Package 'anansi'

November 13, 2025

Type Package

Title Annotation-Based Analysis of Specific Interactions

Version 1.1.0

Description Studies including both microbiome and metabolomics data are becoming more common. Often, it would be helpful to integrate both datasets in order to see if they corroborate each others patterns. All vs all association is imprecise and likely to yield spurious associations. This package takes a knowledge-based approach to constrain association search space, only considering metabolite-function pairs that have been recorded in a pathway database. This package also provides a framework to assess differential association.

Depends R (>= 4.5.0)

Imports S7, stats, methods, igraph, Matrix, forcats, S4Vectors, SummarizedExperiment, MultiAssayExperiment, SingleCellExperiment, TreeSummarizedExperiment, rlang, ggplot2, ggforce, patchwork, ggraph, tidygraph

Suggests BiocStyle, dplyr, tidyr, graph, mia, KEGGREST, testthat (>= 3.0.0), knitr, rmarkdown

License GPL-3

Encoding UTF-8

LazyData false

RoxygenNote 7.3.3

Config/testthat/edition 3

biocViews Microbiome, Metabolomics, Regression, Pathways, KEGG

URL https://github.com/thomazbastiaanssen/anansi, https://thomazbastiaanssen.github.io/anansi

BugReports https://github.com/thomazbastiaanssen/anansi/issues

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

git_url https://git.bioconductor.org/packages/anansi

git_branch devel

git_last_commit d5ff74a

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2025-11-13

Author Thomaz Bastiaanssen [aut, cre] (ORCID: <https://orcid.org/0000-0001-6891-734X>), Thomas Quinn [aut] (ORCID: <https://orcid.org/0000-0003-0286-6329>), Giulio Benedetti [aut] (ORCID: <https://orcid.org/0000-0002-8732-7692>), Tuomas Borman [aut] (ORCID: <https://orcid.org/0000-0002-8563-8884>), Leo Lahti [aut] (ORCID: <https://orcid.org/0000-0001-5537-637X>)

Maintainer Thomaz Bastiaanssen <thomazbastiaanssen@gmail.com>

Contents

`anansi` *anansi: Annotation-based Analysis of Specific Interactions.*

Description

The anansi package package provides tools to prepare and facilitate integrative association analysis between the features of two data sets that are known to interact.

1. Input for `anansi()` with `AnansiWeb()` and `MultiFactor()`:

- randomAnansi, `kegg_link()`: Generate example input
- AnansiWeb, MultiFactor: Handle and manipulate input

2. Output and cross-compatibility:

- `getGraph()`: Compatibility with igraph::igraph
- `plotAnansi()`: Plot output in the style of miaViz::miaViz

3. Vignettes:

- 1. Getting started with anansi
- 2. Adjacency matrices
- 3. Association testing

Description: The `anansi()` function:

The main workspider function in the anansi package is called `anansi`. It manages the individual functionalities of anansi, including correlation analysis, correlation by group and differential associations.

Usage

```
anansi(
  web,
  formula,
  groups = NULL,
  metadata = NULL,
  adjust.method = "BH",
  verbose = TRUE,
  return.format = "table",
  ...
)
```

Arguments

web	An AnansiWeb object, containing two tables with 'omics data and a dictionary that links them. See weaveWebFromTables() for how to weave a web.
formula	A formula object. Used to assess differential associations.
groups	A vector of the column names of categorical values in the metadata object to control which groups should be assessed for simple correlations. If no argument provided, anansi will let you know and still to regular correlations according to your dictionary.
metadata	A vector or data.frame of categorical or continuous value necessary for differential correlations. Typically a state or treatment. If no argument provided, anansi will let you know and still to regular correlations according to your dictionary.
adjust.method	Method to adjust p-values for multiple comparisons. adjust.method = "BH" is the default value. See p.adjust() in the base R stats package.
verbose	Logical scalar. Whether to print diagnostic information (Default: TRUE). while running. Useful for debugging errors on large datasets.
return.format	Character scalar. Should be one of "table", "list", or "raw". Should the output of anansi() respectively be a wide data.frame of results, a list containing the results and input, or a list of raw output (used for testing purposes). convenient use. (Default: "table")
...	additional arguments (currently not used).

Value

A list of lists containing correlation coefficients, p-values and q-values for all operations.

