

Package ‘metacoder’

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Title Tools for Parsing, Manipulating, and Graphing Taxonomic
Abundance Data

Version 0.3.1

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Description A set of tools for parsing, manipulating, and graphing data
classified by a hierarchy (e.g. a taxonomy).

Depends R (>= 3.0.2), taxa

License GPL-2 | GPL-3

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R topics documented:

as_phyloseq	3
calc_group_mean	4
calc_group_median	6
calc_group_rsd	7
calc_group_stat	9
calc_n_samples	11
calc_obs_props	13
calc_prop_samples	15
compare_groups	17
complement	19
counts_to_presence	20
diverging_palette	21
filter_ambiguous_taxa	22
heat_tree	23
heat_tree_matrix	31
hmp_otus	32
hmp_samples	33
is_ambiguous	34
layout_functions	35
make_dada2_asv_table	36
make_dada2_tax_table	36
metacoder	37
ncbi_taxon_sample	39
parse_dada2	40
parse_greenegenes	41
parse_mothur_taxonomy	42
parse_mothur_tax_summary	43
parse_newick	45
parse_phylo	45
parse_phyloseq	46
parse_qiime_biom	47
parse_rdp	48
parse_silva_fasta	49
parse_ubioime	50
parse_unite_general	51
primersearch	52
primersearch_raw	55
qualitative_palette	58
quantative_palette	59
rarefy_obs	60
read_fasta	61
reverse	62
rev_comp	63
write_greenegenes	63
write_mothur_taxonomy	64
write_rdp	65

write_silva_fasta	66
write_unite_general	67
zero_low_counts	68

Index	71
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as_phyloseq	<i>Convert taxmap to phyloseq</i>
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Description

Convert a taxmap object to a phyloseq object.

Usage

```
as_phyloseq(obj, otu_table = NULL, otu_id_col = "otu_id",
            sample_data = NULL, sample_id_col = "sample_id", phy_tree = NULL)
```

Arguments

obj	The taxmap object.
otu_table	The table in ‘obj\$data’ with OTU counts. Must be one of the following: NULL Look for a table named "otu_table" in ‘obj\$data’ with taxon IDs, OTU IDs, and OTU counts. If it exists, use it. character The name of the table stored in ‘obj\$data’ with taxon IDs, OTU IDs, and OTU counts data.frame A table with taxon IDs, OTU IDs, and OTU counts FALSE Do not include an OTU table, even if "otu_table" exists in ‘obj\$data’
otu_id_col	The name of the column storing OTU IDs in the otu table.
sample_data	A table containing sample data with sample IDs matching column names in the OTU table. Must be one of the following: NULL Look for a table named "sample_data" in ‘obj\$data’. If it exists, use it. character The name of the table stored in ‘obj\$data’ with sample IDs data.frame A table with sample IDs FALSE Do not include a sample data table, even if "sample_data" exists in ‘obj\$data’
sample_id_col	The name of the column storing sample IDs in the sample data table.
phy_tree	A phylogenetic tree of class phylo from the ape package with tip labels matching OTU ids. Must be one of the following: NULL Look for a tree named "phy_tree" in ‘obj\$data’ with tip labels matching OTU ids. If it exists, use it. character The name of the tree stored in ‘obj\$data’ with tip labels matching OTU ids. phylo A tree with tip labels matching OTU ids. FALSE Do not include a tree, even if "phy_tree" exists in ‘obj\$data’

Examples

```
## Not run:
# Install phyloseq to get example data
# source('http://bioconductor.org/biocLite.R')
# biocLite('phyloseq')

# Parse example dataset
library(phyloseq)
data(GlobalPatterns)
x <- parse_phyloseq(GlobalPatterns)

# Convert back to a phyloseq object
as_phyloseq(x)

## End(Not run)
```

calc_group_mean

Calculate means of groups of columns

Description

For a given table in a [taxmap](#) object, split columns by a grouping factor and return row means in a table.

Usage

```
calc_group_mean(obj, data, groups, cols = NULL, other_cols = FALSE,
  out_names = NULL, dataset = NULL)
```

Arguments

obj	A taxmap object
data	The name of a table in obj\$data.
groups	Group multiple columns per treatment/group. This should be a vector of group IDs (e.g. character, integer) the same length as cols that defines which samples go in which group. When used, there will be one column in the output for each unique value in groups.
cols	The columns in data to use. By default, all numeric columns are used. Takes one of the following inputs: TRUE/FALSE: All/No columns will used. Character vector: The names of columns to use Numeric vector: The indexes of columns to use Vector of TRUE/FALSE of length equal to the number of columns: Use the columns corresponding to TRUE values.

other_cols	<p>Preserve in the output non-target columns present in the input data. New columns will always be on the end. The "taxon_id" column will be preserved in the front. Takes one of the following inputs:</p> <p>NULL: No columns will be added back, not even the taxon id column.</p> <p>TRUE/FALSE: All/None of the non-target columns will be preserved.</p> <p>Character vector: The names of columns to preserve</p> <p>Numeric vector: The indexes of columns to preserve</p> <p>Vector of TRUE/FALSE of length equal to the number of columns: Preserve the columns corresponding to TRUE values.</p>
out_names	The names of count columns in the output. Must be the same length as cols (or unique(groups), if groups is used).
dataset	DEPRECATED. use "data" instead.

Value

A tibble

See Also

Other calculations: [calc_group_median](#), [calc_group_rsd](#), [calc_group_stat](#), [calc_n_samples](#), [calc_obs_props](#), [calc_prop_samples](#), [calc_taxon_abund](#), [compare_groups](#), [counts_to_presence](#), [rarefy_obs](#), [zero_low_counts](#)

Examples

```
## Not run:
# Parse data for examples
x = parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
                  class_key = c(tax_rank = "info", tax_name = "taxon_name"),
                  class_regex = "^(.+)_(.+)")

# Calculate the means for each group
calc_group_mean(x, "tax_data", hmp_samples$sex)

# Use only some columns
calc_group_mean(x, "tax_data", hmp_samples$sex[4:20],
               cols = hmp_samples$sample_id[4:20])

# Including all other columns in output
calc_group_mean(x, "tax_data", groups = hmp_samples$sex,
               other_cols = TRUE)

# Including specific columns in output
calc_group_mean(x, "tax_data", groups = hmp_samples$sex,
               other_cols = 2)
calc_group_mean(x, "tax_data", groups = hmp_samples$sex,
               other_cols = "otu_id")

# Rename output columns
calc_group_mean(x, "tax_data", groups = hmp_samples$sex,
```

```
out_names = c("Women", "Men"))
```

```
## End(Not run)
```

calc_group_median *Calculate medians of groups of columns*

Description

For a given table in a [taxmap](#) object, split columns by a grouping factor and return row medians in a table.

Usage

```
calc_group_median(obj, data, groups, cols = NULL, other_cols = FALSE,
  out_names = NULL, dataset = NULL)
```

Arguments

obj	A taxmap object
data	The name of a table in obj\$data.
groups	Group multiple columns per treatment/group. This should be a vector of group IDs (e.g. character, integer) the same length as cols that defines which samples go in which group. When used, there will be one column in the output for each unique value in groups.
cols	The columns in data to use. By default, all numeric columns are used. Takes one of the following inputs: TRUE/FALSE: All/No columns will be used. Character vector: The names of columns to use Numeric vector: The indexes of columns to use Vector of TRUE/FALSE of length equal to the number of columns: Use the columns corresponding to TRUE values.
other_cols	Preserve in the output non-target columns present in the input data. New columns will always be on the end. The "taxon_id" column will be preserved in the front. Takes one of the following inputs: NULL: No columns will be added back, not even the taxon id column. TRUE/FALSE: All/None of the non-target columns will be preserved. Character vector: The names of columns to preserve Numeric vector: The indexes of columns to preserve Vector of TRUE/FALSE of length equal to the number of columns: Preserve the columns corresponding to TRUE values.
out_names	The names of count columns in the output. Must be the same length as cols (or unique(groups), if groups is used).
dataset	DEPRECATED. use "data" instead.

