Package ‘dnopath’

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Version 0.6.11
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dnaphath2-package

A short title line describing what the package does

Description

A more detailed description of what the package does. A length of about one to five lines is recommended.

Details

This section should provide a more detailed overview of how to use the package, including the most important functions.

Author(s)

Your Name, email optional.

Maintainer: Your Name <your@email.com>

References

This optional section can contain literature or other references for background information.

See Also

Optional links to other man pages

Examples

## Not run:

## Optional simple examples of the most important functions

## These can be in \dontrun{} and \donttest{} blocks.

## End(Not run)
bimart_hsapiens  Default mapping for entrezgene IDs and HGNC gene symbols

Description

This dataset is used by default if the connection to biomaRt fails. It is highly recommended to retry the function call that attempted to connect to biomaRt. Using this dataset in general may not produce the correct results.

Usage

bimart_hsapiens

Format

A data.frame containing a mapping between entrezgene IDs and HGNC gene symbols.

c.dnapath  Combine two 'dnapath' objects.

Description

This functionality is not implemented and will return an error.

Usage

## S3 method for class \texttt{dnapath}
c(...)

Arguments

\dots  'dnapath' objects to be concatenated.

Value

Concatenation is not defined; an error is generated.
**c.dnapath_list**

Combine two 'dnapath_list' objects.

---

**Description**

This functionality is not implemented and will return an error.

**Usage**

```r
## S3 method for class 'dnapath_list'
c(…)
```

**Arguments**

... 'dnapath_list' objects to be concatenated.

**Value**

Concatenation is not defined; an error is generated.

---

**dnapath**

*Differential Network Analysis Using Gene Pathways*

---

**Description**

Integrates pathways into the differential network analysis of gene expression data (Grimes et al. 2019).

**Usage**

```r
dnapath(
  x,
  pathway_list,
  groups = NULL,
  network_inference = run_pcor,
  n_perm = 100,
  lp = 2,
  seed = NULL,
  verbose = FALSE,
  ...
)
```

---
Arguments

x
The gene expression data to be analyzed. This can be either (1) a list of two matrices or data frames that contain the gene expression profile from each of two populations (groups) – with rows corresponding to samples and columns to genes – or (2) a single matrix or data frame that contains the expression profiles for both groups. For case (2), the groups argument must be specified to identify which rows belong to which group.

pathway_list
A single vector or list of vectors containing gene names to indicate pathway membership. The vectors are used to subset the columns of the matrices in x. A pathway list can be obtained using get_reactome_pathways. If NULL, then the entire expression dataset is analyzed as a single network (this approach is not recommended unless there are only a small number of genes).

groups
If x is a single matrix or data frame, groups must be specified to label each row. groups is a vector of length equal to the number of rows in x, and it should contain two unique elements (the two group names).

network_inference
A function used to infer the pathway network. It should take in an n by p matrix and return a p by p matrix of association scores. (Built-in options include: run_aracne, run_bc3net, run_c3net, run_clr, run_corr, run_dwlasso, run_genie3, run_glasso, run_mrnnet, run_pcor, and run_silencer.) Defaults to run_pcor for partial correlations.

n_perm
The number of random permutations to perform during permutation testing. If n_perm == 1, the permutation tests are not performed. If n_perm is larger than the number of possible permutations, n_perm will be set to this value with a warning message.

lp
The lp value used to compute differential connectivity scores. (Note: If a vector is provided, then the results are returned as a list of dnapath_list objects, one result for each value of lp. This option is available so that network inference methods only need to be run once for each pathway when multiple values of lp are being considered. This may be useful when conducting simulation studies).

seed
(Optional) Used to set.seed prior to permutation test for each pathway. This allows results for individual pathways to be easily reproduced.

verbose
Set to TRUE to turn on messages.

...
Additional arguments are passed into the network inference function.

Value

A 'dnapath_list' or 'dnapath' object containing results for each pathway in pathway_list.

References

d_edgesC

See Also

filter_pathways, summary.dnpath_list, subset.dnpath_list, sort.dnpath_list, plot.dnpath, rename_genes

Examples

data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
       groups = meso$groups, n_perm = 10)
results
summary(results) # Summary over all pathways in the pathway list.
# Remove results for pathways with p-values above 0.2.
top_results <- filter_pathways(results, 0.2)
# Sort the top results by the pathway DC score.
top_results <- sort(top_results, by = "dc_score")
top_results
summary(top_results[[1]]) # Summary of pathway 1.
plot(results[[1]]) # Plot of the differential network for pathway 1.

# Use ... to adjust arguments in the network inference function.
# For example, using run_corr() with method = "spearman":
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
       groups = meso$groups, n_perm = 10,
       network_inference = run_corr,
       method = "spearman")

results

---

d_edgesC

C++ implementation of d_edges

Description

Calculates differential network score for each edge in a network

Usage

d_edgesC(nw1, nw2, lp)

Arguments

nw1
    The association scores for network 1
nw2
    The association scores for network 2
lp
    The lp value to use.

Value

A matrix of differential network scores for the edges.
**d_genesC**

*Description*

Calculates differential network score for a set of genes

*Usage*

```c
d_genesC(nw1, nw2, lp)
```

*Arguments*

- `nw1`: The association scores for network 1
- `nw2`: The association scores for network 2
- `lp`: The lp value to use.

*Value*

A vector of differential network scores for the genes.

---

**d_pathwayC**

*Description*

Calculates differential network score for an entire pathway.

*Usage*

```c
d_pathwayC(nw1, nw2, lp)
```

*Arguments*

- `nw1`: The association scores for network 1
- `nw2`: The association scores for network 2
- `lp`: The lp value to use.

*Value*

The differential network score for the pathway.
entrez_to_symbol

Obtain gene symbols for entrezgene IDs

Description

Uses biomaRt (Durinck et al. 2009) to map entrezgene IDs to gene symbols for a given species. Obtains MGI symbols for mouse species and HGNC symbols for other species. (Note: this mapping may not work for all species.) The output of this function can be used in rename_genes.

Usage

entrez_to_symbol(
  x,
  species,
  symbol_name = NULL,
  dir_save = tempdir(),
  verbose = TRUE
)

Arguments

x
  A vector of entrezgene IDs.

species
  The species used to obtain the entrezgene IDs. For example: "Homo sapiens", "m musculus", "C. elegans", or "S cerevisiae". "Human" and "mouse" can also be used and will be converted to the correct species name.

symbol_name
  The type of gene symbol to use. If NULL, then "hgnc_symbol" is used for HGNC symbols, unless species is "mmusculus", in which case

dir_save
  The directory to store annotation reference. Future calls to this function will use the stored annotations. This speeds up the operation and allows for reproducibility in the event that the biomaRt database is updated. Set to NULL to disable. By default, it uses a temporary directory to store files during the R session. "mgi_symbol" is used.

verbose
  Set to FALSE to avoid messages.

Details

If entrezgene IDs are used in a dnapath_list or dnapath object, or a pathway list, then get_genes can be used to extract them and used for the x argument here.

Value

A data frame with two columns: the first contains the original entrezgene IDs, and the second contains the corresponding gene symbols. MGI symbols are returned when species = "Mus musculus" and HGNC symbols are returned otherwise.
Note

Internet connection is required to connect to biomaRt. If unavailable, the default biomart and default species contained in the package is used, but this may not match the desired species.

References


See Also

symbol_to_entrez, get_genes

Examples

data(meso)
# The meso gene expression data contains entrezgene IDs.
# These can be converted to gene symbols.
gene_mat <- entrez_to_symbol(colnames(meso$gene_expression), species = "human")

filter_pathways

Remove pathways with non-significant DC scores.

Description

Remove pathways with non-significant DC scores.