Author(s)

Maintainer: Thomaz Bastiaanssen <thomazbastiaanssen@gmail.com> (ORCID)

Authors:

- Thomas Quinn <contacttomquinn@gmail.com> (ORCID)
- Giulio Benedetti <giulio.benedetti@utu.fi> (ORCID)
- Tuomas Borman <tuomas.v.borman@utu.fi> (ORCID)
- Leo Lahti <leo.lahti@utu.fi> (ORCID)

See Also

Useful links:

- https://github.com/thomazbastiaanssen/anansi
- https://thomazbastiaanssen.github.io/anansi
- Report bugs at https://github.com/thomazbastiaanssen/anansi/issues

Examples

```
# Load example data:

data(FMT_data)

# Make sure that columns are features and rows are samples.

t1 <- t(FMT_metab)
t2 <- t(FMT_KOs)

# Run anansi pipeline.

web <- weaveWeb(
    cpd ~ ko,
    tableY = t1,
    tableX = t2,
    link = kegg_link()
)

anansi_out <- anansi(
    web = web,
    formula = ~Legend,
    groups = "Legend",
    metadata = FMT_metadata,
    adjust.method = "BH",
    verbose = TRUE
)


library(tidyr)

# Use tidyr to wrangle the correlation r-values to a single column
anansiLong <- anansi_out |>
    pivot_longer(starts_with("All") | contains("FMT")) |>
    separate_wider_delim(
        name,
        delim = "_", names = c("cor_group", "param")
    ) |>
    pivot_wider(names_from = param, values_from = value)

# Only consider interactions where the entire model fits well enough.
library(ggplot2)
anansiLong <- anansiLong[anansiLong$full_p.values < 0.05, ]



ggplot(
    data = anansiLong,
    aes(
        x = r.values,
        y = feature_X,
        fill = cor_group,
```

```
        alpha = disjointed_Legend_p.values < 0.05
    )
) +

    # Make a vertical dashed red line at x = 0
    geom_vline(xintercept = 0, linetype = "dashed", colour = "red") +

    # Points show  raw correlation coefficients
    geom_point(shape = 21, size = 3) +

    # facet per compound
    ggforce::facet_col(~feature_Y, space = "free", scales = "free_y") +
    scale_fill_manual(values = c(
        "Young yFMT" = "#2166ac",
        "Aged oFMT" = "#b2182b",
        "Aged yFMT" = "#ef8a62",
        "All" = "gray"
    )) +
    theme_bw()

# Using miaViz style function:

p <- plotAnansi(anansi_out,
    association.type = "disjointed",
    model.var = "Legend",
    fill_by = "group",
    signif.threshold = 0.05,
    x_lab = "Pearson's rho"
)
p <- p +
    scale_fill_manual(values = c(
        "Young yFMT" = "#2166ac",
        "Aged oFMT" = "#b2182b",
        "Aged yFMT" = "#ef8a62",
        "All" = "gray"
    )) +
    theme_bw()

p
```

---

anansi-coercion *Coercion functions for anansi*

Description

Coercion functions for anansi

Usage

```
## S3 method for class '`anansi::AnansiWeb`'
as.list(x, ...)

## S3 method for class '`anansi::MultiFactor`'
as.list(x, ..., use.names = TRUE)

## S3 method for class '`anansi::AnansiWeb`'
as.data.frame(x, row.names, optional, ...)

asMAE(x)

asTSE(x)
```

Arguments

x	input object
...	additional arguments (currently not used).
use.names	Logical scalar, whether output list should contain character (Default) or integer data frame. If FALSE, returns unfactor(x).
row.names, optional	Not used. See ?base::data.frame

Value

An object of the desired class.

See Also

unfactor()

Examples

```
# AnansiWeb
x <- randomWeb(
    n_samples = 5,
    n_features_x = 4,
    n_features_y = 6
)

as.list(x)
as.data.frame(x)

# AnansiWeb to MultiAssayExperiment
asMAE(x)
asTSE(x)

# MultiFactor
x <- randomMultiFactor(n_types = 3, n_features = 3)
as.list(x, use.names = TRUE)
```

`anansiCor` *Compute r-statistics for each featureY-featureX pair in the dictionary. Typically, the main* `anansi()` *function will run this for you.*

Description

Compute r-statistics for each featureY-featureX pair in the dictionary. Typically, the main `anansi()` function will run this for you.

Usage

```
anansiCor(web, group.bool)
```

Arguments

`web`	An `AnansiWeb` object, containing two tables with omics data and a dictionary that links them. See `weaveWebFromTables()` for how to weave a web.
`group.bool`	A boolean vector used to select which samples should be included in the correlations.

Value

A matrix of r-statistics.

See Also

`anansi()`
`anansiCorTestByGroup()`

`anansiCorPvalue` *Compute r-statistics for each featureY-featureX pair in the dictionary. Typically, the main* `anansi()` *function will run this for you.*

Description

Compute r-statistics for each featureY-featureX pair in the dictionary. Typically, the main `anansi()` function will run this for you.

