

Package ‘mina’

December 27, 2024

Title Microbial community dIversity and Network Analysis

Version 1.15.0

Description An increasing number of microbiome datasets have been generated and analyzed with the help of rapidly developing sequencing technologies. At present, analysis of taxonomic profiling data is mainly conducted using composition-based methods, which ignores interactions between community members. Besides this, a lack of efficient ways to compare microbial interaction networks limited the study of community dynamics. To better understand how community diversity is affected by complex interactions between its members, we developed a framework (Microbial community dIversity and Network Analysis, mina), a comprehensive framework for microbial community diversity analysis and network comparison. By defining and integrating network-derived community features, we greatly reduce noise-to-signal ratio for diversity analyses. A bootstrap and permutation-based method was implemented to assess community network dissimilarities and extract discriminative features in a statistically principled way.

Depends R (>= 4.0.0)

LinkingTo Rcpp, RcppParallel, RcppArmadillo

License GPL

Encoding UTF-8

Imports methods, stats, Rcpp, MCL, RSpectra, apcluster, bigmemory, foreach, ggplot2, parallel, parallelDist, reshape2, plyr, biganalytics, stringr, Hmisc, utils

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Enhances doMC

VignetteBuilder knitr

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.adj<-	<i>Setter for the slot 'adj' and 'adj_sig', the adjacency matrix of 'norm' and corresponding significant value matrix with 'sig' is 'TRUE'.</i>
--------	---

Description

Setter for the slot 'adj' and 'adj_sig', the adjacency matrix of 'norm' and corresponding significant value matrix with 'sig' is 'TRUE'.

Get the slot 'adj'.

Get the slot 'adj_sig'.

Usage

```
.adj(x) <- value

## S4 replacement method for signature 'mina'
.adj(x) <- value

.adj(x)

adj_sig(x) <- value

## S4 replacement method for signature 'mina'
adj_sig(x) <- value

adj_sig(x)
```

Arguments

x	The 'mina' object.
value	The value to set for the slot of the 'mina' object 'x'.

Value

The 'adj' slot of the 'mina' object.

The slot 'adj_sig' of the object.

<code>.dmr<-</code>	<i>Setter and getter for the slot 'dmr'.</i>
------------------------	--

Description

Setter and getter for the slot 'dmr'.

Usage

```
.dmr(x) <- value  
  
.dmr(x)  
  
## S4 replacement method for signature 'mina'  
.dmr(x) <- value  
  
## S4 method for signature 'mina'  
.dmr(x)
```

Arguments

<code>x</code>	The 'mina' object.
<code>value</code>	The value to set for the slot of the 'mina' object 'x'.

Value

The 'dmr' slot of the 'mina' object.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)  
maize <- norm_tab(maize, method = "raref")  
maize <- fit_tabs(maize)  
maize <- com_dis(maize, method = "bray")  
maize <- dmr(maize)  
asv_dmr <- .dmr(maize)
```

adj *Calculate the correlation adjacency matrix.*

Description

Calculate the correlation adjacency matrix.

Usage

```
adj(x, method, ...)
```

Arguments

x An object of the class `mina` with ‘norm’ defined or a ‘norm’ matrix.
 method The correlation coefficient used for adjacency matrix.
 ... Additional parameters.

Value

Adjacency matrix.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref", depth = 1000)
maize <- fit_tabs(maize)
maize <- adj(maize, method = "spearman", sig = FALSE)
```

adj,matrix,ANY-method *Calculate the adjacency matrix of ‘norm’ by correlation with matrix as input.*

Description

Calculate the adjacency matrix of ‘norm’ by correlation with matrix as input.

Usage

```
## S4 method for signature 'matrix,ANY'
adj(x, method, sig = FALSE, threads = 80, nblocks = 400, ...)

## S4 method for signature 'matrix,character'
adj(x, method, sig = FALSE, threads = 80, nblocks = 400, ...)
```

Arguments

x	An object of the class mina with 'norm' defined or a 'norm' matrix.
method	The correlation coefficient used for adjacency matrix.
sig	(optional) The asymptotic P-values, only applicable for Pearson and Spearman methods with 'mina' object as input, always FALSE here.
threads	The number of threads used for parallel running, 80 by default.
nblocks	The number of row/column for splitting sub-matrix, 400 by default.
...	Additional parameters.

Value

y The adjacency matrix.

Examples

```
asv_norm <- norm_tab(maize_asv2, method = "raref", depth = 1000)
asv_adj <- adj(asv_norm, method = "pearson")
```

adj,mina,ANY-method *Calculate the adjacency matrix of 'norm' by correlation with 'mina' class object as input.*

Description

Calculate the adjacency matrix of 'norm' by correlation with 'mina' class object as input.

Usage

```
## S4 method for signature 'mina,ANY'
adj(x, method, sig = FALSE, threads = 80, nblocks = 400, ...)

## S4 method for signature 'mina,character'
adj(x, method, sig = FALSE, threads = 80, nblocks = 400, ...)
```

Arguments

x	An object of the class mina with 'norm' defined or a 'norm' matrix.
method	The correlation coefficient used for adjacency matrix.
sig	The asymptotic P-values, only applicable for Pearson and Spearman methods, FALSE by default.
threads	The number of threads used for parallel running, 80 by default.
nblocks	The number of row/column for splitting sub-matrix, 400 by default.
...	Additional parameters.

Value

x The same 'mina' object with 'adj' added.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- adj(maize, method = "spearman", sig = FALSE)
```

adj_method_list	<i>List of adjacency matrix calculation methods/ orrelations supported in</i> adj
-----------------	--

Description

Correlation methods should be specified by exact string match.

Usage

```
adj_method_list
```

Format

A list of character vectors.

pearson Pearson correlation.

spearman Spearman correlation.

sparcce SparCC correlation by spearman.

See Also

[adj](#)

Examples

```
? adj_method_list
```

bs_pm	<i>Inferring the network of different group of samples and test significance by permutation.</i>
-------	--

Description

Inferring the network of different group of samples and test significance by permutation.

Usage

```
bs_pm(x, group, ...)
```

Arguments

x	An object of class 'mina' with 'norm' and 'des' defined.
group	The column name of descriptive file 'des' for comparison.
...	Additional parameters.

Value

The network bootstrap and permutation result.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- get_rep(maize, top = 5)
maize <- bs_pm(maize, group = "Compartment", per = 0.5)
```

bs_pm, mina, ANY-method	<i>Inferring the network of different group of samples and test significance by permutation.</i>
-------------------------	--

Description

Inferring the network of different group of samples and test significance by permutation.

Usage

```
## S4 method for signature 'mina,ANY'
bs_pm(
  x,
  group,
  g_size = 88,
  s_size = 30,
  rm = TRUE,
  per = 0.1,
  sig = TRUE,
  bs = 6,
  pm = 6,
  individual = FALSE,
  out_dir = "./",
  ...
)

## S4 method for signature 'mina,character'
bs_pm(
  x,
  group,
  g_size = 88,
  s_size = 30,
  rm = TRUE,
  per = 0.1,
  sig = TRUE,
  bs = 6,
  pm = 6,
  individual = FALSE,
  out_dir = "./",
  ...
)
```

Arguments

<code>x</code>	An object of class 'mina' with @norm and @des defined.
<code>group</code>	The column name of descriptive file @des for comparison.
<code>g_size</code>	The cutoff of group size used for filtering, default is 88.
<code>s_size</code>	The number of samples used for network inference during bootstrap and permutation (when 'sig' is TRUE), it should be smaller than $g_size / 2$ to make sure the randomness; default is 30.
<code>rm</code>	Filtering the components present in less than 'per' of the samples from compared groups, default TRUE.
<code>per</code>	The percentage of present samples for filtering, default is 0.1.
<code>sig</code>	Whether to test the significance, skip the permutation when set as FALSE, default is TRUE.

bs	The times for bootstrap network inference, default is 6.
pm	The times for permuatated samples network inference, default is 6.
individual	Whether to output the bootstrap and permutation results of each comparison individually, default is FALSE.
out_dir	The output directory if 'individual' is TRUE, default is the current working directory
...	Additional parameters.

