporary directory.
- **threads**: Number of threads to use. Default: 1.
- **compare**: Character scalar indicating which comparisons should be made when running DIAMOND. Possible modes are "all" (all-vs-all comparisons), "intraspecies" (intraspecies comparisons only), or "interspecies" (interspecies comparisons only). Alternatively, users can pass a 2-column data frame as input with the names of species to be compared.
- **lastD**: last option D: query letters per random alignment. Default: 1e6.
- **...**: Any additional arguments to `diamond blastp`.

Value

A list of data frames containing last’s tabular output for each pairwise combination of species. For n species, the list length will be $n^2$. 

---

**run_last**

Wrapper to run last from an R session
Examples

```r
data(proteomes)
data(annotation)
seq <- process_input(proteomes, annotation)$seq[1:2]
if(last_is_installed()) {
  last_results <- run_last(seq)
}
```

---

**scerevisiae_annot**  
*Genome annotation of the yeast species* *S. cerevisiae*

**Description**

Data obtained from Ensembl Fungi. Only annotation data for primary transcripts were included.

**Usage**

```r
data(scerevisiae_annot)
```

**Format**

A GRangesList as returned by `process_input()` containing the element `Scerevisiae`.

**Examples**

```r
data(scerevisiae_annot)
```

---

**scerevisiae_diamond**  
*Intraspecies DIAMOND output for* *S. cerevisiae*

**Description**

List obtained with `run_diamond()`.

**Usage**

```r
data(scerevisiae_diamond)
```

**Format**

A list of data frames (length 1) containing the whole paranome of *S. cerevisiae* resulting from intragenome similarity searches.

**Examples**

```r
data(scerevisiae_diamond)
```
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