Usage

filter_pathways(x, alpha_pathway = NULL, monotonized = FALSE)

Arguments

x
A ‘dnapath_list’ object from dnapath.

alpha_pathway
Threshold for pathway p-values to determine significance. If NULL, defaults to 0.05 or the minimum possible threshold (based on the number of permutations that were run).

monotonized
If TRUE, monotonized p-values are used.

Value

A ‘dnapath_list’ object containing only those pathways with differential connectivity p-values below alpha.
get_genes

Examples

```r
data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
                   groups = meso$groups, n_perm = 10)
results_sig <- filter_pathways(results)
```

get_genes

Get the gene names from a differential network analysis

Description

Get the gene names from a differential network analysis

Usage

```r
get_genes(x)
```

Arguments

x

A `dnapath_list` or `dnapath` object from `dnapath`, or a pathway list.

Value

Returns a vector containing all the genes in x.

See Also

`rename_genes`, `entrez_to_symbol`, `symbol_to_entrez`

Examples

```r
data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
                   groups = meso$groups, n_perm = 10)
genesis <- get_genes(results)
```
get_min_alpha  
Get the minimum alpha level for the permutation test

Description
This method is used internally by several methods to determine the minimum significance threshold (alpha value) that can be applied to the permutation p-values obtained in the differential network analysis.

Usage
get_min_alpha(x)

Arguments
x  
A `dnapath_list` or `dnapath` object from dnapath.

Value
The minimum alpha level that can be used based on the number of permutations performed in the analysis.

Examples
```r
data(meso)
data(p53_pathways)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
                   groups = meso$groups, n_perm = 5)
get_min_alpha(results) # 1 / (5 + 1) = 0.167
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
                   groups = meso$groups, n_perm = 10)
get_min_alpha(results) # 1 / (10 + 1) = 0.091
```

get_networks  
Get the two association networks

Description
Extracts the estimated association network for each group from the differential network analysis results.

Usage
get_networks(x)
**get_reactome_pathways**

**Description**

Connects to reactome.db (Ligtenberg 2019) to obtain a list of pathways for a given species. The pathway list is processed by combining any two pathways that have substantial overlap (default is over 90% overlap). This output if this function can be used for the pathway_list argument in dnapath.

**Arguments**

- `x` A `dnapath` object from dnapath.

**Value**

A list of two association matrices.

**Note**

The two matrices can be plotted using the `plot_network` function from the SeqNet package, as illustrated in the examples below.

**Examples**

```r
data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
groups = meso$groups, n_perm = 10)
# Extract the two estimated association networks for the first pathway
nw <- get_networks(results[[1]])
# Plot the networks using the SeqNet::plot_network function.
# Note that the `compare_graph` argument is used so that the same node layout
# is used across all of the plots.
# Plot the two networks (in separate plots)
g <- SeqNet::plot_network(nw[[1]])
SeqNet::plot_network(nw[[1]], compare_graph = g)
# Plot of the differential network for pathway 1.
plot(results[[1]], compare_graph = g)
# We see that genes 51230 and 7311 show strong differential connectivity.
# The plot_pair() function can be used to investigate these two genes further.
plot_pair(results[[1]], "51230", "7311")
```
Usage

get_reactome_pathways(
  species,
  overlap_limit = 0.9,
  min_size = 10,
  max_size = 50,
  verbose = TRUE
)

Arguments

species A string, for example "Homo sapiens" or "Mus musculus", indicating the species to use.
overlap_limit (Optional) Any pathways that have an overlap greater than overlap_limit are combined. Set to NULL to disable this option.
min_size The minimum pathway size. Any Reactome pathways with fewer than min_size genes are removed from the list. Defaults to 10.
max_size The maximum pathway size. Any Reactome pathways with more than max_size genes are removed from the list. Defaults to 50.
verbose Set to FALSE to turn off messages.

Value

A named list of vectors. Each vector corresponds to a Reactome pathway and contains the entrez-gene IDs of the genes in that pathway.

References


See Also

The genes in the Reactome pathways use entrezgene IDs. These can be converted to gene symbols, if desired, using the entrez_to_symbol and rename_genes functions.

Examples

# Obtaining a pathway list for human (Homo sapiens).
# In this example, overlapping pathways are not combined (this is specified by setting overlap_limit to NULL).
pathway_list <- get_reactome_pathways("Homo sapiens", overlap_limit = NULL,
                                 min_size = 10, max_size = 20)
head.dnapath_list

Return the first part of the dnapath results.

Description
Return the first part of the dnapath results.

Usage
## S3 method for class 'dnapath_list'
head(x, ...)

Arguments

x
A 'dnapath_list' object.

... Additional parameters are passed into summary.dnapath_list.

Value
Returns the first five rows of the summary table of the 'dnapath_list' object.

Examples
data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
  groups = meso$groups, n_perm = 10)
head(results)

length.dnapath_list

The number of pathways in a 'dnapath_list' object.

Description
The number of pathways in a 'dnapath_list' object.

Usage
## S3 method for class 'dnapath_list'
length(x)

Arguments

x
A 'dnapath_list' object from dnapath.
Value

The number of pathways.

Examples

data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
                   groups = meso$groups, n_perm = 10)
length(results)

Description

meso is a list containing gene expression data from Mesothelioma tumors generated by The Cancer Genome Atlas (TCGA) and obtained using the LinkedOmics portal. The first element in the list, named "gene_expression", contains 32 samples (rows) with 150 genes (columns). The second element, named "groups", is a vector of length 32 indicating which group (stage ii or stage iv) each gene expression sample belongs to. See the "Package data" vignette for details.

Usage

meso

Format

A list containing two items:

$gene_expression A 32 by 150 matrix of gene expression values

$groups A vector of length 32 indicating which group (stage ii or stage iv) each of the rows in the gene expression data belong to.

Source

http://www.linkedomics.org/data_download/TCGA-GBMLGG/
names.dnapath

The pathway names in a 'dnapath' object.

Description

The pathway names in a 'dnapath' object.

Usage

## S3 method for class 'dnapath'
names(x)

Arguments

x

A 'dnapath' object from dnapath or from subsetting a 'dnapath_list'.

Value

The pathway's name.

Examples

data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
groups = meso$groups, n_perm = 10)
names(results[[1]])

names.dnapath_list

The pathway names in a 'dnapath_list' object.

Description

The pathway names in a 'dnapath_list' object.

Usage

## S3 method for class 'dnapath_list'
names(x)

Arguments

x

A 'dnapath_list' object from dnapath.
plot.dnapath

Value

The pathway names.

Examples

data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
                   groups = meso$groups, n_perm = 10)
names(results)

p53_pathways

Reactome pathway list for Homo sapiens

Description

This is a pathway list obtained from get_reactome_pathways with species = "human" (used reactome.db version 1.68.0). Only pathways with "p53" in their name are retained (to subset on some cancer-related pathways). The list contains 13 total pathways. See the "Package data" vignette for details.

Usage

p53_pathways

Format

A list of 13 vectors each containing a set of entregene IDs.

plot.dnapath

Plot function for 'dnapath' object.

Description

Uses the plotting functions for networks from the SeqNet package (Grimes and Datta 2019)
Usage

```r
## S3 method for class 'dnapath'
plot(
  x,
  alpha = NULL,
  monotonized = FALSE,
  only_dc = FALSE,
  require_dc_genes = FALSE,
  scale_edges = 1,
  scale_nodes = 1,
  ...
)
```

Arguments

- `x`: A `dnapath` object from `dnapath`.
- `alpha`: Threshold for p-values to infer differentially connected edges. If NULL (the default) then no edges are removed from the plot.
- `monotonized`: If TRUE, monotonized (i.e. step-down) p-values from the permutation test will be used.
- `only_dc`: If TRUE, only differentially connected edges will be shown; any edges that are present in both groups are hidden. If FALSE, the edges shared by both groups are shown. If a non-sparse estimator for network edges is used, then the graph may be dense and setting this argument to TRUE will be useful for highlighting the DC edges.
- `require_dc_genes`: If TRUE, the gene-level differential connectivity p-value of the two genes for a given edge are also considered when deciding whether an edge is differentially connected. If neither gene is significantly differentially connected, then the edge between them will not be either.
- `scale_edges`: (Optional) multiplier for edge widths.
- `scale_nodes`: (Optional) multiplier for node radius
- `...`: Additional arguments are passed into the plotting function `plot_network`.