Value

x The same object with @multi and @perm defined.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- bs_pm(maize, group = "Compartment", per = 0.5)
```

check_mina	<i>Check the tab and des file. Return TRUE if they are NULL or both quantitative and descriptive files of same samples are included (i.e. the object is valid).</i>
------------	---

Description

Check the tab and des file. Return TRUE if they are NULL or both quantitative and descriptive files of same samples are included (i.e. the object is valid).

Usage

```
check_mina(x)
```

Arguments

x An object of class mina.

Value

TRUE if the object is valid.

Examples

```
data(maize)
check_mina(maize)
```

check_mina_de	<i>Check the object and return TRUE if the object includes descriptive table contains the same samples as quantitative table.</i>
---------------	---

Description

Check the object and return TRUE if the object includes descriptive table contains the same samples as quantitative table.

Usage

```
check_mina_de(x)
```

Arguments

x An object of class mina with 'tab' and 'des' defined.

Value

TRUE if the object contains non-empty descriptive table and has the same samples as quantitative table.

Examples

```
data(maize)
check_mina_de(maize)
```

check_mina_qu	<i>Check the object and return TRUE if the object includes quantitative table.</i>
---------------	--

Description

Check the object and return TRUE if the object includes quantitative table.

Usage

```
check_mina_qu(x)
```

Arguments

x An object of class mina with 'tab' defined.

Value

TRUE if the object contains quantitative table and is not empty.

Examples

```
data(maize)
check_mina_qu(maize)
```

cls	<i>Get the slot 'cls'.</i>
-----	----------------------------

Description

Get the slot 'cls'.

Usage

```
cls(x)
```

Arguments

x The 'mina' object.

Value

The 'cls' slot of the object.

cls<-	<i>Setter for the slot 'cls'.</i>
-------	-----------------------------------

Description

Setter for the slot 'cls'.

Usage

```
cls(x) <- value

## S4 replacement method for signature 'mina'
cls(x) <- value
```

Arguments

x The 'mina' object.
value The value to set for the slot of the 'mina' object 'x'.

Value

The 'cls' slot of the 'mina' object.

cls_tab	<i>Get the slot 'cls_tab'.</i>
---------	--------------------------------

Description

Get the slot 'cls_tab'.

Usage

```
cls_tab(x)
```

Arguments

x The 'mina' object.

Value

The 'cls_tab' slot of the object.

Examples

```
cls_tab(maize)
```

cls_tab<-	<i>Setter for the slot 'cls_tab'.</i>
-----------	---------------------------------------

Description

Setter for the slot 'cls_tab'.

Usage

```
cls_tab(x) <- value

## S4 replacement method for signature 'mina'
cls_tab(x) <- value
```

Arguments

x The 'mina' object.
value The value to set for the slot of the 'mina' object 'x'.

Value

The 'cls_tab' slot of the 'mina' object.

com_dis	<i>Calculate the community dissimilarity / distance matrix.</i>
---------	---

Description

Calculate the community dissimilarity / distance matrix.

Usage

```
com_dis(x, method = "bray", ...)
```

Arguments

x	An object of the class <code>mina</code> with 'norm' defined or any quantitative matrix.
method	The dissimilarity / distance method used, default 'bray'.
...	Additional parameters.

Value

The distance / dissimilarity matrix.

Examples

```
asv_norm <- norm_tab(maize_asv2, method = "raref", depth = 1000)
asv_dis <- com_dis(asv_norm, method = "bray")
```

com_dis,matrix,ANY-method	<i>Calculate the community dissimilarity / distance matrix of the input matrix.</i>
---------------------------	---

Description

Calculate the community dissimilarity / distance matrix of the input matrix.

Usage

```
## S4 method for signature 'matrix,ANY'
com_dis(x, method = "bray", threads = 80, nblocks = 400, ...)

## S4 method for signature 'matrix,character'
com_dis(x, method = "bray", threads = 80, nblocks = 400, ...)
```

Arguments

x	A matrix of the quantitative table.
method	The dissimilarity / distance method used, default 'bray'.
threads	(optional, only needed when method == "tina") The number of threads used for parallel running.
nblocks	(optional, only needed when method == "tina") The number of row / column for splitted sub-matrix.
...	Additional parameters.

Value

y The dissimilarity / distance matrix.

Examples

```
asv_norm <- norm_tab(maize_asv2, method = "raref", depth = 1000)
asv_dis <- com_dis(asv_norm, method = "bray")
```

com_dis,mina,ANY-method

Calculate the community dissimilarity / distance matrix of 'norm' with 'mina' class object as input.

Description

Calculate the community dissimilarity / distance matrix of 'norm' with 'mina' class object as input.

Usage

```
## S4 method for signature 'mina,ANY'
com_dis(x, method = "bray", threads = 80, nblocks = 400, ...)

## S4 method for signature 'mina,character'
com_dis(x, method = "bray", threads = 80, nblocks = 400, ...)
```

Arguments

x	An object of the class 'mina' with 'norm' defined.
method	The dissimilarity / distance method used, default 'bray'.
threads	(optional, only needed when method == "tina") The number of threads used for parallel running.
nblocks	(optional, only needed when method == "tina") The number of row / column for splitted sub-matrix.
...	Additional parameters.

Value

x The same 'mina' object with @dis added.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "total")
maize <- fit_tabs(maize)
maize <- com_dis(maize, method = "bray")
```

com_dis_list	<i>List of dissimilarity / distance supported in com_dis. Dissimilarity / distance should be specified by exact string match.</i>
--------------	---

Description

List of dissimilarity / distance supported in [com_dis](#). Dissimilarity / distance should be specified by exact string match.

Usage

```
com_dis_list
```

Format

A list of character vectors indicate the dissimilarity / distance method used.

tina TINA from Schmidt_et_al_2016

Jaccard Jaccard defined by [vegdist](#)

weighted Dissimilarity / distance method for weighted matrix:

bhjattacharyya from [parDist](#)

canberra from [parDist](#)

bray from [parDist](#)

chord from [parDist](#)

divergence from [parDist](#)

euclidean from [parDist](#)

fJaccard from [parDist](#)

geodesic from [parDist](#)

hellinger from [parDist](#)

kullback from [parDist](#)

manhattan from [parDist](#)

maximum from [parDist](#)

minkowski from [parDist](#)

podani from [parDist](#)

soergel from [parDist](#)

wave from [parDist](#)

whittaker from [parDist](#)

unweighted Dissimilarity / Distance for unweighted matrix:

binary from [parDist](#)

braun-blanquet from [parDist](#)

consine from [parDist](#)

dice from [parDist](#)

fager from [parDist](#)

faith from [parDist](#)

hamman from [parDist](#)

hamming from [parDist](#)

kulczynski1 from [parDist](#)

kulczynski2 from [parDist](#)

michael from [parDist](#)

mountford from [parDist](#)

mozley from [parDist](#)

ochiai from [parDist](#)

phi from [parDist](#)

russel from [parDist](#)

simple matching from [parDist](#)

simpson from [parDist](#)

stiles from [parDist](#)

tanimoto from [parDist](#)

yule from [parDist](#)

yule2 from [parDist](#)

Examples

? com_dis_list

com_plot	<i>Visualization of components distance / dissimilarity in k dimension.</i>
----------	---

Description

Visualization of components distance / dissimilarity in k dimension.

Usage

```
com_plot(x, match, ...)
```

Arguments

x	An object of class 'mina' with 'dmr' and 'des' defined.
match	The column name of the components IDs in 'des' which exactly the same indicated in 'dmr'.
...	Additional parameters.

Value

The PCoA plot.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref", depth = 5000)
maize <- fit_tabs(maize)
maize <- com_dis(maize, method = "bray")
maize <- dmr(maize)
p1a <- com_plot(maize, match = "Sample_ID", color = "Compartment")
p1b <- com_plot(maize, match = "Sample_ID", d1 = 3, d2 = 4,
color = "Compartment")
p2a <- com_plot(maize, match = "Sample_ID", color = "Host_genotype")
p2b <- com_plot(maize, match = "Sample_ID", d1 = 1, d2 = 3, color =
"Host_genotype")
p3a <- com_plot(maize, match = "Sample_ID", color = "Compartment", shape =
"Soil")
p3b <- com_plot(maize, match = "Sample_ID", d1 = 1, d2 = 4, color =
"Compartment", shape = "Soil")
```

 com_plot,mina,ANY-method

Visualization of components distance / dissimilarity in k dimension.

Description

Visualization of components distance / dissimilarity in k dimension.

Usage

```
## S4 method for signature 'mina,ANY'
com_plot(x, match, d1 = 1, d2 = 2, color, shape = NULL, ...)

