

# Package ‘microbiome’

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**Description** Utilities for microbiome analysis.

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**License** BSD\_2\_clause + file LICENSE

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**URL** <http://microbiome.github.io/microbiome>

**MailingList** microbiome <microbiome-devel@googlegroups.com>

**BugReports** <https://github.com/microbiome/microbiome/issues>

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**R topics documented:**

microbiome-package	4
abundances	4
add_besthit	5
add_refseq	6
aggregate_rare	7
aggregate_taxa	8
alpha	9
associate	10
atlas1006	11
baseline	12
bimodality	13
bimodality_sarle	15
boxplot_abundance	16
boxplot_alpha	17
cmat2table	18
collapse_replicates	19
core	20
core_abundance	21
core_heatmap	22
core_matrix	23
core_members	24
coverage	25
default_colors	26
densityplot	26
dietswap	28
divergence	29
diversity	30
dominance	31
dominant	33
evenness	34
find_optima	35
gktau	36
group_age	37
group_bmi	38
heat	40
hitchip.taxonomy	41
hotplot	42
inequality	43
intermediate_stability	44
is_compositional	45
log_modulo_skewness	46
low_abundance	47
map_levels	48
merge_taxa2	49
meta	50
multimodality	50

neat . . . . .	52
neatsort . . . . .	53
overlap . . . . .	54
peerj32 . . . . .	55
plot_atlas . . . . .	56
plot_composition . . . . .	57
plot_core . . . . .	58
plot_density . . . . .	59
plot_frequencies . . . . .	60
plot_landscape . . . . .	61
plot_regression . . . . .	63
plot_taxa_prevalence . . . . .	65
plot_tipping . . . . .	66
potential_analysis . . . . .	67
potential_univariate . . . . .	68
prevalence . . . . .	70
psmelt2 . . . . .	71
rare . . . . .	72
rare_abundance . . . . .	73
rare_members . . . . .	74
rarity . . . . .	75
readcount . . . . .	76
read_biom2phyloseq . . . . .	77
read_csv2phyloseq . . . . .	78
read_mothur2phyloseq . . . . .	79
read_phyloseq . . . . .	80
remove_samples . . . . .	81
remove_taxa . . . . .	82
richness . . . . .	83
spreadplot . . . . .	84
summarize_phyloseq . . . . .	85
taxa . . . . .	85
TibbleUtilites . . . . .	86
timesplit . . . . .	87
time_normalize . . . . .	88
time_sort . . . . .	88
top . . . . .	89
top_taxa . . . . .	90
transform . . . . .	91

---

microbiome-package      *R package for microbiome studies*

---

### Description

Brief summary of the microbiome package

### Details

Package:      microbiome  
Type:          Package  
Version:      See sessionInfo() or DESCRIPTION file  
Date:          2014-2017  
License:      FreeBSD  
LazyLoad:    yes

R package for microbiome studies

### Author(s)

Leo Lahti et al. <microbiome-admin@googlegroups.com>

### References

See citation('microbiome') <http://microbiome.github.io>

### Examples

```
citation('microbiome')
```

---

abundances                      *Abundance Matrix from Phyloseq*

---

### Description

Retrieves the taxon abundance table from phyloseq-class object and ensures it is systematically returned as taxa x samples matrix.

### Usage

```
abundances(x, transform = "identity")
```

**Arguments**

x [phyloseq-class](#) object

transform Transformation to apply. The options include: 'compositional' (ie relative abundance), 'Z', 'log10', 'log10p', 'hellinger', 'identity', 'clr', 'alr', or any method from the `vegan::decostand` function.

**Value**

Abundance matrix (OTU x samples).

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation('microbiome')

**Examples**

```
data(dietswap)
a <- abundances(dietswap)
# b <- abundances(dietswap, transform='compositional')
```

---

add\_besthit *Adds best\_hist to a [phyloseq-class](#) Object*

---

**Description**

Add the lowest classification for an OTU or ASV.

**Usage**

```
add_besthit(x, sep = ":")
```

**Arguments**

x [phyloseq-class](#) object

sep separator e.g. ASV161:Roseburia

**Details**

Most commonly it is observed that taxa names are either OTU ids or ASV ids. In such cases it is useful to know the taxonomic identity. For this purpose, `best_hist` identifies the best available taxonomic identity and adds it to the OTU ids or ASV ids. If genus and species columns are present in input the function internally combines the names.

**Value**

[phyloseq-class](#) object [phyloseq-class](#)

**Author(s)**

Contact: Sudarshan A. Shetty <sudarshanshetty9@gmail.com>

**Examples**

```
## Not run:
# Example data
library(microbiome)
data(dietswap)
p0.f <- add_besthit(atlas1006, sep=":")

## End(Not run)
```

---

add\_refseq

*Add refseq Slot for dada2 based phyloseq Object*

---

**Description**

Utility to add refseq slot for dada2 based phyloseq Object. Here, the taxa\_names which are unique sequences, are stored in refseq slot of phyloseq. Sequence ids are converted to ids using tag option.

**Usage**

```
add_refseq(x, tag = "ASV")
```

**Arguments**

x [phyloseq-class](#) object with sequences as rownames.  
tag Provide name for Ids, Default="ASV".

**Value**

[phyloseq-class](#) object

**Author(s)**

Contact: Sudarshan A. Shetty <sudarshanshetty9@gmail.com>

**Examples**

```
# ps <- add_refseq(p0, tag="ASV")
# ps
```

---

aggregate\_rare      *Aggregate Rare Groups*

---

### Description

Combining rare taxa.

### Usage

```
aggregate_rare(x, level, detection, prevalence, include.lowest = FALSE, ...)
```

### Arguments

x	phyloseq-class object
level	Summarization level (from rank_names(pseq))
detection	Detection threshold for absence/presence (strictly greater by default).
prevalence	Prevalence threshold (in [0, 1]). The required prevalence is strictly greater by default. To include the limit, set include.lowest to TRUE.
include.lowest	Include the lower boundary of the detection and prevalence cutoffs. FALSE by default.
...	Arguments to pass.

### Value

phyloseq-class object

### Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

### References

See citation('microbiome')

### Examples

```
data(dietswap)
s <- aggregate_rare(dietswap, level = 'Phylum',
  detection = 0.1/100, prevalence = 5/100)
```

---

aggregate_taxa	<i>Aggregate Taxa</i>
----------------	-----------------------

---

### Description

Summarize phyloseq data into a higher phylogenetic level.

### Usage

```
aggregate_taxa(x, level, verbose = FALSE)
```

### Arguments

x	phyloseq-class object
level	Summarization level (from rank_names(pseq))
verbose	verbose

### Details

This provides a convenient way to aggregate phyloseq OTUs (or other taxa) when the phylogenetic tree is missing. Calculates the sum of OTU abundances over all OTUs that map to the same higher-level group. Removes ambiguous levels from the taxonomy table. Returns a phyloseq object with the summarized abundances.

### Value

Summarized phyloseq object

### Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

### References

See citation('microbiome')

### Examples

```
data(dietswap)
s <- aggregate_taxa(dietswap, 'Phylum')
```



---

alpha	<i>Global Ecosystem State Variables</i>
-------	---

---

**Description**

Global indicators of the ecosystem state, including richness, evenness, diversity, and other indicators

**Usage**

```
alpha(x, index = "all", zeroes = TRUE)
```

**Arguments**

x	A species abundance vector, or matrix (taxa/features x samples) with the absolute count data (no relative abundances), or <a href="#">phyloseq-class</a> object
index	Default is 'NULL', meaning that all available indices will be included. For specific options, see details.
zeroes	Include zero counts in the diversity estimation.

**Details**

This function returns various indices of the ecosystem state. The function is named alpha (global in some previous versions of this package) as these indices can be viewed as measures of alpha diversity. The function uses default choices for detection, prevalence and other parameters for simplicity and standardization. See the individual functions for more options. All indicators from the richness, diversity, evenness, dominance, and rarity functions are available. Some additional measures, such as Chao1 and ACE are available via [estimate\\_richness](#) function in the **phyloseq** package but not included here. The index names are given the prefix richness\_, evenness\_, diversity\_, dominance\_, or rarity\_ in the output table to avoid confusion between similarly named but different indices (e.g. Simpson diversity and Simpson dominance). All parameters are set to their default. To experiment with different parameterizations, see the more specific index functions (richness, diversity, evenness, dominance, rarity).

**Value**

A data.frame of samples x alpha diversity indicators

**Author(s)**

Contact: Leo Lahti <[microbiome-admin@googlegroups.com](mailto:microbiome-admin@googlegroups.com)>

**References**

See [citation\('microbiome'\)](#)

**See Also**

[dominance](#), [rarity](#), [phyloseq::estimate\\_richness](#)

**Examples**

```
data(dietswap)
d <- alpha(dietswap, index='shannon')
# d <- alpha(dietswap, index='all')
```

---

 associate

*Cross Correlation Wrapper*


---

**Description**

Cross-correlate columns of the input matrices.

**Usage**

```
associate(
  x,
  y = NULL,
  method = "spearman",
  p.adj.threshold = Inf,
  cth = NULL,
  order = FALSE,
  n.signif = 0,
  mode = "table",
  p.adj.method = "fdr",
  verbose = FALSE,
  filter.self.correlations = FALSE
)
```

**Arguments**

x	matrix (samples x features if annotation matrix)
y	matrix (samples x features if cross-correlated with annotations)
method	association method ('pearson', or 'spearman' for continuous)
p.adj.threshold	q-value threshold to include features
cth	correlation threshold to include features
order	order the results
n.signif	minimum number of significant correlations for each element
mode	Specify output format ('table' or 'matrix')
p.adj.method	p-value multiple testing correction method. One of the methods in p.adjust function ('BH' and others; see help(p.adjust)). Default: 'fdr'
verbose	verbose
filter.self.correlations	Filter out correlations between identical items.

**Details**

The p-values in the output table depend on the method. For the spearman and pearson correlation values, the p-values are provided by the default method in the cor.test function.

**Value**

List with cor, pval, pval.adjusted

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation('microbiome')

**Examples**

```
data(peerj32)
d1 <- peerj32$microbes[1:20, 1:10]
d2 <- peerj32$lipids[1:20,1:10]
cc <- associate(d1, d2, method='pearson')
```

---

atlas1006

*HITChip Atlas with 1006 Western Adults*

---

**Description**

This data set contains genus-level microbiota profiling with HITChip for 1006 western adults with no reported health complications, reported in Lahti et al. (2014) <https://doi.org/10.1038/ncomms5344>.

**Usage**

```
data(atlas1006)
```

**Format**

The data set in [phyloseq-class](#) format.

**Details**

The data is also available for download from the Data Dryad <http://doi.org/10.5061/dryad.pk75d>.

**Value**

Loads the data set in R.

**Author(s)**

Leo Lahti <microbiome-admin@googlegroups.com>

**References**

Lahti et al. Tipping elements of the human intestinal ecosystem. Nature Communications 5:4344, 2014. To cite the microbiome R package, see `citation('microbiome')`

---

baseline

*Pick Baseline Timepoint Samples*

---

**Description**

Identify and select the baseline timepoint samples in a `phyloseq` object.

**Usage**

```
baseline(x, na.omit = TRUE)
```

**Arguments**

<code>x</code>	phyloseq object. Assuming that the <code>sample_data(x)</code> has the fields 'time', 'sample' and 'subject'
<code>na.omit</code>	Logical. Ignore samples with no time point information. If this is FALSE, the first sample for each subject is selected even when there is no time information.

**Details**

Arranges the samples by time and picks the first sample for each subject. Compared to simple subsetting at time point zero, this checks NAs and possibility for multiple samples at the baseline, and guarantees that a single sample per subject is selected.

**Value**

Phyloseq object with only baseline time point samples selected.

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See `citation('microbiome')`

**Examples**

```
data(peerj32)
a <- baseline(peerj32$phyloseq)
```

---

bimodality

*Bimodality Analysis*


---

**Description**

Estimate bimodality scores.

**Usage**

```
bimodality(
  x,
  method = "potential_analysis",
  peak.threshold = 1,
  bw.adjust = 1,
  bs.iter = 100,
  min.density = 1,
  verbose = TRUE
)
```

**Arguments**

x	A vector, matrix, or a phyloseq object
method	bimodality quantification method ('potential_analysis', 'Sarle.finite.sample', or 'Sarle.asymptotic'). If method='all', then a data.frame with all scores is returned.
peak.threshold	Mode detection threshold
bw.adjust	Bandwidth adjustment
bs.iter	Bootstrap iterations
min.density	minimum accepted density for a maximum; as a multiple of kernel height
verbose	Verbose

**Details**

- Sarle.finite.sample Coefficient of bimodality for finite sample. See SAS 2012.
- Sarle.asymptotic Coefficient of bimodality, used and described in Shade et al. (2014) and Ellison AM (1987).
- potential\_analysis Repeats potential analysis (Livina et al. 2010) multiple times with bootstrap sampling for each row of the input data (as in Lahti et al. 2014) and returns the bootstrap score.

The coefficient lies in (0, 1).

The 'Sarle.asymptotic' version is defined as

$$b = (g^2 + 1)/k$$

. This is coefficient of bimodality from Ellison AM Am. J. Bot. 1987, for microbiome analysis it has been used for instance in Shade et al. 2014. The formula for 'Sarle.finite.sample' (SAS 2012):

$$b = \frac{g^2 + 1}{k + (3(n - 1)^2)/((n - 2)(n - 3))}$$

where  $n$  is sample size and In both formulas,  $g$  is sample skewness and  $k$  is the  $k$ th standardized moment (also called the sample kurtosis, or excess kurtosis).