Value

Plots the differential network and returns the graph object. See `plot_network` for details.

References


Examples

```r
data(meso)
data(p53_pathways)
```
```r
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
                     groups = meso$groups, n_perm = 10)
# Plot of the differential network for pathway 1.
plot(results[[1]])
# Plot of the differential network for pathway 1; remove any edges from
# the plot that have p-values above 0.1.
plot(results[[1]], alpha = 0.1)
```

---

**plot_pair**

### Plot the expression values of two genes

**Description**

Inspired by the plotCors function from the DGCA package, this function is used to plot the expression values of two genes contained in the differential network analysis results. This is useful for comparing the marginal relationship between two genes. Note, however, that this visualization is not able to show conditional associations.

**Usage**

```r
plot_pair(
  x,
  gene_A,
  gene_B,
  method = "loess",
  alpha = 0.5,
  se_alpha = 0.1,
  use_facet = FALSE,
  scales = "fixed"
)
```

**Arguments**

- `x`: A `dnapath` or `dnapath_list` object from `dnapath`.
- `gene_A`: The name of the first gene to plot. Must be one of the names in `get_genes(x)`.
- `gene_B`: The name of the second gene to plot. Must be one of the names in `get_genes(x)`.
- `method`: A character string, either "lm" or "loess" (the default) used by `geom_smooth` to summarize the marginal gene-gene association. For no line, set method = NULL.
- `alpha`: Sets the transparency of the points, used to set alpha in `geom_point`.
- `se_alpha`: Sets the transparency of the confidence band around the association trend line. Set to 0 to remove the band.
- `use_facet`: If TRUE, the groups are plotted in separate graphs using the link[ggplot2]{facet_wrap} method.
- `scales`: Only used if do_facet_wrap is TRUE. See link[ggplot2]{facet_wrap} for details.
Value

Plots the differential network and returns the ggplot object. Additional modifications can be applied to this object just like any other ggplot.

References


Examples

data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
groups = meso$groups, n_perm = 10)
# Plot of the marginal association between the first two genes.
genes <- get_genes(results)[1:2]
g <- plot_pair(results, genes[1], genes[2])
# The ggplot object, g, can be further modified.
# Here we move the legend and use a log scale for the expression values
# (the log scale doesn't help with these data but is shown for demonstration).
g <- g +
ggplot2::theme(legend.position = "bottom") +
ggplot2::scale_x_log10() +
ggplot2::scale_y_log10()
g

print.dnapath

Print function for 'dnapath' object.

Description

Print function for 'dnapath' object.

Usage

## S3 method for class 'dnapath'
print(x, ...)

Arguments

x A 'dnapath' object from dnapath.

... Additional arguments are ignored.

Value

Prints a summary of the module.
print.dnapath_list  
*Print function for 'dnapath_list' object.*

### Description

Print function for 'dnapath_list' object.

### Usage

```r
## S3 method for class 'dnapath_list'
print(x, ...)
```

### Arguments

- `x`  A 'dnapath_list' object from `dnapath`.
- `...` Additional arguments are ignored.

### Value

Prints a summary of the module.

---

rename_genes  *
*Rename genes in the differential network analysis*

### Description

Rename genes in the differential network analysis

### Usage

```r
rename_genes(x, gene_mat = NULL, to = NULL, species = NULL, ...)
```

### Arguments

- `x`  A 'dnapath_list' or 'dnapath' object from `dnapath`, a pathway list, or a vector of gene names.
- `gene_mat`  (Optional) A matrix of key value pairs. The first column should contain current gene names, and the second column the new names. Any genes that are not in this matrix will retain their current names. This can be any user-defined mapping, or the mapping obtained using `entrez_to_symbol` or `symbol_to_entrez`.
- `to`  (Optional) Setting `to = "symbol"` will rename entrezgene IDs to gene symbols; this will automatically call the `entrez_to_symbol()` function to obtain the mapping for `gene_mat`. The `species` argument must also be specified when `to` is used.
rev.dnapath_list

Reverse the order of pathways in a 'dnapath_list' object.

Description
Reverse the order of pathways in a 'dnapath_list' object.

Usage
## S3 method for class 'dnapath_list'
rev(x, ...)

Arguments
x  A 'dnapath_list' object from dnapath.
... Additional arguments are ignored.
run_aracne

Wrapper for ARACNE method

Description

Conducts co-expression analysis using ARACNE (Margolin et al. 2006). Uses the implementation from the minet package (Meyer et al. 2008). Can be used for the network_inference argument in dnapath.

Usage

run_aracne(
  x,
  estimator = "spearman",
  disc = "none",
  nbins = NULL,
  eps = 0,
  ...
)

Arguments

x A n by p matrix of gene expression data (n samples and p genes).
estimator Argument is passed into build.mim.
disc Argument is passed into build.mim.
nbins Argument is passed into build.mim.
eps Argument is passed into aracne.
... Additional arguments are ignored.

Value

A p by p matrix of association scores.
References


See Also

*run_bc3net*, *run_c3net*, *run_clr*, *run_corr*, *run_dwlasso*, *run_genie3*, *run_glasso*, *run_mrnet*, *run_pcor*, and *run_silencer*

Examples

data(meso)
data(p53_pathways)

# To create a short example, we subset on two pathways from the p53 pathway list, # and will only run 5 permutations for significance testing.
pathway_list <- p53_pathways[c(8, 13)]
n_perm <- 5

# Use this method to perform differential network analysis.
# The parameters in run_aracne() can be adjusted using the ... argument.
# For example, the 'estimator' parameter can be specified as shown here.
results <- dnapath(x = meso$gene_expression,
                   pathway_list = pathway_list,
                   groups = meso$groups,
                   n_perm = n_perm,
                   network_inference = run_aracne,
                   estimator = "spearman")

summary(results)

# The group-specific association matrices can be extracted using get_networks().
nw_list <- get_networks(results[[1]]) # Get networks for pathway 1.

# nw_list has length 2 and contains the inferred networks for the two groups.
# The gene names are the Entrezgene IDs from the original expression dataset.
# Renaming the genes in the dnapath results to rename those in the networks.
# NOTE: The temporary directory, tempdir(), is used in this example. In practice,
# this argument can be removed or changed to an existing directory
results <- rename_genes(results, to = "symbol", species = "human",
                        dir_save = tempdir())
nw_list <- get_networks(results[[1]]) # The genes (columns) will have new names.

# (Optional) Plot the network using SeqNet package (based on igraph plotting).
# First rename entrezgene IDs into gene symbols.
SeqNet::plot_network(nw_list[[1]])
run_bc3net  
Wrapper for BC3Net method

Description
Conducts co-expression analysis using BC3Net (Matos Simoes and Emmert-Streib 2012). Uses the implementation from the bc3net package (de Matos Simoes and Emmert-Streib 2016). Can be used for the network_inference argument in dnapath.