## S4 method for signature 'mina,character'
com_plot(x, match, d1 = 1, d2 = 2, color, shape = NULL, ...)

## S4 method for signature 'mina,character'
com_plot(x, match, d1 = 1, d2 = 2, color, shape = NULL, ...)
```

Arguments

x	An object of 'mina' with list 'dmr' defined.
match	The column name of the components IDs in 'des' with exactly the same as rownames in x.
d1	The dimension be visualized in x-axis, default '1'.
d2	The dimension be visualized in y-axis, default '2'.
color	The column name in 'des' to be used for different color groups.
shape	The column name in 'des' to be used for different shape groups, default 'NULL'.
...	Additional parameters.

Value

p The plotted figure.
The PCoA plot.

Examples

```
maize <- new("mina", tab = maize_asv, des = maize_des)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- com_dis(maize, method = "bray")
maize <- dmr(maize)
p1a <- com_plot(maize, match = "Sample_ID", color = "Compartment")
p1b <- com_plot(maize, match = "Sample_ID", d1 = 3, d2 = 4,
color = "Compartment")
p2a <- com_plot(maize, match = "Sample_ID", color = "Host_genotype")
```

```
p2b <- com_plot(maize, match = "Sample_ID", d1 = 1, d2 = 3, color =  
"Host_genotype")  
p3a <- com_plot(maize, match = "Sample_ID", color = "Compartment", shape =  
"Soil")  
p3b <- com_plot(maize, match = "Sample_ID", d1 = 1, d2 = 4, color =  
"Compartment", shape = "Soil")
```

com_r2	<i>Calculate the unexplained variance ratio using formula indicated in: Anderson, M.J. 2001. A new method for non-parametric multivariate analysis of variance. Austral Ecology, 26: 32–46.</i>
--------	---

Description

Calculate the unexplained variance ratio using formula indicated in: Anderson, M.J. 2001. A new method for non-parametric multivariate analysis of variance. Austral Ecology, 26: 32–46.

Usage

```
com_r2(x, group)
```

Arguments

x	An object of class 'mina' with 'dis' and 'des' defined.
group	The name(s) of column(s) defined as experimental setup group(s).

Value

Unexplained variance ratio.

Examples

```
data(maize)  
maize <- norm_tab(maize, method = "raref", depth = 5000)  
maize <- fit_tabs(maize)  
maize <- com_dis(maize, method = "bray")  
com_r2(maize, group = c("Compartment", "Soil", "Host_genotype"))
```

com_r2,mina,ANY-method

Function for unexplained variance ratio calculation indicated in Anderson, M.J. 2001. A new method for non-parametric multivariate analysis of variance. Austral Ecology, 26: 32–46.

Description

Function for unexplained variance ratio calculation indicated in Anderson, M.J. 2001. A new method for non-parametric multivariate analysis of variance. Austral Ecology, 26: 32–46.

Usage

```
## S4 method for signature 'mina,ANY'
com_r2(x, group)

## S4 method for signature 'mina,character'
com_r2(x, group)
```

Arguments

x An mina object with 'dis' and 'des' defined.
 group The name(s) of column(s) defined as experimental setup group(s).

Value

r2 The variance ratio cannot be explained by given groups.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- com_dis(maize, method = "bray")
com_r2(maize, group = c("Compartment", "Soil", "Host_genotype"))
```

cp_cor

Function for correlation coefficient calculation.

Description

Function for correlation coefficient calculation.

Usage

```
cp_cor(mat)
```

Arguments

mat The input matrix for correlation calculation.

Value

The output correlation matrix.

data-hmp	<i>Internal testing data of HMP project, including quantitative table (hmp_otu) and descriptive table (hmp_des) for testing.</i>
----------	--

Description

Internal testing data of HMP project, including quantitative table (hmp_otu) and descriptive table (hmp_des) for testing.

Examples

```
data(hmp)
```

data-maize	<i>Internal testing data of maize project, vegetative stage samples only, including quantitative table (maize_asv.rds) and descriptive table (maize_des.txt) for testing.</i>
------------	---

Description

Internal testing data of maize project, vegetative stage samples only, including quantitative table (maize_asv.rds) and descriptive table (maize_des.txt) for testing.

Examples

```
data(maize)
```

des<- *Setter and getter for the slot 'des', which is the description and meta data of rows in 'tab'.*

Description

Setter and getter for the slot 'des', which is the description and meta data of rows in 'tab'.

Usage

```
des(x) <- value

## S4 replacement method for signature 'mina'
des(x) <- value

des(x)

## S4 method for signature 'mina'
des(x)
```

Arguments

x The 'mina' object.
value The value to set for the slot of the 'mina' object 'x'.

Value

The 'des' slot of the 'mina' object.

Examples

```
des(maize) <- maize_des2
head(des(maize))
```

dis<- *Setter and getter for the slot 'dis'.*

Description

Setter and getter for the slot 'dis'.
Get the slot 'dis'

Usage

```
dis(x) <- value

dis(x)

## S4 replacement method for signature 'mina'
dis(x) <- value

## S4 method for signature 'mina'
dis(x)
```

Arguments

x	The 'mina' object.
value	The value to set for the slot of the 'mina' object 'x'.

Value

The 'dis' slot of the 'mina' object.

Examples

```
maize_norm <- norm_tab(maize_asv2, method = "total")
dis(maize) <- com_dis(maize_norm, method = "bray")
dis(maize)[1:5, 1:5]
```

dis_bs

Getter for the slots 'dis_bs', 'dis_pm' and 'dis_stat'.

Description

Getter for the slots 'dis_bs', 'dis_pm' and 'dis_stat'.

Usage

```
dis_bs(x)

dis_pm(x)

dis_stat(x)
```

Arguments

x	The 'mina' object.
---	--------------------

Value

The 'dis_bs', 'dis_pm' and 'dis_stat' slots of the 'mina' object.

dmr	<i>Dimensionality reduction of community dissimilarity / distance for visualization.</i>
-----	--

Description

Dimensionality reduction of community dissimilarity / distance for visualization.

Usage

```
dmr(x, k = 2)
```

Arguments

x	An object of class 'mina' with 'dis' defined or a distance matrix.
k	The dimension number after reduction.

Value

The dimensionality reduction results.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- com_dis(maize, method = "bray")
maize <- dmr(maize)
```

dmr,matrix-method	<i>Dimensionality reduction of the distance matrix.</i>
-------------------	---

Description

Dimensionality reduction of the distance matrix.

Usage

```
## S4 method for signature 'matrix'
dmr(x, k = 4)
```

Arguments

x	A distance matrix.
k	The number of dimensionality after reduction, 4 by default.

Value

y The coordinates of components indicated in distance matrix in k dimension.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- com_dis(maize, method = "bray")
asv_dis <- dis(maize)
asv_dis_dmr <- dmr(asv_dis, k = 4)
```

dmr,mina-method	<i>Dimensionality reduction of the 'dis' included in mina.</i>
-----------------	--

Description

Dimensionality reduction of the 'dis' included in mina.

Usage

```
## S4 method for signature 'mina'
dmr(x, k = 4)
```

Arguments

x An object of the class 'mina' with 'dis' defined.
k The number of dimensionality after reduction, 4 by default.