### Value

A list with following elements:

- scoreFraction of bootstrap samples where multiple modes are observed
- nmodes The most frequently observed number of modes in bootstrap sampling results.
- results Full results of potential\_analysis for each row of the input matrix.

### Author(s)

Leo Lahti <leo.lahti@iki.fi>

### References

- Livina et al. (2010). Potential analysis reveals changing number of climate states during the last 60 kyr. *Climate of the Past*, 6, 77-82.
- Lahti et al. (2014). Tipping elements of the human intestinal ecosystem. *Nature Communications* 5:4344.
- Shade et al. mBio 5(4):e01371-14, 2014.
- AM Ellison, Am. J. Bot 74:1280-8, 1987.
- SAS Institute Inc. (2012). SAS/STAT 12.1 user's guide. Cary, NC.
- To cite the microbiome R package, see citation('microbiome')

### See Also

A classical test of multimodality is provided by `dip.test` in the **DIP** package.

### Examples

```
# In practice, use more bootstrap iterations
b <- bimodality(c(rnorm(100, mean=0), rnorm(100, mean=5)),
  method = "Sarle.finite.sample", bs.iter=5)
# The classical DIP test:
# quantifies unimodality. Values range between 0 to 1.
# dip.test(x, simulate.p.value=TRUE, B=200)$statistic
# Values less than 0.05 indicate significant deviation from unimodality.
# Therefore, to obtain an increasing multimodality score, use
# library(diptest)
# multimodality.dip <- apply(abundances(pseq), 1,
# function(x) {1 - unname(dip.test(x)$p.value)})
```

---

bimodality_sarle	<i>Sarle's Bimodality Coefficient</i>
------------------	---------------------------------------

---

**Description**

Sarle's bimodality coefficient.

**Usage**

```
bimodality_sarle(x, bs.iter = 1, type = "Sarle.finite.sample")
```

**Arguments**

x	Data vector for which bimodality will be quantified
bs.iter	Bootstrap iterations
type	Score type ('Sarle.finite.sample' or 'Sarle.asymptotic')

**Details**

The coefficient lies in (0, 1).

The 'Sarle.asymptotic' version is defined as

$$b = (g^2 + 1)/k$$

. This is coefficient of bimodality from Ellison AM Am. J. Bot. 1987, for microbiome analysis it has been used for instance in Shade et al. 2014.

The formula for 'Sarle.finite.sample' (SAS 2012):

$$b = \frac{g^2 + 1}{k + (3(n - 1)^2)/((n - 2)(n - 3))}$$

where n is sample size and

In both formulas,  $g$  is sample skewness and  $k$  is the kth standardized moment (also called the sample kurtosis, or excess kurtosis).

**Value**

Bimodality score

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

- Shade et al. mBio 5(4):e01371-14, 2014.
- Ellison AM (1987) Am J Botany 74(8):1280-1288.
- SAS Institute Inc. (2012). SAS/STAT 12.1 user's guide. Cary, NC.
- To cite the microbiome R package, see citation('microbiome')

**See Also**

Check the `dip.test` from the **DIP** package for a classical test of multimodality.

**Examples**

```
# b <- bimodality_sarle(rnorm(50), type='Sarle.finite.sample')
```

---

boxplot\_abundance      *Abundance Boxplot*

---

**Description**

Plot phyloseq abundances.

**Usage**

```
boxplot_abundance(
  d,
  x,
  y,
  line = NULL,
  violin = FALSE,
  na.rm = FALSE,
  show.points = TRUE
)
```

**Arguments**

<code>d</code>	<a href="#">phyloseq-class</a> object
<code>x</code>	Metadata variable to map to the horizontal axis.
<code>y</code>	OTU to map on the vertical axis
<code>line</code>	The variable to map on lines
<code>violin</code>	Use violin version of the boxplot
<code>na.rm</code>	Remove NAs
<code>show.points</code>	Include data points in the figure



**Details**

The directionality of change in paired boxplot is indicated by the colors of the connecting lines.

**Value**

A `ggplot` plot object

**Examples**

```
data(peerj32)
p <- boxplot_abundance(peerj32$phyloseq, x='time', y='Akkermansia',
  line='subject')
```

---

 boxplot\_alpha

*Alpha Boxplot*


---

**Description**

Plot alpha index.

**Usage**

```
boxplot_alpha(
  x,
  x_var = NULL,
  index = NULL,
  violin = FALSE,
  na.rm = FALSE,
  show.points = TRUE,
  zeroes = TRUE,
  element.alpha = 0.5,
  element.width = 0.2,
  fill.colors = NA,
  outlier.fill = "grey50"
)
```

**Arguments**

x	<code>phyloseq-class</code> object
x_var	Metadata variable to map to the horizontal axis.
index	Alpha index to plot. See function <code>alpha</code> .
violin	Use violin version of the boxplot
na.rm	Remove NAs
show.points	Include data points in the figure
zeroes	Include zero counts in diversity estimation. Default is TRUE

<code>element.alpha</code>	Alpha value for plot elements. Controls the transparency of plots elements.
<code>element.width</code>	Width value for plot elements. Controls the transparency of plots elements.
<code>fill.colors</code>	Specify a list of colors passed on to <code>ggplot2 scale_fill_manual</code>
<code>outlier.fill</code>	If using boxplot and and points together how to deal with outliers. See <code>ggplot2 outlier.fill</code> argument in <code>geom_</code> elements.

### Details

A simple wrapper to visualize alpha diversity index.

### Value

A `ggplot` plot object

### Examples

```
data("dietswap")
p <- boxplot_alpha(dietswap, x_var = "sex", index="observed", violin=FALSE,
  na.rm=FALSE, show.points=TRUE, zeroes=TRUE,
  element.alpha=0.5, element.width=0.2,
  fill.colors= c("steelblue", "firebrick"),
  outlier.fill="white")

p
```

---

`cmat2table`

*Convert Correlation Matrix into a Table*

---

### Description

Arrange correlation matrices from associate into a table format.

### Usage

```
cmat2table(res, verbose = FALSE)
```

### Arguments

<code>res</code>	Output from associate
<code>verbose</code>	verbose

### Value

Correlation table

### Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

## References

See citation('microbiome')

## Examples

```
data(peerj32)
d1 <- peerj32$microbes[1:20, 1:10]
d2 <- peerj32$lipids[1:20,1:10]
cc <- associate(d1, d2, mode='matrix', method='pearson')
cmat <- associate(d1, d2, mode='table', method='spearman')
```

---

collapse\_replicates    *Collapse Replicate Samples*

---

## Description

Collapse samples, mostly meant for technical replicates.

## Usage

```
collapse_replicates(
  x,
  method = "sample",
  replicate_id = NULL,
  replicate_fields = NULL
)
```

## Arguments

**x**                    [phyloseq-class](#) object

**method**              Collapsing method. Only random sampling ("sample") implemented.

**replicate\_id**        Replicate identifier. A character vector.

**replicate\_fields**    Metadata fields used to determine replicates.

## Value

Collapsed phyloseq object.

## Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

## References

To cite the microbiome R package, see citation('microbiome')

## Examples

```
data(atlas1006)
pseq <- collapse_replicates(atlas1006,
  method = "sample",
  replicate_fields = c("subject", "time"))
```

---

core

*Core Microbiota*

---

## Description

Filter the phyloseq object to include only prevalent taxa.

## Usage

```
core(x, detection, prevalence, include.lowest = FALSE, ...)
```

## Arguments

x	<a href="#">phyloseq-class</a> object
detection	Detection threshold for absence/presence (strictly greater by default).
prevalence	Prevalence threshold (in [0, 1]). The required prevalence is strictly greater by default. To include the limit, set include.lowest to TRUE.
include.lowest	Include the lower boundary of the detection and prevalence cutoffs. FALSE by default.
...	Arguments to pass.

## Value

Filtered phyloseq object including only prevalent taxa

## Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

## References

Salonen A, Salojarvi J, Lahti L, de Vos WM. The adult intestinal core microbiota is determined by analysis depth and health status. *Clinical Microbiology and Infection* 18(S4):16-20, 2012 To cite the microbiome R package, see citation('microbiome')

## See Also

core\_members, rare\_members

**Examples**

```

data(dietswap)
# Detection threshold 0 (strictly greater by default);
# Prevalence threshold 50 percent (strictly greater by default)
pseq <- core(dietswap, 0, 50/100)
# Detection threshold 0 (strictly greater by default);
# Prevalence threshold exactly 100 percent; for this set
# include.lowest=TRUE, otherwise the required prevalence is
# strictly greater than 100
pseq <- core(dietswap, 0, 100/100, include.lowest = TRUE)

```

---

core_abundance	<i>Core Abundance</i>
----------------	-----------------------

---

**Description**

Calculates the community core abundance index.

**Usage**

```

core_abundance(
  x,
  detection = 0.1/100,
  prevalence = 50/100,
  include.lowest = FALSE
)

```

**Arguments**

x	<a href="#">phyloseq-class</a> object
detection	Detection threshold for absence/presence (strictly greater by default).
prevalence	Prevalence threshold (in [0, 1]). The required prevalence is strictly greater by default. To include the limit, set include.lowest to TRUE.
include.lowest	Include the lower boundary of the detection and prevalence cutoffs. FALSE by default.

**Details**

The core abundance index gives the relative proportion of the core species (in [0,1]). The core taxa are defined as those that exceed the given population prevalence threshold at the given detection level.

**Value**

A vector of core abundance indices

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**See Also**

rarity

**Examples**

```
data(dietswap)
d <- core_abundance(dietswap, detection=0.1/100, prevalence=50/100)
```

---

core\_heatmap

*Core Heatmap*

---

**Description**

Core heatmap.

**Usage**

```
core_heatmap(x, dets, cols, min.prev, taxa.order)
```

**Arguments**

x	OTU matrix
dets	A vector or a scalar indicating the number of intervals in (0, log10(max(data))). The dets are calculated for relative abundancies.
cols	colours for the heatmap
min.prev	If minimum prevalence is set, then filter out those rows (taxa) and columns (dets) that never exceed this prevalence. This helps to zoom in on the actual core region of the heatmap.
taxa.order	Ordering of the taxa.

**Value**

Used for its side effects

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

A Salonen et al. The adult intestinal core microbiota is determined by analysis depth and health status. *Clinical Microbiology and Infection* 18(S4):16 20, 2012. To cite the microbiome R package, see citation('microbiome')

---

core_matrix	<i>Core Matrix</i>
-------------	--------------------

---

## Description

Creates the core matrix.

## Usage

```
core_matrix(x, prevalences = seq(0.1, 1, , 1), detections = NULL)
```

## Arguments

`x` [phyloseq](#) object or a taxa x samples abundance matrix  
`prevalences` a vector of prevalence percentages in [0,1]  
`detections` a vector of intensities around the data range

## Value

Estimated core microbiota

## Author(s)

Contact: Jarkko Salojarvi <microbiome-admin@googlegroups.com>

## References

A Salonen et al. The adult intestinal core microbiota is determined by analysis depth and health status. *Clinical Microbiology and Infection* 18(S4):16 20, 2012. To cite the microbiome R package, see `citation('microbiome')`

## Examples

```
# Not exported  
#data(peerj32)  
#core <- core_matrix(peerj32$phyloseq)
```

---

`core_members`*Core Taxa*

---

**Description**

Determine members of the core microbiota with given abundance and prevalences

**Usage**

```
core_members(x, detection = 1/100, prevalence = 50/100, include.lowest = FALSE)
```

**Arguments**

<code>x</code>	phyloseq-class object
<code>detection</code>	Detection threshold for absence/presence (strictly greater by default).
<code>prevalence</code>	Prevalence threshold (in [0, 1]). The required prevalence is strictly greater by default. To include the limit, set <code>include.lowest</code> to TRUE.
<code>include.lowest</code>	Include the lower boundary of the detection and prevalence cutoffs. FALSE by default.

**Details**

For phyloseq object, lists taxa that are more prevalent with the given detection threshold. For matrix, lists columns that satisfy these criteria.

**Value**

Vector of core members

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

A Salonen et al. The adult intestinal core microbiota is determined by analysis depth and health status. *Clinical Microbiology and Infection* 18(S4):16-20, 2012. To cite the microbiome R package, see `citation('microbiome')`

**Examples**

```
data(dietswap)
# Detection threshold 1 (strictly greater by default);
# Note that the data (dietswap) is here in absolute counts
# (and not compositional, relative abundances)
# Prevalence threshold 50 percent (strictly greater by default)
a <- core_members(dietswap, 1, 50/100)
```



---

coverage	<i>Coverage Index</i>
----------	-----------------------

---

### Description

Community coverage index.

### Usage

```
coverage(x, threshold = 0.5)
```

### Arguments

x	A species abundance vector, or matrix (taxa/features x samples) with the absolute count data (no relative abundances), or <a href="#">phyloseq-class</a> object
threshold	Indicates the fraction of the ecosystem to be occupied by the N most abundant species (N is returned by this function). If the detection argument is a vector, then a data.frame is returned, one column for each detection threshold.

### Details

The coverage index gives the number of groups needed to have a given proportion of the ecosystem occupied (by default 0.5 ie 50

### Value

A vector of coverage indices

### Author(s)

Contact: Leo Lahti <[microbiome-admin@googlegroups.com](mailto:microbiome-admin@googlegroups.com)>

### See Also

dominance, alpha

### Examples

```
data(dietswap)
d <- coverage(dietswap, threshold=0.5)
```

---

default_colors	<i>Default Colors</i>
----------------	-----------------------

---

**Description**

Default colors for different variables.

**Usage**

```
default_colors(x, v = NULL)
```

**Arguments**

x	Name of the variable type ("Phylum")
v	Optional. Vector of elements to color.