Usage

```r
run_bc3net(
  x,
  boot = 100,
  estimator = "spearman",
  disc = "equalwidth",
  mtc1 = TRUE,
  adj1 = "bonferroni",
  alpha1 = 0.05,
  mtc2 = TRUE,
  adj2 = "bonferroni",
  alpha2 = 0.05,
  ...)
```

Arguments

- **x**: A n by p matrix of gene expression data (n samples and p genes).
- **boot**: Argument is passed into bc3net.
- **estimator**: Argument is passed into bc3net.
- **disc**: Argument is passed into bc3net.
- **mtc1**: Argument is passed into bc3net.
- **adj1**: Argument is passed into bc3net.
- **alpha1**: Argument is passed into bc3net.
- **mtc2**: Argument is passed into bc3net.
- **adj2**: Argument is passed into bc3net.
- **alpha2**: Argument is passed into bc3net.
- **...**: Additional arguments are ignored.

Value

A p by p matrix of association scores.
run_bc3net

References


See Also

*run_aracne, run_c3net, run_clr, run_corr, run_dwllasso, run_genie3, run_glasso, run_mrnet, run_pcor, and run_silencer*

Examples

```r
data(meso)
data(p53_pathways)

# To create a short example, we subset on one pathway from the p53 pathway list, # and will only run 1 permutation for significance testing.
pathway_list <- p53_pathways[13]
n_perm <- 1

# Use this method to perform differential network analysis. # The parameters in run_bc3net() can be adjusted using the ... argument. # For example, the ’estimator’ and ’boot’ parameter can be specified as shown here.
results <- dnapath(x = meso$gene_expression, 
pathway_list = pathway_list, 
groups = meso$groups, 
n_perm = n_perm, 
network_inference = run_bc3net, 
boot = 10, 
estimator = "pearson", 
mtc1 = FALSE, 
mtc2 = FALSE)

summary(results)

# The group-specific association matrices can be extracted using get_networks().
nw_list <- get_networks(results) # Get networks for pathway 1.

# nw_list has length 2 and contains the inferred networks for the two groups. # The gene names are the Entrezgene IDs from the original expression dataset. # Renaming the genes in the dnapath results to rename those in the networks. # NOTE: The temporary directory, tempdir(), is used in this example. In practice, # this argument can be removed or changed to an existing directory
results <- rename_genes(results, to = "symbol", species = "human", 
dir_save = tempdir())
nw_list <- get_networks(results) # The genes (columns) will have new names.

# (Optional) Plot the network using SeqNet package (based on igraph plotting). # First rename entrezgene IDs into gene symbols.
SeqNet::plot_network(nw_list[[1]])```
run_c3net  

Wrapper for C3Net method

Description

Conducts co-expression analysis using C3Net (Altay and Emmert-Streib 2010). Uses the implementation from the bc3net package (de Matos Simoes and Emmert-Streib 2016). Can be used for the network_inference argument in dnapath.

Usage

run_c3net(
  x,
  estimator = "spearman",
  disc = "equalwidth",
  mtc = TRUE,
  adj = "bonferroni",
  alpha = 0.05,
  ...)

Arguments

  x  A n by p matrix of gene expression data (n samples and p genes).
  estimator  Argument is passed into c3mtc.
  disc  Argument is passed into c3mtc.
  mtc  Argument is passed into c3mtc.
  adj  Argument is passed into c3mtc.
  alpha  Argument is passed into c3mtc.
  ...  Additional arguments are ignored.

Value

  A p by p matrix of association scores.

References


run_clr

See Also

run_aracne, run_bc3net, run_clr, run_corr, run_dwlasso, run_genie3, run_glasso, run_mrnet, run_pcor, and run_silencer

Examples

data(meso)
data(p53_pathways)

# To create a short example, we subset on one pathway from the p53 pathway list,
# and will only run 1 permutation for significance testing.
pathway_list <- p53_pathways[13]
n_perm <- 1

# Use this method to perform differential network analysis.
# The parameters in run_c3net() can be adjusted using the ... argument.
# For example, the `estimator` parameter can be specified as shown here.
results <- dnapath(x = meso$gene_expression,
                   pathway_list = pathway_list,
                   groups = meso$groups,
                   n_perm = n_perm,
                   network_inference = run_c3net,
                   estimator = "pearson",
                   mtc = FALSE)
summary(results)

# The group-specific association matrices can be extracted using get_networks().
nw_list <- get_networks(results) # Get networks for the pathway.

# nw_list has length 2 and contains the inferred networks for the two groups.
# The gene names are the Entrezgene IDs from the original expression dataset.
# Renaming the genes in the dnapath results to rename those in the networks.
# NOTE: The temporary directory, tempdir(), is used in this example. In practice,
# this argument can be removed or changed to an existing directory
results <- rename_genes(results, to = "symbol", species = "human",
                        dir_save = tempdir())
nw_list <- get_networks(results) # The genes (columns) will have new names.

# (Optional) Plot the network using SeqNet package (based on igraph plotting).
# First rename entrezgene IDs into gene symbols.
SeqNet::plot_network(nw_list[[1]])
Description

Conducts co-expression analysis using CLR (Faith et al. 2007). Uses the implementation from the minet package (Meyer et al. 2008). Can be used for the network_inference argument in dnapath.

Usage

run_clr(x, estimator = "spearman", ...)

Arguments

x
A n by p matrix of gene expression data (n samples and p genes).
estimator
Argument is passed into build.mim.
...
Additional arguments are ignored.

Value

A p by p matrix of association scores.

References


See Also

run_aracne, run_bc3net, run_c3net, run_corr, run_dwlasso, run_genie3, run_glasso, run_mrnet, run_pcor, and run_silencer

Examples

data(meso)
data(p53_pathways)

# To create a short example, we subset on two pathways from the p53 pathway list, # and will only run 5 permutations for significance testing.
pathway_list <- p53_pathways[c(8, 13)]
n_perm <- 5

# Use this method to perform differential network analysis. # The parameters in run_clr() can be adjusted using the ... argument. # For example, the 'estimator' parameter can be specified as shown here.
results <- dnapath(x = meso$gene_expression, 
    pathway_list = pathway_list, 
    groups = meso$groups, 
    n_perm = n_perm, 
    network_inference = run_clr, 

run_corr

estimator = "spearman")

summary(results)

# The group-specific association matrices can be extracted using get_networks().
nw_list <- get_networks(results[[1]]) # Get networks for pathway 1.

# nw_list has length 2 and contains the inferred networks for the two groups.
# The gene names are the Entrezgene IDs from the original expression dataset.
# Renaming the genes in the dnapath results to rename those in the networks.
# NOTE: The temporary directory, tempdir(), is used in this example. In practice,
# this argument can be removed or changed to an existing directory
results <- rename_genes(results, to = "symbol", species = "human",
   dir_save = tempdir())
nw_list <- get_networks(results[[1]]) # The genes (columns) will have new names.

# (Optional) Plot the network using SeqNet package (based on igraph plotting).
# First rename entrezgene IDs into gene symbols.
SeqNet::plot_network(nw_list[[1]])

run_corr

Wrapper for correlation co-expression

Description
Conducts co-expression analysis using correlation for association measure. Can be used for the
network_inference argument in dnapath.

Usage
run_corr(x, threshold = NULL, method = c("pearson", "spearman"), ...)

Arguments

x A n by p matrix of gene expression data (n samples and p genes).
threshold Cutoff for significant associations. If NULL, all correlations are returned. Oth-
   erwise, correlations of magnitude at or below this threshold are set to zero.
method Argument is passed into cor. Should be one of "pearson" or "spearman".
... Additional arguments are ignored.

Value
A p by p matrix of association scores.

See Also
run_aracne, run_bc3net, run_c3net, run_clr, run_dwlasso, run_genie3, run_glasso, run_mrnet,
run_pcor, and run_silencer
Examples

data(meso)
data(p53_pathways)

# To create a short example, we subset on two pathways from the p53 pathway list,
# and will only run 5 permutations for significance testing.
pathway_list <- p53_pathways[c(8, 13)]
n_perm <- 5

# Use this method to perform differential network analysis.
# The parameters in run_corr() can be adjusted using the ... argument.
# For example, the 'method' parameter can be specified as shown here.
results <- dnapath(x = meso$gene_expression,
                  pathway_list = pathway_list,
                  groups = meso$groups,
                  n_perm = n_perm,
                  network_inference = run_corr,
                  method = "spearman")

summary(results)

# The group-specific association matrices can be extracted using get_networks().
nw_list <- get_networks(results[[1]]) # Get networks for pathway 1.

# nw_list has length 2 and contains the inferred networks for the two groups.
# The gene names are the Entrezgene IDs from the original expression dataset.
# Renaming the genes in the dnapath results to rename those in the networks.
# NOTE: The temporary directory, tempdir(), is used in this example. In practice,
# this argument can be removed or changed to an existing directory
results <- rename_genes(results, to = "symbol", species = "human",
                        dir_save = tempdir())

nw_list <- get_networks(results[[1]]) # The genes (columns) will have new names.

# (Optional) Plot the network using SeqNet package (based on igraph plotting).
# First rename entrezgene IDs into gene symbols.
SeqNet::plot_network(nw_list[[1]])

run_dwlasso

Wrapper for degree-weighted lasso method

Description

Conducts co-expression analysis using DWLasso (Sulaimanov et al. 2018). Uses the implementation
from the DWLasso package (Sulaimanov et al. 2017). Can be used for the network_inference
argument in dnapath.

Usage

run_dwlasso(x, lambda1 = 0.4, lambda2 = 2, ...)
**Arguments**

- **x**: A n by p matrix of gene expression data (n samples and p genes).
- **lambda1**: A penalty parameter that controls degree sparsity of the inferred network. See `DWLasso` for details.
- **lambda2**: A penalty parameter that controls overall sparsity of the inferred network. See `DWLasso` for details.
- **...**: Additional arguments are ignored.

**Value**

A p by p matrix of association scores.

**References**


**See Also**

`run_aracne`, `run_bc3net`, `run_c3net`, `run_clr`, `run_corr`, `run_genie3`, `run_glasso`, `run_mrnet`, `run_pcor`, and `run_silencer`

**Examples**

data(meso)
data(p53_pathways)

# To create a short example, we subset on two pathways from the p53 pathway list,
# and will only run 1 permutation for significance testing.
pathway_list <- p53_pathways[c(8, 13)]
n_perm <- 1

# Use this method to perform differential network analysis.
# The parameters in run_dwlasso() can be adjusted using the ... argument.
# For example, the 'lambda1' parameter can be specified as shown here.
results <- dnapath(x = meso[, gene_expression],
                   pathway_list = pathway_list,
                   groups = meso[, groups],
                   n_perm = n_perm,
                   network_inference = run_dwlasso,
                   lambda1 = 0.5)

summary(results)

# The group-specific association matrices can be extracted using get_networks().
mw_list <- get_networks(results[[1]]) # Get networks for pathway 1.
# nw_list has length 2 and contains the inferred networks for the two groups.
# The gene names are the Entrezgene IDs from the original expression dataset.
# Renaming the genes in the dnapath results to rename those in the networks.
# NOTE: The temporary directory, tempdir(), is used in this example. In practice,
# this argument can be removed or changed to an existing directory
results <- rename_genes(results, to = "symbol", species = "human",
dir_save = tempdir())
nw_list <- get_networks(results[[1]]) # The genes (columns) will have new names.

# (Optional) Plot the network using SeqNet package (based on igraph plotting).
# First rename entrezgene IDs into gene symbols.
SeqNet::plot_network(nw_list[[1]])

run_genie3  
Wrapper for GENIE3 method

Description
Conducts co-expression analysis using GENIE3 (Huynh-Thu et al. 2010). Uses the implementation
from the GENIE3 package. Can be used for the network_inference argument in dnapath.

Usage
run_genie3(x, nTrees = 200, ...)

Arguments

x  A n by p matrix of gene expression data (n samples and p genes).
nTrees  Argument is passed into GENIE3.
...  Additional arguments are ignored.

Value
A p by p matrix of association scores.

References
Expression Data using Tree-Based Methods.” Plos ONE, 5(9), e12776.

See Also
run_aracne, run_bc3net, run_c3net, run_clr, run_corr, run_dwlasso, run_glasso, run_mrnet,
run_pcor, and run_silencer
Examples