Value

x The same object with 'dmr' added.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- com_dis(maize, method = "bray")
maize <- dmr(maize)
```

filter_mat	<i>Function for filtering of matrix, rows present in less than 'p' columns will be removed. After row filtering, columns with a sum of 0 will be removed.</i>
------------	---

Description

Function for filtering of matrix, rows present in less than 'p' columns will be removed. After row filtering, columns with a sum of 0 will be removed.

Usage

```
filter_mat(x, p)
```

Arguments

x	The input matrix to be filtered.
p	The cutoff for non-zero column number.

Value

x The same matrix after filtering.

fit_tabs	<i>Filter the quantitative and descriptive table to make them have the same samples, the intersect samples will be remained.</i>
----------	--

Description

Filter the quantitative and descriptive table to make them have the same samples, the intersect samples will be remained.

Usage

```
fit_tabs(x)
```

Arguments

x	An object of the class mina with 'tab' and 'des' defined or a quantitative matrix(need parameter des in this case).
---	---

Value

Same 'mina' object but fitted 'tab' and 'des' (as well as 'norm' if defined)

Examples

```
data(maize)
maize <- fit_tabs(maize)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
```

`fit_tabs,mina-method` *Filter the quantitative and descriptive table to make them have the same samples, samples present in both tables are remained. If 'norm' table exist in the 'mina' object, descriptive table will be filtered again to only keep samples present in 'norm'.*

Description

Filter the quantitative and descriptive table to make them have the same samples, samples present in both tables are remained. If 'norm' table exist in the 'mina' object, descriptive table will be filtered again to only keep samples present in 'norm'.

Usage

```
## S4 method for signature 'mina'
fit_tabs(x)
```

Arguments

x An object of class `mina`.

Value

x The same object as input with fitted 'tab', 'des' and 'norm' (if defined).

Examples

```
{
  data(maize)
  maize <- fit_tabs(maize)
  maize <- norm_tab(maize, method = "total")
  maize <- fit_tabs(maize)
}
```

get_contrast	<i>Get the contrast between two networks / adjacency matrices.</i>
--------------	--

Description

Get the contrast between two networks / adjacency matrices.

Usage

```
get_contrast(x, y)
```

Arguments

x	The network/adjacency matrix of one of the compared condition.
y	The other network/adjacency matrix.

Value

The contrast between two matrices.

get_contrast_grp	<i>Get the contrast of groups of nodes between two networks/adjacency matrices.</i>
------------------	---

Description

Get the contrast of groups of nodes between two networks/adjacency matrices.

Usage

```
get_contrast_grp(x, y, grp)
```

Arguments

x	The network/adjacency matrix of one of the compared condition.
y	The other network/adjacency matrix.
grp	The group information.

Value

The contrast between two matrices.

get_dis_df	<i>Function for getting distance data frame from 'dist'.</i>
------------	--

Description

Function for getting distance data frame from 'dist'.

Usage

```
get_dis_df(x)
```

Arguments

x The object of class 'dist'.

Value

The data frame of distance matrix.

get_ja	<i>Get the Jaccard distance between two networks / adjacency matrices.</i>
--------	--

Description

Get the Jaccard distance between two networks / adjacency matrices.

Usage

```
get_ja(x, y)
```

Arguments

x The network/adjacency matrix of one of the compared condition.

y The other network/adjacency matrix.

Value

The Jaccard distance between two matrices.

get_ja0	<i>Get the Jaccard0 distance between two networks / adjacency matrices.</i>
---------	---

Description

Get the Jaccard0 distance between two networks / adjacency matrices.

Usage

```
get_ja0(x, y)
```

Arguments

x	The network/adjacency matrix of one of the compared condition.
y	The other network/adjacency matrix.

Value

The Jaccard0 distance between two matrices.

get_ja0_grp	<i>Get the Jaccard0 distance between two networks / adjacency matrices.</i>
-------------	---

Description

Get the Jaccard0 distance between two networks / adjacency matrices.

Usage

```
get_ja0_grp(x, y, grp)
```

Arguments

x	The network/adjacency matrix of one of the compared condition.
y	The other network/adjacency matrix.
grp	The table with group information.

Value

The Jaccard0 distance between two matrices.

get_ja_grp	<i>Get the Jaccard distance between two networks / adjacency matrices.</i>
------------	--

Description

Get the Jaccard distance between two networks / adjacency matrices.

Usage

```
get_ja_grp(x, y, grp)
```

Arguments

x	The network/adjacency matrix of one of the compared condition.
y	The other network/adjacency matrix.
grp	The table with group information.

Value

The Jaccard distance between two matrices.

get_net_cls_tab	<i>Get the cluster table 'cls_tab' from quantitative table 'norm' and network clustering results 'cls'.</i>
-----------------	---

Description

Get the cluster table 'cls_tab' from quantitative table 'norm' and network clustering results 'cls'.

Usage

```
get_net_cls_tab(x_norm, x_cls, uw = FALSE)
```

Arguments

x_norm	The normalized quantitative table used for network inference and clustering.
x_cls	The network clustering table.
uw	By summing up the number of present components of each cluster instead of relative abundance, default is FALSE.

Value

x_cls The quantitative table with clusters in rows.

Examples

```

maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref", depth = 1000)
maize <- fit_tabs(maize)
maize_norm <- norm(maize)
maize_adj <- adj(maize_norm, method = "spearman")
maize_cls <- net_cls(maize_adj, method = "ap", cutoff = 0.5)
maize_cls_tab <- get_net_cls_tab(maize_norm, maize_cls)

```

```
get_net_cls_tab,matrix,data.frame-method
```

Get the cluster table 'cls_tab' from quantitative table 'norm' and network clustering results 'cls'.

Description

Get the cluster table 'cls_tab' from quantitative table 'norm' and network clustering results 'cls'.

Usage

```

## S4 method for signature 'matrix,data.frame'
get_net_cls_tab(x_norm, x_cls, uw = FALSE)

```

Arguments

x_norm	The normalized quantitative table used for network inference and clustering.
x_cls	The network clustering table.
uw	By summing up the number of present components of each cluster instead of relative abundance, default is FALSE.

Value

x_cls The quantitative table with clusters in rows.

Examples

```

maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref", depth = 1000)
maize <- fit_tabs(maize)
maize_norm <- norm(maize)
maize_adj <- adj(maize_norm, method = "spearman")
maize_cls <- net_cls(maize_adj, method = "ap", cutoff = 0.5)
maize_cls_tab <- get_net_cls_tab(maize_norm, maize_cls)

```

get_r2	<i>Same function as 'com_r2' with matrix and corresponding descriptive table as input.</i>
--------	--

Description

Same function as 'com_r2' with matrix and corresponding descriptive table as input.

Usage

```
get_r2(x, des, group)
```

Arguments

x	Dissimilarity / distance matrix which indicate variances.
des	The descriptive table of samples which define the groups.
group	The name(s) of column(s) used as experimental setup group(s) in descriptive file.

Value

r2 The variance ratio cannot be explained by given groups.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- com_dis(maize, method = "bray")
get_r2(dis(maize), des(maize), group = c("Compartment", "Soil"))
```

get_r2,matrix,ANY,ANY-method

Function for unexplained variance ratio calculation indicated in Anderson, M.J. 2001. A new method for non-parametric multivariate analysis of variance. Austral Ecology, 26: 32–46.

Description

Function for unexplained variance ratio calculation indicated in Anderson, M.J. 2001. A new method for non-parametric multivariate analysis of variance. Austral Ecology, 26: 32–46.

Usage

```
## S4 method for signature 'matrix,ANY,ANY'
get_r2(x, des, group)

## S4 method for signature 'matrix,data.frame,ANY'
get_r2(x, des, group)

## S4 method for signature 'matrix,data.frame,character'
get_r2(x, des, group = c("Host_genotype", "Compartment", "Soil", "Management"))
```

Arguments

x	Dissimilarity / distance matrix which indicate variances.
des	The descriptive table of samples which define the groups.
group	The name(s) of column(s) used as experimental setup group(s) in descriptive file.

Value

r2 The variance ratio cannot be explained by given groups.

Examples

```
maize <- new("maize", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- com_dis(maize, method = "bray")
x <- dis(maize)
des <- des(maize)
get_r2(x, des, group = c("Compartment", "Soil"))
```

get_rep	<i>Get the representative community members by extracting the most abundant and prevalent compositions.</i>
---------	---

Description

Get the representative community members by extracting the most abundant and prevalent compositions.

Get the representative community members.

Usage

```
get_rep(x, ...)

## S4 method for signature 'matrix'
get_rep(x, top = 5)
```

Arguments

`x` A quantitative matrix with samples in columns and compositions in rows.
`...` Additional parameters.
`top` The percent of the most abundant and prevalent members.

Value

The matrix with samples in columns and representative compositions in rows.
The matrix with samples in columns and representative compositions in rows.