Value

A tibble

See Also

Other calculations: [calc_group_mean](#), [calc_group_rsd](#), [calc_group_stat](#), [calc_n_samples](#), [calc_obs_props](#), [calc_prop_samples](#), [calc_taxon_abund](#), [compare_groups](#), [counts_to_presence](#), [rarefy_obs](#), [zero_low_counts](#)

Examples

```
## Not run:
# Parse data for examples
x = parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
                  class_key = c(tax_rank = "info", tax_name = "taxon_name"),
                  class_regex = "^(.+)_(.+)$")

# Calculate the medians for each group
calc_group_median(x, "tax_data", hmp_samples$sex)

# Use only some columns
calc_group_median(x, "tax_data", hmp_samples$sex[4:20],
                 cols = hmp_samples$sample_id[4:20])

# Including all other columns in output
calc_group_median(x, "tax_data", groups = hmp_samples$sex,
                 other_cols = TRUE)

# Including specific columns in output
calc_group_median(x, "tax_data", groups = hmp_samples$sex,
                 other_cols = 2)
calc_group_median(x, "tax_data", groups = hmp_samples$sex,
                 other_cols = "otu_id")

# Rename output columns
calc_group_median(x, "tax_data", groups = hmp_samples$sex,
                 out_names = c("Women", "Men"))

## End(Not run)
```

calc_group_rsd

Relative standard deviations of groups of columns

Description

For a given table in a [taxmap](#) object, split columns by a grouping factor and return the relative standard deviation for each row in a table. The relative standard deviation is the standard deviation divided by the mean of a set of numbers. It is useful for comparing the variation when magnitude of sets of number are very different.

Usage

```
calc_group_rsd(obj, data, groups, cols = NULL, other_cols = FALSE,
  out_names = NULL, dataset = NULL)
```

Arguments

obj	A taxmap object
data	The name of a table in obj\$data.
groups	Group multiple columns per treatment/group. This should be a vector of group IDs (e.g. character, integer) the same length as cols that defines which samples go in which group. When used, there will be one column in the output for each unique value in groups.
cols	The columns in data to use. By default, all numeric columns are used. Takes one of the following inputs: TRUE/FALSE: All/No columns will be used. Character vector: The names of columns to use Numeric vector: The indexes of columns to use Vector of TRUE/FALSE of length equal to the number of columns: Use the columns corresponding to TRUE values.
other_cols	Preserve in the output non-target columns present in the input data. New columns will always be on the end. The "taxon_id" column will be preserved in the front. Takes one of the following inputs: NULL: No columns will be added back, not even the taxon id column. TRUE/FALSE: All/None of the non-target columns will be preserved. Character vector: The names of columns to preserve Numeric vector: The indexes of columns to preserve Vector of TRUE/FALSE of length equal to the number of columns: Preserve the columns corresponding to TRUE values.
out_names	The names of count columns in the output. Must be the same length as cols (or unique(groups), if groups is used).
dataset	DEPRECATED. use "data" instead.

Value

A tibble

See Also

Other calculations: [calc_group_mean](#), [calc_group_median](#), [calc_group_stat](#), [calc_n_samples](#), [calc_obs_props](#), [calc_prop_samples](#), [calc_taxon_abund](#), [compare_groups](#), [counts_to_presence](#), [rarefy_obs](#), [zero_low_counts](#)

Examples

```
## Not run:
# Parse data for examples
x = parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
                  class_key = c(tax_rank = "info", tax_name = "taxon_name"),
                  class_regex = "^(.+)_(.+)$")

# Calculate the RSD for each group
calc_group_rsd(x, "tax_data", hmp_samples$sex)

# Use only some columns
calc_group_rsd(x, "tax_data", hmp_samples$sex[4:20],
              cols = hmp_samples$sample_id[4:20])

# Including all other columns in output
calc_group_rsd(x, "tax_data", groups = hmp_samples$sex,
              other_cols = TRUE)

# Including specific columns in output
calc_group_rsd(x, "tax_data", groups = hmp_samples$sex,
              other_cols = 2)
calc_group_rsd(x, "tax_data", groups = hmp_samples$sex,
              other_cols = "otu_id")

# Rename output columns
calc_group_rsd(x, "tax_data", groups = hmp_samples$sex,
              out_names = c("Women", "Men"))

## End(Not run)
```

calc_group_stat	<i>Apply a function to groups of columns</i>
-----------------	--

Description

For a given table in a [taxmap](#) object, apply a function to rows in groups of columns. The result of the function is used to create new columns. This is equivalent to splitting columns of a table by a factor and using `apply` on each group.

Usage

```
calc_group_stat(obj, data, func, groups = NULL, cols = NULL,
               other_cols = FALSE, out_names = NULL, dataset = NULL)
```

Arguments

obj	A taxmap object
data	The name of a table in <code>obj\$data</code> .

func	The function to apply. It should take a vector and return a single value. For example, <code>max</code> or <code>mean</code> could be used.
groups	Group multiple columns per treatment/group. This should be a vector of group IDs (e.g. character, integer) the same length as <code>cols</code> that defines which samples go in which group. When used, there will be one column in the output for each unique value in groups.
cols	The columns in data to use. By default, all numeric columns are used. Takes one of the following inputs: TRUE/FALSE: All/No columns will be used. Character vector: The names of columns to use Numeric vector: The indexes of columns to use Vector of TRUE/FALSE of length equal to the number of columns: Use the columns corresponding to TRUE values.
other_cols	Preserve in the output non-target columns present in the input data. New columns will always be on the end. The "taxon_id" column will be preserved in the front. Takes one of the following inputs: NULL: No columns will be added back, not even the taxon id column. TRUE/FALSE: All/None of the non-target columns will be preserved. Character vector: The names of columns to preserve Numeric vector: The indexes of columns to preserve Vector of TRUE/FALSE of length equal to the number of columns: Preserve the columns corresponding to TRUE values.
out_names	The names of count columns in the output. Must be the same length as <code>cols</code> (or <code>unique(groups)</code> , if <code>groups</code> is used).
dataset	DEPRECATED. use "data" instead.