**Value**

Named character vector of default colors

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("microbiome")

**Examples**

```
col <- default_colors("Phylum")
```

---

densityplot	<i>Density Plot</i>
-------------	---------------------

---

**Description**

Density visualization for data points overlaid on cross-plot.

**Usage**

```
densityplot(  
  x,  
  main = NULL,  
  x.ticks = 10,  
  rounding = 0,  
  add.points = TRUE,  
  col = "black",  
  adjust = 1,  
  size = 1,  
  legend = FALSE,  
  shading = TRUE,  
  shading.low = "white",  
  shading.high = "black",  
  point.opacity = 0.75  
)
```

**Arguments**

x	Data matrix to plot. The first two columns will be visualized as a cross-plot.
main	title text
x.ticks	Number of ticks on the X axis
rounding	Rounding for X axis tick values
add.points	Plot the data points as well
col	Color of the data points. NAs are marked with darkgray.
adjust	Kernel width adjustment
size	point size
legend	plot legend TRUE/FALSE
shading	Shading
shading.low	Color for shading low density regions
shading.high	Color for shading high density regions
point.opacity	Transparency-level for points

**Value**

ggplot2 object

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation('microbiome')

**Examples**

```
# p <- densityplot(cbind(rnorm(100), rnorm(100)))
```

---

dietswap

*Diet Swap Data*

---

**Description**

The diet swap data set represents a study with African and African American groups undergoing a two-week diet swap. For details, see [dx.doi.org/10.1038/ncomms7342](https://doi.org/10.1038/ncomms7342).

**Usage**

```
data(dietswap)
```

**Format**

The data set in [phyloseq-class](#) format.

**Details**

The data is also available for download from the Data Dryad repository <http://datadryad.org/resource/doi:10.5061/dryad.1mn1n>.

**Value**

Loads the data set in R.

**Author(s)**

Leo Lahti <[microbiome-admin@googlegroups.com](mailto:microbiome-admin@googlegroups.com)>

**References**

O'Keefe et al. Nature Communications 6:6342, 2015. [dx.doi.org/10.1038/ncomms7342](https://doi.org/10.1038/ncomms7342) To cite the microbiome R package, see `citation('microbiome')`

---

divergence                      *Divergence within a Sample Group*

---

### Description

Quantify microbiota divergence (heterogeneity) within a given sample set with respect to a reference.

### Usage

```
divergence(x, y, method = "bray")
```

### Arguments

x	phyloseq object or a vector
y	Reference sample. A vector.
method	dissimilarity method: any method available via <code>phyloseq::distance</code> function. Note that some methods ("jsd" and 'unifrac' for instance) do not work with the group divergence.

### Details

Microbiota divergence (heterogeneity / spread) within a given sample set can be quantified by the average sample dissimilarity or beta diversity with respect to a given reference sample.

This measure is sensitive to sample size. Subsampling or bootstrapping can be applied to equalize sample sizes between comparisons.

### Value

Vector with dissimilarities; one for each sample, quantifying the dissimilarity of the sample from the reference sample.

### Author(s)

Leo Lahti <microbiome-admin@googlegroups.com>

### References

To cite this R package, see `citation('microbiome')`

### See Also

the `vegdist` function from the **vegan** package provides many standard beta diversity measures

**Examples**

```
# Assess beta diversity among the African samples
# in a diet swap study (see \code{help(dietswap)} for references)
data(dietswap)
pseq <- subset_samples(dietswap, nationality == 'AFR')
reference <- apply(abundances(pseq), 1, median)
b <- divergence(pseq, reference, method = "bray")
```

diversity

*Diversity Index***Description**

Various community diversity indices.

**Usage**

```
diversity(x, index = "all", zeroes = TRUE)
```

**Arguments**

x	A species abundance vector, or matrix (taxa/features x samples) with the absolute count data (no relative abundances), or <a href="#">phyloseq-class</a> object
index	Diversity index. See details for options.
zeroes	Include zero counts in the diversity estimation.

**Details**

By default, returns all diversity indices. The available diversity indices include the following:

- `inverse_simpson` Inverse Simpson diversity:  $1/\lambda$  where  $\lambda = \sum(p^2)$  and  $p$  are relative abundances.
- `gini_simpson` Gini-Simpson diversity  $1 - \lambda$ . This is also called Gibbs–Martin, or Blau index in sociology, psychology and management studies.
- `shannon` Shannon diversity ie entropy
- `fisher` Fisher alpha; as implemented in the **vegan** package
- `coverage` Number of species needed to cover 50% of the ecosystem. For other quantiles, apply the function `coverage` directly.

**Value**

A vector of diversity indices

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

## References

- Beisel J-N. et al. A Comparative Analysis of Diversity Index Sensitivity. *Internal Rev. Hydrobiol.* 88(1):3-15, 2003. URL: [https://portais.ufg.br/up/202/o/2003-comparative\\_evennes\\_index.pdf](https://portais.ufg.br/up/202/o/2003-comparative_evennes_index.pdf)
- Bulla L. An index of diversity and its associated diversity measure. *Oikos* 70:167–171, 1994
- Magurran AE, McGill BJ, eds (2011) *Biological Diversity: Frontiers in Measurement and Assessment* (Oxford Univ Press, Oxford), Vol 12.
- Smith B and Wilson JB. A Consumer's Guide to Diversity Indices. *Oikos* 76(1):70-82, 1996.

## See Also

dominance, richness, evenness, rarity, alpha

## Examples

```
data(dietswap)
d <- alpha(dietswap, 'shannon')
```

---

dominance

*Dominance Index*

---

## Description

Calculates the community dominance index.

## Usage

```
dominance(x, index = "all", rank = 1, relative = TRUE, aggregate = TRUE)
```

## Arguments

- |           |   |
|-----------|---|
| x         | A species abundance vector, or matrix (taxa/features x samples) with the absolute count data (no relative abundances), or <code>phyloseq-class</code> object  |
| index     | If the index is given, it will override the other parameters. See the details below for description and references of the standard dominance indices. By default, this function returns the Berger-Parker index, ie relative dominance at rank 1. |
| rank      | Optional. The rank of the dominant taxa to consider.  |
| relative  | Use relative abundances (default: TRUE)   |
| aggregate | Aggregate (TRUE; default) the top members or not. If aggregate=TRUE, then the sum of relative abundances is returned. Otherwise the relative abundance is returned for the single taxa with the indicated rank.                                   |

**Details**

The dominance index gives the abundance of the most abundant species. This has been used also in microbiomics context (Locey & Lennon (2016)). The following indices are provided:

- 'absolute' This is the most simple variant, giving the absolute abundance of the most abundant species (Magurran & McGill 2011). By default, this refers to the single most dominant species (rank=1) but it is possible to calculate the absolute dominance with rank n based on the abundances of top-n species by tuning the rank argument.
- 'relative' Relative abundance of the most abundant species. This is with rank=1 by default but can be calculated for other ranks.
- 'DBP' Berger–Parker index, a special case of relative dominance with rank 1; This also equals the inverse of true diversity of the infinite order.
- 'DMN' McNaughton's dominance. This is the sum of the relative abundance of the two most abundant taxa, or a special case of relative dominance with rank 2
- 'simpson' Simpson's index ( $\sum(p^2)$ ) where p are relative abundances has an interpretation as a dominance measure. Also the version ( $\sum(q * (q-1)) / S(S-1)$ ) based on absolute abundances q has been proposed by Simpson (1949) but not included here as it is not within [0,1] range, and it is highly correlated with the simpler Simpson dominance. Finally, it is also possible to calculate dominances up to an arbitrary rank by setting the rank argument
- 'core\_abundance' Relative proportion of the core species that exceed detection level 0.2% in over 50% of the samples
- 'gini' Gini index is calculated with the function `inequality`.

By setting `aggregate=FALSE`, the abundance for the single n'th most dominant taxa (n=rank) is returned instead the sum of abundances up to that rank (the default).

**Value**

A vector of dominance indices

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

- Kenneth J. Locey and Jay T. Lennon. Scaling laws predict global microbial diversity. PNAS 2016 113 (21) 5970-5975; doi:10.1073/pnas.1521291113.
- Magurran AE, McGill BJ, eds (2011) Biological Diversity: Frontiers in Measurement and Assessment (Oxford Univ Press, Oxford), Vol 12

**See Also**

coverage, core\_abundance, rarity, alpha



**Examples**

```
data(dietswap)
# vector
d <- dominance(abundances(dietswap)[,1], rank=1, relative=TRUE)
# matrix
# d <- dominance(abundances(dietswap), rank=1, relative=TRUE)
# Phyloseq object
# d <- dominance(dietswap, rank=1, relative=TRUE)
```

---

dominant	<i>Dominant taxa</i>
----------	----------------------

---

**Description**

Returns the dominant taxonomic group for each sample.

**Usage**

```
dominant(x, level = NULL)
```

**Arguments**

x	A <a href="#">phyloseq-class</a> object
level	Optional. Taxonomic level.

**Value**

A vector of dominance indices

**Author(s)**

Leo Lahti <[microbiome-admin@googlegroups.com](mailto:microbiome-admin@googlegroups.com)>

**Examples**

```
data(dietswap)
# vector
d <- dominant(dietswap)
```

---

evenness	<i>Evenness Index</i>
----------	-----------------------

---

### Description

Various community evenness indices.

### Usage

```
evenness(x, index = "all", zeroes = TRUE, detection = 0)
```

### Arguments

x	A species abundance vector, or matrix (taxa/features x samples) with the absolute count data (no relative abundances), or <code>phyloseq-class</code> object
index	Evenness index. See details for options.
zeroes	Include zero counts in the evenness estimation.
detection	Detection threshold

### Details

By default, Pielou's evenness is returned.

The available evenness indices include the following: 1) 'camargo': Camargo's evenness (Camargo 1992) 2) 'simpson': Simpson's evenness (inverse Simpson diversity / S) 3) 'pielou': Pielou's evenness (Pielou, 1966), also known as Shannon or Shannon-Weaver/Wiener/Weiner evenness;  $H/\ln(S)$ . The Shannon-Weaver is the preferred term; see A tribute to Claude Shannon (1916 –2001) and a plea for more rigorous use of species richness, species diversity and the 'Shannon–Wiener' Index. Spellerberg and Fedor. *Alpha Ecology & Biogeography* (2003) 12, 177–197 4) 'evar': Smith and Wilson's Evar index (Smith & Wilson 1996) 5) 'bulla': Bulla's index (O) (Bulla 1994)

Desirable statistical evenness metrics avoid strong bias towards very large or very small abundances; are independent of richness; and range within [0,1] with increasing evenness (Smith & Wilson 1996). Evenness metrics that fulfill these criteria include at least camargo, simpson, smith-wilson, and bulla. Also see Magurran & McGill (2011) and Beisel et al. (2003) for further details.

### Value

A vector of evenness indices

### Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

## References

- Beisel J-N. et al. A Comparative Analysis of Evenness Index Sensitivity. *Internal Rev. Hydrobiol.* 88(1):3-15, 2003. URL: [https://portais.ufg.br/up/202/o/2003-comparative\\_evennes\\_index.pdf](https://portais.ufg.br/up/202/o/2003-comparative_evennes_index.pdf)
- Bulla L. An index of evenness and its associated diversity measure. *Oikos* 70:167–171, 1994
- Camargo, JA. New diversity index for assessing structural alterations in aquatic communities. *Bull. Environ. Contam. Toxicol.* 48:428–434, 1992.
- Locey KJ and Lennon JT. Scaling laws predict global microbial diversity. *PNAS* 113(21):5970-5975, 2016; doi:10.1073/pnas.1521291113.
- Magurran AE, McGill BJ, eds (2011) *Biological Diversity: Frontiers in Measurement and Assessment* (Oxford Univ Press, Oxford), Vol 12.
- Pielou, EC. The measurement of diversity in different types of biological collections. *Journal of Theoretical Biology* 13:131–144, 1966.
- Smith B and Wilson JB. A Consumer's Guide to Evenness Indices. *Oikos* 76(1):70-82, 1996.

## See Also

coverage, core\_abundance, rarity, alpha

## Examples

```
data(dietswap)
# phyloseq object
#d <- evenness(dietswap, 'pielou')
# matrix
#d <- evenness(abundances(dietswap), 'pielou')
# vector
d <- evenness(abundances(dietswap)[,1], 'pielou')
```

---

find\_optima

*Find Optima*

---

## Description

Detect optima, excluding local optima below peak.threshold.

## Usage

```
find_optima(f, peak.threshold = 0, bw = 1, min.density = 1)
```

## Arguments

f	density
peak.threshold	Mode detection threshold
bw	bandwidth
min.density	Minimum accepted density for a maximum; as a multiple of kernel height

**Value**

A list with min (minima), max (maxima), and peak.threshold (minimum detection density)

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation('microbiome')

**Examples**

```
# Not exported
# o <- find_optima(rnorm(100), bw=1)
```

---

gktau

*gktau*

---

**Description**

Measure association between nominal (no order for levels) variables

**Usage**

```
gktau(x, y)
```

**Arguments**

x	first variable
y	second variable

**Details**

Measure association between nominal (no order for levels) variables using Goodman and Kruskal tau. Code modified from the original source: [r-bloggers.com/measuring-associations-between-non-numeric-variables/](http://r-bloggers.com/measuring-associations-between-non-numeric-variables/) An important feature of this procedure is that it allows missing values in either of the variables x or y, treating 'missing' as an additional level. In practice, this is sometimes very important since missing values in one variable may be strongly associated with either missing values in another variable or specific non-missing levels of that variable. An important characteristic of Goodman and Kruskal's tau measure is its asymmetry: because the variables x and y enter this expression differently, the value of a(y,x) is not the same as the value of a(x, y), in general. This stands in marked contrast to either the product-moment correlation coefficient or the Spearman rank correlation coefficient, which are both symmetric, giving the same association between x and y as that between y and x. The fundamental reason for the asymmetry of the general class of measures defined above is that they quantify the extent to which the variable x is useful in predicting y, which may be very different than the extent to which the variable y is useful in predicting x.