Examples

```
data(maize_asv)
maize_asv_rep <- get_rep(maize_asv)
data(maize_asv)
maize_asv_rep <- get_rep(maize_asv, top = 5)
```

`get_rep,mina-method` *Get the representative community members.*

Description

Get the representative community members.

Usage

```
## S4 method for signature 'mina'
get_rep(x, top = 5)
```

Arguments

`x` An object of the class ‘mina’ with @norm define.
`top` The percent of the most abundant and prevalent members.

Value

The same object with @norm replaced by the representative members.

Examples

```
maize <- new("mina", tab = maize_asv, des = maize_des)
maize <- norm_tab(maize, method = "raref")
maize <- get_rep(maize, top = 5)
```

`get_spectra`*Function for calculation of eigenvalue of given matrix.*

Description

Function for calculation of eigenvalue of given matrix.

Usage

```
get_spectra(x, k = 100)
```

Arguments

x	The input matrix.
k	Get the first k eigenvalues.

Value

y The vector of the first k eigenvalues.

`get_stat`*Function for distance statistic and significance test.*

Description

Function for distance statistic and significance test.

Usage

```
get_stat(x, p = NULL)
```

Arguments

x	The bootstrap distance data frame.
p	The permutation distance data frame.

Value

The statistics of network comparison.

hmp_des	<i>Design file for HMP project, including 2711 samples in total.</i>
---------	--

Description

Design file for HMP project, including 2711 samples in total.

Format

A data frame with columns:

Sample_ID The unique ID of the microbial profiling sample.

Sex The gender of the host human.

Run_center The lab processing the sample sequencing.

Subsite The subsite of body where samples were collected.

Site The site of body where samples were collected.

Description The further details about the samples.

Source

HMP project.

Examples

```
data(hmp_des)
```

hmp_otu	<i>OTU table of HMP project, data downloaded from https://www.hmpdacc.org/hmp/HMQCP/</i>
---------	---

Description

OTU table of HMP project, data downloaded from <https://www.hmpdacc.org/hmp/HMQCP/>

Format

A matrix with samples in columns and OTUs in rows.

Source

HMP project.

Examples

```
data(hmp_otu)
```

maize_asv	<i>ASV table of maize project, vegetative stage samples only.</i>
-----------	---

Description

ASV table of maize project, vegetative stage samples only.

Format

A matrix with samples in columns and ASVs in rows. Unnormalized table including 12765 ASVs from 420 samples.

Source

RECONSTRUCT project, maize microbiome part.

Examples

```
data(maize_asv)
```

maize_asv2	<i>Subset of ASV table of maize project, ASVs appear in less than 100 samples were filtered for later analysis.</i>
------------	---

Description

Subset of ASV table of maize project, ASVs appear in less than 100 samples were filtered for later analysis.

Format

A matrix with samples in columns and ASVs in rows. Unnormalized table including 1219 ASVs from 313 samples.

Source

RECONSTRUCT project, maize microbiome part.

Examples

```
data(maize_asv2)
```

maize_des	<i>Design file of maize project, vegetative stage samples only, including 528 samples in total.</i>
-----------	---

Description

Design file of maize project, vegetative stage samples only, including 528 samples in total.

Format

A data frame with columns:

Sample_ID The unique ID of the microbial profiling sample.

Host_genotype The genotype of the plant host maize.

Compartment The compartment of the microbial sample comes from.

Soil The soil of the sampled microbiome.

Management The management of the soil where microbial sample from.

Source

RECONSTRUCT project, maize microbiome part.

Examples

```
data(maize_des)
```

maize_des2	<i>Subset of design file of maize project, 313 samples are included.</i>
------------	--

Description

Subset of design file of maize project, 313 samples are included.

Format

A data frame with columns:

Sample_ID The unique ID of the microbial profiling sample.

Host_genotype The genotype of the plant host maize.

Compartment The compartment of the microbial sample comes from.

Soil The soil of the sampled microbiome.

Management The management of the soil where microbial sample from.

Source

RECONSTRUCT project, maize microbiome part.

Examples

```
data(maize_des2)
```

mat_or_NULL-class	<i>Modified from https://github.com/joey711/phyloseq/blob/master/R/allClasses.R Use <code>setClassUnion</code> to define the unholy NULL-data union as a virtual class. This is a way of dealing with the expected scenarios in which one or more of the component data classes is not available, in which case NULL will be used instead.</i>
-------------------	---

Description

Modified from <https://github.com/joey711/phyloseq/blob/master/R/allClasses.R> Use `setClassUnion` to define the unholy NULL-data union as a virtual class. This is a way of dealing with the expected scenarios in which one or more of the component data classes is not available, in which case NULL will be used instead.

mina-class	<i>Class "mina" includes the quantitative table and descriptive table.</i>
------------	--

Description

Class "mina" includes the quantitative table and descriptive table.

Slots

`tab` The quantitative table of the dataset.

`des` The descriptive table of the samples listed in `@tab`.

`norm` The normalized quantitative table of `@tab`.

`dis` The distance / dissimilarity matrix between samples in `@tab`.

`dmr` The list of dimensionality reduction result, includes points and variance.

`adj` The adjacency matrix between pairwise compositions (e.g. OTUs/ASVs)

`adj_sig` The P-value matrix of adjacency matrix, only applicable for Pearson and Spearman correlation adjacency matrices.

`cls` The cluster information for each composition.

`cls_tab` The cluster quantitative table.

`multi` The list of subsampled adjacency matrices for each environment.

perm The list of permuted adjacency matrices for each pairwise environmental comparison.
 dis_bs The distance between networks of different environmental communities.
 dis_pm The distance between networks of permuted groups.
 dis_stat The average distance between subsampled environmental community networks, permuted networks and corresponding significance.

Author(s)

Rui Guan <https://github.com/Guan06>

Examples

```
maize <- new("mina", tab = maize_asv, des = maize_des)
```

multi<- *Setter and getter for the slot 'multi' and 'perm'.*

Description

Setter and getter for the slot 'multi' and 'perm'.

Usage

```
multi(x) <- value

multi(x)

## S4 replacement method for signature 'mina'
multi(x) <- value

## S4 method for signature 'mina'
multi(x)

perm(x) <- value

perm(x)

## S4 replacement method for signature 'mina'
perm(x) <- value

## S4 method for signature 'mina'
perm(x)
```

Arguments

x The 'mina' object.
 value The value to set for the slot of the 'mina' object 'x'.

Value

The 'multi' or/and 'perm' slot of the 'mina' object.

net_cls	<i>Network clustering of sparsed adjacency matrix.</i>
---------	--

Description

Network clustering of sparsed adjacency matrix.

Usage

```
net_cls(x, method, ...)
```

Arguments

x	An object of class 'mina' with 'adj' defined.
method	The clustering method used.
...	Additional parameters.

Value

The network clustering results.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref", depth = 1000)
maize <- fit_tabs(maize)
maize <- adj(maize, method = "spearman")
maize <- net_cls(maize, method = "mcl", cutoff = 0.4, neg = FALSE)
```

net_cls,matrix,ANY-method	<i>Network clustering based on the sparsed adjacency matrix.</i>
---------------------------	--

Description

Network clustering based on the sparsed adjacency matrix.

Usage

```
## S4 method for signature 'matrix,ANY'
net_cls(x, method, cutoff = 0.4, neg = FALSE, ...)

## S4 method for signature 'matrix,character'
net_cls(x, method, cutoff = 0.4, neg = FALSE, ...)
```

Arguments

x	Adjacency matrix used for clustering.
method	The clustering method used.
cutoff	The cutoff for the sparsed adjacency matrix, default 0.4.
neg	Whether to keep the negative edges, cannot be TRUE when using 'mcl' for clustering. Default FALSE.
...	Additional parameters.

Value

y The cluster table.

Examples

```
asv_norm <- norm_tab(maize_asv2, method = "raref", depth = 1000)
asv_adj <- adj(asv_norm, method = "spearman")
asv_cls <- net_cls(asv_adj, method = "mcl")
```

net_cls,mina,ANY-method

Network clustering based on the sparsed adjacency matrix.

Description

Network clustering based on the sparsed adjacency matrix.

Usage

```
## S4 method for signature 'mina,ANY'
net_cls(x, method, cutoff = 0.4, neg = FALSE, ...)