Value

A tibble

See Also

Other calculations: [calc_group_mean](#), [calc_group_median](#), [calc_group_rsd](#), [calc_n_samples](#), [calc_obs_props](#), [calc_prop_samples](#), [calc_taxon_abund](#), [compare_groups](#), [counts_to_presence](#), [rarefy_obs](#), [zero_low_counts](#)

Examples

```
## Not run:
# Parse data for examples
x = parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
                  class_key = c(tax_rank = "info", tax_name = "taxon_name"),
                  class_regex = "^(.+)_(.+)$")

# Apply a function to every value without grouping
calc_group_stat(x, "tax_data", function(v) v > 3)
```

```

# Calculate the means for each group
calc_group_stat(x, "tax_data", mean, groups = hmp_samples$sex)

# Calculate the variation for each group
calc_group_stat(x, "tax_data", sd, groups = hmp_samples$body_site)

# Different ways to use only some columns
calc_group_stat(x, "tax_data", function(v) v > 3,
               cols = c("700035949", "700097855", "700100489"))
calc_group_stat(x, "tax_data", function(v) v > 3,
               cols = 4:6)
calc_group_stat(x, "tax_data", function(v) v > 3,
               cols = startsWith(colnames(x$data$tax_data), "70001"))

# Including all other columns in output
calc_group_stat(x, "tax_data", mean, groups = hmp_samples$sex,
               other_cols = TRUE)

# Including specific columns in output
calc_group_stat(x, "tax_data", mean, groups = hmp_samples$sex,
               other_cols = 2)
calc_group_stat(x, "tax_data", mean, groups = hmp_samples$sex,
               other_cols = "otu_id")

# Rename output columns
calc_group_stat(x, "tax_data", mean, groups = hmp_samples$sex,
               out_names = c("Women", "Men"))

## End(Not run)

```

calc_n_samples	<i>Count the number of samples</i>
----------------	------------------------------------

Description

For a given table in a [taxmap](#) object, count the number of samples (i.e. columns) with greater than a minimum value.

Usage

```

calc_n_samples(obj, data, cols = NULL, groups = "n_samples",
               other_cols = FALSE, out_names = NULL, drop = FALSE,
               more_than = 0, dataset = NULL)

```

Arguments

obj	A taxmap object
data	The name of a table in obj\$data.

cols	<p>The columns in data to use. By default, all numeric columns are used. Takes one of the following inputs:</p> <p>TRUE/FALSE: All/No columns will be used.</p> <p>Character vector: The names of columns to use</p> <p>Numeric vector: The indexes of columns to use</p> <p>Vector of TRUE/FALSE of length equal to the number of columns: Use the columns corresponding to TRUE values.</p>
groups	<p>Group multiple columns per treatment/group. This should be a vector of group IDs (e.g. character, integer) the same length as cols that defines which samples go in which group. When used, there will be one column in the output for each unique value in groups.</p>
other_cols	<p>Preserve in the output non-target columns present in the input data. New columns will always be on the end. The "taxon_id" column will be preserved in the front. Takes one of the following inputs:</p> <p>NULL: No columns will be added back, not even the taxon id column.</p> <p>TRUE/FALSE: All/None of the non-target columns will be preserved.</p> <p>Character vector: The names of columns to preserve</p> <p>Numeric vector: The indexes of columns to preserve</p> <p>Vector of TRUE/FALSE of length equal to the number of columns: Preserve the columns corresponding to TRUE values.</p>
out_names	<p>The names of count columns in the output. Must be the same length as cols (or unique(groups), if groups is used).</p>
drop	<p>If groups is not used, return a vector of the results instead of a table with one column.</p>
more_than	<p>A sample must have greater than this value for it to be counted as present.</p>
dataset	<p>DEPRECATED. use "data" instead.</p>

Value

A tibble

See Also

Other calculations: [calc_group_mean](#), [calc_group_median](#), [calc_group_rsd](#), [calc_group_stat](#), [calc_obs_props](#), [calc_prop_samples](#), [calc_taxon_abund](#), [compare_groups](#), [counts_to_presence](#), [rarefy_obs](#), [zero_low_counts](#)

Examples

```
## Not run:
# Parse data for example
x = parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
                  class_key = c(tax_rank = "info", tax_name = "taxon_name"),
                  class_regex = "^(.+)__(.+)$$")

# Count samples with at least one read
```

```

calc_n_samples(x, data = "tax_data")

# Count samples with at least 5 reads
calc_n_samples(x, data = "tax_data", more_than = 5)

# Return a vector instead of a table
calc_n_samples(x, data = "tax_data", drop = TRUE)

# Only use some columns
calc_n_samples(x, data = "tax_data", cols = hmp_samples$sample_id[1:5])

# Return a count for each treatment
calc_n_samples(x, data = "tax_data", groups = hmp_samples$body_site)

# Rename output columns
calc_n_samples(x, data = "tax_data", groups = hmp_samples$body_site,
               out_names = c("A", "B", "C", "D", "E"))

# Preserve other columns from input
calc_n_samples(x, data = "tax_data", other_cols = TRUE)
calc_n_samples(x, data = "tax_data", other_cols = 2)
calc_n_samples(x, data = "tax_data", other_cols = "otu_id")

## End(Not run)

```

calc_obs_props

Calculate proportions from observation counts

Description

For a given table in a [taxmap](#) object, convert one or more columns containing counts to proportions. This is meant to be used with counts associated with observations (e.g. OTUs), as opposed to counts that have already been summed per taxon.

Usage

```

calc_obs_props(obj, data, cols = NULL, groups = NULL,
               other_cols = FALSE, out_names = NULL, dataset = NULL)

```

Arguments

obj	A taxmap object
data	The name of a table in obj\$data.
cols	The columns in data to use. By default, all numeric columns are used. Takes one of the following inputs: TRUE/FALSE: All/No columns will used. Character vector: The names of columns to use

	Numeric vector: The indexes of columns to use
	Vector of TRUE/FALSE of length equal to the number of columns: Use the columns corresponding to TRUE values.
groups	Group multiple columns per treatment/group. This should be a vector of group IDs (e.g. character, integer) the same length as cols that defines which samples go in which group. When used, there will be one column in the output for each unique value in groups.
other_cols	Preserve in the output non-target columns present in the input data. New columns will always be on the end. The "taxon_id" column will be preserved in the front. Takes one of the following inputs: NULL: No columns will be added back, not even the taxon id column. TRUE/FALSE: All/None of the non-target columns will be preserved. Character vector: The names of columns to preserve Numeric vector: The indexes of columns to preserve Vector of TRUE/FALSE of length equal to the number of columns: Preserve the columns corresponding to TRUE values.
out_names	The names of count columns in the output. Must be the same length as cols (or unique(groups), if groups is used).
dataset	DEPRECATED. use "data" instead.

Value

A tibble

See Also

Other calculations: [calc_group_mean](#), [calc_group_median](#), [calc_group_rsd](#), [calc_group_stat](#), [calc_n_samples](#), [calc_prop_samples](#), [calc_taxon_abund](#), [compare_groups](#), [counts_to_presence](#), [rarefy_obs](#), [zero_low_counts](#)

Examples

```
## Not run:
# Parse data for examples
x = parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
                  class_key = c(tax_rank = "info", tax_name = "taxon_name"),
                  class_regex = "^(.+)_(.+)$")

# Calculate proportions for all numeric columns
calc_obs_props(x, "tax_data")

# Calculate proportions for a subset of columns
calc_obs_props(x, "tax_data", cols = c("700035949", "700097855", "700100489"))
calc_obs_props(x, "tax_data", cols = 4:6)
calc_obs_props(x, "tax_data", cols = startsWith(colnames(x$data$tax_data), "70001"))

# Including all other columns in output
calc_obs_props(x, "tax_data", other_cols = TRUE)
```

```

# Including specific columns in output
calc_obs_props(x, "tax_data", cols = c("700035949", "700097855", "700100489"),
              other_cols = 2:3)

# Rename output columns
calc_obs_props(x, "tax_data", cols = c("700035949", "700097855", "700100489"),
              out_names = c("a", "b", "c"))

# Get proportions for groups of samples
calc_obs_props(x, "tax_data", groups = hmp_samples$sex)
calc_obs_props(x, "tax_data", groups = hmp_samples$sex,
              out_names = c("Women", "Men"))

## End(Not run)

```

calc_prop_samples *Calculate the proportion of samples*

Description

For a given table in a [taxmap](#) object, calculate the proportion of samples (i.e. columns) with greater than a minimum value.

