Package 'mina'

April 10, 2023

Title Microbial community dIversity and Network Analysis

Version 1.6.0

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

LazyData true

Suggests knitr, rmarkdown

Enhances doMC

VignetteBuilder knitr

RoxygenNote 7.1.1

Collate 'RcppChk.R' 'RcppExports.R' 'all_classes.R' 'all_generics.R' 'adj.R' 'all_accessors.R' 'bs_pm.R' 'check.R' 'com_dis.R' 'com_plot.R' 'com_r2.R' 'data.R' 'dmr.R' 'fit_tabs.R' 'get_rep.R' 'net_cls.R' 'net_cls_tab.R' 'net_dis.R' 'net_dis_indi.R' 'net_dis_pcoa.R' 'net_dis_plot.R' 'net_grp_cmp.R' 'net_node_cmp.R' 'norm_tab.R'

biocViews Software, WorkflowStep

BugReports https://github.com/Guan06/mina

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R topics documented:

`adj` *Calculate the correlation adjacacency matrix.*

Description

Calculate the correlation adjacacency matrix.

Usage

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

Arguments

x	An object of the class mina with ‘norm‘ defined or a ‘norm‘ matrix.
method	The correlation coeffient used for adjacacency 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 coeffient used for adjacacency matrix.
sig	(optional) The asymtotic P-values, only applicable for Pearson and Spearman methods with ‘mina‘ object as input, alwasy 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 coeffient used for adjacacency matrix.
`sig`	The asymtotic 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 — *List of adjacency matix calculation methods/ orrelations supported in 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.

sparcc SparCC correlation by spearman.

See Also

adj

Examples

```
? adj_method_list
```

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

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

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

x	An object of class 'mina' with @norm and @des defined.
group	The column name of descriptive file @des for comparison.
g_size	The cutoff of group size used for filtering, default is 88.
s_size	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.
rm	Filtering the components present in less than 'per' of the samples from compared groups, default TRUE.
per	The percentage of present samples for filtering, default is 0.1.
sig	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` *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).*

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

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

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_tab *Get the slot ‘cls_tab‘.*

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)
```

---

com_dis *Calculate the community dissimilarity / distance matrix.*

Description

Calculate the community dissimilarity / distance matrix.

Usage

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

Arguments

x	An object of the class mina 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 *Calculate the community dissimilarity / distance matrix of the input matrix.*

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 *List of dissimilarity / distance supported in com_dis. Dissimilarity / distance should be specified by exact string match.*

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

Description

Visulization 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

Visulization of components distance / dissimilarity in k dimension.

Description

Visulization 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 *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.*

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

Description

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

Examples

```
data(hmp)
```

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

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.

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)
maize <- net_dis(maize, method = "Jaccard")
dis_bs(maize)
dis_pm(maize)
dis_stat(maize)
```

`dmr` *Dimensionality reduction of community dissimilarity / distance for visulization.*

Description

Dimensionality reduction of community dissimilarity / distance for visulization.

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 dimentionality 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 *Dimensionality reduction of the distance matrix.*

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 *Dimensionality reduction of the 'dis' included in mina.*

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)
```

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

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_net_cls_tab` *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

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

Arguments

x_norm	The normalized quantitative table used for netowrk 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 netowrk 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` *Same function as 'com_r2' with matrix and corresponding descriptive table as input.*

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("mina", 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 *Get the representative community members by extracting the most abundant and prevalent compositions.*

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)
```

---

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

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 proccessing the sample sequencing.

Subsite The subsite of body where samples were collected.

Site The site of body where samples were collectec.

Description The further details about the samples.

Source

HMP project.

Examples

```
data(hmp_des)
```

hmp_otu — *OTU table of HMP project, data downloaded from https://www.hmpdacc.org/hmp/HMQCP/*

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 — *ASV table of maize project, vegetative stage samples only.*

Description

ASV table of maize project, vegetative stage samples only.

Format

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

Source

RECONSTRUCT project, maize microbiome part.

Examples

```
data(maize_asv)
```

maize_asv2 *Subset of ASV table of maize project, ASVs appear in less than 100 samples were filtered for later analysis.*

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. Unormalized table including 1219 ASVs from 313 samples.

Source

RECONSTRUCT project, maize microbiome part.

Examples

```
data(maize_asv2)
```

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

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

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)
```

`mina-class` *Class "mina" includes the quantitative table and descriptive table.*

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 permutated adjacency matrices for each pairwise environmental comparison.

`dis_bs` The distance between networks of different environmental communities.

`dis_pm` The distance between networks of permutated groups.

`dis_stat` The average distance between subsampled environmental community networks, permutated networks and corresponding significance.

Author(s)

Rui Guan https://github.com/Guan06

Examples

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

---

net_cls *Network clustering of sparsed adjacacency matrix.*

Description

Network clustering of sparsed adjacacency 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

Network clustering based on the sparsed adjacacency matrix.

Description

Network clustering based on the sparsed adjacacency 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 adjacacency 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 adjacacency matrix.*

Description

Network clustering based on the sparsed adjacacency 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 adjacacency 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 *Get the cluster table 'cls_tab' from 'norm' and 'cls'.*

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 netowrk 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	Wheather to output the eigenvectors for Spectral distance, the defult 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 dimenstion 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 *Calculate the network distance of bootstrap and permutation when appliable.*

Description

Calculate the network distance of bootstrap and permutation when appliable.

Calculate the network distance of bootstrap and permutation when appliable.

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 dimenstion of adjacency matrix is smaller than setted ‘evk‘, default TRUE.
egv	Wheather to output the eigenvectors for Spectral distance, the defult 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 *Visulization 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 *Visulization of network distance, average distances are used for tile plot.*

Description

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

Visulization 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 *Compare the node features between networks.*

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_tab` *Normalize the slot ‘tab‘ for later analysis.*

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

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

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

---

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

Description

Setter and getter for the slot 'tab'.

Usage

```
tab(x) <- value

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

tab(x)

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

Arguments

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

Value

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

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

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

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

Examples

```
tab(maize) <- maize_asv2
tab(maize)[1:5, 1:5]
```

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

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` *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.*

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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