**Value**

Dependency measure

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

Code modified from the original source: <http://r-bloggers.com/measuring-associations-between-non-numeric-v>  
To cite the microbiome R package, see citation('microbiome')

**Examples**

```
data(peerj32)
v1 <- factor(peerj32$microbes[,1])
v2 <- factor(peerj32$meta$gender)
tc <- gktau(v1, v2)
```

---

group\_age

*Age Classes*

---

**Description**

Cut age information to discrete factors.

**Usage**

```
group_age(  
  x,  
  breaks = "decades",  
  n = 10,  
  labels = NULL,  
  include.lowest = TRUE,  
  right = FALSE,  
  dig.lab = 3,  
  ordered_result = FALSE  
)
```

**Arguments**

x	Numeric vector (age in years)
breaks	Class break points. Either a vector of breakpoints, or one of the predefined options ("years", "decades", "even").
n	Number of groups for the breaks = "even" option.

labels	labels for the levels of the resulting category. By default, labels are constructed using "(a,b]" interval notation. If labels = FALSE, simple integer codes are returned instead of a factor.
include.lowest	logical, indicating if an 'x[i]' equal to the lowest (or highest, for right = FALSE) 'breaks' value should be included.
right	logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa.
dig.lab	integer which is used when labels are not given. It determines the number of digits used in formatting the break numbers.
ordered_result	logical: should the result be an ordered factor?

### Details

Regarding the breaks arguments, the "even" option aims to cut the samples in groups with approximately the same size (by quantiles). The "years" and "decades" options are self-explanatory.

### Value

Factor of age groups.

### Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

### References

See citation('microbiome')

### See Also

base::cut

### Examples

```
data(atlas1006)
age.numeric <- meta(atlas1006)$age
age.factor <- group_age(age.numeric)
```

---

group\_bmi

*Body-Mass Index (BMI) Classes*

---

### Description

Cut BMI information to standard discrete factors.

**Usage**

```
group_bmi(  
  x,  
  breaks = "standard",  
  n = 10,  
  labels = NULL,  
  include.lowest = TRUE,  
  right = FALSE,  
  dig.lab = 3,  
  ordered_result = FALSE  
)
```

**Arguments**

x	Numeric vector (BMI)
breaks	Class break points. Either a vector of breakpoints, or one of the predefined options ("standard", "standard_truncated", "even").
n	Number of groups for the breaks = "even" option.
labels	labels for the levels of the resulting category. By default, labels are constructed using "(a,b]" interval notation. If labels = FALSE, simple integer codes are returned instead of a factor.
include.lowest	logical, indicating if an 'x[i]' equal to the lowest (or highest, for right = FALSE) 'breaks' value should be included.
right	logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa.
dig.lab	integer which is used when labels are not given. It determines the number of digits used in formatting the break numbers.
ordered_result	logical: should the result be an ordered factor?

**Details**

Regarding the breaks arguments, the "even" option aims to cut the samples in groups with approximately the same size (by quantiles). The "standard" option corresponds to standard obesity categories defined by the cutoffs <18.5 (underweight); <25 (lean); <30 (obese); <35 (severe obese); <40 (morbid obese); <45 (super obese). The standard\_truncated combines the severe, morbid and super obese into a single group.

**Value**

Factor of BMI groups.

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation('microbiome')

**See Also**

base::cut

**Examples**

```
bmi.numeric <- range(rnorm(100, mean = 25, sd = 3))
bmi.factor <- group_bmi(bmi.numeric)
```

---

 heat

*Association Heatmap*


---

**Description**

Visualizes  $n \times m$  association table as heatmap.

**Usage**

```
heat(
  df,
  Xvar = names(df)[[1]],
  Yvar = names(df)[[2]],
  fill = names(df)[[3]],
  star = NULL,
  p.adj.threshold = 1,
  association.threshold = 0,
  step = 0.2,
  colours = c("darkblue", "blue", "white", "red", "darkred"),
  limits = NULL,
  legend.text = "",
  order.rows = TRUE,
  order.cols = TRUE,
  filter.significant = TRUE,
  star.size = NULL,
  plot.values = FALSE
)
```

**Arguments**

df	Data frame. Each row corresponds to a pair of associated variables. The columns give variable names, association scores and significance estimates.
Xvar	X axis variable column name. For instance 'X'.
Yvar	Y axis variable column name. For instance 'Y'.
fill	Column to be used for heatmap coloring. For instance 'association'.
star	Column to be used for cell highlighting. For instance 'p.adj'.
p.adj.threshold	Significance threshold for the stars.



association.threshold	Include only elements that have absolute association higher than this value
step	color interval
colours	heatmap colours
limits	colour scale limits
legend.text	legend text
order.rows	Order rows to enhance visualization interpretability. If this is logical, then hclust is applied. If this is a vector then the rows are ordered using this index.
order.cols	Order columns to enhance visualization interpretability. If this is logical, then hclust is applied. If this is a vector then the rows are ordered using this index.
filter.significant	Keep only the elements with at least one significant entry
star.size	NULL Determine size of the highlight symbols
plot.values	Show values as text

**Value**

ggplot2 object

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation('microbiome')

**Examples**

```
data(peerj32)
d1 <- peerj32$lipids[, 1:10]
d2 <- peerj32$microbes[, 1:10]
cc <- associate(d1, d2, method='pearson')
p <- heat(cc, 'X1', 'X2', 'Correlation', star='p.adj')
```

---

hitchip.taxonomy

*HITChip Taxonomy*

---

**Description**

HITChip taxonomy table.

**Usage**

```
data(hitchip.taxonomy)
```

**Format**

List with the element 'filtered', including a simplified version of the HITChip taxonomy.

**Value**

Loads the data set in R.

**Author(s)**

Leo Lahti <microbiome-admin@googlegroups.com>

**References**

Lahti et al. Tipping elements of the human intestinal ecosystem. Nature Communications 5:4344, 2014. To cite the microbiome R package, see citation('microbiome')

---

hotplot

*Univariate Bimodality Plot*

---

**Description**

Coloured bimodality plot.

**Usage**

```
hotplot(  
  x,  
  taxon,  
  tipping.point = NULL,  
  lims = NULL,  
  shift = 0.001,  
  log10 = TRUE  
)
```

**Arguments**

x	<a href="#">phyloseq-class</a> object
taxon	Taxonomic group to visualize.
tipping.point	Indicate critical point for abundance variations to be highlighted.
lims	Optional. Figure X axis limits.
shift	Small constant to avoid problems with zeroes in log10
log10	Use log10 abundances for the OTU table and tipping point

**Value**

[ggplot](#) object

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation('microbiome')

**Examples**

```
data(atlas1006)
pseq <- subset_samples(atlas1006, DNA_extraction_method == 'r')
pseq <- transform(pseq, 'compositional')
# Set a tipping point manually
tipp <- .3/100 # .3 percent relative abundance
# Bimodality is often best visible at log10 relative abundances
p <- hotplot(pseq, 'Dialister', tipping.point=tipp, log10=TRUE)
```

---

inequality

*Gini Index*

---

**Description**

Calculate Gini indices for a phyloseq object.

**Usage**

```
inequality(x)
```

**Arguments**

x [phyloseq-class](#) object

**Details**

Gini index is a common measure for relative inequality in economical income, but can also be used as a community diversity measure. Gini index is between [0,1], and increasing gini index implies increasing inequality.

**Value**

A vector of Gini indices

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

## References

Relative Distribution Methods in the Social Sciences. Mark S. Handcock and Martina Morris, Springer-Verlag, Inc., New York, 1999. ISBN 0387987789.

## See Also

diversity, reldist::gini (inspired by that implementation but independently written here to avoid external dependencies)

## Examples

```
data(dietswap)
d <- inequality(dietswap)
```

---

intermediate\_stability

*Intermediate Stability*

---

## Description

Quantify intermediate stability with respect to a given reference point.

## Usage

```
intermediate_stability(
  x,
  reference.point = NULL,
  method = "correlation",
  output = "scores"
)
```

## Arguments

x	<b>phyloseq</b> object. Includes abundances (variables x samples) and sample_data data.frame (samples x features) with 'subject' and 'time' field for each sample.
reference.point	Calculate stability of the data w.r.t. this point. By default the intermediate range is used ( $\min + (\max - \min)/2$ ). If a vector of points is provided, then the scores will be calculated for every point and a data.frame is returned.
method	'lm' (linear model) or 'correlation'; the linear model takes time into account as a covariate
output	Specify the return mode. Either the 'full' set of stability analysis outputs, or the 'scores' of intermediate stability.

## Details

Decomposes each column in  $x$  into differences between consecutive time points. For each variable and time point we calculate for the data values: (i) the distance from reference point; (ii) distance from the data value at the consecutive time point. The 'correlation' method calculates correlation between these two variables. Negative correlations indicate that values closer to reference point tend to have larger shifts in the consecutive time point. The 'lm' method takes the time lag between the consecutive time points into account as this may affect the comparison and is not taken into account by the straightforward correlation. Here the coefficients of the following linear model are used to assess stability:  $\text{abs}(\text{change}) \sim \text{time} + \text{abs}(\text{start.reference.distance})$ . Samples with missing data, and subjects with less than two time point are excluded. The absolute count data  $x$  is logarithmized before the analysis with the  $\log_{10}(1 + x)$  trick to circumvent logarithmization of zeroes.

## Value

A list with following elements: stability: estimated stability data: processed data set used in calculations

## Author(s)

Leo Lahti <leo.lahti@iki.fi>

## Examples

```
data(atlas1006)
x <- subset_samples(atlas1006, DNA_extraction_method == 'r')
x <- prune_taxa(c('Akkermansia', 'Dialister'), x)
res <- intermediate_stability(x, reference.point=NULL)
```

---

is_compositional	<i>Test Compositionality</i>
------------------	------------------------------

---

## Description

Test if phyloseq object is compositional.

## Usage

```
is_compositional(x, tolerance = 1e-06)
```

## Arguments

$x$  [phyloseq-class](#) object  
tolerance Tolerance for detecting compositionality.

## Details

This function tests that the sum of abundances within each sample is almost zero, within the tolerance of  $1e-6$  by default.

**Value**

Logical TRUE/FALSE

**See Also**

transform

**Examples**

```
data(dietswap)
a <- is_compositional(dietswap)
b <- is_compositional(transform(dietswap, "identity"))
c <- is_compositional(transform(dietswap, "compositional"))
```

---

log\_modulo\_skewness    *Log-Modulo Skewness Rarity Index*

---

**Description**

Calculates the community rarity index by log-modulo skewness.

**Usage**

```
log_modulo_skewness(x, q = 0.5, n = 50)
```

**Arguments**

x	Abundance matrix (taxa x samples) with counts
q	Arithmetic abundance classes are evenly cut up to to this quantile of the data. The assumption is that abundances higher than this are not common, and they are classified in their own group.
n	The number of arithmetic abundance classes from zero to the quantile cutoff indicated by q.

**Details**

The rarity index characterizes the concentration of species at low abundance. Here, we use the skewness of the frequency distribution of arithmetic abundance classes (see Magurran & McGill 2011). These are typically right-skewed; to avoid taking log of occasional negative skews, we follow Locey & Lennon (2016) and use the log-modulo transformation that adds a value of one to each measure of skewness to allow logarithmization.

**Value**

A vector of rarity indices

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

Kenneth J. Locey and Jay T. Lennon. Scaling laws predict global microbial diversity. PNAS 2016 113 (21) 5970-5975; doi:10.1073/pnas.1521291113.

Magurran AE, McGill BJ, eds (2011) Biological Diversity: Frontiers in Measurement and Assessment (Oxford Univ Press, Oxford), Vol 12

**See Also**

core\_abundance, low\_abundance, alpha

**Examples**

```
data(dietswap)
d <- log_modulo_skewness(dietswap)
```

---

low\_abundance

*Low Abundance Index*

---

**Description**

Calculates the concentration of low-abundance taxa below the indicated detection threshold.

**Usage**

```
low_abundance(x, detection = 0.2/100)
```

**Arguments**

x                    [phyloseq-class](#) object  
detection            Detection threshold for absence/presence (strictly greater by default).

**Details**

The low\_abundance index gives the concentration of species at low abundance, or the relative proportion of rare species in [0,1]. The species that are below the indicated detection threshold are considered rare. Note that population prevalence is not considered. If the detection argument is a vector, then a data.frame is returned, one column for each detection threshold.

**Value**

A vector of indicators.

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**See Also**

core\_abundance, rarity, global

**Examples**

```
data(dietswap)
d <- low_abundance(dietswap, detection=0.2/100)
```

---

map\_levels

*Map Taxonomic Levels*

---

**Description**

Map taxa between hierarchy levels.

**Usage**

```
map_levels(taxa = NULL, from, to, data)
```

**Arguments**

taxa	taxa to convert; if NULL then considering all taxa in the tax.table
from	convert from taxonomic level
to	convert to taxonomic level
data	Either a <a href="#">phyloseq</a> object or its <a href="#">taxonomyTable-class</a> , see the <b>phyloseq</b> package.

**Value**

mappings

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation('microbiome')



## Examples

```
data(dietswap)
m <- map_levels('Akkermansia', from='Genus', to='Phylum',
tax_table(dietswap))
m <- map_levels('Verrucomicrobia', from='Phylum', to='Genus',
tax_table(dietswap))
```

---

merge\_taxa2

*Merge Taxa*

---

## Description

Merge taxonomic groups into a single group.