Usage

```

calc_prop_samples(obj, data, cols = NULL, groups = "n_samples",
                 other_cols = FALSE, out_names = NULL, drop = FALSE,
                 more_than = 0, dataset = NULL)

```

Arguments

obj	A taxmap object
data	The name of a table in obj\$data.
cols	The columns in data to use. By default, all numeric columns are used. Takes one of the following inputs: TRUE/FALSE: All/No columns will used. Character vector: The names of columns to use Numeric vector: The indexes of columns to use Vector of TRUE/FALSE of length equal to the number of columns: Use the columns corresponding to TRUE values.
groups	Group multiple columns per treatment/group. This should be a vector of group IDs (e.g. character, integer) the same length as cols that defines which samples go in which group. When used, there will be one column in the output for each unique value in groups.

other_cols	<p>Preserve in the output non-target columns present in the input data. New columns will always be on the end. The "taxon_id" column will be preserved in the front. Takes one of the following inputs:</p> <p>NULL: No columns will be added back, not even the taxon id column.</p> <p>TRUE/FALSE: All/None of the non-target columns will be preserved.</p> <p>Character vector: The names of columns to preserve</p> <p>Numeric vector: The indexes of columns to preserve</p> <p>Vector of TRUE/FALSE of length equal to the number of columns: Preserve the columns corresponding to TRUE values.</p>
out_names	The names of count columns in the output. Must be the same length as cols (or unique(groups), if groups is used).
drop	If groups is not used, return a vector of the results instead of a table with one column.
more_than	A sample must have greater than this value for it to be counted as present.
dataset	DEPRECATED. use "data" instead.

Value

A tibble

See Also

Other calculations: [calc_group_mean](#), [calc_group_median](#), [calc_group_rsd](#), [calc_group_stat](#), [calc_n_samples](#), [calc_obs_props](#), [calc_taxon_abund](#), [compare_groups](#), [counts_to_presence](#), [rarefy_obs](#), [zero_low_counts](#)

Examples

```
## Not run:
# Parse data for example
x = parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
                  class_key = c(tax_rank = "info", tax_name = "taxon_name"),
                  class_regex = "^(.+)__(.+)$")

# Count samples with at least one read
calc_prop_samples(x, data = "tax_data")

# Count samples with at least 5 reads
calc_prop_samples(x, data = "tax_data", more_than = 5)

# Return a vector instead of a table
calc_prop_samples(x, data = "tax_data", drop = TRUE)

# Only use some columns
calc_prop_samples(x, data = "tax_data", cols = hmp_samples$sample_id[1:5])

# Return a count for each treatment
calc_prop_samples(x, data = "tax_data", groups = hmp_samples$body_site)
```



```

# Rename output columns
calc_prop_samples(x, data = "tax_data", groups = hmp_samples$body_site,
  out_names = c("A", "B", "C", "D", "E"))

# Preserve other columns from input
calc_prop_samples(x, data = "tax_data", other_cols = TRUE)
calc_prop_samples(x, data = "tax_data", other_cols = 2)
calc_prop_samples(x, data = "tax_data", other_cols = "otu_id")

## End(Not run)

```

compare_groups

Compare groups of samples

Description

Apply a function to compare data, usually abundance, from pairs of treatments/groups. By default, every pairwise combination of treatments are compared. A custom function can be supplied to perform the comparison. The plotting function [heat_tree_matrix](#) is useful for visualizing these results.

Usage

```

compare_groups(obj, data, cols, groups, func = NULL,
  combinations = NULL, other_cols = FALSE, dataset = NULL)

```

Arguments

obj	A taxmap object
data	The name of a table in obj that contains data for each sample in columns.
cols	The names/indexes of columns in data to use. By default, all numeric columns are used. Takes one of the following inputs: TRUE/FALSE: All/No columns will used. Character vector: The names of columns to use Numeric vector: The indexes of columns to use Vector of TRUE/FALSE of length equal to the number of columns: Use the columns corresponding to TRUE values.
groups	A vector defining how samples are grouped into "treatments". Must be the same order and length as cols.
func	The function to apply for each comparison. For each row in data, for each combination of groups, this function will receive the data for each treatment, passed as two character vectors. Therefore the function must take at least 2 arguments corresponding to the two groups compared. The function should return a vector or list of results of a fixed length. If named, the names will be used in the output. The names should be consistent as well. A simple example is <code>function(x, y) mean(x) - mean(y)</code> . By default, the following function is used:

```
function(abund_1, abund_2) {
  log_ratio <- log2(median(abund_1) / median(abund_2))
  if (is.nan(log_ratio)) {
    log_ratio <- 0
  }
  list(log2_median_ratio = log_ratio,
       median_diff = median(abund_1) - median(abund_2),
       mean_diff = mean(abund_1) - mean(abund_2),
       wilcox_p_value = wilcox.test(abund_1, abund_2)$p.value)
}
```

combinations Which combinations of groups to use. Must be a list of vectors, each containing the names of 2 groups to compare. By default, all pairwise combinations of groups are compared.

other_cols If TRUE, preserve all columns not in cols in the output. If FALSE, dont keep other columns. If a column names or indexes are supplied, only preserve those columns.

dataset DEPRECATED. use "data" instead.

Value

A tibble

See Also

Other calculations: [calc_group_mean](#), [calc_group_median](#), [calc_group_rsd](#), [calc_group_stat](#), [calc_n_samples](#), [calc_obs_props](#), [calc_prop_samples](#), [calc_taxon_abund](#), [counts_to_presence](#), [rarefy_obs](#), [zero_low_counts](#)

Examples

```
## Not run:
# Parse data for plotting
x = parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
                  class_key = c(tax_rank = "info", tax_name = "taxon_name"),
                  class_regex = "^(.+)_(.+)$")

# Convert counts to proportions
x$data$otu_table <- calc_obs_props(x, data = "tax_data", cols = hmp_samples$sample_id)

# Get per-taxon counts
x$data$tax_table <- calc_taxon_abund(x, data = "otu_table", cols = hmp_samples$sample_id)

# Calculate difference between groups
x$data$diff_table <- compare_groups(x, data = "tax_table",
                                   cols = hmp_samples$sample_id,
                                   groups = hmp_samples$body_site)

# Plot results (might take a few minutes)
heat_tree_matrix(x,
                 data = "diff_table",
```

```
node_size = n_obs,  
node_label = taxon_names,  
node_color = log2_median_ratio,  
node_color_range = diverging_palette(),  
node_color_trans = "linear",  
node_color_interval = c(-3, 3),  
edge_color_interval = c(-3, 3),  
node_size_axis_label = "Number of OTUs",  
node_color_axis_label = "Log2 ratio median proportions")  
  
## End(Not run)
```

complement	<i>Find complement of sequences</i>
------------	-------------------------------------

Description

Find the complement of one or more sequences stored as a character vector. This is a wrapper for [comp](#) for character vectors instead of lists of character vectors with one value per letter. IUPAC ambiguity code are handled and the upper/lower case is preserved.

Usage

```
complement(seqs)
```

Arguments

seqs A character vector with one element per sequence.

See Also

Other sequence transformations: [rev_comp](#), [reverse](#)

Examples

```
complement(c("aagtgGGTGaa", "AAGTGGT"))
```

counts_to_presence *Apply a function to groups of columns*

Description

For a given table in a `taxmap` object, apply a function to rows in groups of columns. The result of the function is used to create new columns. This is equivalent to splitting columns of a table by a factor and using `apply` on each group.