Usage

```
anansiCorPvalue(web, group.bool, verbose)
```

Arguments

web	An AnansiWeb object, containing two tables with omics data and a dictionary that links them. See weaveWebFromTables() for how to weave a web.
group.bool	A categorical or continuous value necessary for differential correlations. Typically a state or treatment score. If no argument provided, anansi will let you know and still to regular correlations according to your dictionary.
verbose	A boolean. Toggles whether to print diagnostic information while running. Useful for debugging errors on large datasets.

Value

An AnansiTale result object.

See Also

anansi()
anansiCorTestByGroup()

---

anansiCorTestByGroup *Run correlations for all interacting metabolites and functions.*

Description

If the groups argument is suitable, will also run correlation analysis per group. Typically, the main anansi() function will run this for you.

Usage

```
anansiCorTestByGroup(web, group.vec, verbose = TRUE)
```

Arguments

web	An AnansiWeb object, containing two tables with omics data and a dictionary that links them. See weaveWebFromTables() for how to weave a web.
group.vec	A character vector denoting group membership. Typically a state or treatment score.
verbose	A boolean. Toggles whether to print diagnostic information while running. Useful for debugging errors on large datasets.

Value

a list of AnansiTale result objects, one for the total dataset and per group if applicable.

See Also

anansi()

`anansiDiffCor` *Run differential correlation analysis for all interacting metabolites and functions.*

Description

Can either take continuous or categorical data. Typically, the main `anansi()` function will run this for you.

Usage

```
anansiDiffCor(web, sat_model, errorterm, int.terms, metadata, verbose)
```

Arguments

`web`	An `AnansiWeb` object, containing two tables with omics data and a dictionary that links them. See `weaveWebFromTables()` for how to weave a web.
`sat_model`	A `formula` object, containing the full model
`errorterm`	A `character vector`, containing the metadata col.name denoting repeated measures.
`int.terms`	A `character vector`, containing the metadata col.names denoting covariates interacting with X to be tested for differential associations.
`metadata`	A vector or data.frame of categorical or continuous value necessary for differential correlations. Often a state or treatment score. If no argument provided, anansi will let you know and still to regular correlations according to your dictionary.
`verbose`	A boolean. Toggles whether to print diagnostic information while running. Useful for debugging errors on large datasets.

Value

a list of `AnansiTale` result objects, one for the total model, one for emergent correlations and one for disjointed correlations.

`AnansiTale` *AnansiTale S7 container class. Not intended for general use.*

Description

`AnansiTale` is the main container that will hold your stats output data coming out of the `anansi` pipeline.

Usage

```
AnansiTale(
  subject = character(0),
  type = character(0),
  df = integer(0),
  estimates = integer(0),
  f.values = integer(0),
  t.values = integer(0),
  p.values = integer(0)
)
```

Arguments

subject	A character that describes the data that was queried.
type	A character that describes type of parameter contained in the estimates slot. For example r.values for correlations or r.squared for models.
df	a vector of length 2, containing df1 and df2 corresponding to the F-ratio considered.
estimates	A matrix containing the estimates for the parameters named in the type slot.
f.values	A matrix containing the f-values, for least-squares.
t.values	A matrix containing the t-values, for correlations.
p.values	A matrix containing the p.values for the parameters named in the type slot.

Value

an AnansiTale

Slots

subject A character that describes the data that was queried.

type A character that describes type of parameter contained in the estimates slot. For example r.values for correlations or r.squared for models.

df a vector of length 2, containing df1 and df2 corresponding to the F-ratio considered.

estimates A matrix containing the estimates for the parameters named in the type slot.

f.values A matrix containing the f-values, for least-squares.

t.values A matrix containing the t-values, for correlations.

p.values A matrix containing the p.values for the parameters named in the type slot.

Examples

```
AnansiTale
```

AnansiWeb *AnansiWeb S7 container class*

Description

AnansiWeb is an S7 class containing two feature tables as well as a dictionary to link them. AnansiWeb is the main container that will hold your input data throughout the anansi pipeline.

Typical use of the anansi package will involve generating an AnansiWeb object using the weaveWeb() function.

The function AnansiWeb() constructs an AnansiWeb object from two feature tables and an adjacency matrix.

Usage

```
## Constructor for `AnansiWeb` objects
AnansiWeb(tableX, tableY, dictionary, metadata = data.frame())
```

Arguments

tableY, tableX	A table containing features of interest. Rows should be samples and columns should be features. Y and X refer to the position of the features in a formula: Y ~ X.
dictionary	A binary adjacency matrix of class Matrix, or coercible to Matrix
metadata	list of metadata. Optional.

Value

an AnansiWeb object, with sparse binary biadjacency matrix with features from y as rows and features from x as columns in dictionary slot.

Slots

tableY,tableX Two matrix objects of measurements, data. Rows are samples and columns are features. Access with @tableY and @tableX.

dictionary Matrix, binary adjacency matrix. Optionally sparse. Typically generated using the weaveWeb() function. Access with @dictionary.

metadata Optional data.frame of sample metadata. Access with @metadata.