## S4 method for signature 'mina,character'
net_cls(x, method, cutoff = 0.4, neg = FALSE, ...)
```

Arguments

x	An object of class 'mina' with 'adj' defined.
method	The clustering method used.
cutoff	The cutoff for the sparsed adjacency matrix, default 0.4.
neg	Whether to keep the negative edges, cannot be TRUE when using 'mcl' for clustering. Default FALSE.
...	Additional parameters.

Value

x The same 'mina' class with @cls added.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref", depth = 1000)
maize <- fit_tabs(maize)
maize <- adj(maize, method = "spearman")
maize <- net_cls(maize, method = "mcl", cutoff = 0.4, neg = FALSE)
maize <- net_cls(maize, method = "ap", cutoff = 0.4, neg = FALSE)
```

net_cls_tab	<i>Get the cluster table 'cls_tab' from 'norm' and 'cls'.</i>
-------------	---

Description

Get the cluster table 'cls_tab' from 'norm' and 'cls'.

Usage

```
net_cls_tab(x, uw = FALSE)
```

Arguments

x	An object of class 'mina' with 'norm' and 'cls' defined.
uw	By summing up the number of present components of each cluster instead of relative abundances, default is FALSE.

Value

The network cluster relative abundance table.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref", depth = 1000)
maize <- fit_tabs(maize)
maize <- adj(maize, method = "spearman")
maize <- net_cls(maize, method = "ap", cutoff = 0.5)
maize <- net_cls_tab(maize)
```

```
net_cls_tab, mina-method
```

Get the cluster table 'cls_tab' from quantitative table 'norm' and network clustering results 'cls'.

Description

Get the cluster table 'cls_tab' from quantitative table 'norm' and network clustering results 'cls'.

Usage

```
## S4 method for signature 'mina'
net_cls_tab(x, uw = FALSE)
```

Arguments

x An object of class 'mina' with 'norm' and 'cls' defined.

uw By summing up the number of present components of each cluster instead of relative abundance, default is FALSE.

Value

x The same 'mina' object with 'cls_tab' added.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref", depth = 1000)
maize <- fit_tabs(maize)
maize <- adj(maize, method = "spearman")
maize <- net_cls(maize, method = "mcl", cutoff = 0.5)
maize <- net_cls_tab(maize)
```

```
net_dis
```

Calculate the network distance of 'multi' and test the significance when 'perm' is defined.

Description

Calculate the network distance of 'multi' and test the significance when 'perm' is defined.

Usage

```
net_dis(x, method, ...)
```


Arguments

x An object of class 'mina' with 'multi' (and 'perm' if 'sig' is TRUE) defined.
 method The distance to be calculated, "spectra" and "Jaccard" are available.
 ... Additional parameters.

Value

The network comparison result.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- get_rep(maize, top = 5)
maize <- bs_pm(maize, group = "Compartment")
maize <- net_dis(maize, method = "spectra", evk = 30)
```

net_dis,mina,ANY-method

Calculate the network distance of 'multi' and test the significance when 'perm' is defined.

Description

Calculate the network distance of 'multi' and test the significance when 'perm' is defined.

Usage

```
## S4 method for signature 'mina,ANY'
net_dis(
  x,
  method,
  evk = 100,
  egv = TRUE,
  dir = "./",
  sig = TRUE,
  skip = TRUE,
  ...
)

## S4 method for signature 'mina,character'
net_dis(
  x,
  method,
  evk = 100,
  egv = TRUE,
```

```

  dir = "./",
  sig = TRUE,
  skip = TRUE,
  ...
)

```

Arguments

x	An object of class 'mina' with 'multi' (and 'perm' if sig is TRUE) defined.
method	The distance to be calculated, "spectra" and "Jaccard" are available.
evk	The first 'evk' eigenvalues will be used for 'spectra' distance, the default is 100.
egv	Whether to output the eigenvectors for Spectral distance, the default is TRUE, only validate when 'method == "spectra"'.
dir	The folder to output the eigenvectors, only validate when 'egv == TRUE'.
sig	Whether to test the significance, if TRUE (by default), 'perm' is needed.
skip	Whether to skip the comparison when the dimension of adjacency matrix is smaller than setted 'evk'.
...	Additional parameters.

Value

x The same 'mina' object with 'net_dis' defined.

Examples

```

maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- bs_pm(maize, group = "Compartment")
maize <- net_dis(maize, method = "Jaccard")

```

net_dis_indi	<i>Calculate the network distance of bootstrap and permutation when applicable.</i>
--------------	---

Description

Calculate the network distance of bootstrap and permutation when applicable.

Calculate the network distance of bootstrap and permutation when applicable.

Usage

```
net_dis_indi(x, method, ...)

## S4 method for signature 'character,ANY'
net_dis_indi(
  x,
  method,
  evk = 100,
  sig = TRUE,
  skip = TRUE,
  egv = TRUE,
  dir = "./",
  ...
)

## S4 method for signature 'character,character'
net_dis_indi(
  x,
  method,
  evk = 100,
  sig = TRUE,
  skip = TRUE,
  egv = TRUE,
  dir = "./",
  ...
)
```

Arguments

x	The folder store the network inference results. defined.
method	The distance to be calculated, "spectra" and "Jaccard" are available.
...	Additional parameters.
evk	The first 'evk' eigenvalues will be used for 'spectra' distance, the default is 100.
sig	Whether to test the significance, if TRUE (by default), permutation results should be included in the folder 'x'.
skip	Whether to skip the comparison when the dimension of adjacency matrix is smaller than setted 'evk', default TRUE.
egv	Whether to output the eigenvectors for Spectral distance, the default is TRUE, only validate when 'method == "spectra"'.
dir	The folder to output the eigenvectors, only validate when 'egv == TRUE'.

Value

y The 'mina' object with 'dis_bs', 'dis_pm' and 'dis_stat'.

y The 'mina' object with 'dis_bs', 'dis_pm' and 'dis_stat'.

Examples

```
## Not run:
data(maize)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- get_rep(maize, top = 5)
maize <- bs_pm(maize, group = "Compartment", individual = TRUE, out_dir =
"./individual_bs_pm/")
maize_stat1 <- net_dis_indi(x = "./individual_bs_pm/", method = "spectra")
maize_stat2 <- net_dis_indi(x = "./individual_bs_pm/", method = "Jaccard")
maize_stat3 <- net_dis_indi(x = "./individual_bs_pm/", method = "spectra",
evk = 100, skip = TRUE)

## End(Not run)
## Not run:
data(maize)
norm(maize) <- maize_asv2
maize <- fit_tabs(maize)
maize <- get_rep(maize, top= 5)
maize <- bs_pm(maize, group = "Compartment", individual = TRUE, out_dir =
"./individual_bs_pm/")
maize_stat1 <- net_dis_indi("./individual_bs_pm/", method = "spectra")
maize_stat2 <- net_dis_indi("./individual_bs_pm/", method = "Jaccard")
maize_stat3 <- net_dis_indi("./individual_bs_pm/", method = "spectra",
evk = 100, skip = TRUE)

## End(Not run)
```

net_dis_pcoa

Visualization of spectra network distance as PCoA.

Description

Visulization of spectra network distance as PCoA.

Visulization of spectra network distance as PCoA.

Usage

```
net_dis_pcoa(x)

## S4 method for signature 'character'
net_dis_pcoa(x)
```

Arguments

x The folder with all egv files generated by net_dis_indi().

Value

p The plotted figure.

p The plotted figure.

Examples

```
## Not run:
data(maize)
norm(maize) <- maize_asv2
maize <- fit_tabs(maize)
maize <- bs_pm(maize, group = "Compartment", individual = TRUE, out_dir =
"./individual_bs_pm/")
maize <- net_dis_indi("./individual_bs_pm/", method = "spectra", egv = TRUE,
dir = "./egv_folder/")
p <- net_dis_pcoa("./egv_folder/")

## End(Not run)
## Not run:
data(maize)
maize <- norm_tab(maize)
maize <- fit_tabs(maize)
maize <- get_rep(maize, top = 5)
maize <- bs_pm(maize, group = "Compartment", individual = TRUE, out_dir =
"./individual_bs_pm/")
maize <- net_dis_indi("./individual_bs_pm/", method = "spectra", egv = TRUE,
dir = "./egv_folder/")
p <- net_dis_pcoa("./egv_folder/")

## End(Not run)
```

net_dis_plot

Visualization of network distance, average distances are used for tile plot.

Description

Visualization of network distance, average distances are used for tile plot.

Visualization of network distance, average distances are used for tile plot.

Usage

```
net_dis_plot(x, d = "BS", ...)
```

```
## S4 method for signature 'mina'
net_dis_plot(x, d = "BS", sig = TRUE)
```

Arguments

x	An object of 'mina' with slot 'dis_stat' defined.
d	The distance to be plotted, could be "BS" or "PM".
...	Additional parameters.
sig	If 'TRUE', indicating significant distance with gold guild.

Value

p The plotted figure.
p The plotted figure.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- bs_pm(maize, group = "Compartment")
maize <- net_dis(maize, method = "Jaccard")
p <- net_dis_plot(maize)
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- bs_pm(maize, group = "Compartment")
maize <- net_dis(maize, method = "Jaccard")
p <- net_dis_plot(maize, d = "BS")
```

net_grp_cmp

Compare the group features between networks.