Usage

```
counts_to_presence(obj, data, threshold = 0, groups = NULL,
  cols = NULL, other_cols = FALSE, out_names = NULL,
  dataset = NULL)
```

Arguments

<code>obj</code>	A <code>taxmap</code> object
<code>data</code>	The name of a table in <code>obj\$data</code> .
<code>threshold</code>	The value a number must be greater than to count as present. By default, anything above 0 is considered present.
<code>groups</code>	Group multiple columns per treatment/group. This should be a vector of group IDs (e.g. character, integer) the same length as <code>cols</code> that defines which samples go in which group. When used, there will be one column in the output for each unique value in groups.
<code>cols</code>	The columns in <code>data</code> to use. By default, all numeric columns are used. Takes one of the following inputs: TRUE/FALSE: All/No columns will used. Character vector: The names of columns to use Numeric vector: The indexes of columns to use Vector of TRUE/FALSE of length equal to the number of columns: Use the columns corresponding to TRUE values.
<code>other_cols</code>	Preserve in the output non-target columns present in the input data. New columns will always be on the end. The "taxon_id" column will be preserved in the front. Takes one of the following inputs: NULL: No columns will be added back, not even the taxon id column. TRUE/FALSE: All/None of the non-target columns will be preserved. Character vector: The names of columns to preserve Numeric vector: The indexes of columns to preserve Vector of TRUE/FALSE of length equal to the number of columns: Preserve the columns corresponding to TRUE values.
<code>out_names</code>	The names of count columns in the output. Must be the same length as <code>cols</code> (or <code>unique(groups)</code> , if <code>groups</code> is used).
<code>dataset</code>	DEPRECATED. use "data" instead.

Value

A tibble

See Also

Other calculations: [calc_group_mean](#), [calc_group_median](#), [calc_group_rsd](#), [calc_group_stat](#), [calc_n_samples](#), [calc_obs_props](#), [calc_prop_samples](#), [calc_taxon_abund](#), [compare_groups](#), [rarefy_obs](#), [zero_low_counts](#)

Examples

```
## Not run:
# Parse data for examples
x = parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
                  class_key = c(tax_rank = "info", tax_name = "taxon_name"),
                  class_regex = "^(.+)__(.+)$")

# Convert count to presence/absence
counts_to_presence(x, "tax_data")

# Check if there are any reads in each group of samples
counts_to_presence(x, "tax_data", groups = hmp_samples$body_site)

## End(Not run)
```

diverging_palette *The default diverging color palette*

Description

Returns the default color palette for diverging data

Usage

```
diverging_palette()
```

Value

character of hex color codes

Examples

```
diverging_palette()
```

filter_ambiguous_taxa *Filter ambiguous taxon names*

Description

Filter out taxa with ambiguous names, such as "unknown" or "uncultured". NOTE: some parameters of this function are passed to `filter_taxa` with the "invert" option set to TRUE. Works the same way as `filter_taxa` for the most part.

Usage

```
filter_ambiguous_taxa(obj, unknown = TRUE, uncultured = TRUE,
  name_regex = ".", ignore_case = TRUE, subtaxa = FALSE,
  drop_obs = TRUE, reassign_obs = TRUE, reassign_taxa = TRUE)
```

Arguments

obj	A <code>taxmap</code> object
unknown	If TRUE, Remove taxa with names the suggest they are placeholders for unknown taxa (e.g. "unknown ...").
uncultured	If TRUE, Remove taxa with names the suggest they are assigned to uncultured organisms (e.g. "uncultured ...").
name_regex	The regex code to match a valid character in a taxon name. For example, "[a-z]" would mean taxon names can only be lower case letters.
ignore_case	If TRUE, dont consider the case of the text when determining a match.
subtaxa	(logical or numeric of length 1) If TRUE, include subtaxa of taxa passing the filter. Positive numbers indicate the number of ranks below the target taxa to return. 0 is equivalent to FALSE. Negative numbers are equivalent to TRUE.
drop_obs	(logical) This option only applies to <code>taxmap()</code> objects. If FALSE, include observations (i.e. user-defined data in <code>obj\$data</code>) even if the taxon they are assigned to is filtered out. Observations assigned to removed taxa will be assigned to NA. This option can be either simply TRUE/FALSE, meaning that all data sets will be treated the same, or a logical vector can be supplied with names corresponding one or more data sets in <code>obj\$data</code> . For example, <code>c(abundance = FALSE, stats = TRUE)</code> would include observations whose taxon was filtered out in <code>obj\$data\$abundance</code> , but not in <code>obj\$data\$stats</code> . See the <code>reassign_obs</code> option below for further complications.
reassign_obs	(logical of length 1) This option only applies to <code>taxmap()</code> objects. If TRUE, observations (i.e. user-defined data in <code>obj\$data</code>) assigned to removed taxa will be reassigned to the closest supertaxon that passed the filter. If there are no supertaxa of such an observation that passed the filter, they will be filtered out if <code>drop_obs</code> is TRUE. This option can be either simply TRUE/FALSE, meaning that all data sets will be treated the same, or a logical vector can be supplied with names corresponding one or more data sets in <code>obj\$data</code> . For example, <code>c(abundance = TRUE, stats = FALSE)</code> would reassign observations in <code>obj\$data\$abundance</code> , but not in <code>obj\$data\$stats</code> .

`reassign_taxa` (logical of length 1) If TRUE, subtaxa of removed taxa will be reassigned to the closest supertaxon that passed the filter. This is useful for removing intermediate levels of a taxonomy.

Details

If you encounter a taxon name that represents an ambiguous taxon that is not filtered out by this function, let us know and we will add it.

Value

A `taxmap` object

Examples

```
obj <- parse_tax_data(c("Plantae;Solanaceae;Solanum;lycopersicum",
  "Plantae;Solanaceae;Solanum;tuberosum",
  "Plantae;Solanaceae;Solanum;unknown",
  "Plantae;Solanaceae;Solanum;uncultured",
  "Plantae;UNIDENTIFIED"))
filter_ambiguous_taxa(obj)
```

heat_tree

Plot a taxonomic tree

Description

Plots the distribution of values associated with a taxonomic classification/heirarchy. Taxonomic classifications can have multiple roots, resulting in multiple trees on the same plot. A tree consists of elements, element properties, conditions, and mapping properties which are represented as parameters in the `heat_tree` object. The elements (e.g. nodes, edges, lables, and individual trees) are the infrastructure of the heat tree. The element properties (e.g. size and color) are characteristics that are manipulated by various data conditions and mapping properties. The element properties can be explicitly defined or automatically generated. The conditions are data (e.g. taxon statistics, such as abundance) represented in the `taxmap/metacoder` object. The mapping properties are parameters (e.g. transformations, range, interval, and layout) used to change the elements/element properties and how they are used to represent (or not represent) the various conditions.

