

# Package ‘microbiome’

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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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microbiome-package	<i>R package for microbiome studies</i>
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## 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	<a href="#">phyloseq-class</a> object
transform	Transformation to apply. The options include: 'compositional' (ie relative abundance), 'Z', 'log10', 'log10p', 'hellinger', 'identity', 'clr', or any method from the <code>vegan::decostand</code> 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')
```

---

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

---

### Description

Summarize phyloseq data into a higher phylogenetic level.

### Usage

```
aggregate_taxa(x, level, top = NULL)
```

### Arguments

x	<a href="#">phyloseq-class</a> object
level	Summarization level (from <code>rank_names(pseq)</code> )
top	Keep the top-n taxa, and merge the rest under the category 'Other'. Instead of top-n numeric this can also be a character vector listing the groups to combine.

### 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](mailto:microbiome-admin@googlegroups.com)>

### References

See citation('microbiome')

### Examples

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

---

 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; categorical for discrete)
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

As the method=categorical (discrete) association measure for nominal (no order for levels) variables we use Goodman and Kruskal tau based on [r-bloggers.com/measuring-associations-between-non-numeric-variables/](http://r-bloggers.com/measuring-associations-between-non-numeric-variables/)

## Value

List with cor, pval, pval.adjusted

## Author(s)

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

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

```
## Not run:
b <- bimodality_sarle(rnorm(100), type='Sarle.finite.sample')

## End(Not run)
```

---

boxplot_abundance	<i>Abundance Boxplot</i>
-------------------	--------------------------

---

### Description

Plot phyloseq abundances.

### Usage

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

### Arguments

d	phyloseq-class object
x	Metadata variable to map to the horizontal axis.
y	OTU to map on the vertical axis
line	The variable to map on lines
violin	Use violin version of the boxplot
na.rm	Remove NAs
show.points	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')
```

---

cmat2table	<i>Convert Correlation Matrix into a Table</i>
------------	------------------------------------------------

---

### Description

Arrange correlation matrices from associate into a table format.

### Usage

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

**Arguments**

res                    Output from associate  
 verbose                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')
```

---

 core

*Core Microbiota*


---

**Description**

Filter the phyloseq object to include only prevalent taxa.

**Usage**

```
core(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. 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, variable\_members, noncore\_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)
```

---

core\_abundance

*Core Abundance*

---

## Description

Calculates the community core abundance index.

## Usage

```
core_abundance(x, detection = 0.1/100, prevalence = 50/100)
```

## 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)

## 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	<i>Core Heatmap</i>
--------------	---------------------

---

**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 run:  
# Not exported  
data(peerj32)  
core <- core_matrix(peerj32$phyloseq)  
  
## End(Not run)
```



---

`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>	<code>phyloseq-class</code> object
<code>detection</code>	Detection threshold for absence/presence (strictly greater by default).
<code>prevalence</code>	Prevalence threshold (in [0, 1]; strictly greater by default)
<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, global

### Examples

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

---

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)
```

**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

**Value**

ggplot2 object

**Author(s)**

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

**References**

See citation('microbiome')

**Examples**

```
## Not run:  
  p <- densityplot(cbind(rnorm(100), rnorm(100)))  
  
## End(Not run)
```

---

 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

*Diversity within a Sample Group*


---

### Description

Quantify microbiota divergence (heterogeneity) within a given sample set.

### Usage

```
divergence(x, method = "bray", coreset = NULL)
```

### Arguments

x	phyloseq object
method	dissimilarity method: any method available via <code>stats::cor</code> or <code>phyloseq::distance</code> function. Note that some methods ("jsd" for instance) do not work with the group divergence.
coreset	phyloseq object; the samples to be used to define the centroid

## Details

Microbiota divergence (heterogeneity / spread) within a given sample set can be quantified by the average sample dissimilarity or beta diversity. Taking average over all pairwise dissimilarities is sensitive to sample size and heavily biased as the similarity values are not independent. To reduce this bias, the dissimilarity of each sample against the group mean is calculated. This generates one value per sample. These can be compared between groups in order to compare differences in group homogeneity.

Note that this measure is still affected by sample size. Subsampling or bootstrapping can be applied to equalize sample sizes between comparisons.

The spearman mode is a simple indicator that returns average spearman correlation between samples of the input data and the overall group-wise average. The inverse of this measure (ie rho instead of 1-rho as in here) was used in Salonen et al. (2014) to quantify group homogeneity.

## Value

Vector with dissimilarities; one for each sample, quantifying the dissimilarity of the sample from the group-level mean.

## Author(s)

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

## References

The inter- and intra-individual homogeneity measures used in Salonen et al. ISME J. 8:2218-30, 2014 were obtained as  $1 - \beta$  where  $\beta$  is the group diversity as quantified by the spearman method.

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)
b <- divergence(subset_samples(dietswap, nationality == 'AFR'))
```

---

diversities

*Diversity Index*

---

## Description

Various community diversity indices.