## Usage

```
merge_taxa2(x, taxa = NULL, pattern = NULL, name = "Merged")
```

## Arguments

x	phyloseq-class object
taxa	A vector of taxa names to merge.
pattern	Taxa that match this pattern will be merged.
name	Name of the merged group.

## Details

In some cases it is necessary to place certain OTUs or other groups into an "other" category. For instance, unclassified groups. This wrapper makes this easy. This function differs from phyloseq::merge\_taxa by the last two arguments. Here, in merge\_taxa2 the user can specify the name of the new merged group. And the merging can be done based on common pattern in the name.

## Value

Modified phyloseq object

## Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

## References

See citation('microbiome')

## Examples

```
data(dietswap)
s <- merge_taxa(dietswap, c())
```

---

meta	<i>Retrieve Phyloseq Metadata as Data Frame</i>
------	---

---

**Description**

The output of the `phyloseq::sample_data()` function does not return `data.frame`, which is needed for many applications. This function retrieves the sample data as a `data.frame`

**Usage**

```
meta(x)
```

**Arguments**

x                    a phyloseq object

**Value**

Sample metadata as a `data.frame`

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**See Also**

[sample\\_data](#) in the **phyloseq** package

**Examples**

```
data(dietswap); df <- meta(dietswap)
```

---

multimodality	<i>Multimodality Score</i>
---------------	----------------------------

---

**Description**

Multimodality score based on bootstrapped potential analysis.

**Usage**

```
multimodality(  
  x,  
  peak.threshold = 1,  
  bw.adjust = 1,  
  bs.iter = 100,  
  min.density = 1,  
  verbose = TRUE  
)
```

**Arguments**

x	A vector, or data matrix (variables x samples)
peak.threshold	Mode detection threshold
bw.adjust	Bandwidth adjustment
bs.iter	Bootstrap iterations
min.density	minimum accepted density for a maximum; as a multiple of kernel height
verbose	Verbose

**Details**

Repeats potential analysis (Livina et al. 2010) multiple times with bootstrap sampling for each row of the input data (as in Lahti et al. 2014) and returns the specified results.

**Value**

A list with following elements:

- scoreFraction of bootstrap samples with multiple observed modes
- nmodesThe most frequently observed number of modes in bootstrap
- resultsFull results of potential\_analysis for each row of the input matrix.

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

- Livina et al. (2010). Potential analysis reveals changing number of climate states during the last 60 kyr. *Climate of the Past*, 6, 77-82.
- Lahti et al. (2014). Tipping elements of the human intestinal ecosystem. *Nature Communications* 5:4344.

**Examples**

```
#data(peerj32)
#s <- multimodality(t(peerj32$microbes[, c('Akkermansia', 'Dialister'))])
```

---

`neat`*Neatmap Sorting*

---

## Description

Order matrix or phyloseq OTU table based on the neatmap approach.

## Usage

```
neat(  
  x,  
  arrange = "both",  
  method = "NMDS",  
  distance = "bray",  
  first.feature = NULL,  
  first.sample = NULL,  
  ...  
)
```

## Arguments

<code>x</code>	A matrix or phyloseq object.
<code>arrange</code>	Order 'features', 'samples' or 'both' (for matrices). For matrices, it is assumed that the samples are on the columns and features are on the rows. For phyloseq objects, features are the taxa of the OTU table.
<code>method</code>	Ordination method. Only NMDS implemented for now.
<code>distance</code>	Distance method. See <a href="#">vegdist</a> function from the <b>vegan</b> package.
<code>first.feature</code>	Optionally provide the name of the first feature to start the ordering
<code>first.sample</code>	Optionally provide the name of the first sample to start the ordering
<code>...</code>	Arguments to pass.

## Details

Borrows elements from the heatmap implementation in the **phyloseq** package. The row/column sorting is not available there as a separate function. Therefore I implemented this function to provide an independent method for easy sample/taxon reordering for phyloseq objects. The ordering is cyclic so we can start at any point. The choice of the first sample may somewhat affect the overall ordering

## Value

Sorted matrix

## References

This function is partially based on code derived from the **phyloseq** package. However for the original neatmap approach for heatmap sorting, see (and cite): Rajaram, S., & Oono, Y. (2010). NeatMap—non-clustering heat map alternatives in R. *BMC Bioinformatics*, 11, 45.

## Examples

```
data(peerj32)
# Take subset to speed up example
x <- peerj32$microbes[1:10,1:10]
xo <- neat(x, 'both', method='NMDS', distance='bray')
```

---

neatsort	<i>Neatmap Sorting</i>
----------	------------------------

---

## Description

Sort samples or features based on the neatmap approach.

## Usage

```
neatsort(x, target, method = "NMDS", distance = "bray", first = NULL, ...)
```

## Arguments

x	<a href="#">phyloseq-class</a> object or a matrix
target	For <a href="#">phyloseq-class</a> input, the target is either 'sites' (samples) or 'species' (features) (taxa/OTUs); for matrices, the target is 'rows' or 'cols'.
method	Ordination method. See <a href="#">ordinate</a> from <b>phyloseq</b> package. For matrices, only the NMDS method is available.
distance	Distance method. See <a href="#">ordinate</a> from <b>phyloseq</b> package.
first	Optionally provide the name of the first sample/taxon to start the ordering (the ordering is cyclic so we can start at any point). The choice of the first sample may somewhat affect the overall ordering.
...	Arguments to be passed.

## Details

This function borrows elements from the heatmap implementation in the **phyloseq** package. The row/column sorting is there not available as a separate function at present, however, hindering reuse in other tools. Implemented in the microbiome package to provide an independent method for easy sample/taxon reordering for phyloseq objects.

## Value

Vector of ordered elements

## References

This function is partially based on code derived from the **phyloseq** package. For the original neatmap approach for heatmap sorting, see (and cite): Rajaram, S., & Oono, Y. (2010). NeatMap—non-clustering heat map alternatives in R. *BMC Bioinformatics*, 11, 45.

## Examples

```
data(peerj32)
pseq <- peerj32$phyloseq
# For Phyloseq
sort.otu <- neatsort(pseq, target='species')
# For matrix
# sort.rows <- neatsort(abundances(pseq), target='rows')
```

---

overlap

*Overlap Measure*

---

## Description

Quantify microbiota 'overlap' between samples.

## Usage

```
overlap(x, detection = 0)
```

## Arguments

x                    **phyloseq-class** object  
detection            Detection threshold.

## Value

Overlap matrix

## Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

## References

Bashan, A., Gibson, T., Friedman, J. et al. Universality of human microbial dynamics. *Nature* 534, 259–262 (2016). <https://doi.org/10.1038/nature18301>

## Examples

```
data(atlas1006)
o <- overlap(atlas1006, detection = 0.1/100)
```

**Description**

The peerj32 data set contains high-through profiling data from 389 human blood serum lipids and 130 intestinal genus-level bacteria from 44 samples (22 subjects from 2 time points; before and after probiotic/placebo intervention). The data set can be used to investigate associations between intestinal bacteria and host lipid metabolism. For details, see <http://dx.doi.org/10.7717/peerj.32>.

**Usage**

```
data(peerj32)
```

**Format**

List of the following data matrices as described in detail in Lahti et al. (2013):

- lipids: Quantification of 389 blood serum lipids across 44 samples
- microbes: Quantification of 130 genus-like taxa across 44 samples
- meta: Sample metadata including time point, sex, subjectID, sampleID and treatment group (probiotic LGG / Placebo)
- phyloseq The microbiome data set converted into a `phyloseq-class` object.

**Value**

Loads the data set in R.

**Author(s)**

Leo Lahti <microbiome-admin@googlegroups.com>

**References**

Lahti et al. (2013) PeerJ 1:e32 <http://dx.doi.org/10.7717/peerj.32>

---

`plot_atlas`*Visualize Samples of a Microbiota Atlas*

---

**Description**

Show all samples of a microbiota collection, colored by specific factor levels (x axis) and signal (y axis).

**Usage**

```
plot_atlas(pseq, x, y, ncol = 2)
```

**Arguments**

<code>pseq</code>	phyloseq object
<code>x</code>	Sorting variable for X axis and sample coloring
<code>y</code>	Signal variable for Y axis
<code>ncol</code>	Number of legend columns.

**Details**

Arranges the samples based on the given grouping factor (x), and plots the signal (y) on the Y axis. The samples are randomly ordered within each factor level. The factor levels are ordered by standard deviation of the signal (y axis).

**Value**

ggplot object

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation('microbiome'); Visualization inspired by Kilpinen et al. 2008, Genome Biology 9:R139.  
DOI: 10.1186/gb-2008-9-9-r139

**Examples**

```
data(atlas1006)
p <- plot_atlas(atlas1006, 'DNA_extraction_method', 'diversity')
p <- plot_atlas(atlas1006, 'DNA_extraction_method', 'Bifidobacterium')
```



---

plot_composition	<i>Taxonomic Composition Plot</i>
------------------	-----------------------------------

---

## Description

Plot taxon abundance for samples.

## Usage

```
plot_composition(
  x,
  sample.sort = NULL,
  otu.sort = NULL,
  x.label = "sample",
  plot.type = "barplot",
  verbose = FALSE,
  average_by = NULL,
  group_by = NULL,
  ...
)
```

## Arguments

x	phyloseq-class object
sample.sort	Order samples. Various criteria are available: <ul style="list-style-type: none"> <li>• NULL or 'none': No sorting</li> <li>• A single character string: indicate the metadata field to be used for ordering. Or: if this string is found from the tax_table, then sort by the corresponding taxonomic group.</li> <li>• A character vector: sample IDs indicating the sample ordering.</li> <li>• 'neatmap' Order samples based on the neatmap approach. See <a href="#">neatsort</a>. By default, 'NMDS' method with 'bray' distance is used. For other options, arrange the samples manually with the function.</li> </ul>
otu.sort	Order taxa. Same options as for the sample.sort argument but instead of metadata, taxonomic table is used. Also possible to sort by 'abundance'.
x.label	Specify how to label the x axis. This should be one of the variables in sample_variables(x).
plot.type	Plot type: 'barplot' or 'heatmap'
verbose	verbose (but not in sample/taxon ordering). The options are 'Z-OTU', 'Z-Sample', 'log10' and 'compositional'. See the <a href="#">transform</a> function.
average_by	Average the samples by the average_by variable
group_by	Group by this variable (in plot.type "barplot")
...	Arguments to be passed (for <a href="#">neatsort</a> function)

**Value**

A `ggplot` plot object.

**Examples**

```
library(dplyr)
data(atlas1006)
pseq <- atlas1006 %>%
  subset_samples(DNA_extraction_method == "r") %>%
  aggregate_taxa(level = "Phylum") %>%
  transform(transform = "compositional")
p <- plot_composition(pseq, sample.sort = "Firmicutes",
  otu.sort = "abundance", verbose = TRUE) +
  scale_fill_manual(values = default_colors("Phylum")[taxa(pseq)])
```

---

plot\_core

*Visualize OTU Core*

---

**Description**

Core visualization (2D).

**Usage**

```
plot_core(
  x,
  prevalences = seq(0.1, 1, 0.1),
  detections = 20,
  plot.type = "lineplot",
  colours = NULL,
  min.prevalence = NULL,
  taxa.order = NULL,
  horizontal = FALSE
)
```

**Arguments**

x	A <a href="#">phyloseq</a> object or a core matrix
prevalences	a vector of prevalence percentages in [0,1]
detections	a vector of intensities around the data range, or a scalar indicating the number of intervals in the data range.
plot.type	Plot type ('lineplot' or 'heatmap')
colours	colours for the heatmap
min.prevalence	If minimum prevalence is set, then filter out those rows (taxa) and columns (detections) that never exceed this prevalence. This helps to zoom in on the actual core region of the heatmap. Only affects the plot.type='heatmap'.
taxa.order	Ordering of the taxa: a vector of names.
horizontal	Logical. Horizontal figure.

**Value**

A list with three elements: the ggplot object and the data. The data has a different form for the lineplot and heatmap. Finally, the applied parameters are returned.

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

A Salonen et al. The adult intestinal core microbiota is determined by analysis depth and health status. *Clinical Microbiology and Infection* 18(S4):16 20, 2012. To cite the microbiome R package, see `citation('microbiome')`

**Examples**

```
data(dietswap)
p <- plot_core(transform(dietswap, "compositional"),
  prevalences=seq(0.1, 1, .1), detections=seq(0.01, 1, length = 10))
```

---

plot\_density

*Plot Density*

---

**Description**

Plot abundance density across samples for a given taxon.

**Usage**

```
plot_density(
  x,
  variable = NULL,
  log10 = FALSE,
  adjust = 1,
  kernel = "gaussian",
  trim = FALSE,
  na.rm = FALSE,
  fill = "gray",
  tipping.point = NULL,
  xlim = NULL
)
```

**Arguments**

x	phyloseq-class object or an OTU matrix (samples x phylotypes)
variable	OTU or metadata variable to visualize
log10	Logical. Show log10 abundances or not.
adjust	see stat_density
kernel	see stat_density
trim	see stat_density
na.rm	see stat_density
fill	Fill color
tipping.point	Optional. Indicate critical point for abundance variations to be highlighted.
xlim	X axis limits

**Value**

A `ggplot` plot object.