See Also

- AnansiWeb-methods
- randomAnansi: For generation of random AnansiWeb objects.
- kegg_link(): For examples of input for link argument.

Examples

```
# Use AnansiWeb() to construct an AnansiWeb object from components:
tX <- `dimnames<-`(replicate(5, (rnorm(36))),
    value = list(
        as.character(seq_len(36)),
        letters[1:5]
    )
)
tY <- `dimnames<-`(replicate(3, (rnorm(36))),
    value = list(
        as.character(seq_len(36)),
        LETTERS[1:3]
    )
)

d <- matrix(TRUE,
    nrow = NCOL(tY), ncol = NCOL(tX),

    # Note: Dictionary should have named dimensions
    dimnames = list(
        y_names = colnames(tY),
        x_names = colnames(tX)
    )
)
web <- AnansiWeb(tableX = tX, tableY = tY, dictionary = d)
```

AnansiWeb-methods *Methods for AnansiWeb S7 container class*

Description

Methods for AnansiWeb S7 container class

Arguments

x	input, AnansiWeb object

Value

The desired information from an AnansiWeb object

See Also

- weaveWeb(): for general use.
- AnansiWeb-pairwise: for methods for pairwise operations

Examples

```
# Setup
web <- randomWeb(n_samp = 36)

# Accessors
dimnames(web)
dim(web)
names(web)

# Getters and setters:

tableX(web)[1:5, 1:5]
tableY(web)[1:5, 1:5]
dictionary(web)
head(metadata(web))

# Assign some random metadata
metadata(web) <- data.frame(
    id = row.names(tableY(web)),
    a = rnorm(36),
    b = sample(c("a", "b"), 36, TRUE),
    row.names = "id"
)

# Coerce to list
weblist <- as.list(web)

# Coerce to Data.frame
webdf <- as.data.frame(web)

# Coerce to MultiAssayExperiment
mae <- asMAE(web)

# Coerce to TreeSummarizedExperiment
tse <- asTSE(web)
```

`AnansiWeb-pairwise` *Methods for pairwise operations on AnansiWeb objects*

Description

Methods to run pairwise analysis on multi-modal data.

Arguments

`X`, `x`	input, AnansiWeb object
`...`	additional arguments
`FUN`	a function with at least two arguments. The variables `x` and `y`, in order, refer to the corresponding values of feature pairs in `tableX` and `tableY`.

MoreArgs, SIMPLIFY, USE.NAMES
: see ?base::mapply

which
: integer matrix, indicating pair positions in x@tableY and x@tableX, respectively. If NULL (default): Matrix::which(x@dictionary, TRUE).

with.metadata
: Logical scalar whether to append metadata to output

Value

pairs: A two-column array index, corresponding to i,j coordinates in matrix notation.
getFeaturePairs: A list of data.frames with the paired data

Examples

```
web <- randomWeb()
# Extract data.frames in pairs (only show first)
getFeaturePairs(web)[1L]

pairs(x = web)

getFeaturePairs(x = web, which = NULL, with.metadata = FALSE)

pairwiseApply(
    X = web,
    FUN = function(x, y) cor(x, y),
    MoreArgs = NULL, SIMPLIFY = TRUE, USE.NAMES = TRUE
)
```

---

dictionary *Get dictionary*

Description

Get dictionary

Usage

```
dictionary(x, ...)
```

Arguments

x
: input object

...
: additional arguments

Value

dictionary slot of x

Examples

```
x <- randomWeb(10)
dictionary(x)
```

---

ec2ko *Use linking data from the KEGG database.*

Description

kegg_link() is a convenience function to return a list containing two data.frames; ec2cpd and ec2ko. This will be their most likely use. ec2cpd and ec2ko are two data.frames, used to link ko, ecs and cpd identifiers in the KEGG database.

Usage

```
data("ec2ko", package = "anansi")

data("ec2cpd", package = "anansi")

kegg_link()
```

Format

ec2ko: a data.frame of two columns, named "ec" and "ko". The IDs refer to KEGG orthologues. Enzyme commission numbers, ecs, typically describe reactions captured by them.

ec2cpd: a data.frame of two columns, named "ec" and "cpd". The IDs refer to compounds in the KEGG database. Enzyme commission numbers, ecs, typically describe reactions either producing or requiring them.

Value

kegg_link() returns a list containing the two aforementioned data.frames, ec2cpd and ec2ko.

Source

ec2ko: Adapted from https://www.genome.jp/kegg/, using KEGGREST. Script to generate available in example.

ec2cpd: Adapted from https://www.genome.jp/kegg/ using KEGGREST. Script to generate available in example.