Usage

```
heat_tree(...)

## S3 method for class 'Taxmap'
heat_tree(.input, ...)

## Default S3 method:
heat_tree(taxon_id, supertaxon_id, node_label = NA,
```

```

edge_label = NA, tree_label = NA, node_size = 1,
edge_size = node_size, node_label_size = node_size,
edge_label_size = edge_size, tree_label_size = as.numeric(NA),
node_color = "#999999", edge_color = node_color, tree_color = NA,
node_label_color = "#000000", edge_label_color = "#000000",
tree_label_color = "#000000", node_size_trans = "area",
edge_size_trans = node_size_trans,
node_label_size_trans = node_size_trans,
edge_label_size_trans = edge_size_trans,
tree_label_size_trans = "area", node_color_trans = "area",
edge_color_trans = node_color_trans, tree_color_trans = "area",
node_label_color_trans = "area", edge_label_color_trans = "area",
tree_label_color_trans = "area", node_size_range = c(NA, NA),
edge_size_range = c(NA, NA), node_label_size_range = c(NA, NA),
edge_label_size_range = c(NA, NA), tree_label_size_range = c(NA, NA),
node_color_range = quantitative_palette(),
edge_color_range = node_color_range,
tree_color_range = quantitative_palette(),
node_label_color_range = quantitative_palette(),
edge_label_color_range = quantitative_palette(),
tree_label_color_range = quantitative_palette(),
node_size_interval = range(node_size, na.rm = TRUE, finite = TRUE),
node_color_interval = NULL, edge_size_interval = range(edge_size,
na.rm = TRUE, finite = TRUE), edge_color_interval = NULL,
node_label_max = 500, edge_label_max = 500, tree_label_max = 500,
overlap_avoidance = 1, margin_size = c(0, 0, 0, 0),
layout = "reingold-tilford", initial_layout = "fruchterman-reingold",
make_node_legend = TRUE, make_edge_legend = TRUE, title = NULL,
title_size = 0.08, node_color_axis_label = NULL,
node_size_axis_label = NULL, edge_color_axis_label = NULL,
edge_size_axis_label = NULL, background_color = "#FFFFFF00",
output_file = NULL, aspect_ratio = 1, repel_labels = TRUE,
repel_force = 1, repel_iter = 1000, verbose = FALSE, ...)

```

Arguments

...	(other named arguments) Passed to the igraph layout function used.
.input	An object of type taxmap
taxon_id	The unique ids of taxa.
supertaxon_id	The unique id of supertaxon taxon_id is a part of.
node_label	See details on labels. Default: no labels.
edge_label	See details on labels. Default: no labels.
tree_label	See details on labels. The label to display above each graph. The value of the root of each graph will be used. Default: None.
node_size	See details on size. Default: constant size.
edge_size	See details on size. Default: relative to node size.

node_label_size	See details on size. Default: relative to vertex size.
edge_label_size	See details on size. Default: relative to edge size.
tree_label_size	See details on size. Default: relative to graph size.
node_color	See details on colors. Default: grey.
edge_color	See details on colors. Default: same as node color.
tree_color	See details on colors. The value of the root of each graph will be used. Overwrites the node and edge color if specified. Default: Not used.
node_label_color	See details on colors. Default: black.
edge_label_color	See details on colors. Default: black.
tree_label_color	See details on colors. Default: black.
node_size_trans	See details on transformations. Default: "area".
edge_size_trans	See details on transformations. Default: same as node_size_trans.
node_label_size_trans	See details on transformations. Default: same as node_size_trans.
edge_label_size_trans	See details on transformations. Default: same as edge_size_trans.
tree_label_size_trans	See details on transformations. Default: "area".
node_color_trans	See details on transformations. Default: "area".
edge_color_trans	See details on transformations. Default: same as node color transformation.
tree_color_trans	See details on transformations. Default: "area".
node_label_color_trans	See details on transformations. Default: "area".
edge_label_color_trans	See details on transformations. Default: "area".
tree_label_color_trans	See details on transformations. Default: "area".
node_size_range	See details on ranges. Default: Optimize to balance overlaps and range size.
edge_size_range	See details on ranges. Default: relative to node size range.
node_label_size_range	See details on ranges. Default: relative to node size.
edge_label_size_range	See details on ranges. Default: relative to edge size.

tree_label_size_range	See details on ranges. Default: relative to tree size.
node_color_range	See details on ranges. Default: Color-blind friendly palette.
edge_color_range	See details on ranges. Default: same as node color.
tree_color_range	See details on ranges. Default: Color-blind friendly palette.
node_label_color_range	See details on ranges. Default: Color-blind friendly palette.
edge_label_color_range	See details on ranges. Default: Color-blind friendly palette.
tree_label_color_range	See details on ranges. Default: Color-blind friendly palette.
node_size_interval	See details on intervals. Default: The range of values in node_size.
node_color_interval	See details on intervals. Default: The range of values in node_color.
edge_size_interval	See details on intervals. Default: The range of values in edge_size.
edge_color_interval	See details on intervals. Default: The range of values in edge_color.
node_label_max	The maximum number of node labels. Default: 20.
edge_label_max	The maximum number of edge labels. Default: 20.
tree_label_max	The maximum number of tree labels. Default: 20.
overlap_avoidance	(numeric) The relative importance of avoiding overlaps vs maximizing size range. Higher numbers will cause node size optimization to avoid overlaps more. Default: 1.
margin_size	(numeric of length 2) The horizontal and vertical margins. c(left, right, bottom, top). Default: 0, 0, 0, 0.
layout	The layout algorithm used to position nodes. See details on layouts. Default: "reingold-tilford".
initial_layout	he layout algorithm used to set the initial position of nodes, passed as input to the layout algorithm. See details on layouts. Default: Not used.
make_node_legend	if TRUE, make legend for node size/color mappings.
make_edge_legend	if TRUE, make legend for edge size/color mappings.
title	Name to print above the graph.
title_size	The size of the title relative to the rest of the graph.
node_color_axis_label	The label on the scale axis corresponding to node_color. Default: The expression given to node_color.

node_size_axis_label	The label on the scale axis corresponding to node_size. Default: The expression given to node_size.
edge_color_axis_label	The label on the scale axis corresponding to edge_color. Default: The expression given to edge_color.
edge_size_axis_label	The label on the scale axis corresponding to edge_size. Default: The expression given to edge_size.
background_color	The background color of the plot. Default: Transparent
output_file	The path to one or more files to save the plot in using ggsave . The type of the file will be determined by the extension given. Default: Do not save plot.
aspect_ratio	The aspect_ratio of the plot.
repel_labels	If TRUE (Default), use the ggrepel package to spread out labels.
repel_force	The force of which overlapping labels will be repelled from eachother.
repel_iter	The number of iterations used when repelling labels
verbose	If TRUE print progress reports as the function runs.

labels

The labels of nodes, edges, and trees can be added. Node labels are centered over their node. Edge labels are displayed over edges, in the same orientation. Tree labels are displayed over their tree.

Accepts a vector, the same length `taxon_id` or a factor of its length.

sizes

The size of nodes, edges, labels, and trees can be mapped to various conditions. This is useful for displaying statistics for taxa, such as abundance. Only the relative size of the condition is used, not the values themselves. The `<element>_size_trans` (transformation) parameter can be used to make the size mapping non-linear. The `<element>_size_range` parameter can be used to proportionately change the size of an element based on the condition mapped to that element. The `<element>_size_interval` parameter can be used to change the limit at which a condition will be graphically represented as the same size as the minimum/maximum `<element>_size_range`.

Accepts a numeric vector, the same length `taxon_id` or a factor of its length.

colors

The colors of nodes, edges, labels, and trees can be mapped to various conditions. This is useful for visually highlighting/clustering groups of taxa. Only the relative size of the condition is used, not the values themselves. The `<element>_color_trans` (transformation) parameter can be used to make the color mapping non-linear. The `<element>_color_range` parameter can be used to proportionately change the color of an element based on the condition mapped to that element. The `<element>_color_interval` parameter can be used to change the limit at which a condition will be graphically represented as the same color as the minimum/maximum `<element>_color_range`.

Accepts a vector, the same length `taxon_id` or a factor of its length. If a numeric vector is given, it is mapped to a color scale. Hex values or color names can be used (e.g. `#000000` or `"black"`).