**Examples**

```
# Load gut microbiota data on 1006 western adults
# (see help(atlas1006) for references and details)
data(dietswap)
# Use compositional abundances instead of absolute signal
pseq.rel <- transform(dietswap, 'compositional')
# Population density for Dialister spp.; with log10 on the abundance (X)
# axis
library(ggplot2)
p <- plot_density(pseq.rel, variable='Dialister') + scale_x_log10()
```

---

plot\_frequencies      *Plot Frequencies*

---

**Description**

Plot relative frequencies within each Group for the levels of the given factor.

**Usage**

```
plot_frequencies(x, Groups, Factor)
```

**Arguments**

x	data.frame
Groups	Name of the grouping variable
Factor	Name of the frequency variable

### Details

For table with the indicated frequencies, see the returned phyloseq object.

### Value

`ggplot` plot object.

### Examples

```
data(dietswap)
p <- plot_frequencies(meta(dietswap), 'group', 'sex')
```

---

plot_landscape	<i>Landscape Plot</i>
----------------	-----------------------

---

### Description

Wrapper for visualizing sample similarity landscape ie. sample density in various 2D projections.

### Usage

```
plot_landscape(  
  x,  
  method = "PCoA",  
  distance = "bray",  
  transformation = "identity",  
  col = NULL,  
  main = NULL,  
  x.ticks = 10,  
  rounding = 0,  
  add.points = TRUE,  
  adjust = 1,  
  size = 1,  
  legend = FALSE,  
  shading = TRUE,  
  shading.low = "#ebf4f5",  
  shading.high = "#e9b7ce",  
  point.opacity = 0.75  
)
```

### Arguments

x	<code>phyloseq-class</code> object or a data matrix (samples x features; eg. samples vs. OTUs). If the input x is a 2D matrix then it is plotted as is.
method	Ordination method, see <code>phyloseq::plot_ordination</code> ; or "PCA", or "t-SNE" (from the <b>Rtsne</b> package)

distance	Ordination distance, see phyloseq::plot_ordination; for method = "PCA", only euclidean distance is implemented now.
transformation	Transformation applied on the input object x
col	Variable name to highlight samples (points) with colors
main	title text
x.ticks	Number of ticks on the X axis
rounding	Rounding for X axis tick values
add.points	Plot the data points as well
adjust	Kernel width adjustment
size	point size
legend	plot legend TRUE/FALSE
shading	Add shading in the background.
shading.low	Color for shading low density regions
shading.high	Color for shading high density regions
point.opacity	Transparency-level for points

### Details

For consistent results, set random seed (set.seed) before function call. Note that the distance and transformation arguments may have a drastic effect on the outputs.

### Value

A `ggplot` plot object.

### Examples

```
data(dietswap)

# PCoA
p <- plot_landscape(transform(dietswap, "compositional"),
  distance = "bray", method = "PCoA")

p <- plot_landscape(dietswap, method = "t-SNE", distance = "bray",
  transformation = "compositional")

# PCA
p <- plot_landscape(dietswap, method = "PCA", transformation = "clr")
```

---

plot_regression	<i>Visually Weighted Regression Plot</i>
-----------------	--

---

### Description

Draw regression curve with smoothed error bars with Visually-Weighted Regression by Solomon M. Hsiang; see <http://www.fight-entropy.com/2012/07/visually-weighted-regression.html> The R is modified from Felix Schonbrodt's original code <http://www.nicebread.de/visually-weighted-watercolor-plots-new-variants-please-vote>

### Usage

```
plot_regression(
  formula,
  data,
  B = 1000,
  shade = TRUE,
  shade.alpha = 0.1,
  spag = FALSE,
  mweight = TRUE,
  show.lm = FALSE,
  show.median = TRUE,
  median.col = "white",
  show.CI = FALSE,
  method = loess,
  slices = 200,
  ylim = NULL,
  quantize = "continuous",
  show.points = TRUE,
  color = NULL,
  pointsize = NULL,
  ...
)
```

### Arguments

formula	formula
data	data
B	number bootstrapped smoothers
shade	plot the shaded confidence region?
shade.alpha	shade.alpha: should the CI shading fade out at the edges? (by reducing alpha; 0=no alpha decrease, 0.1=medium alpha decrease, 0.5=strong alpha decrease)
spag	plot spaghetti lines?
mweight	visually weight the median smoother
show.lm	plot the linear regression line

show.median	show median smoother
median.col	median color
show.CI	should the 95% CI limits be plotted?
method	the fitting function for the spaghettis; default: loess
slices	number of slices in x and y direction for the shaded region. Higher numbers make a smoother plot, but takes longer to draw. I wouldn't go beyond 500
ylim	restrict range of the watercoloring
quantize	either 'continuous', or 'SD'. In the latter case, we get three color regions for 1, 2, and 3 SD (an idea of John Mashey)
show.points	Show points.
color	Point colors
pointsize	Point sizes
...	further parameters passed to the fitting function, in the case of loess, for example, 'span=.9', or 'family='symmetric''

**Value**

ggplot2 object

**Author(s)**

Based on the original version from F. Schonbrodt. Modified by Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation('microbiome')

**Examples**

```
data(atlas1006)
pseq <- subset_samples(atlas1006,
  DNA_extraction_method == 'r' &
  sex == "female" &
  nationality == "UKIE",
  B=10, slices=10 # non-default used here to speed up examples
)
p <- plot_regression(diversity ~ age, meta(pseq)[1:20,], slices=10, B=10)
```



---

plot\_taxa\_prevalence *Visualize Prevalence Distributions for Taxa*

---

### Description

Create taxa prevalence plots at various taxonomic levels.

### Usage

```
plot_taxa_prevalence(x, level, detection = 0)
```

### Arguments

x	phyloseq-class object, OTU data must be counts and not relative abundance or other transformed data.
level	Phylum/Order/Class/Family
detection	Detection threshold for presence (prevalance)

### Details

This helps to obtain first insights into how is the taxa distribution in the data. It also gives an idea about the taxonomic affiliation of rare and abundant taxa in the data. This may be helpful for data filtering or other downstream analysis.

### Value

A `ggplot` plot object.

### Author(s)

Sudarshan A. Shetty <sudarshanshetty9@gmail.com>

### Examples

```
data(atlas1006)
# Pick data subset just to speed up example
p0 <- subset_samples(atlas1006, DNA_extraction_method == "r")
p0 <- prune_taxa(taxa(p0)[grep("Bacteroides", taxa(p0))], p0)
# Detection threshold (0 by default; higher especially with HITChip)
p <- plot_taxa_prevalence(p0, 'Phylum', detection = 1)
print(p)
```

---

`plot_tipping`*Variation Line Plot*

---

## Description

Plot variation in taxon abundance for many subjects.

## Usage

```
plot_tipping(  
  x,  
  taxon,  
  tipping.point = NULL,  
  lims = NULL,  
  shift = 0.001,  
  xlim = NULL  
)
```

## Arguments

<code>x</code>	<a href="#">phyloseq-class</a> object
<code>taxon</code>	Taxonomic group to visualize.
<code>tipping.point</code>	Optional. Indicate critical point for abundance variations to be highlighted.
<code>lims</code>	Optional. Figure X axis limits.
<code>shift</code>	Small constant to avoid problems with zeroes in log10
<code>xlim</code>	Horizontal axis limits

## Details

Assuming the `sample_data(x)` has 'subject' field and some subjects have multiple time points.

## Value

[ggplot](#) object

## Author(s)

Contact: Leo Lahti <[microbiome-admin@googlegroups.com](mailto:microbiome-admin@googlegroups.com)>

## References

See `citation('microbiome')`

## Examples

```
data(atlas1006)
pseq <- subset_samples(atlas1006, DNA_extraction_method == 'r')
pseq <- transform(pseq, 'compositional')
p <- plot_tipping(pseq, 'Dialister', tipping.point=1)
```

---

potential\_analysis      *Bootstrapped Potential Analysis*

---

## Description

Analysis of multimodality based on bootstrapped potential analysis of Livina et al. (2010) as described in Lahti et al. (2014).

## Usage

```
potential_analysis(  
  x,  
  peak.threshold = 0,  
  bw.adjust = 1,  
  bs.iter = 100,  
  min.density = 1  
)
```

## Arguments

x	Input data vector
peak.threshold	Mode detection threshold
bw.adjust	Bandwidth adjustment
bs.iter	Bootstrap iterations
min.density	minimum accepted density for a maximum; as a multiple of kernel height

## Value

List with following elements:

- **modes**Number of modes for the input data vector (the most frequent number of modes from bootstrap)
- **minima**Average of potential minima across the bootstrap samples (for the most frequent number of modes)
- **maxima**Average of potential maxima across the bootstrap samples (for the most frequent number of modes)
- **unimodality.support**Fraction of bootstrap samples exhibiting unimodality
- **bws**Bandwidths

## References

- Livina et al. (2010). Potential analysis reveals changing number of climate states during the last 60 kyr. *Climate of the Past*, 6, 77-82.
- Lahti et al. (2014). Tipping elements of the human intestinal ecosystem. *Nature Communications* 5:4344.

## See Also

plot\_potential

## Examples

```
# Example data; see help(peerj32) for details
data(peerj32)

# Log10 abundance of Dialister
x <- abundances(transform(peerj32$phyloseq, "clr"))['Dialister',]

# Bootstrapped potential analysis
# In practice, use more bootstrap iterations
# res <- potential_analysis(x, peak.threshold=0, bw.adjust=1,
#   bs.iter=9, min.density=1)
```

---

potential\_univariate *Potential Analysis for Univariate Data*

---

## Description

One-dimensional potential estimation for univariate timeseries.

## Usage

```
potential_univariate(
  x,
  std = 1,
  bw = "nrd",
  weights = c(),
  grid.size = NULL,
  peak.threshold = 1,
  bw.adjust = 1,
  density.smoothing = 0,
  min.density = 1
)
```

**Arguments**

x	Univariate data (vector) for which the potentials shall be estimated
std	Standard deviation of the noise (defaults to 1; this will set scaled potentials)
bw	kernel bandwidth estimation method
weights	optional weights in ksdensity (used by potential_slidingaverages).
grid.size	Grid size for potential estimation. of density kernel height $d_{norm}(0, sd=bandwidth)/N$
peak.threshold	Mode detection threshold
bw.adjust	The real bandwidth will be $bw.adjust*bw$ ; defaults to 1
density.smoothing	Add a small constant density across the whole observation range to regularize density estimation (and to avoid zero probabilities within the observation range). This parameter adds uniform density across the observation range, scaled by density.smoothing.
min.density	minimum accepted density for a maximum; as a multiple of kernel height

**Value**

potential\_univariate returns a list with the following elements:

- xi the grid of points on which the potential is estimated
- pot The estimated potential:  $-\log(f)*std^2/2$ , where f is the density.
- density Density estimate corresponding to the potential.
- min.inds indices of the grid points at which the density has minimum values; (-potentials; neglecting local optima)
- max.inds indices the grid points at which the density has maximum values; (-potentials; neglecting local optima)
- bw bandwidth of kernel used
- min.points grid point values at which the density has minimum values; (-potentials; neglecting local optima)
- max.points grid point values at which the density has maximum values; (-potentials; neglecting local optima)

**Author(s)**

Based on Matlab code from Egbert van Nes modified by Leo Lahti. Extended from the initial version in the **earlywarnings** R package.

**References**

- Livina et al. (2010). Potential analysis reveals changing number of climate states during the last 60 kyr. *Climate of the Past*, 6, 77-82.
- Lahti et al. (2014). Tipping elements of the human intestinal ecosystem. *Nature Communications* 5:4344.

**Examples**

```
# res <- potential_univariate(x)
```

---

prevalence	<i>OTU Prevalence</i>
------------	-----------------------

---

**Description**

Simple prevalence measure.

**Usage**

```
prevalence(
  x,
  detection = 0,
  sort = FALSE,
  count = FALSE,
  include.lowest = FALSE
)
```

**Arguments**

<code>x</code>	A vector, data matrix or <a href="#">phyloseq</a> object
<code>detection</code>	Detection threshold for absence/presence (strictly greater by default).
<code>sort</code>	Sort the groups by prevalence
<code>count</code>	Logical. Indicate prevalence as fraction of samples (in percentage [0, 1]; default); or in absolute counts indicating the number of samples where the OTU is detected (strictly) above the given abundance threshold.
<code>include.lowest</code>	Include the lower boundary of the detection and prevalence cutoffs. FALSE by default.

**Details**

For vectors, calculates the fraction (`count=FALSE`) or number (`count=TRUE`) of samples that exceed the detection. For matrices, calculates this for each matrix column. For `phyloseq` objects, calculates this for each OTU. The relative prevalence (`count=FALSE`) is simply the absolute prevalence (`count=TRUE`) divided by the number of samples.

**Value**

For each OTU, the fraction of samples where a given OTU is detected. The output is readily given as a percentage.

**Author(s)**

Contact: Leo Lahti <[microbiome-admin@googlegroups.com](mailto:microbiome-admin@googlegroups.com)>

## References

A Salonen et al. The adult intestinal core microbiota is determined by analysis depth and health status. *Clinical Microbiology and Infection* 18(S4):16 20, 2012. To cite the microbiome R package, see `citation('microbiome')`

## Examples

```
data(peerj32)
pr <- prevalence(peerj32$phyloseq, detection=0, sort=TRUE, count=TRUE)
```

---

psmelt2

*Convert [phyloseq-class](#) object to long data format*

---

## Description

An alternative to `psmelt` function from [phyloseq-class](#) object.

## Usage

```
psmelt2(x, sample.column = NULL, feature.column = NULL)
```

## Arguments

`x` [phyloseq-class](#) object

`sample.column` A single character string specifying name of the column to hold sample names.

`feature.column` A single character string specifying name of the column to hold OTU or ASV names.