Description

Compare the group features between networks.
Compare the group features between networks.

Usage

```
net_grp_cmp(x, cmp = "contrast", dir = "./", grp)

## S4 method for signature 'character'
net_grp_cmp(x, cmp = "contrast", dir = "./", grp)
```

Arguments

x	The folder with all network inference results generated by bs_pm()
cmp	The compared feature of grp, default 'contrast'.
dir	The directory to store the alculated node features.
grp	The table with group information.

Examples

```
## Not run:
net_node_cmp("./individual_bs_pm/", f = "contrast", dir = "./", grp =
cls_tab(maize))

## End(Not run)
## Not run:
net_node_cmp("./individual_bs_pm/", f = "contrast", dir = "./", grp =
cls_tab(maize))

## End(Not run)
```

net_node_cmp	<i>Compare the node features between networks.</i>
--------------	--

Description

Compare the node features between networks.

Compare the node features between networks.

Usage

```
net_node_cmp(x, cmp = "contrast", dir = "./")

## S4 method for signature 'character,character'
net_node_cmp(x, cmp = "contrast", dir = "./")
```

Arguments

x	The folder with all network inference results generated by bs_pm()
cmp	The compared feature of node, default 'contrast'.
dir	The directory to store the alculated node features.

Examples

```
## Not run:
net_node_cmp("./individual_bs_pm/", f = "contrast", dir = "./")

## End(Not run)
## Not run:
net_node_cmp("./individual_bs_pm/", f = "contrast", dir = "./")

## End(Not run)
```

norm<- *Setter and getters for the slot 'norm', normalized 'tab' matrix.*

Description

Setter and getters for the slot 'norm', normalized 'tab' matrix.

Usage

```
norm(x) <- value

## S4 replacement method for signature 'mina'
norm(x) <- value

norm(x)

## S4 method for signature 'mina'
norm(x)
```

Arguments

x The 'mina' object.
value The value to set for the slot of the 'mina' object 'x'.

Value

The 'norm' slot of the 'mina' object.

Examples

```
norm(maize) <- norm_tab(maize_asv2, method = "total")
norm(maize)[1:5, 1:5]
```

norm_by_raref *Function for normalization by rarefying the samples into the same depth, modified from **phyloseq**, find it [here](https://rdrr.io/bioc/phyloseq/man/rarefy_even_depth.html).*

Description

Function for normalization by rarefying the samples into the same depth, modified from **phyloseq**, find it [here](#).

Usage

```
norm_by_raref(x, depth = 1000, replace = TRUE)
```


Arguments

x	A quantitative table with sample in columns and compositions in rows.
depth	The depth for rarefying, 1000 by default.
replace	Whether to sample with replacement (TRUE) or without replacement (FALSE). Default TRUE for computational efficiency.

Value

A normalized quantitative table.

norm_by_total	<i>Function for normalization, by total number of the reads in each sample.</i>
---------------	---

Description

Function for normalization, by total number of the reads in each sample.

Usage

```
norm_by_total(x)
```

Arguments

x	A quantitative table with samples in columns and compositions in rows.
---	--

Value

A normalized quantitative table.

norm_tab	<i>Normalize the slot 'tab' for later analysis.</i>
----------	---

Description

Normalize the slot 'tab' for later analysis.

Usage

```
norm_tab(x, method, ...)
```

Arguments

x	The input mina object with quantitative tab / a matrix needed to be normalized.
method	The method used for the normalization of quantitative table.
...	Additional parameters.

Value

Normalized quantitative table.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "total")
```

norm_tab,matrix,character-method

Normalize the quantitative matrix.

Description

Normalize the quantitative matrix.

Usage

```
## S4 method for signature 'matrix,character'
norm_tab(x, method, depth = 1000, replace = TRUE, multi = 1, ...)
```

Arguments

<code>x</code>	A quantitative matrix with samples in columns and compositions in rows.
<code>method</code>	The method used for normalization.
<code>depth</code>	The depth for rarefying, 1000 by default.
<code>replace</code>	Whether to sample with replacement (TRUE by default) or without replacement (FALSE) when using method 'raref'.
<code>multi</code>	Rarefy the table for multiple times, 1 by default, indicate the times of rarefaction want to be repeated, only validate for rarefaction.
<code>...</code>	Additional parameters.

Value

The normalized quantitative matrix.

`x_norm` Normalized matrix of the quantitative table.

Examples

```
data(maize_asv2)
maize_asv_norm <- norm_tab(maize_asv2, method = "total")
maize_asv_norm <- norm_tab(maize_asv2, method = "raref", depth = 1000,
replace = TRUE, multi = 3)
```

`norm_tab,mina,ANY-method`*Normalize the quantitative table with mina input.*

Description

Normalize the quantitative table with mina input.

Usage

```
## S4 method for signature 'mina,ANY'  
norm_tab(x, method, depth = 1000, replace = TRUE, multi = 1, ...)  
  
## S4 method for signature 'mina,character'  
norm_tab(x, method, depth = 1000, replace = TRUE, multi = 1, ...)
```

Arguments

<code>x</code>	An object of the class <code>mina</code> with <code>@tab</code> defined.
<code>method</code>	The method used for normalization.
<code>depth</code>	The depth for subsampling by rarefying, 1000 by default.
<code>replace</code>	Whether to sample with replacement (TRUE by default) or without replacement (FALSE) when using method 'raref'.
<code>multi</code>	Rarefy the table for multiple times, FALSE by default, indicate the times of rarefaction want to be repeated, only validate for rarefaction.
<code>...</code>	Additional parameters.

Value

`x` An object of the class `mina` with `@norm` added.

Examples

```
maize <- new("mina", tab = maize_asv2, des = maize_des2)  
maize <- norm_tab(maize, method = "raref", depth = 1000, replace = TRUE,  
multi = 3)
```

norm_tab_method_list *List of normalization methods supported in [norm_tab](#)*

Description

Normalization methods should be specified by exact string match.

Usage

```
norm_tab_method_list
```

Format

A list of character vectors.

raref By downsampling all samples to specific depth.

total Devided by the total read of each sample.

See Also

[norm_tab](#)

Examples

```
? norm_tab_method_list
```

pcoa_plot *Visulization of components distance / dissimilarity in k dimension.*

Description

Visulization of components distance / dissimilarity in k dimension.

Visulization of components distance / dissimilarity in k dimension.

Usage

```
pcoa_plot(x, des, match, ...)
```

```
## S4 method for signature 'list,data.frame,character'
```

```
pcoa_plot(x, des, match, d1 = 1, d2 = 2, color, shape = NULL, ...)
```

Arguments

x	A list generated by 'dmr'.
des	The corresponding descriptive table.
match	The column name of the components IDs in 'des' with exactly the same as rownames in x.
...	Additional parameters.
d1	The dimension be visualized in x-axis, default '1'.
d2	The dimension be visualized in y-axis, default '2'.
color	The column name in 'des' to be used for different color groups.
shape	The column name in 'des' to be used for different shape groups, default 'NULL'.

Value

- p The plotted figure.
- p The plotted PCoA.

Examples