```r
if(!requireNamespace("GENIE3", quietly = TRUE)) {
  data(meso)
  data(p53_pathways)

  # To create a short example, we subset on two pathways from the p53 pathway list,
  # and will only run 5 permutations for significance testing.
  pathway_list <- p53_pathways[c(8, 13)]
  n_perm <- 5

  # Use this method to perform differential network analysis.
  # The parameters in run_genie3() can be adjusted using the ... argument.
  # For example, the 'nTrees' parameter can be specified as shown here.
  results <- dnapath(x = meso$gene_expression,
                      pathway_list = pathway_list,
                      groups = meso$groups,
                      n_perm = n_perm,
                      network_inference = run_genie3,
                      nTrees = 100)
  summary(results)

  # The group-specific association matrices can be extracted using get_networks().
  nw_list <- get_networks(results[[1]]) # Get networks for pathway 1.

  # nw_list has length 2 and contains the inferred networks for the two groups.
  # The gene names are the Entrezgene IDs from the original expression dataset.
  # Renaming the genes in the dnapath results to rename those in the networks.
  # NOTE: The temporary directory, tempdir(), is used in this example. In practice,
  # this argument can be removed or changed to an existing directory
  results <- rename_genes(results, to = "symbol", species = "human",
                          dir_save = tempdir())
  nw_list <- get_networks(results[[1]]) # The genes (columns) will have new names.

  # (Optional) Plot the network using SeqNet package (based on igraph plotting).
  # First rename entrezgene IDs into gene symbols.
  SeqNet::plot_network(nw_list[[1]])
}
```

---

**run_glasso**

*Wrapper for glasso method*

**Description**

Conducts co-expression analysis using glasso (Friedman et al. 2018). Uses the implementation from the huge package (Jiang et al. 2019). Can be used for the network_inference argument in dnapath.
run_glasso

Usage

run_glasso(
  x,
  method = c("glasso", "mb", "ct"),
  criterion = c("ric", "stars"),
  verbose = FALSE,
  ...
)

Arguments

- x: A n by p matrix of gene expression data (n samples and p genes).
- method: Argument is passed into huge.
- criterion: Argument is passed into huge.select.
- verbose: Argument is passed into huge and huge.select
- ...: Additional arguments are ignored.

Value

A p by p matrix of association scores.

References


See Also

run_aracne, run_bc3net, run_c3net, run_clr, run_corr, run_dwlasso, run_genie3, run_mrnet, run_pcor, and run_silencer

Examples

data(meso)
data(p53_pathways)

# To create a short example, we subset on one pathway from the p53 pathway list,
# and will only run 1 permutation for significance testing.
pathway_list <- p53_pathways[13]
n_perm <- 1

# Use this method to perform differential network analysis.
# The parameters in run_glasso() can be adjusted using the ... argument.
# For example, the 'criterion' parameter can be specified as shown here.
results <- dnapath(x = meso$gene_expression,
                   pathway_list = pathway_list,
groups = meso$groups,
n_perm = n_perm,
network_inference = run_glasso,
criterion = "ric")

summary(results)

# The group-specific association matrices can be extracted using get_networks().
nw_list <- get_networks(results) # Get networks for pathway 1.

# nw_list has length 2 and contains the inferred networks for the two groups.
# The gene names are the Entrezgene IDs from the original expression dataset.
# Renaming the genes in the dnapath results to rename those in the networks.
# NOTE: The temporary directory, tempdir(), is used in this example. In practice,
# this argument can be removed or changed to an existing directory
results <- rename_genes(results, to = "symbol", species = "human",
dir_save = tempdir())
nw_list <- get_networks(results) # The genes (columns) will have new names.

# (Optional) Plot the network using SeqNet package (based on igraph plotting).
# First rename entrezgene IDs into gene symbols.
SeqNet::plot_network(nw_list[[1]])

---

**run_mrnet**

*Wrapper for MRNET method*

**Description**

Conducts co-expression analysis using MRNET (Meyer et al. 2007). Uses the implementation from the `minet` package (Meyer et al. 2008). Can be used for the `network_inference` argument in `dnapath`.

**Usage**