## Value

A tibble in long format

## Author(s)

Contact: Sudarshan A. Shetty <[sudarshanshetty9@gmail.com](mailto:sudarshanshetty9@gmail.com)>

## Examples

```
data("dietswap")
ps.melt <- psmelt2(dietswap, sample.column="SampleID",
                  feature.column="Feature")
head(ps.melt)
```

---

rare

*Rare Microbiota*

---

### Description

Filter the phyloseq object to include only rare (non-core) taxa.

### Usage

```
rare(x, detection, prevalence, include.lowest = FALSE, ...)
```

### Arguments

x	phyloseq-class object
detection	Detection threshold for absence/presence (strictly greater by default).
prevalence	Prevalence threshold (in [0, 1]; strictly greater by default)
include.lowest	Include the lower boundary of the detection and prevalence cutoffs in core calculation. FALSE by default.
...	Arguments to pass.

### Value

Filtered phyloseq object including only rare taxa

### Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

### References

Salonen A, Salojarvi J, Lahti L, de Vos WM. The adult intestinal core microbiota is determined by analysis depth and health status. *Clinical Microbiology and Infection* 18(S4):16-20, 2012 To cite the microbiome R package, see citation('microbiome')

### See Also

core\_members

### Examples

```
data(dietswap)
# Detection threshold 0 (strictly greater by default);
# Prevalence threshold 50 percent (strictly greater by default)
pseq <- rare(dietswap, 0, 50/100)
```



---

rare_abundance	<i>Rare (Non-Core) Abundance Index</i>
----------------	--

---

**Description**

Calculates the rare abundance community index.

**Usage**

```
rare_abundance(  
  x,  
  detection = 0.1/100,  
  prevalence = 50/100,  
  include.lowest = FALSE  
)
```

**Arguments**

x	<a href="#">phyloseq-class</a> object
detection	Detection threshold for absence/presence (strictly greater by default).
prevalence	Prevalence threshold (in [0, 1]). The required prevalence is strictly greater by default. To include the limit, set include.lowest to TRUE.
include.lowest	Include the lower boundary of the detection and prevalence cutoffs. FALSE by default.

**Details**

This index gives the relative proportion of rare species (ie. those that are not part of the core microbiota) in the interval [0,1]. This is the complement (1-x) of the core abundance. The rarity function provides the abundance of the least abundant taxa within each sample, regardless of the population prevalence.

**Value**

A vector of indices

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**See Also**

core\_abundance, rarity, diversity

**Examples**

```
data(dietswap)  
d <- rare_abundance(dietswap, detection=0.1/100, prevalence=50/100)
```

---

rare_members	<i>Rare Taxa</i>
--------------	------------------

---

### Description

Determine members of the rare microbiota with given abundance and prevalence threshold.

### Usage

```
rare_members(x, detection = 1/100, prevalence = 50/100, include.lowest = FALSE)
```

### Arguments

x	phyloseq-class object
detection	Detection threshold for absence/presence (strictly greater by default).
prevalence	Prevalence threshold (in [0, 1]). The required prevalence is strictly greater by default. To include the limit, set include.lowest to TRUE.
include.lowest	Include the lower boundary of the detection and prevalence cutoffs. FALSE by default.

### Details

For phyloseq object, lists taxa that are less prevalent than the given prevalence threshold. Optionally, never exceeds the given abundance threshold (by default, all abundances accepted). For matrix, lists columns that satisfy these criteria.

### Value

Vector of rare taxa

### Author(s)

Leo Lahti <microbiome-admin@googlegroups.com>

### References

To cite the microbiome R package, see citation('microbiome')

### See Also

core\_members

### Examples

```
data(dietswap)
# Detection threshold: the taxa never exceed the given detection threshold
# Prevalence threshold 20 percent (strictly greater by default)
a <- rare_members(dietswap, detection=100/100, prevalence=20/100)
```

---

rarity	<i>Rarity Index</i>
--------	---------------------

---

**Description**

Calculates the community rarity index.

**Usage**

```
rarity(x, index = "all", detection = 0.2/100, prevalence = 20/100)
```

**Arguments**

x	phyloseq-class object
index	If the index is given, it will override the other parameters. See the details below for description and references of the standard rarity indices.
detection	Detection threshold for absence/presence (strictly greater by default).
prevalence	Prevalence threshold (in [0, 1]). The required prevalence is strictly greater by default. To include the limit, set include.lowest to TRUE.

**Details**

The rarity index characterizes the concentration of species at low abundance.

The following rarity indices are provided:

- `log_modulo_skewness` Quantifies the concentration of the least abundant species by the log-modulo skewness of the arithmetic abundance classes (see Magurran & McGill 2011). These are typically right-skewed; to avoid taking log of occasional negative skews, we follow Locey & Lennon (2016) and use the log-modulo transformation that adds a value of one to each measure of skewness to allow logarithmization. The values  $q=0.5$  and  $n=50$  are used here.
- `low_abundance` Relative proportion of the least abundant species, below the detection level of 0.2%. The least abundant species are determined separately for each sample regardless of their prevalence.
- `rare_abundance` Relative proportion of the non-core species, exceed the given detection level (default 20 at the given prevalence (default 20 This is complement of the core with the same thresholds.

**Value**

A vector of rarity indices

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

## References

Kenneth J. Locey and Jay T. Lennon. Scaling laws predict global microbial diversity. PNAS 2016 113 (21) 5970-5975; doi:10.1073/pnas.1521291113.

Magurran AE, McGill BJ, eds (2011) Biological Diversity: Frontiers in Measurement and Assessment (Oxford Univ Press, Oxford), Vol 12

## See Also

alpha, log\_modulo\_skewness, rare\_abundance, low\_abundance

## Examples

```
data(dietswap)
d <- rarity(dietswap, index='low_abundance')
# d <- rarity(dietswap, index='all')
```

---

readcount	<i>Total Read Count</i>
-----------	-------------------------

---

## Description

Total Read Count

## Usage

```
readcount(x)
```

## Arguments

x [phyloseq-class](#) object

## Value

Vector of read counts.

## Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

## References

See citation('microbiome')

## Examples

```
data(dietswap)
d <- readcount(dietswap)
```

---

read\_biom2phyloseq     *Read BIOM File into a Phyloseq Object*

---

## Description

Read biom and mapping files into a [phyloseq-class](#) object.

## Usage

```
read_biom2phyloseq(  
  biom.file = NULL,  
  taxonomy.file = NULL,  
  metadata.file = NULL,  
  ...  
)
```

## Arguments

biom.file	A biom file with '.biom' extension
taxonomy.file	NULL the latest version has taxonomic information within the biom
metadata.file	A simple metadata/mapping file with .csv extension
...	Arguments to pass for import_biom

## Details

Biom file and mapping files will be converted to [phyloseq-class](#).

## Value

[phyloseq-class](#) object.

## Author(s)

Sudarshan A. Shetty <sudarshanshetty9@gmail.com>

## Examples

```
p0 <- read_biom2phyloseq()  
#biom.file <- qiita1629.biom"  
#meta.file <- qiita1629_mapping.csv"  
#p0 <- read_biom2phyloseq(biom.file = biom.file,  
#                          metadata.file = meta.file,  
#                          taxonomy.file = NULL)
```

---

read\_csv2phyloseq      *Read Simple OTU Tables into a Phyloseq Object*

---

## Description

Read simple OTU tables, mapping and taxonomy files into a [phyloseq-class](#) object.

## Usage

```
read_csv2phyloseq(  
  otu.file = NULL,  
  taxonomy.file = NULL,  
  metadata.file = NULL,  
  sep = ", "  
)
```

## Arguments

otu.file	A simple otu_table with '.csv' extension
taxonomy.file	A simple taxonomy file with '.csv' extension
metadata.file	A simple metadata/mapping file with .csv extension
sep	CSV file separator

## Details

Simple OTU tables, mapping and taxonomy files will be converted to [phyloseq-class](#).

## Value

[phyloseq-class](#) object.

## Author(s)

Sudarshan A. Shetty <sudarshanshetty9@gmail.com>

## Examples

```
# NOTE: the system.file command reads these example files from the  
# microbiome R package. To use your own local files, simply write  
# otu.file <- "/path/to/my/file.csv" etc.  
  
#otu.file <-  
#  system.file("extdata/qiita1629_otu_table.csv",  
#  package='microbiome')  
  
#tax.file <- system.file("extdata/qiita1629_taxonomy_table.csv",  
#  package='microbiome')
```

```
#meta.file <- system.file("extdata/qiita1629_mapping_subset.csv",  
#   package='microbiome')  
  
#p0 <- read_csv2phyloseq(  
#   otu.file=otu.file,  
#   taxonomy.file=tax.file,  
#   metadata.file=meta.file)
```

---

read\_mothur2phyloseq *Read Mothur Output into a Phyloseq Object*

---

## Description

Read mothur shared and consensus taxonomy files into a [phyloseq-class](#) object.

## Usage

```
read_mothur2phyloseq(shared.file, consensus.taxonomy.file, mapping.file = NULL)
```

## Arguments

`shared.file` A **shared file** produced by *mothur*. Identified from the `.shared` extension  
`consensus.taxonomy.file` Consensus taxonomy file produced by *mothur*. Identified from with the `.taxonomy` extension. See [http://www.mothur.org/wiki/ConTaxonomy\\_file](http://www.mothur.org/wiki/ConTaxonomy_file).  
`mapping.file` Metadata/mapping file with `.csv` extension

## Details

Mothur shared and consensus taxonomy files will be converted to [phyloseq-class](#).

## Value

[phyloseq-class](#) object.

## Author(s)

Sudarshan A. Shetty <[sudarshanshetty9@gmail.com](mailto:sudarshanshetty9@gmail.com)>

## Examples

```
#otu.file <- system.file(  
#"extdata/Baxter_FITs_Microbiome_2016_fit.final.tx.1.subsample.shared",  
#   package='microbiome')  
  
#tax.file <- system.file(  
#"extdata/Baxter_FITs_Microbiome_2016_fit.final.tx.1.cons.taxonomy",  
#   package='microbiome')
```

```
#meta.file <- system.file(
#"extdata/Baxter_FITs_Microbiome_2016_mapping.csv",
# package='microbiome')

#p0 <- read_mothur2phyloseq(
#   shared.file=otu.file,
#   consensus.taxonomy.file=tax.file,
#   mapping.file=meta.file)
```

---

read\_phyloseq      *Import phyloseq Data*

---

## Description

Read the otu, taxonomy and metadata from various formats.

## Usage

```
read_phyloseq(
  otu.file = NULL,
  taxonomy.file = NULL,
  metadata.file = NULL,
  type = c("simple", "mothur", "biom"),
  sep = ",")
```

## Arguments

otu.file	File containing the OTU table (for mothur this is the file with the .shared extension)
taxonomy.file	(for mothur this is typically the consensus taxonomy file with the .taxonomy extension)
metadata.file	File containing samples x variables metadata.
type	Input data type: 'mothur' or 'simple' or 'biom' type.
sep	CSV file separator

## Details

See `help(read_mothur2phyloseq)` for details on the Mothur input format; and `help(read_biom2phyloseq)` for details on the biom format. The simple format refers to the set of CSV files.

## Value

`phyloseq-class` object



**Author(s)**

Sudarshan A. Shetty <sudarshanshetty9@gmail.com>

**Examples**

```
# pseq <- read_phyloseq(otu.file,  
#                       taxonomy.file,  
#                       metadata.file,  
#                       type=c('mothur', 'simple', 'biom'))
```

---

remove_samples	<i>Exclude Samples</i>
----------------	------------------------

---

**Description**

Filter out selected samples from a phyloseq object.

**Usage**

```
remove_samples(samples = NULL, x)
```

**Arguments**

samples	Names of samples to be removed.
x	<a href="#">phyloseq-class</a> object

**Details**

This complements the phyloseq function `prune_samples` by providing a way to exclude given groups from a phyloseq object.

**Value**

Filtered phyloseq object.

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

To cite the microbiome R package, see `citation('microbiome')`

**See Also**

`phyloseq::prune_samples`, `phyloseq::subset_samples`

**Examples**

```
data(dietswap)
pseq <- remove_samples(c("Sample-182", "Sample-222"), dietswap)
```

---

remove\_taxa

*Exclude Taxa*

---

**Description**

Filter out selected taxa from a phyloseq object.

**Usage**

```
remove_taxa(taxa = NULL, x)
```

**Arguments**

taxa	Names of taxa to be removed.
x	<a href="#">phyloseq-class</a> object

**Details**

This complements the phyloseq function `prune_taxa` by providing a way to exclude given groups from a phyloseq object.

**Value**

Filtered phyloseq object.

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

To cite the microbiome R package, see `citation('microbiome')`

**See Also**

`phyloseq::prune_taxa`, `phyloseq::subset_taxa`

**Examples**

```
data(dietswap)
pseq <- remove_taxa(c("Akkermansia", "Dialister"), dietswap)
```

---

richness	<i>Richness Index</i>
----------	-----------------------

---

**Description**

Community richness index.

**Usage**

```
richness(x, index = c("observed", "chao1"), detection = 0)
```

**Arguments**

x	A species abundance vector, or matrix (taxa/features x samples) with the absolute count data (no relative abundances), or <a href="#">phyloseq-class</a> object
index	"observed" or "chao1"
detection	Detection threshold. Used for the "observed" index.

**Details**

By default, returns the richness for multiple detection thresholds defined by the data quantiles. If the detection argument is provided, returns richness with that detection threshold. The "observed" richness corresponds to index="observed", detection=0.