Examples

```
kegg_link()

# Generate ec2ko and ec2cpd:
# Don't download during tests. set to `TRUE` to download.
dry_run <- TRUE

if (!dry_run) {
    ec2ko <- KEGGREST::keggLink("ec", "ko")
    ec2ko <- data.frame(
        ec = gsub("ec:", "", x = ec2ko, fixed = TRUE),
        ko = gsub("ko:", "", x = names(ec2ko), fixed = TRUE),
        row.names = NULL
    )

    ec2cpd <- KEGGREST::keggLink("ec", "cpd")
    ec2cpd <- data.frame(
        ec = gsub("ec:", "", x = ec2cpd, fixed = TRUE),
        cpd = gsub("cpd:", "", x = names(ec2cpd), fixed = TRUE),
        row.names = NULL
    )
}
```

FMT_KOs *Snippet of the CLR-transformed inferred functional data from the FMT Aging study.*

Description

Piphillin was used to infer functions from the 16S sequencing data in terms of KOs. Unfortunately, the Piphillin algorithm is proprietary and has since been taken down.

Usage

```
data("FMT_data", package = "anansi")
```

Format

A marix object with 6468 rows, KOs, and 36 columns, samples.

Source

doi:10.1038/s43587021000939

FMT_metab *Snippet of the CLR-transformed hippocampal metabolomics data from the FMT Aging study.*

Description

Snippet of the CLR-transformed hippocampal metabolomics data from the FMT Aging study.

Usage

```
data("FMT_data", package = "anansi")
```

Format

A matrix object with three rows, compounds, and 36 columns, samples.

Source

doi:10.1038/s43587021000939

FMT_metadata *Snippet of the metadata from the FMT Aging study.*

Description

There were three treatment groups in the study that all received faecal microbiota transplantation (FMT). Young mice that received FMT from young mice (Young yFMT), aged mice that received FMT from aged mice (Aged oFMT) and aged mice that received FMT from young mice (Aged yFMT).

Usage

```
data("FMT_data", package = "anansi")
```

Format

A data.frame object with 36 rows, samples, and two columns, denoting sample ID and treatment group, respectively.

Source

doi:10.1038/s43587021000939

getEdgeList *Get a listof edges*

Description

Get a listof edges

Usage

```
getEdgeList(x, ...)
```

Arguments

x	input object
...	additional arguments

Value

a two-column data.frame that lists the content of each entry in the input MultiFactor

Examples

```
x <- randomMultiFactor(n_features = 10)
getEdgeList(x)
```

getFeaturePairs *Get a list of all pairs of features*

Description

Get a list of all pairs of features

Usage

```
getFeaturePairs(x, ...)
```

Arguments

x	input object
...	additional arguments for specific methods

Value

an list of two-column data.frames that represent all feature pairs.

Examples

```
x <- randomWeb(10)
head(getFeaturePairs(x), 3)
```

---

getGraph *Get a graph object.*

Description

Get a graph object.

Usage

```
getGraph(x, ...)
```

Arguments

x	input
...	additional arguments (currently not used).

Value

a specified graph object.

See Also

MultiFactor-methods

Examples

```
# Show methods
getGraph
```

---

krebs *Simplified snippet of the Krebs cycle*

Description

Enzymes and metabolites that make up the Krebs cycle. Features share a row when they play a role in the same reaction. Used in vignettes, exported to facilitate user exploration.

Usage

```
data("krebs", package = "anansi")
```

Format

A data.frame of two factors, named "Enzyme" and "Metabolite", which contain these respective components of the krebs cycle.

Source

Generated by hand based on the krebs cycle.

See Also

krebsDemoWeb()

---

linkBiobakeryMap *make a link data.frame for biobakery mapping files input*

Description

make a link data.frame for biobakery mapping files input

Usage

```
linkBiobakeryMap(map)
```

Arguments

map	Character, result from readLines() on uncompressed humann mapping files.

Value

a two-column data.frame that can be converted into an adjacency matrix used as input for weaveWeb().

See Also

weaveWeb()

Examples

```
# some dummy input, as a character vector of IDs separated by tabs.
x <- c("x_1\ty_1\ty_2\ty_4", "x_2\ty_1\ty_3", "x_3\ty_2\ty_y")
linkBiobakeryMap(x)
```

metadata *Get metadata.*

Description

Get metadata.

Arguments

x	input object
...	additional arguments

Details

Compatible with S4Vectors generic.

Value

metadata slot of x

Examples

```
x <- randomWeb(10)
metadata(x)
```

metadata<- *Set metadata.*

Description

Set metadata.

Arguments

x	input object
...	additional arguments
value	replacement value, coerced to data.frame

Details

Compatible with S4Vectors generic.