## Usage

```
diversities(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 <code>phyloseq-class</code> 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\\_evenness\\_index.pdf](https://portais.ufg.br/up/202/o/2003-comparative_evenness_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, global

**Examples**

```
data(dietswap)
d <- diversities(dietswap, 'shannon')
# d <- diversities(dietswap, 'all')
```

---

dominance	<i>Dominance Index</i>
-----------	------------------------

---

### 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 <a href="#">phyloseq-class</a> 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, global

**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)
```

---

evenness

*Evenness Index*

---

**Description**

Various community evenness indices.

**Usage**

```
evenness(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	Evenness index. See details for options.
zeroes	Include zero counts in the evenness estimation.



## 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. *Global Ecology & Biogeography* (2003) 12, 177–197 4) 'evan': 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\\_evenness\\_index.pdf](https://portais.ufg.br/up/202/o/2003-comparative_evenness_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, global

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

## End(Not run)
```

---

 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](mailto:microbiome-admin@googlegroups.com)>

**References**

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

**Examples**

```
data(peerj32)
v1 <- unlist(peerj32$microbes[,1])
v2 <- unlist(peerj32$lipids[,1])
tc <- gktau(v1, v2)
```

---

global

*Global Ecosystem State Variables*

---

**Description**

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

**Usage**

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

## 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	Default is 'NULL', meaning that all available global indices will be included. For specific options, see details.
rarity.detection	Detection threshold for determining rare taxa.
rarity.prevalence	Prevalence threshold for determining rare taxa.

## Details

This function returns global indices of the ecosystem state using default choices for detection, prevalence and other parameters for simplicity and standardization. See the individual functions for more options. All indicators from the richness, diversities, 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_`, `diversities_`, `dominance_`, or `rarity_` in the output table to avoid confusion between similarly named but different indices (e.g. Simpson diversity and Simpson dominance).

## Value

A data.frame of samples x global indicators

## Author(s)

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

## References

See citation('microbiome')

## See Also

global, dominance, rarity, phyloseq::estimate\_richness

## Examples

```
data(dietswap)
d <- global(dietswap, index='gini')
# d <- global(dietswap, index='all')
```

---

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	<i>Body-Mass Index (BMI) Classes</i>
-----------	--------------------------------------

---

**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**

<code>x</code>	Numeric vector (BMI)
<code>breaks</code>	Class break points. Either a vector of breakpoints, or one of the predefined options ("standard", "standard_truncated", "even").
<code>n</code>	Number of groups for the breaks = "even" option.
<code>labels</code>	labels for the levels of the resulting category. By default, labels are constructed using "(a,b]" interval notation. If <code>labels = FALSE</code> , simple integer codes are returned instead of a factor.
<code>include.lowest</code>	logical, indicating if an 'x[i]' equal to the lowest (or highest, for <code>right = FALSE</code> ) 'breaks' value should be included.
<code>right</code>	logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa.
<code>dig.lab</code>	integer which is used when labels are not given. It determines the number of digits used in formatting the break numbers.
<code>ordered_result</code>	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, text.size = 10,
      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.

text.size	Adjust text size
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	<i>HITChip Taxonomy</i>
------------------	-------------------------

---

**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	<i>Univariate Bimodality Plot</i>
---------	-----------------------------------

---

**Description**

Coloured bimodality plot.

**Usage**

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

**Arguments**

x	phyloseq-class 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

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

---

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, global

**Examples**

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

---

low_abundance	<i>Low Abundance Index</i>
---------------	----------------------------

---

**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	<i>Map Taxonomic Levels</i>
------------	-----------------------------

---

### 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	<i>Merge Taxa</i>
-------------	-------------------

---

### Description

Merge taxonomic groups into a single group.

### Usage

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

### Arguments

x	<a href="#">phyloseq-class</a> 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](mailto: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**

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

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

## End(Not run)
```

---

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**

x	A matrix or phyloseq object.
arrange	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.
method	Ordination method. Only NMDS implemented for now.

distance	Distance method. See <a href="#">vegdist</a> function from the <b>vegan</b> package.
first.feature	Optionally provide the name of the first feature to start the ordering
first.sample	Optionally provide the name of the first sample to start the ordering
...	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

*Neatmap Sorting*

---

### 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')
```

---

noncore\_abundance            *Non-Core Abundance Index*

---

### Description

Calculates the noncore\_abundance community index.