**Value**

A vector of richness indices

**Author(s)**

Contact: Leo Lahti <[microbiome-admin@googlegroups.com](mailto:microbiome-admin@googlegroups.com)>

**See Also**

alpha

**Examples**

```
data(dietswap)
d <- richness(dietswap, detection=0)
```

---

spreadplot	<i>Abundance Spread Plot</i>
------------	------------------------------

---

### Description

Visualize abundance spread for OTUs

### Usage

```
spreadplot(x, trunc = 0.001/100, alpha = 0.15, width = 0.35)
```

### Arguments

x	<a href="#">phyloseq-class</a> object; or a data.frame with fields "otu" (otu name); "sample" (sample name); and "abundance" (otu abundance in the given sample)
trunc	Truncate abundances lower than this to zero
alpha	Alpha level for point transparency
width	Width for point spread

### Value

ggplot2 object

### Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

### References

See citation('microbiome')

### Examples

```
data(dietswap)
p <- spreadplot(transform(dietswap, "compositional"))
```

---

summarize_phyloseq	<i>Summarize phyloseq object</i>
--------------------	----------------------------------

---

**Description**

Prints basic information of data.

**Usage**

```
summarize_phyloseq(x)
```

**Arguments**

x                    Input is a [phyloseq-class](#) object.

**Details**

The summarize\_phyloseq function will give information on whether data is compositional or not, reads (min, max, median, average), sparsity, presence of singletons and sample variables.

**Value**

Prints basic information of [phyloseq-class](#) object.

**Author(s)**

Contact: Sudarshan A. Shetty <[sudarshanshetty9@gmail.com](mailto:sudarshanshetty9@gmail.com)>

**Examples**

```
data(dietswap)
summarize_phyloseq(dietswap)
```

---

taxa	<i>Taxa Names</i>
------	-------------------

---

**Description**

List the names of taxonomic groups in a phyloseq object.

**Usage**

```
taxa(x)
```

**Arguments**

x                    [phyloseq-class](#) object

**Details**

A handy shortcut for `phyloseq::taxa_names`, with a potential to add to add some extra tweaks later.

**Value**

A vector with taxon names.

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

To cite the microbiome R package, see `citation('microbiome')`

**Examples**

```
data(dietswap)
x <- taxa(dietswap)
```

---

TibbleUtilites

*Utilities For `phyloseq-class` Slots to Tibbles*

---

**Description**

Utility to convert phyloseq slots to tibbles.

**Usage**

```
otu_tibble(x, column.id = "FeatureID")
tax_tibble(x, column.id = "FeatureID")
sample_tibble(x, column.id = "SampleID")
combine_otu_tax(x, column.id = "FeatureID")
```

**Arguments**

`x` `phyloseq-class` object.  
`column.id` Provide name for the column which will hold the rownames. of slot.

**Details**

Convert different phyloseq slots into tibbles. `otu_tibble` gets the `otu_table` in tibble format. `tax_tibble` gets the `taxa_table` in tibble format. `combine_otu_tax` combines `otu_table` and `taxa_table` into one tibble.

**Value**

A tibble

**Author(s)**

Contact: Sudarshan A. Shetty <sudarshanshetty9@gmail.com>

**Examples**

```
library(microbiome)
data("dietswap")
otu_tib <- otu_tibble(dietswap, column.id="FeatureID")
tax_tib <- tax_tibble(dietswap, column.id="FeatureID")
sample_tib <- sample_tibble(dietswap, column.id="SampleID")
otu_tax <- combine_otu_tax(dietswap, column.id = "FeatureID")
head(otu_tax)
```

---

timesplit

*Time Split*

---

**Description**

For each subject, return temporally consecutive sample pairs together with the corresponding time difference.

**Usage**

```
timesplit(x)
```

**Arguments**

x                    **phyloseq** object.

**Value**

data.frame

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**Examples**

```
data(atlas1006)
x <- timesplit(subset_samples(atlas1006,
  DNA_extraction_method == 'r' & sex == "male"))
```

---

time_normalize	<i>Normalize Phyloseq Metadata Time Field</i>
----------------	---

---

**Description**

Shift the time field in phyloseq sample\_data such that the first time point of each subject is always 0.

**Usage**

```
time_normalize(x)
```

**Arguments**

x phyloseq object. The sample\_data(x) should contain the following fields: subject, time

**Value**

Phyloseq object with a normalized time field

**Examples**

```
data(peerj32)
pseq <- time_normalize(peerj32$phyloseq)
```

---

time_sort	<i>Temporal Sorting Within Subjects</i>
-----------	---

---

**Description**

Within each subject, sort samples by time and calculate distance from the baseline point (minimum time).

**Usage**

```
time_sort(x)
```

**Arguments**

x A metadata data.frame including the following columns: time, subject, sample, signal. Or a phyloseq object.

**Value**

A list with sorted metadata (data.frame) for each subject.



**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation('microbiome')

**Examples**

```
data(atlas1006)
pseq <- subset_samples(atlas1006, DNA_extraction_method == "r")
ts <- time_sort(meta(pseq))
```

---

top *Identify Top Entries*

---

**Description**

Identify top entries in a vector or given field in data frame.

**Usage**

```
top(
  x,
  field = NULL,
  n = NULL,
  output = "vector",
  round = NULL,
  na.rm = FALSE,
  include.rank = FALSE
)
```

**Arguments**

x	data.frame, matrix, or vector
field	Field or column to check for a data.frame or matrix
n	Number of top entries to show
output	Output format: vector or data.frame
round	Optional rounding
na.rm	Logical. Remove NA before calculating the statistics.
include.rank	Include ranking if the output is data.frame. Logical.

**Value**

Vector of top counts, named by the corresponding entries

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("bibliographica")

**Examples**

```
data(dietswap)
p <- top(meta(dietswap), "group", 10)
```

---

top\_taxa

*Top Taxa*

---

**Description**

Return n most abundant taxa (based on total abundance over all samples), sorted by abundance

**Usage**

```
top_taxa(x, n = ntaxa(x))
```

**Arguments**

x                    phyloseq object  
n                    Number of top taxa to return (default: all)

**Value**

Character vector listing the top taxa

**Examples**

```
data(dietswap)
topx <- top_taxa(dietswap, n=10)
```

---

transform	<i>Data Transformations for phyloseq Objects</i>
-----------	--

---

## Description

Standard transforms for [phyloseq-class](#).

## Usage

```
transform(
  x,
  transform = "identity",
  target = "OTU",
  shift = 0,
  scale = 1,
  log10 = TRUE,
  reference = 1,
  ...
)
```

## Arguments

x	<a href="#">phyloseq-class</a> object
transform	Transformation to apply. The options include: 'compositional' (ie relative abundance), 'Z', 'log10', 'log10p', 'hellinger', 'identity', 'clr', 'alr', or any method from the <code>vegan::decostand</code> function.
target	Apply the transform for 'sample' or 'OTU'. Does not affect the log transform.
shift	A constant indicating how much to shift the baseline abundance (in <code>transform='shift'</code> )
scale	Scaling constant for the abundance values when <code>transform = "scale"</code> .
log10	Used only for Z transformation. Apply log10 before Z.
reference	Reference feature for the alr transformation.
...	arguments to be passed

## Details

In transformation typ, the 'compositional' abundances are returned as relative abundances in [0, 1] (convert to percentages by multiplying with a factor of 100). The Hellinger transform is square root of the relative abundance but instead given at the scale [0,1]. The log10p transformation refers to  $\log_{10}(1 + x)$ . The log10 transformation is applied as  $\log_{10}(1 + x)$  if the data contains zeroes. CLR transform applies a pseudocount of  $\min(\text{relative abundance})/2$  to exact zero relative abundance entries in OTU table before taking logs.

## Value

Transformed [phyloseq](#) object

**Examples**

```
data(dietswap)
x <- dietswap

# No transformation
xt <- transform(x, 'identity')

# OTU relative abundances
# xt <- transform(x, 'compositional')

# Z-transform for OTUs
# xt <- transform(x, 'Z', 'OTU')

# Z-transform for samples
# xt <- transform(x, 'Z', 'sample')

# Log10 transform (log10(1+x) if the data contains zeroes)
# xt <- transform(x, 'log10')

# Log10p transform (log10(1+x) always)
# xt <- transform(x, 'log10p')

# CLR transform
# Note that small pseudocount is added if data contains zeroes
xt <- microbiome::transform(x, 'clr')

# ALR transform
# The pseudocount must be specified explicitly
# The reference feature is 1 by default
xt <- microbiome::transform(x, 'alr', shift=1, reference=1)

# Shift the baseline
# xt <- transform(x, 'shift', shift=1)

# Scale
# xt <- transform(x, 'scale', scale=1)
```

# Index

## \* data

- atlas1006, 11
- dietswap, 28
- hitchip.taxonmy, 41
- peerj32, 55

## \* early-warning

- potential\_univariate, 68

## \* package

- microbiome-package, 4

## \* utilities

- abundances, 4
- add\_besthit, 5
- add\_refseq, 6
- aggregate\_rare, 7
- aggregate\_taxa, 8
- alpha, 9
- associate, 10
- baseline, 12
- bimodality, 13
- bimodality\_sarle, 15
- boxplot\_abundance, 16
- boxplot\_alpha, 17
- cmat2table, 18
- collapse\_replicates, 19
- core, 20
- core\_abundance, 21
- core\_heatmap, 22
- core\_matrix, 23
- core\_members, 24
- coverage, 25
- default\_colors, 26
- densityplot, 26
- divergence, 29
- diversity, 30
- dominance, 31
- dominant, 33
- evenness, 34
- find\_optima, 35
- gktau, 36

- group\_age, 37
- group\_bmi, 38
- heat, 40
- hotplot, 42
- inequality, 43
- intermediate\_stability, 44
- is\_compositional, 45
- log\_modulo\_skewness, 46
- low\_abundance, 47
- map\_levels, 48
- merge\_taxa2, 49
- meta, 50
- multimodality, 50
- neat, 52
- neatsort, 53
- overlap, 54
- plot\_atlas, 56
- plot\_composition, 57
- plot\_core, 58
- plot\_density, 59
- plot\_frequencies, 60
- plot\_landscape, 61
- plot\_regression, 63
- plot\_taxa\_prevalence, 65
- plot\_tipping, 66
- prevalence, 70
- psmelt2, 71
- rare, 72
- rare\_abundance, 73
- rare\_members, 74
- rarity, 75
- read\_biom2phyloseq, 77
- read\_csv2phyloseq, 78
- read\_mothur2phyloseq, 79
- read\_phyloseq, 80
- readcount, 76
- remove\_samples, 81
- remove\_taxa, 82
- richness, 83

- spreadplot, 84
  - summarize\_phyloseq, 85
  - taxa, 85
  - time\_sort, 88
  - timesplit, 87
  - top, 89
  - transform, 91
- ab, (abundances), 4
- abundances, 4
- add\_besthit, 5
- add\_refseq, 6
- aggregate\_rare, 7
- aggregate\_taxa, 8
- alpha, 9
- associate, 10
- atlas1006, 11
- baseline, 12
- bimodality, 13
- bimodality\_sarle, 15
- boxplot\_abundance, 16
- boxplot\_alpha, 17
- cmat2table, 18
- collapse\_replicates, 19
- combine\_otu\_tax (TibbleUtilites), 86
- core, 20
- core\_abundance, 21
- core\_heatmap, 22
- core\_matrix, 23
- core\_members, 24
- coverage, 25
- cross\_correlate (associate), 10
- data.frame, 60
- default\_colors, 26
- densityplot, 26
- dietswap, 28
- divergence, 29
- diversity, 30
- dominance, 31
- dominant, 33
- estimate\_richness, 9
- evenness, 34
- filter\_prevalent (core), 20
- find\_optima, 35
- ggplot, 17, 18, 42, 58, 60–62, 65, 66
- gktau, 36
- group\_age, 37
- group\_bmi, 38
- heat, 40
- hitchip.taxonomy, 41
- hotplot, 42
- inequality, 43
- intermediate\_stability, 44
- is\_compositional, 45
- log\_modulo\_skewness, 46
- low\_abundance, 47
- map\_levels, 48
- merge\_taxa2, 49
- meta, 50
- microbiome (microbiome-package), 4
- microbiome-package, 4
- multimodality, 50
- neat, 52
- neatsort, 53, 57
- ordinate, 53
- otu (abundances), 4
- otu\_tibble (TibbleUtilites), 86
- overlap, 54
- peerj32, 55
- phyloseq, 12, 23, 48, 58, 70, 91
- phyloseq-class, 5, 71, 86
- plot\_atlas, 56
- plot\_composition, 57
- plot\_core, 58
- plot\_density, 59
- plot\_frequencies, 60
- plot\_landscape, 61
- plot\_regression, 63
- plot\_taxa\_prevalence, 65
- plot\_tipping, 66
- potential\_analysis, 67
- potential\_univariate, 68
- prevalence, 70
- prevalent\_taxa (core\_members), 24
- psmelt2, 71
- rare, 72

rare\_abundance, [73](#)  
rare\_members, [74](#)  
rarity, [75](#)  
read\_biom2phyloseq, [77](#)  
read\_csv2phyloseq, [78](#)  
read\_mothur2phyloseq, [79](#)  
read\_phyloseq, [80](#)  
readcount, [76](#)  
remove\_samples, [81](#)  
remove\_taxa, [82](#)  
richness, [83](#)

sample\_data, [50](#)  
sample\_tibble (TibbleUtilites), [86](#)  
spreadplot, [84](#)  
summarize\_phyloseq, [85](#)

tax\_tibble (TibbleUtilites), [86](#)  
taxa, [85](#)  
TibbleUtilites, [86](#)  
time\_normalize, [88](#)  
time\_sort, [88](#)  
timesplit, [87](#)  
top, [89](#)  
top\_taxa, [90](#)  
transform, [57, 91](#)

vegdist, [52](#)