Value

x with modified metadata slot.

Examples

```
x <- randomWeb(10)
metadata(x) <- cbind(
    metadata(x),
    new_groups = c("A", "B")
)
```

`MultiFactor` *MultiFactor S7 container class*

Description

`MultiFactor` is an S7 class to organize and manage multiple sets of factors, for instance when tracing or converting feature IDs across databases. Methods for `MultiFactor` aim to follow `factor` behaviour.

Usage

```
MultiFactor(x, levels = NULL, drop.unmatched = FALSE)

## Constructor for `MultiFactor` objects
MultiFactor(x, levels = NULL, drop.unmatched = FALSE)
```

Arguments

`x`	`MultiFactor`
`levels`	an optional named list of vectors of the unique values (as character strings) that x might have taken. The default is the unique set of values taken by lapply(x, as.character), sorted into increasing order of x.
`drop.unmatched`	`Logical scalar` If `TRUE` (Default), for feature types that are seen at least twice, exclude features that only present in one of their respective link data frames.

Details

The most straightforward way to construct a `MultiFactor` object is as a named list of named data.frames. The columns of the data.frames indicate the category of factor in that column.

A `MultiFactor` object presents itself similar to a `data.frame`, in the sense that level types can be called as columns and individual data.frame components can be called as rows.

Value

a MultiFactor object.

Slots

`index` Named `list` of named integer data frames of at least two columns each. The column names correspond to names in the `levels` slot. Similar to `factors`, the integers in those columns correspond to the characters in that level. Accessed through regular list methods (e.g., `[`, `[[`).

`levels` `Named list of character vectors`. Accessed through `levels(x)`

`map` `(sparse) Matrix` specifying which elements contain which levels. Accesses through `x@dictionary`.

See Also

`MultiFactor-methods()`

- `kegg_link()`: for an example of valid input.

Examples

```
# Generate some random linkage input
x <- data.frame(
    a = sample(letters[seq(3)], 10, replace = TRUE),
    A = sample(LETTERS[seq(3)], 10, replace = TRUE)
)
MultiFactor(x)
```

`MultiFactor-methods` *Methods for MultiFactor S7 container class*

Description

`droplevels()` `droplevels(MultiFactor)` returns a `MultiFactor` with unused levels removed, Analogous to the `factor` method.

Arguments

`...`	`i,j` indices specifying elements to extract or replace. Indices are numeric or character vectors or empty (missing) or NULL. Numeric values are coerced to integer or whole numbers as by as.integer or for large values by trunc (and hence truncated towards zero). Character vectors will be matched to the names of the object.
`value`	Replacement value, typically of same type as that which is to be replaced.
`exclude`	`NULL` or `Named character list` of similar structure as `levels(MultiFactor)`. Which levels to drop from output.
`select`	`NULL` or `Named character list` of similar structure as `levels(MultiFactor)`. Which levels to keep in output.
`use.names, ignore.mcols`	For compatibility, not used.
`x`	`MultiFactor`
`format`	`Character scalar`, controls output format by package name. `"igraph"` and `"graph"` are supported.

Details

Only one of `select` and `exclude` should be provided, as they are each others complement.

Value

A MultiFactor

a specified graph object.

See Also

`igraph::graph_from_data_frame()` and `igraph::as_graphnel()`, which are used under the hood, from `igraph::igraph()` package.

Examples

```
# Setup
x <- MultiFactor(kegg_link())
x

# Basic properties
dim(x)
dimnames(x)

# Factor-like properties
head(levels(x)$ko)
droplevels(x)
head(unfactor(x)$ec2ko)

# Extract common output formats
getEdgeList(x)

droplevels(x, exclude = list(ko = "K00001"))
droplevels(x, select = list(ko = "K00001"))
# Generate an igraph object
g <- getGraph(x = kegg_link(), format = "igraph")
plot(g)
```

---

pairwiseApply *Apply a function on each pair of features*

Description

Apply a function on each pair of features

Usage

```
pairwiseApply(X, ...)
```

Arguments

X	input object
...	additional arguments

Value

a list containing the output of applying the function to each feature pair. See ?base::mapply()

Examples

```
web <- randomWeb(10)

# For each feature pair, was the value for x higher than the value for y?
pairwise_gt <- pairwiseApply(
    X = web,
    FUN = function(x, y) x > y,
    MoreArgs = NULL, SIMPLIFY = FALSE, USE.NAMES = TRUE
)

head(pairwise_gt)

# Run cor.test() on each pair of features
pairwise_cor <- pairwiseApply(
    X = web,
    FUN = function(x, y) cor.test(x, y),
    MoreArgs = NULL, SIMPLIFY = FALSE, USE.NAMES = TRUE
)

pairwise_cor[1]
```

---

plotAnansi *Dissociation plot*

Description

plotAnansi generates an association plot from the output of anansi() in the table format. It provides a convenient way to visually assess relevant results from the anansi analysis, either in the form of a dotplot or a graph.