Mapping Properties

transformations

Before any conditions specified are mapped to an element property (color/size), they can be transformed to make the mapping non-linear. Any of the transformations listed below can be used by specifying their name. A customized function can also be supplied to do the transformation.

"linear" Proportional to radius/diameter of node

"area" circular area; better perceptual accuracy than `"linear"`

"log10" Log base 10 of radius

"log2" Log base 2 of radius

"ln" Log base e of radius

"log10 area" Log base 10 of circular area

"log2 area" Log base 2 of circular area

"ln area" Log base e of circular area

ranges

The displayed range of colors and sizes can be explicitly defined or automatically generated. When explicitly used, the size range will proportionately increase/decrease the size of a particular element. Size ranges are specified by supplying a numeric vector with two values: the minimum and maximum. The units used should be between 0 and 1, representing the proportion of a dimension of the graph. Since the dimensions of the graph are determined by layout, and not always square, the value that 1 corresponds to is the square root of the graph area (i.e. the side of a square with the same area as the plotted space). Color ranges can be any number of color values as either HEX codes (e.g. `#000000`) or color names (e.g. `"black"`).

layout

Layouts determine the position of node elements on the graph. They are implemented using the `igraph` package. Any additional arguments passed to `heat_tree` are passed to the `igraph` function used. The following character values are understood:

"automatic" Use `nicely`. Let `igraph` choose the layout.

"reingold-tilford" Use `as_tree`. A circular tree-like layout.

"davidson-harel" Use `with_dh`. A type of simulated annealing.

"gem" Use `with_gem`. A force-directed layout.

"graphopt" Use `with_graphopt`. A force-directed layout.

"mds" Use `with_mds`. Multidimensional scaling.

"fruchterman-reingold" Use `with_fr`. A force-directed layout.

"kamada-kawai" Use `with_kk`. A layout based on a physical model of springs.

"large-graph" Use `with_lgl`. Meant for larger graphs.

"drl" Use `with_drl`. A force-directed layout.

intervals

This is the minimum and maximum of values displayed on the legend scales. Intervals are specified by supplying a numeric vector with two values: the minimum and maximum. When explicitly used, the `<element>_<property>_interval` will redefine the way the actual conditional values are being represented by setting a limit for the `<element>_<property>`. Any condition below the minimum `<element>_<property>_interval` will be graphically represented the same as a condition AT the minimum value in the full range of conditional values. Any value above the maximum `<element>_<property>_interval` will be graphically represented the same as a value AT the maximum value in the full range of conditional values. By default, the minimum and maximum equals the `<element>_<property>_range` used to infer the value of the `<element>_<property>`. Setting a custom interval is useful for making `<element>_<properties>` in multiple graphs correspond to the same conditions, or setting logical boundaries (such as `c(0, 1)` for proportions). Note that this is different from the `<element>_<property>_range` mapping property, which determines the size/color of graphed elements.

Acknowledgements

This package includes code from the R package `ggrepel` to handle label overlap avoidance with permission from the author of `ggrepel` Kamil Slowikowski. We included the code instead of depending on `ggrepel` because we are using internal functions to `ggrepel` that might change in the future. We thank Kamil Slowikowski for letting us use his code and would like to acknowledge his implementation of the label overlap avoidance used in `metacoder`.

Examples

```
## Not run:
# Parse dataset for plotting
x = parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
                  class_key = c(tax_rank = "info", tax_name = "taxon_name"),
                  class_regex = "^(.+)_(.+)$")

# Default appearance:
# No parameters are needed, but the default tree is not too useful
heat_tree(x)

# A good place to start:
# There will always be "taxon_names" and "n_obs" variables, so this is a
# good place to start. This will show the number of OTUs in this case.
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = n_obs)

# Plotting read depth:
# To plot read depth, you first need to add up the number of reads per taxon.
# The function `calc_taxon_abund` is good for this.
x$data$taxon_counts <- calc_taxon_abund(x, data = "tax_data")
x$data$taxon_counts$total <- rowSums(x$data$taxon_counts[, -1]) # -1 = taxon_id column
heat_tree(x, node_label = taxon_names, node_size = total, node_color = total)

# Plotting multiple variables:
# You can plot up to 4 quantitative variables use node/edge size/color, but it
# is usually best to use 2 or 3. The plot below uses node size for number of
```

```

# OTUs and color for number of reads and edge size for number of samples
x$data$n_samples <- calc_n_samples(x, data = "taxon_counts")
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = total,
          edge_color = n_samples)

# Different layouts:
# You can use any layout implemented by igraph. You can also specify an
# initial layout to seed the main layout with.
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = n_obs,
          layout = "davidson-harel")
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = n_obs,
          layout = "davidson-harel", initial_layout = "reingold-tilford")

# Axis labels:
# You can add custom labels to the legends
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = total,
          edge_color = n_samples, node_size_axis_label = "Number of OTUs",
          node_color_axis_label = "Number of reads",
          edge_color_axis_label = "Number of samples")

# Overlap avoidance:
# You can change how much node overlap avoidance is used.
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = n_obs,
          overlap_avoidance = .5)

# Label overlap avoidance
# You can modify how label scattering is handled using the `repel_force` and
# `repel_iter` options. You can turn off label scattering using the `repel_labels` option.
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = n_obs,
          rebel_force = 2, rebel_iter = 20000)
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = n_obs,
          rebel_labels = FALSE)

# Setting the size of graph elements:
# You can force nodes, edges, and labels to be a specific size/color range instead
# of letting the function optimize it. These options end in `_range`.
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = n_obs,
          node_size_range = c(0.01, .1))
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = n_obs,
          edge_color_range = c("black", "#FFFFFF"))
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = n_obs,
          node_label_size_range = c(0.02, 0.02))

# Setting the transformation used:
# You can change how raw statistics are converted to color/size using options
# ending in `_trans`.
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = n_obs,
          node_size_trans = "log10 area")

# Setting the interval displayed:
# By default, the whole range of the statistic provided will be displayed.
# You can set what range of values are displayed using options ending in `_interval`.
heat_tree(x, node_label = taxon_names, node_size = n_obs, node_color = n_obs,

```

```
node_size_interval = c(10, 100))
```

```
## End(Not run)
```

```
heat_tree_matrix      Plot a matrix of heat trees
```

Description

Plot a matrix of heat trees for showing pairwise comparisons. A larger, labelled tree serves as a key for the matrix of smaller unlabelled trees. The data for this function is typically created with [compare_groups](#),

Usage

```
heat_tree_matrix(obj, data, label_small_trees = FALSE, key_size = 0.6,
  seed = 1, output_file = NULL,
  row_label_color = diverging_palette()[3],
  col_label_color = diverging_palette()[1], row_label_size = 12,
  col_label_size = 12, ..., dataset = NULL)
```

Arguments

obj	A taxmap object
data	The name of a table in obj\$data that is the output of compare_groups or in the same format.
label_small_trees	If TRUE add labels to small trees as well as the key tree. Otherwise, only the key tree will be labeled.
key_size	The size of the key tree relative to the whole graph. For example, 0.5 means half the width/height of the graph.
seed	That random seed used to make the graphs.
output_file	The path to one or more files to save the plot in using ggsave . The type of the file will be determined by the extension given. Default: Do not save plot.
row_label_color	The color of the row labels on the right side of the matrix. Default: based on the <code>node_color_range</code> .
col_label_color	The color of the columns labels along the top of the matrix. Default: based on the <code>node_color_range</code> .
row_label_size	The size of the row labels on the right side of the matrix. Default: 12.
col_label_size	The size of the columns labels along the top of the matrix. Default: 12.
...	Passed to heat_tree . Some options will be overwritten.
dataset	DEPRECATED. use "data" instead.