```r
run_mrnet(x, estimator = "spearman", ...)
```

**Arguments**

- `x` : A n by p matrix of gene expression data (n samples and p genes).
- `estimator` : Argument is passed into `build.mim`.
- `...` : Additional arguments are ignored.

**Value**

A p by p matrix of association scores.
References


See Also

run_aracne, run_bc3net, run_c3net, run_clr, run_corr, run_dwlasso, run_genie3, run_glasso, run_pcor, and run_silencer

Examples

data(meso)
data(p53_pathways)

# To create a short example, we subset on two pathways from the p53 pathway list, # and will only run 3 permutations for significance testing.
pathway_list <- p53_pathways[c(8, 13)]
n_perm <- 3

# Use this method to perform differential network analysis.
# The parameters in run_mrnet() can be adjusted using the ... argument.
# For example, the 'estimator' parameter can be specified as shown here.
results <- dnapath(x = meso$gene_expression,
                   pathway_list = pathway_list,
                   groups = meso$groups,
                   n_perm = n_perm,
                   network_inference = run_mrnet,
                   estimator = "spearman")

summary(results)

# The group-specific association matrices can be extracted using get_networks().
nw_list <- get_networks(results[[1]]) # Get networks for pathway 1.

# nw_list has length 2 and contains the inferred networks for the two groups.
# The gene names are the Entrezgene IDs from the original expression dataset.
# Renaming the genes in the dnapath results to rename those in the networks.
# NOTE: The temporary directory, tempdir(), is used in this example. In practice,
# this argument can be removed or changed to an existing directory
results <- rename_genes(results, to = "symbol", species = "human",
                         dir_save = tempdir())
nw_list <- get_networks(results[[1]]) # The genes (columns) will have new names.

# (Optional) Plot the network using SeqNet package (based on igraph plotting).
# First rename entrezgene IDs into gene symbols.
SeqNet::plot_network(nw_list[[1]])
**Description**

Conducts co-expression analysis using full partial correlations; these are computed using the shrinkage approach for covariance estimation (Schäfer and Strimmer 2005) from the corpcor package (Schafer et al. 2017). Can be used for the network_inference argument in dnapath.

**Usage**

```r
run_pcor(x, ranks = TRUE, verbose = FALSE, ...)
```

**Arguments**

- `x`: A n by p matrix of gene expression data (n samples and p genes).
- `ranks`: If TRUE, the gene expression values will be converted to ranks (across samples) prior to covariance estimation.
- `verbose`: Argument is passed into pcor.shrink.
- `...`: Additional arguments are ignored.

**Value**

A p by p matrix of association scores.

**References**


**See Also**

`run_aracne`, `run_bc3net`, `run_c3net`, `run_clr`, `run_corr`, `run_dwlasso`, `run_genie3`, `run_glasso`, `run_mrnet`, and `run_silencer`

**Examples**

```r
data(meso)
data(p53_pathways)