Arguments

x	a data.frame object output of anansi() in the table format.
...	additional parameters
layout	Character scalar. Specifies the plot layout to generate. It must be one of c("dotplot, graph). (Default: dotplot)

association.type
: Character scalar. Specifies the type of association to show in the plot. One of "disjointed", "emergent" and "full". (Default: NULL)

model.var
: Character scalar. Specifies the name of a variable in the anansi model. It is relevant only when association.type is "disjointed" or "emergent". (Default: NULL)

group
: Character scalar. Selects one of the groups included in the anansi model. It is relevant only when layout is graph. (Default: All)

signif.threshold
: Numeric scalar. Specifies the threshold to mark the significance of association.type. (Default: NULL)

colour_by
: Character scalar. Specifies one of the groups terms used in the original anansi call, x by which points should be coloured. (Default: NULL)

color_by
: Character scalar. Alias to colour_by.

fill_by
: Character scalar. Specifies one of the groups terms used in the original anansi call, x by which points should be filled (Default: "group")

size_by
: Character scalar. Specifies one of the groups terms used in the original anansi call, x by which points should be sized. (Default: NULL)

shape_by
: Character scalar. Specifies one of the groups terms used in the original anansi call, x by which points should be shaped. (Default: NULL)

x_lab
: Character scalar. Specifies the label of the x axis. (Default: "cor")

y_lab
: Character scalar. Specifies the label of the y axis. (Default: "")

y_position
: Character scalar. Specifies the position of the y labels. It should be either "left" or "right". (Default: "right")

show.cor
: Logical scalar. Whether correlation edges should be labelled with correlation coefficients when layout is graph. (Default: FALSE)

Details

plotAnansi provides a standardised method to visualise the results of anansi by means of a differential association plot. The input for this function should be generated from anansi() or anansi(), with return.format = "table"

Value

a figure that can be further modified using the ggplot2 suite

A ggplot2 object.

See Also

anansi()

Examples

```
# Import libraries
library(mia)
library(TreeSummarizedExperiment)
library(MultiAssayExperiment)
```

```
library(ggraph)

web <- randomWeb(n_samples = 100)
mae <- asMAE(web)

# Perform anansi analysis
out <- weaveWeb(mae,
    tableY = "y", tableX = "x"
) |> anansi(formula = ~group_ab)

# Select significant interactions
out <- out[out$full_p.values < 0.05, ]

# Visualise disjointed associations filled by group
plotAnansi(out,
    association.type = "disjointed",
    model.var = "group_ab",
    signif.threshold = 0.05,
    fill_by = "group"
)

# Visualise full associations filled by group
plotAnansi(out,
    association.type = "full",
    signif.threshold = 0.05,
    fill_by = "group"
)

# Visualise full associations as graph
plotAnansi(out,
    layout = "graph",
    association.type = "full",
    signif.threshold = 0.05,
    show.cor = TRUE
)

# Visualise disjointed associations as graph
plotAnansi(out,
    layout = "graph",
    association.type = "disjointed",
    model.var = "group_ab",
    signif.threshold = 0.05
)
```

`randomAnansi` *Generate a random AnansiWeb or MultiFactor*

Description

Randomly generate a valid `AnansiWeb` or `MultiFactor` object.

Usage

```
randomWeb(
  n_samples = 10,
  n_reps = 1L,
  n_features_x = 8,
  n_features_y = 12,
  sparseness = 0.5,
  tableY = NULL,
  tableX = NULL,
  dictionary = NULL
)

randomMultiFactor(n_types = 6, n_features = 100, sparseness = 0.5)

krebsDemoWeb(n_samples = 100, n_reps = 4L)
```

Arguments

n_samples, n_reps	Numeric scalar Number of samples and repeated measures of those samples to be generated. Ignored if tableY and tableX are provided. (defaults: 10 samples without repeats)
n_features_y, n_features_x	Numeric scalar Number of features to be generated. Ignored if tableY and tableX are provided.
sparseness	Numeric scalar, proportion: How rare are connections
tableY, tableX	A table containing features of interest. Rows should be samples and columns should be features. Y and X refer to the position of the features in a formula: Y ~ X.
dictionary	A binary adjacency matrix of class Matrix, or coercible to Matrix.
n_types	Numeric scalar, number of types of features to generate
n_features	Numeric scalar, number of features per type

Value

a randomly generated object of the specified class.