### Usage

```
noncore_abundance(x, detection = 0.1/100, prevalence = 50/100)
```

### 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)

## Details

The noncore\_abundance 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 <- noncore_abundance(dietswap, detection=0.1/100, prevalence=50/100)
```

---

noncore\_members

*Select Non-Core Taxa*

---

## Description

Filter the phyloseq object to include only taxa that do not belong to the core set defined by the detection and prevalence thresholds.

## Usage

```
noncore_members(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. FALSE by default.

## Value

Filtered phyloseq object including only rare taxa

## Author(s)

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

## References

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

## Examples

```
data(peerj32)
pseq <- noncore_members(peerj32$phyloseq, 200, 20/100)
```

---

peerj32

*Probiotics Intervention Data*

---

## 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, gender, 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](mailto: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, mar = c(5,
  12, 1, 1), average_by = NULL, ...)
```

## Arguments

x	<a href="#">phyloseq-class</a> 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</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 <code>sample_variables(x)</code> .
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.
mar	Figure margins
average_by	Average the samples by the average_by variable
...	Arguments to be passed (for <a href="#">neatsort</a> function)

## Value

A [ggplot](#) plot object.

## Examples

```
data(dietswap)
pseq <- subset_samples(dietswap, group == 'DI' & nationality == 'AFR')
p <- plot_composition(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(atlas1006)
pseq <- subset_samples(atlas1006, DNA_extraction_method == 'r')
p <- plot_core(transform(pseq, "compositional"),
  prevalences=seq(0.1, 1, .1), detections=seq(0.01, 1, length = 10))
```



---

plot_density	<i>Plot Density</i>
--------------	---------------------

---

### 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	<a href="#">phyloseq-class</a> object or an OTU matrix (samples x phylotypes)
variable	OTU or metadata variable to visualize
log10	Logical. Show log10 abundances or not.
adjust	see <code>stat_density</code>
kernel	see <code>stat_density</code>
trim	see <code>stat_density</code>
na.rm	see <code>stat_density</code>
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	<i>Plot Frequencies</i>
------------------	-------------------------

---

**Description**

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

**Usage**

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

**Arguments**

x	<code>data.frame</code>
Groups	Name of the grouping variable
Factor	Name of the frequency variable

**Value**

A list with two elements:

- `dataTable` with the indicated frequencies.
- `plotggplot` plot object.

**Examples**

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

---

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

---

**Description**

Plot abundance landscape ie. sample density in 2D projection landscape

**Usage**

```
plot_landscape(x, method = "NMDS", distance = "bray", col = NULL,
  main = NULL, x.ticks = 10, rounding = 0, add.points = TRUE,
  adjust = 1, size = 1, legend = FALSE)
```

**Arguments**

x	<code>phyloseq-class</code> object or a data matrix (features x samples; eg. HITChip taxa vs. samples)
method	Ordination method, see <code>phyloseq::plot_ordination</code>
distance	Ordination distance, see <code>phyloseq::plot_ordination</code>
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

**Details**

For consistent results, set random seed (`set.seed`) before function call

**Value**

A `ggplot` plot object.

**Examples**

```
data(dietswap)
p <- plot_landscape(abundances(transform(dietswap, "log10"))[, 1:2])
```

---

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	should the median smoother be visually weighted?
show.lm	should the linear regression line be plotted?
show.median	show median smoother
median.col	median color
show.CI	should the 95% CI limits be plotted?
method	the fitting function for the spaghetti; 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' &
  gender == "female" &
  nationality == "UKIE")
p <- plot_regression(diversity ~ age, meta(pseq))
```

---

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
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>	<code>phyloseq-class</code> 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>

**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:

- modesNumber of modes for the input data vector (the most frequent number of modes from bootstrap)
- minimaAverage of potential minima across the bootstrap samples (for the most frequent number of modes)
- maximaAverage of potential maxima across the bootstrap samples (for the most frequent number of modes)
- unimodality.supportFraction of bootstrap samples exhibiting unimodality
- bwsBandwidths

### 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 <- log10(abundances(peerj32$phyloseq)['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 $\text{dnorm}(0, \text{sd}=\text{bandwidth})/N$
peak.threshold	Mode detection threshold
bw.adjust	The real bandwidth will be $\text{bw.adjust}*\text{bw}$ ; 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:  $-\log(f)*\text{std}^2/2$ , 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

```
## Not run: 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

- |                |                                                                                                                                                                                                                       |
|----------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x              | A vector, data matrix or <a href="#">phyloseq</a> object                                                                                                                                                              |
| detection      | Detection threshold for absence/presence (strictly greater by default).                                                                                                                                               |
| sort           | Sort the groups by prevalence                                                                                                                                                                                         |
| count          | 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. |
| include.lowest | 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>

**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)
```