# To create a short example, we subset on two pathways from the p53 pathway list,
# and will only run 3 permutations for significance testing.
pathway_list <- p53_pathways[c(8, 13)]
```
n_perm <- 3

# Use this method to perform differential network analysis.
results <- dnapath(x = meso$gene_expression,
                    pathway_list = pathway_list,
                    groups = meso$groups,
                    n_perm = n_perm,
                    network_inference = run_pcor)
summary(results)

# The group-specific association matrices can be extracted using get_networks().
w_list <- get_networks(results[[1]]) # Get networks for pathway 1.

# nw_list has length 2 and contains the inferred networks for the two groups.
# The gene names are the Entrezgene IDs from the original expression dataset.
# Renaming the genes in the dnapath results to rename those in the networks.
# NOTE: The temporary directory, tempdir(), is used in this example. In practice,
# this argument can be removed or changed to an existing directory
results <- rename_genes(results, to = "symbol", species = "human",
                        dir_save = tempdir())
w_list <- get_networks(results[[1]]) # The genes (columns) will have new names.

# (Optional) Plot the network using SeqNet package (based on igraph plotting).
# First rename entrezgene IDs into gene symbols.
SeqNet::plot_network(nw_list[[1]])

---

**run_pcor_fdr**

*Wrapper for partial correlations with Empirical Bayes FDR correction*

**Description**

Conducts co-expression analysis using full partial correlations; these are computed using the shrinkage approach for covariance estimation (Schäfer and Strimmer 2005) from the corpcor package (Schafer et al. 2017). Can be used for the network_inference argument in dnapath. This method will use Empirical Bayes FDR to set some estimates to zero.

**Usage**

`run_pcor_fdr(x, ranks = TRUE, thrsh = 1.5, verbose = FALSE, ...)`

**Arguments**

- `x` A n by p matrix of gene expression data (n samples and p genes).
- `ranks` If TRUE, the gene expression values will be converted to ranks (across samples) prior to covariance estimation.
thresh  A positive value (defaults to 1.5). This is used as the cutoff for the likelihood ratio of the estimate local FDR.
verbose  Argument is passed into `pcor.shrink`.

Additional arguments are ignored.

Value

A p by p matrix of association scores.

References


See Also

`run_aracne`, `run_bc3net`, `run_c3net`, `run_clr`, `run_corr`, `run_dwlasso`, `run_genie3`, `run_glasso`, `run_mrnet`, and `run_silencer`

Examples

data(meso)
data(p53_pathways)

# To create a short example, we subset on two pathways from the p53 pathway list, # and will only run 3 permutations for significance testing.
pathway_list <- p53_pathways[c(8, 13)]
n_perm <- 3

# Use this method to perform differential network analysis.
results <- dnapath(x = meso$gene_expression,
                   pathway_list = pathway_list,
                   groups = meso$groups,
                   n_perm = n_perm,
                   network_inference = run_pcor)

summary(results)

# The group-specific association matrices can be extracted using get_networks().
nw_list <- get_networks(results[[1]])  # Get networks for pathway 1.

# nw_list has length 2 and contains the inferred networks for the two groups.
# The gene names are the Entrezgene IDs from the original expression dataset.
# Renaming the genes in the dnapath results to rename those in the networks.
# NOTE: The temporary directory, tempdir(), is used in this example. In practice,
# this argument can be removed or changed to an existing directory
results <- rename_genes(results, to = "symbol", species = "human")
run_silencer

Description

Conducts co-expression analysis using the matrix silencer method (Barzel and Barabási 2013). Can be used for the network_inference argument in dnapath.

Usage

run_silencer(x, method = "spearman", verbose = FALSE, ...)

Arguments

- **x**: A n by p matrix of gene expression data (n samples and p genes).
- **method**: Argument is passed into cor.
- **verbose**: If TRUE, updates are printed during the estimation process.
- **...**: Additional arguments are ignored.

Value

A p by p matrix of association scores.

References


See Also

run_aracne, run_bc3net, run_c3net, run_clr, run_corr, run_dwlasso, run_genie3, run_glasso, run_mrnet, and run_pcor
sort.dnapath_list

Sort function for 'dnapath_list' object.

Description

Sort function for 'dnapath_list' object.

Usage

## S3 method for class 'dnapath_list'
sort(x, decreasing = TRUE, by = "dc_score", ...)

Examples

data(meso)
data(p53_pathways)

# To create a short example, we subset on two pathways from the p53 pathway list,
# and will only run 1 permutation for significance testing.
pathway_list <- p53_pathways[13]
n_perm <- 1

# Use this method to perform differential network analysis.
# The parameters in run_silencer() can be adjusted using the ... argument.
# For example, the 'method' parameter can be specified as shown here.
results <- dnapath(x = meso$gene_expression,
                   pathway_list = pathway_list,
                   groups = meso$groups,
                   n_perm = n_perm,
                   network_inference = run_silencer,
                   method = "spearman")
summary(results)

# The group-specific association matrices can be extracted using get_networks().
nw_list <- get_networks(results) # Get networks for the pathway

# nw_list has length 2 and contains the inferred networks for the two groups.
# The gene names are the Entrezgene IDs from the original expression dataset.
# Renaming the genes in the dnapath results to rename those in the networks.
# NOTE: The temporary directory, tempdir(), is used in this example. In practice,
# this argument can be removed or changed to an existing directory
results <- rename_genes(results, to = "symbol", species = "human",
                       dir_save = tempdir())
nw_list <- get_networks(results) # The genes (columns) will have new names.

# (Optional) Plot the network using SeqNet package (based on igraph plotting).
# First rename entrezgene IDs into gene symbols.
SeqNet::plot_network(nw_list[[1]])
Arguments

x  A 'dnapath_list' object from dnapath.
decreasing Logical. If TRUE (the default), results are sorted in decreasing order.
by  The variable to sort the results by. Must be one of: "mean_expr", the mean expression of each pathway across both groups; "mean_expr1" or "mean_expr2", the mean expression of each pathway in group 1 or 2, respectively; "dc_score", the differential connectivity score of the pathway; "p_value", the p-value of the dc score; "n_genes", the number of genes in each pathway; "pathway", the pathway names; or "n_dc" the number of significantly differentially connected genes in each pathway.

...  Additional arguments are ignored.

Value

The differential network analysis results ordered by DC pathway score.

Examples

data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
groups = meso$groups, n_perm = 10)
# Filter out pathways that have p-values above 0.2.
results_sig <- filter_pathways(results, 0.2)
sort(results_sig, by = "dc_score") # Sort by the pathway DC score.
sort(results_sig, by = "n_genes") # Sort by the pathway size.
sort(results_sig, by = "mean_expr") # Sort by the mean expression.

subset.dnapath_list  Subset function for 'dnapath_list' object.

Description

Subset function for 'dnapath_list' object.

Usage

## S3 method for class 'dnapath_list'
subset(x, pathways = NULL, genes = NULL, ...)

Arguments

x  A 'dnapath_list' object from dnapath.
pathways A set of pathways to index on. This can be (1) a vector of character strings, corresponding to pathway names or regular expressions used to find pathways, (2) a vector of indices to select pathways, (3) a vector of negative indices indicating pathways to remove, or (4) a logical (boolean) vector that is the same length of current number of pathways in x.

genes A set of gene names to index on; exact matching is used. Only pathways containing these genes are retained.

... Additional arguments are ignored.

Value A subset of the differential network analysis results.

Examples

data(meso)
# Obtain a pathway list for this short example:
pathway_list <- get_reactome_pathways("human", overlap_limit = NULL,
  min_size = 13, max_size = 19)

# Run the differential network analysis.
results <- dnapath(x = meso$gene_expression, pathway_list = pathway_list,
  groups = meso$groups, n_perm = 5, seed = 0)
summary(results) # Summary over all pathways in the pathway list.

# Subset on pathways that contain "cell cycle" in its name.
cell_cycle_pathways <- subset(results, pathways = "cell cycle")
summary(cell_cycle_pathways)

# Subset on pathways that contain the gene 1026 (Entrezgene ID).
pathways_with_1026 <- subset(results, genes = "1026")
summary(pathways_with_1026)

# Multiple pathways and/or genes can also be specified.
# Specifying both acts as an "OR" operation. For example, the following subset
# will contain pathways containing the words "acetylation" or "methylation"
# OR pathways that contain the genes "1108" or "11200".
results_OR <- subset(results,
  pathways = c("acetylation", "methylation"),
  genes = c("1108", "11200"))
summary(results_OR)

# To subset on pathways that have both a specific pathway name AND
# certain genes, call the subset function twice: once specifying the
# 'pathways' argument, then pass those results back into subset() with the
# 'genes' argument specified. For example:
results_AND <- subset(results,
  pathways = c("acetylation", "methylation"))
results_AND <- subset(results_AND,
  genes = c("1108", "11200"))
summary(results_AND)
summarize_edges  Summarize differential connections for a pathway

Description
Summarize differential connections for a pathway

Usage
summarize_edges(x, alpha = NULL, monotonized = FALSE, require_dc_genes = FALSE)

Arguments
x  A ‘dnapath’ object from dnapath.
alpha  Threshold for p-values of edge DC scores. If NULL, defaults to 0.05 or the minimum possible threshold (based on the number of permutations that were run).
monotonized  If TRUE, monotonized p-values are used.
require_dc_genes  If TRUE, the gene-level differential connectivity p-value of the two genes for a given edge are also considered when deciding whether an edge is differentially connected. If neither gene is significantly differentially connected, then the edge between them will not be either.

Value
A tibble summarizing the differential connections in the pathway.

See Also
summarize_pathways, summarize_genes

Examples
data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
                   groups = meso$groups, n_perm = 10)
summarize_edges(results[[1]])
Summarize the differential connectivity of genes over all pathways.

Description

Summarize the differential connectivity of genes over all pathways.

Usage

```r
summarize_genes(x, alpha = NULL, monotonized = FALSE)
```

Arguments

- `x`: A `dnapath_list` object from `dnapath`.
- `alpha`: Threshold for p-values of gene DC scores. Used to determine the number of pathways that each gene is differentially connected in. If NULL, defaults to 0.05 or the minimum possible threshold (based on the number of permutations that were run).
- `monotonized`: If TRUE, monotonized p-values are used.

Value

A tibble summarizing the differential connectivity of genes across all pathways.

See Also

`summarize_pathways`, `summarize_edges`

Examples

```r
data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways, 
groups = meso$groups, n_perm = 10)
summarize_genes(results) # Summary of genes across all pathways.
summarize_genes(results[[1]]) # Summary of genes within the first pathway.
```
summarize_pathways  

**Summarize the differential connectivity of pathways.**

**Description**

Summarize the differential connectivity of pathways.

**Usage**

```r
genes <- summarize_pathways(x, alpha = NULL, alpha_gene = NULL, monotonized = FALSE)
```

**Arguments**

- `x`  
  A `dnapath_list` object from `dnapath`.

- `alpha`  
  Threshold for p-values of pathway DC scores. If NULL (or 1), results for all pathways are shown.

- `alpha_gene`  
  Threshold for p-values of gene DC scores. Used to determine the number of genes that are differentially connected within each pathway. If NULL, defaults to 0.05 or the minimum possible threshold (based on the number of permutations that were run).

- `monotonized`  
  If TRUE, monotonized p-values are used.

**Value**

A tibble summarizing the differential connectivity of genes in the pathway.

**See Also**

- `summarize_genes`, `summarize_edges`

**Examples**

```r
data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
groups = meso$groups, n_perm = 10)
summarize_pathways(results)
```
summary.dnapath

Summary function for 'dnapath' object.

Description

Summary function for 'dnapath' object.

Usage

```r
## S3 method for class 'dnapath'
summary(object, by_gene = TRUE, alpha = NULL, monotonized = FALSE, ...)
```

Arguments

- `object` A 'dnapath' object from `dnapath`.
- `by_gene` If TRUE, summarizes the differential network analysis by genes; otherwise, summarizes by gene-gene interactions.
- `alpha` Threshold for p-values to determine significance; defaults to 1 and returns all results. If 'by_gene' is FALSE, then 'alpha' is used to filter edges. If 'by_gene' is TRUE, then 'alpha' is used to filter genes.
- `monotonized` If TRUE, monotonized p-values are used.
- `...` Additional arguments are ignored.

Value

Summarizes the differential network analysis result.

See Also

- `summarize_genes`, `summarize_edges`

Examples