See Also

AnansiWeb(), MultiFactor()

Examples

```
# Make a random AnansiWeb object
randomWeb()
krebsDemoWeb()
randomMultiFactor()
```

tableX *Get tableX*

Description

Get tableX

Usage

```
tableX(x, ...)
```

Arguments

x	input object
...	additional arguments

Value

tableX slot of x

Examples

```
x <- randomWeb(10)
tableX(x)
```

tableY *Get tableY*

Description

Get tableY

Usage

```
tableY(x, ...)
```

Arguments

x	input object
...	additional arguments

Value

tableY slot of x

Examples

```
x <- randomWeb(10)
tableY(x)
```

weaveWeb *Weave an AnansiWeb object*

Description

Weave an AnansiWeb object

Usage

```
weaveWeb(x, ...)

weaveKEGG(x, ...)
```

Arguments

x	input object
...	additional arguments

Value

an AnansiWeb object, with sparse binary biadjacency matrix with features from y as rows and features from x as columns in dictionary slot.

See Also

weaveWeb-methods()

Examples

```
# Setup demo tables
ec2ko <- kegg_link()[["ec2ko"]]
ec2cpd <- kegg_link()[["ec2cpd"]]

# Basic usage
weaveWeb(cpd ~ ko, link = kegg_link())
weaveWeb(x = "ko", y = "ec", link = ec2ko)
weaveWeb(ec ~ cpd, link = ec2cpd)

# A wrapper is available for kegg ko, ec and cpd data
generic <- weaveWeb(cpd ~ ko, link = kegg_link())
kegg_wrapper <- weaveKEGG(cpd ~ ko)

identical(generic, kegg_wrapper)

# The following are equivalent to transposition:
a <- weaveWeb(ko ~ cpd, link = kegg_link()) |> dictionary()
b <- weaveWeb(cpd ~ ko, link = kegg_link()) |> dictionary()

identical(a, Matrix::t(b))
```

weaveWeb-methods *Weave an AnansiWeb*

Description

Generate a biadjacency matrix, linking the features between two tables. Return an AnansiWeb object which contains all three.

weaveWeb() is for general use and has flexible default settings.

weaveKEGG() is a wrapper that sets link to kegg_link(). All variants are special cases of weaveWeb().

Arguments

x, y	Character scalar, names of feature types that should be linked. Should be found in the column names of link.
link	One of the following: • Character scalar with value "none". • data.frame with two columns • list with two such data.frames.
tableY, tableX	A table containing features of interest. Rows should be samples and columns should be features. Y and X refer to the position of the features in a formula: Y ~ X. < For Bioconductor S4 objects > Character scalar or numeric scalar. Selects experiment corresponding to tableY and tableX from experiments(x) of MultiAssayExperiment object by name or index, name is recommended. (Default slots: Y = 1L, X = 2L).
metadata	Optional data.frame of sample metadata, to be included with output. Can be accessed from AnansiWeb generated by weaveWeb() with output@metadata.
verbose	Logical scalar. Whether to print diagnostic information (Default: TRUE).#' @param force_new boolean If x already has a dictionary Matrix in metadata, ignore it and generate a new object anyway? (Default: FALSE).
typeY, typeX	Character scalar or numeric scalar. Selects assay from experiments to tableY and tableX from experiments(x). (Default: 1L - the first assay in that experiment).
experiment1, experiment2	synonymous args to tableY,tableX for compatibility with mia argument style.
assay.type1, assay.type2	synonymous args to typeY,typeX for compatibility with mia argument style.

Details

If the link argument is "none", all features will be considered linked. If one or more data.frames, colnames should be as specified in x and y.

Value

an AnansiWeb object, with sparse binary biadjacency matrix with features from y as rows and features from x as columns in dictionary slot.

See Also

- AnansiWeb: For general constructor and methods.
- kegg_link(): For examples of input for link argument.

Examples

```
# Setup demo tables, see first vignette.
data(FMT_data)

t1 <- t(FMT_metab)
t2 <- t(FMT_KOs)

# Input objects and syntax:
## define `x` and `y` as characters
web <- weaveWeb(
    x = "ko", y = "cpd", link = kegg_link(),
    tableX = t2, tableY = t1,
    metadata = NULL, verbose = TRUE
)

## define `x` and `y` with a formula
web2 <- weaveWeb(
    x = cpd ~ ko, link = kegg_link(),
    tableX = t2, tableY = t1,
    metadata = NULL, verbose = TRUE
)

identical(web, web2)

# Method for MultiAssayExperiment S4 object
mae <- asMAE(web)
weaveWeb(
    x = mae, link = kegg_link(),
    tableY = "cpd", tableX = "ko",
    force_new = FALSE
)

# Method for TreeSummarizedExperiment S4 object
tse <- asTSE(web)
weaveWeb(
    x = tse, link = kegg_link(),
    tableY = "cpd", tableX = "ko",
    force_new = FALSE
)
```

Index