```

maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- com_dis(maize, method = "bray")
maize <- dmr(maize)
asv_dmr <- .dmr(maize)
des <- des(maize)
p1a <- pcoa_plot(asv_dmr, des, match = "Sample_ID", color = "Compartment")
p1b <- pcoa_plot(asv_dmr, des, match = "Sample_ID", d1 = 3, d2 = 4, color =
"Compartment")
p2a <- pcoa_plot(asv_dmr, des, match = "Sample_ID", color = "Host_genotype")
p2b <- pcoa_plot(asv_dmr, des, match = "Sample_ID", d1 = 1, d2 = 3, color =
"Host_genotype")
p3a <- pcoa_plot(asv_dmr, des, match = "Sample_ID", color = "Compartment",
shape = "Soil")
p3b <- pcoa_plot(asv_dmr, des, match = "Sample_ID", d1 = 1, d2 = 4, color =
"Compartment", shape = "Soil")
maize <- new("mina", tab = maize_asv2, des = maize_des2)
maize <- norm_tab(maize, method = "raref")
maize <- fit_tabs(maize)
maize <- com_dis(maize, method = "bray")
maize <- dmr(maize)
asv_dmr <- .dmr(maize)
des <- des(maize)
p1a <- pcoa_plot(asv_dmr, des, match = "Sample_ID", color = "Compartment")
p1b <- pcoa_plot(asv_dmr, des, match = "Sample_ID", d1 = 3, d2 = 4, color =
"Compartment")
p2a <- pcoa_plot(asv_dmr, des, match = "Sample_ID", color = "Host_genotype")
p2b <- pcoa_plot(asv_dmr, des, match = "Sample_ID", d1 = 1, d2 = 3, color =
"Host_genotype")

```

```
p3a <- pcoa_plot(asv_dmr, des, match = "Sample_ID", color = "Compartment",
  shape = "Soil")
p3b <- pcoa_plot(asv_dmr, des, match = "Sample_ID", d1 = 1, d2 = 4, color =
  "Compartment", shape = "Soil")
```

rarefaction_subsample *Rarefaction subsample function, one sample, modified from a internal function in **phyloseq**, find it [here](https://rdrr.io/bioc/phyloseq/man/rarefy_even_depth.html).*

Description

Rarefaction subsample function, one sample, modified from a internal function in **phyloseq**, find it [here](#).

Usage

```
rarefaction_subsample(x, depth = 1000, replace = TRUE)
```

Arguments

x	A column of quantitative table.
depth	The depth for rarefying, 1000 by default.
replace	Whether to sample with or without replacement, TRUE by default for computational efficiency.

Value

The vector rarefied to defined depth.

re_format_AP *Convert APResult (apcluster output) to dataframe.*

Description

Modified from <https://rdrr.io/github/jefferis/flycircuit/src/R/clustering.R#sym-as.data.frame.APResult>

Usage

```
re_format_AP(x)
```

Arguments

x	an APResult object from apcluster .
---	--

Value

y A data frame with columns 'ID', 'Exemplar', 'Cluster' and 'Cluster_size'.

re_format_MCL	<i>Convert mcl (mcl output) to dataframe.</i>
---------------	---

Description

Modified from <https://rdr.io/github/jefferis/flycircuit/src/R/clustering.R> #sym-as.data.frame.APResult

Usage

```
re_format_MCL(x, names)
```

Arguments

x an ‘mcl’ object from [mcl](#).
names The names of clustered components.

Value

y A data frame with columns ‘ID’, ‘Cluster’ and ‘Cluster_size’.

See Also

[mcl](#)

sim_par	<i>Function for community similarity calculation used by ‘tina’, modified from https://github.com/defleury/Schmidt_et_al_2016_community_similarity/blob/master/functions.community_similarity.R</i>
---------	--

Description

Function for community similarity calculation used by ‘tina’, modified from https://github.com/defleury/Schmidt_et_al_2016_community_similarity/blob/master/functions.community_similarity.R

Usage

```
sim_par(x, y, sim_method = "w_ja", threads = 80, nblocks = 400)
```

Arguments

x An quantitative matrix.
y The Cij matrix, which is correlation matrix of adjusted sparcc matrix of x.
sim_method The method for similarity, "w_ja" and "uw_ja" are available for weighted and unweighted Jaccard similarity respectively.
threads The number of threads used for parallel running, 80 by default.
nblocks The number of row / column for splitted sub-matrix, 400 by default.

Value

s The output similarity matrix.

Examples

```
## Not run:
data(maize_asv)
maize_tab <- maize_asv[1 : 1000, 1 : 200]
asv <- norm_tab(maize_tab, method = "raref", depth = 100)
asv[is.na(asv)] <- 0
asv_sparcc <- sparcc(asv, threads = 8, nblocks = 40)
tmp.S <- adj(asv_sparcc, method = "spearman")
y <- 0.5 * (tmp.S + 1)
s <- sim_par(asv_sparcc, y, sim_method = "w_ja", threads = 8, nblocks = 40)

## End(Not run)
```

sparcc	<i>Function for ‘sparcc’ correlation calculation. Modified from Schmidt et al. 2016, find the scripts here and the SparCC paper here.</i>
--------	--

Description

Function for ‘sparcc’ correlation calculation. Modified from Schmidt et al. 2016, find the scripts [here](#) and the SparCC paper [here](#).

Usage

```
sparcc(x, threads = 80, nblocks = 400)
```

Arguments

x	An matrix for correlation calculation.
threads	The number of threads used for parallel running, 80 by default.
nblocks	The number of row /column for splitting sub-matrix, 400 by default.

Value

y The adjacency matrix.

Examples

```
## Not run:
asv_sparcc <- sparcc(maize_asv2, threads = 2, nblocks = 40)

## End(Not run)
```

tina	<i>TINA community dissimilarity used in <code>com_dis</code>. Function for ‘tina’ dissimilarity/distance calculation. Modified from Schmidt et al., 2016.</i>
------	---

Description

TINA community dissimilarity used in `com_dis`. Function for ‘tina’ dissimilarity/distance calculation. Modified from Schmidt et al., 2016.

Usage

```
tina(x, ...)
```

Arguments

x	An matrix for dissimilarity calculation.
...	Additional parameters.

Value

The output ‘tina’ dissimilarity matrix.

Examples

```
## Not run:
asv_norm <- norm_tab(maize_asv2, method = "raref", depth = 1000)
asv_dis <- com_dis(asv_norm, method = "bray")
asv_dis <- com_dis(asv_norm, method = "tina", threads = 8, nblocks = 40)
asv_tina <- tina(asv_norm, cor_method = "spearman", sim_method = "w_ja",
threads = 8, nblocks = 40)

## End(Not run)
```

tina,matrix-method	<i>Function for ‘tina’ dissimilarity calculation. Modified from Schmidt et al., 2016. Person and Spearman could be used for correlation and weighted and unweighted Jaccard could be used for similarity calculation.</i>
--------------------	---

Description

Function for ‘tina’ dissimilarity calculation. Modified from Schmidt et al., 2016. Person and Spearman could be used for correlation and weighted and unweighted Jaccard could be used for similarity calculation.

Usage

```
## S4 method for signature 'matrix'
tina(
  x,
  cor_method = "spearman",
  sim_method = "w_ja",
  threads = 80,
  nblocks = 400,
  ...
)
```

Arguments

x	A matrix for dissimilarity calculation.
cor_method	The method for correlation, "pearson" and "spearman" are available.
sim_method	The method for similarity, "w_ja" and "uw_ja" are available for weighted and unweighted Jaccard similarity respectively.
threads	The number of threads used for parallel running, 80 by default.
nblocks	The number of row and column for splitted sub-matrix, 400 by default.
...	Additional parameters.

Value

t The output 'tina' dissimilarity matrix.

Examples

```
## Not run:
asv_norm <- norm_tab(maize_asv2, method = "raref", depth = 1000)
asv_dis <- com_dis(asv_norm, method = "bray")
asv_dis <- com_dis(asv_norm, method = "tina", threads = 8, nblocks = 40)
asv_tina <- tina(asv_norm, cor_method = "spearman", sim_method = "w_ja",
  threads = 8, nblocks = 40)

## End(Not run)
```

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