```r
data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
groups = meso$groups, n_perm = 10)
summary(results[[1]]) # Summary of the first pathway in the results.
```
Summary function for 'dnapath_list' object.

## S3 method for class 'dnapath_list'
summary(
  object,
  by_gene = FALSE,
  alpha_pathway = NULL,
  alpha_gene = NULL,
  monotonized = FALSE,
  ...
)

**Arguments**

- `object`: A 'dnapath_list' object from `dnapath`.
- `by_gene`: If TRUE, summarizes the differential network analysis by genes instead of by pathways.
- `alpha_pathway`: Threshold for p-values of pathway DC scores; used to subset the results. If NULL (or 1), results for all pathways are shown.
- `alpha_gene`: Threshold for p-values of gene DC scores. Used to determine the number of genes that are differentially connected within each pathway. If NULL, defaults to 0.05 or the minimum possible threshold (based on the number of permutations that were run).
- `monotonized`: If TRUE, monotonized p-values are used.
- `...`: Additional arguments are ignored.

**Value**

Summarizes the differential network analysis results.

**See Also**

`summarize_pathways`, `summarize_genes`
symbol_to_entrez

Examples

```r
data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways, 
groups = meso$groups, n_perm = 10)
summary(results) # Summary across all pathways in the analysis.
```

symbol_to_entrez  Obtain entrezgene IDs for gene symbols

Description

Uses biomaRt (Durinck et al. 2009) to map entrezgene IDs to gene symbols for a given species.
The output of this function can be used in `rename_genes`.

Usage

```r
symbol_to_entrez(
  x, 
  species, 
  symbol_name = NULL, 
  dir_save = tempdir(), 
  verbose = TRUE 
)
```

Arguments

- `x` A vector of gene symbols.
- `species` The species used to obtain the entrezgene IDs. For example: "Homo sapiens", "m musculus", "C. elegans", or "S cerevisiae". "Human" and "mouse" can also be used and will be converted to the correct species name.
- `symbol_name` The type of gene symbol to use. If NULL, then "hgnc_symbol" is used for HGNC symbols, unless species is "mmusculus", in which case "mgi_symbol" is used.
- `dir_save` The directory to store annotation reference. Future calls to this function will use the stored annotations. This speeds up the operation and allows for reproducibility in the event that the biomaRt database is updated. Set to NULL to disable. By default, it uses a temporary directory to store files during the R session.
- `verbose` Set to FALSE to avoid messages.

Details

If entrezgene IDs are used in a dnapath_list or dnapath object, or a pathway list, then `get_genes` can be used to extract them and used for the `x` argument here.
Value

A data frame with two columns: the first contains the original gene symbols, and the second contains a corresponding entrezgene ID. If a gene symbol is not mapped to an entrezgene ID, the entrezgene ID is set to -1.

Note

Internet connection is required to connect to biomaRt. If unavailable, the default biomart and default species contained in the package is used, but this may not match the desired species.

It is assumed that x contains MGI symbols when the biomart species is "Mus musculus" and HGNC symbols otherwise.

References


See Also

entrez_to_symbol, get_genes

Examples

```r
# Convert a set of gene symbols to entrezgene IDs.
# Note that not all may have mapping (such as "MSX" in this example).
gene_mat <- symbol_to_entrez(c("SOX2", "SEMA3E", "COL11A1", "UBB", "MSX"),
                             species = "human")
```

Description

Return the last part of the dnapath results.

Usage

```r
#' S3 method for class 'dnapath_list'
tail(x, ...)
```

Arguments

- `x`  
  A 'dnapath_list' object.
- `...`  
  Additional parameters are passed into `summary.dnapath_list`. 
Value

Returns the last five rows of the summary table of the ‘dnapath_list’ object.

Examples

data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
                   groups = meso$groups, n_perm = 10)
tail(results)

[.dnapath

Extract results of a single pathway from a ‘dnapath’ object.

Description

Extract results of a single pathway from a ‘dnapath’ object.

Usage

## S3 method for class ‘dnapath’
x[i, ...]

Arguments

x     A ‘dnapath’ object.
i     The index specifying which pathway to extract.
...   Additional arguments are ignored.

Value

The ‘dnapath’ object unmodified

Note

In the current implementation, there is nothing to subset on for individual pathway results, so the
original object is returned unmodified.

Examples

data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways[[1]],
                   groups = meso$groups, n_perm = 10)
results[1]
[.dnapath_list

Extract parts of a 'dnapath_list' object.

Description
Extract parts of a 'dnapath_list' object.

Usage
## S3 method for class 'dnapath_list'
x[i, ...]

Arguments
x
A 'dnapath_list' object from dnapath.
i
The indices of pathways to extract.
...
Additional arguments are ignored.

Value
A 'dnapath_list' object containing pathways indexed by 'i'.

[<-.dnapath

Replace parts of a 'dnapath' object.

Description
This functionality is not implemented and will return an error.

Usage
## S3 replacement method for class 'dnapath'
x[...] <- value

Arguments
x
A 'dnapath' object from dnapath.
...
Additional arguments are ignored.
value
A 'dnapath' object.

Value
Replacement is not defined; an error is generated.
[<-\.dnapath_list

Replace parts of a \texttt{\`dnapath\_list\'} object.

\section*{Description}

This functionality is not implemented and will return an error.

\section*{Usage}

\#\# S3 replacement method for class \texttt{\`dnapath\_list\'}
\>[\ldots] <- value

\section*{Arguments}

\begin{itemize}
  \item \texttt{x} \hspace{1cm} A \texttt{\`dnapath\_list\'} object from \texttt{\texttt{\`dnapath}.}
  \item \texttt{\ldots} \hspace{.5cm} Additional arguments are ignored.
  \item \texttt{value} \hspace{.5cm} A \texttt{\`dnapath\_list\'} object.
\end{itemize}

\section*{Value}

Replacement is not defined; an error is generated.

[[\.dnapath

Extract results of a single pathway from a \texttt{\`dnapath\'} object.

\section*{Description}

Extract results of a single pathway from a \texttt{\`dnapath\'} object.

\section*{Usage}

\#\# S3 method for class \texttt{\`dnapath\'}
\>[\[i, \ldots]]

\section*{Arguments}

\begin{itemize}
  \item \texttt{x} \hspace{1cm} A \texttt{\`dnapath\'} object.
  \item \texttt{i} \hspace{1cm} The index specifying which pathway to extract.
  \item \texttt{\ldots} \hspace{.5cm} Additional arguments are ignored.
\end{itemize}

\section*{Value}

The \texttt{\`dnapath\'} object unmodified
Note

In the current implementation, there is nothing to subset on for individual pathway results, so the original object is returned unmodified.

Examples

data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways[[1]],
                groups = meso$groups, n_perm = 10)
results[[1]]

[[.dnaphath_list

Extract results of a single pathway from a 'dnaphath_list' object.

Description

Extract results of a single pathway from a 'dnaphath_list' object.

Usage

## S3 method for class 'dnaphath_list'
x[[i, ...]]

Arguments

x A 'dnaphath_list' object from dnapath.
i The index specifying which pathway to extract.
... Additional arguments are ignored.

Value

A 'dnaphath' object containing a single pathway result.

Examples

data(meso)
data(p53_pathways)
set.seed(0)
results <- dnapath(x = meso$gene_expression, pathway_list = p53_pathways,
                groups = meso$groups, n_perm = 10)
results[[1]]
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