---

rare\_members

*Rare Taxa*

---

**Description**

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

**Usage**

```
rare_members(x, detection = Inf, prevalence = 20/100)
```

**Arguments**

x	<a href="#">phyloseq-class</a> object
detection	Detection threshold for absence/presence (strictly greater by default).
prevalence	Prevalence threshold (in [0, 1]; strictly greater 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`, `noncore_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", rarity.detection = 0.2/100,
       rarity.prevalence = 20/100)
```

**Arguments**

<code>x</code>	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
<code>index</code>	If the index is given, it will override the other parameters. See the details below for description and references of the standard rarity indices.
<code>rarity.detection</code>	Detection threshold for determining rare taxa.
<code>rarity.prevalence</code>	Prevalence threshold for determining rare taxa.

**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 `rarity.detection` level of 0.2%. The least abundant species are determined separately for each sample regardless of their `rarity.prevalence`.
- `noncore_abundance` Relative proportion of the non-core species, exceed the `rarity.detection` level of 0.2% at 50% `rarity.prevalence` at most. This is complement of the core with the same thresholds.
- `rare_abundance` Relative proportion of the rare taxa in [0,1] - the rare taxa are detected with less than 20% `rarity.prevalence`, regardless of abundance.

### 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

`global`, `log_modulo_skewness`, `noncore_abundance`, `low_abundance`

### Examples

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

---

`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

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

**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**

```
## Not run:
biom.file <- qiita1629.biom"
meta.file <- qiita1629_mapping.csv"
p0 <- read_biom2phyloseq(biom.file = biom.file,
                        metadata.file = meta.file,
                        taxonomy.file = NULL)

## End(Not run)
```

---

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

```
## Not run:
# 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)

## End(Not run)
```

---

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>

**Examples**

```
## Not run:

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)

## End(Not run)
```

---

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 written by the `write_phyloseq` function.

**Value**

phyloseq-class object

**Author(s)**

Sudarshan A. Shetty <sudarshanshetty9@gmail.com>

**See Also**

write\_phyloseq

**Examples**

```
## Not run:
pseq <- read_phyloseq(otu.file,
                     taxonomy.file,
                     metadata.file,
                     type=c('mothur', 'simple', 'biom'))

## End(Not run)
```

---

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	phyloseq-class 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("Akkermansia", "Dialister"), 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, detection = NULL)
```

**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
detection	Detection threshold.

**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.

**Value**

A vector of richness indices

**Author(s)**

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

**See Also**

[global](#)

**Examples**

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

---

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>

**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)
```

---

time\_normalize      *Normalize Phyloseq Metadata Time Field*

---

**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              *Temporal Sorting Within Subjects*

---

**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_taxa	<i>Top Taxa</i>
----------	-----------------

---

**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

*Data Transformations for phyloseq Objects***Description**

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

**Usage**

```
transform(x, transform = "identity", target = "OTU", shift = 0,
         scale = 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', 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> .

**Details**

The relative abundance are returned as percentages in [0, 1]. 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.

**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
# xt <- transform(x, 'clr')

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

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

```

---

variable_members	<i>Variable Microbiota</i>
------------------	----------------------------

---

## Description

Filter the phyloseq object to include only variable taxa.

## Usage

```
variable_members(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]; strictly greater by default)
include.lowest	Include the lower boundary of the detection and prevalence cutoffs. FALSE by default.

## Details

Variable taxa are members of the microbiota that are not rare, and not members of the core microbiota. Such taxa reach notable abundance in a notable fraction of the population. The variable members are calculated by using the indicated prevalence threshold to define rare taxa; and its complement 1-prevalence to define core taxa. The remaining taxa are considered variable. The same detection threshold is used in all cases.

## Value

Filtered phyloseq object including only variable taxa.

## Author(s)

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

## References

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

**See Also**

core\_members, core, rare

**Examples**

```
data(dietswap)
# Detection threshold 0 (strictly greater by default);
# Prevalence threshold 50 percent (strictly greater by default)
pseq.rel <- transform(dietswap, 'compositional')
pseq <- variable_members(pseq.rel, 0.5/100, 20/100)
```

---

write_phyloseq	<i>Exporting phyloseq Data in CSV Files</i>
----------------	---------------------------------------------

---

**Description**

Writes the otu, taxonomy and metadata in csv files.

**Usage**

```
write_phyloseq(x, type = "all", path = getwd())
```

**Arguments**

x	phyloseq-class object
type	'OTU' or 'TAXONOMY' or 'METADATA'
path	Path to the directory/folder where the data will be written. Uses the working directory by default.

**Value**

Output file path (a string)

**See Also**

read\_phyloseq

**Examples**

```
## Not run:
data(dietswap)
pseq <- dietswap
# By default writes all info at once (ie OTU/TAXONOMY/METADATA)
write_phyloseq(pseq)
write_phyloseq(pseq, 'OTU')
write_phyloseq(pseq, 'TAXONOMY')
write_phyloseq(pseq, 'METADATA')

## End(Not run)
```



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