Examples

```
## Not run:
# Parse dataset for plotting
x <- parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
                    class_key = c(tax_rank = "info", tax_name = "taxon_name"),
                    class_regex = "^(.+)_(.+)")

# Convert counts to proportions
x$data$otu_table <- calc_obs_props(x, data = "tax_data", cols = hmp_samples$sample_id)

# Get per-taxon counts
x$data$tax_table <- calc_taxon_abund(x, data = "otu_table", cols = hmp_samples$sample_id)

# Calculate difference between treatments
x$data$diff_table <- compare_groups(x, data = "tax_table",
                                    cols = hmp_samples$sample_id,
                                    groups = hmp_samples$body_site)

# Plot results (might take a few minutes)
heat_tree_matrix(x,
                 data = "diff_table",
                 node_size = n_obs,
                 node_label = taxon_names,
                 node_color = log2_median_ratio,
                 node_color_range = diverging_palette(),
                 node_color_trans = "linear",
                 node_color_interval = c(-3, 3),
                 edge_color_interval = c(-3, 3),
                 node_size_axis_label = "Number of OTUs",
                 node_color_axis_label = "Log2 ratio median proportions")

## End(Not run)
```

hmp_otus

A HMP subset

Description

A subset of the Human Microbiome Project abundance matrix produced by QIIME. It contains OTU ids, taxonomic lineages, and the read counts for 50 samples. See [hmp_samples](#) for the matching dataset of sample information.

Format

A 1,000 x 52 tibble.

Details

The 50 samples were randomly selected such that there were 10 in each of 5 treatments: "Saliva", "Throat", "Stool", "Right_Antecubital_fossa", "Anterior_nares". For each treatment, there were 5 samples from men and 5 from women.

Source

Subset from data available at <https://www.hmpdacc.org/hmp/HMQCP/>

See Also

Other hmp_data: [hmp_samples](#)

hmp_samples

Sample information for HMP subset

Description

The sample information for a subset of the Human Microbiome Project data. It contains the sample ID, sex, and body site for each sample in the abundance matrix stored in [hmp_otus](#). The "sample_id" column corresponds to the column names of [hmp_otus](#).

Format

A 50 x 3 tibble.

Details

The 50 samples were randomly selected such that there were 10 in each of 5 treatments: "Saliva", "Throat", "Stool", "Right_Antecubital_fossa", "Anterior_nares". For each treatment, there were 5 samples from men and 5 from women. "Right_Antecubital_fossa" was renamed to "Skin" and "Anterior_nares" to "Nose".

Source

Subset from data available at <https://www.hmpdacc.org/hmp/HMQCP/>

See Also

Other hmp_data: [hmp_otus](#)

is_ambiguous	<i>Find ambiguous taxon names</i>
--------------	-----------------------------------

Description

Find taxa with ambiguous names, such as "unknown" or "uncultured".

Usage

```
is_ambiguous(taxon_names, unknown = TRUE, uncultured = TRUE,  
             name_regex = ".", ignore_case = TRUE)
```

Arguments

taxon_names	A taxmap object
unknown	If TRUE, Remove taxa with names the suggest they are placeholders for unknown taxa (e.g. "unknown ...").
uncultured	If TRUE, Remove taxa with names the suggest they are assigned to uncultured organisms (e.g. "uncultured ...").
name_regex	The regex code to match a valid character in a taxon name. For example, "[a-z]" would mean taxon names can only be lower case letters.
ignore_case	If TRUE, dont consider the case of the text when determining a match.

Details

If you encounter a taxon name that represents an ambiguous taxon that is not filtered out by this function, let us know and we will add it.

Value

TRUE/FALSE vector corresponding to taxon_names

Examples

```
is_ambiguous(c("unknown", "uncultured", "homo sapiens", "kfdsjfdljsdf"))
```

layout_functions	<i>Layout functions</i>
------------------	-------------------------

Description

Functions used to determine graph layout. Calling the function with no parameters returns available function names. Calling the function with only the name of a function returns that function. Supplying a name and a [graph](#) object to run the layout function on the graph.

Usage

```
layout_functions(name = NULL, graph = NULL, initial_coords = NULL,  
  effort = 1, ...)
```

Arguments

name	(character of length 1 OR NULL) name of algorithm. Leave NULL to see all options.
graph	(igraph) The graph to generate the layout for.
initial_coords	(matrix) Initial node layout to base new layout off of.
effort	(numeric of length 1) The amount of effort to put into layouts. Typically determines the the number of iterations.
...	(other arguments) Passed to igraph layout function used.

Value

The name available functions, a layout functions, or a two-column matrix depending on how arguments are provided.

Examples

```
# List available function names:  
layout_functions()  
  
# Execute layout function on graph:  
layout_functions("davidson-harel", igraph::make_ring(5))
```

make_dada2_asv_table *Make a imitation of the dada2 ASV abundance matrix*

Description

Attempts to save the abundance matrix stored as a table in a taxmap object in the dada2 ASV abundance matrix format. If the taxmap object was created using [parse_dada2](#), then it should be able to replicate the format exactly with the default settings.

Usage

```
make_dada2_asv_table(obj, asv_table = "asv_table", asv_id = "asv_id")
```

Arguments

obj	A taxmap object
asv_table	The name of the abundance matrix in the taxmap object to use.
asv_id	The name of the column in asv_table with unique ASV ids or sequences.

Value

A numeric matrix with rows as samples and columns as ASVs

See Also

Other writers: [make_dada2_tax_table](#), [write_greengenes](#), [write_mothur_taxonomy](#), [write_rdp](#), [write_silva_fasta](#), [write_unite_general](#)

make_dada2_tax_table *Make a imitation of the dada2 taxonomy matrix*

Description

Attempts to save the taxonomy information associated with an abundance matrix in a taxmap object in the dada2 taxonomy matrix format. If the taxmap object was created using [parse_dada2](#), then it should be able to replicate the format exactly with the default settings.

Usage

```
make_dada2_tax_table(obj, asv_table = "asv_table", asv_id = "asv_id")
```

Arguments

obj	A taxmap object
asv_table	The name of the abundance matrix in the taxmap object to use.
asv_id	The name of the column in asv_table with unique ASV ids or sequences.

Value

A character matrix with rows as ASVs and columns as taxonomic ranks.

See Also

Other writers: [make_dada2_asv_table](#), [write_greenegenes](#), [write_mothur_taxonomy](#), [write_rdp](#), [write_silva_fasta](#), [write_unite_general](#)

metacoder

Metacoder

Description

A package for planning and analysis of amplicon metagenomics research projects.

Details

The goal of the metacoder package is to provide a set of tools for:

- Standardized parsing of taxonomic information from diverse resources.
- Visualization of statistics distributed over taxonomic classifications.
- Evaluating potential metabarcoding primers for taxonomic specificity.
- Providing flexible functions for analyzing taxonomic and abundance data.

To accomplish these goals, metacoder leverages resources from other R packages, interfaces with external programs, and provides novel functions where needed to allow for entire analyses within R.

Documentation

The full documentation can be found online at http://grunwaldlab.github.io/metacoder_documentation.

There is also a short vignette included for offline use that can be accessed by the following code:

```
browseVignettes(package = "metacoder")
```

Plotting:

- [heat_tree](#)
- [heat_tree_matrix](#)

In silico PCR:

- [primersearch](#)

Analysis:

- [calc_taxon_abund](#)

- `calc_obs_props`
- `rarefy_obs`
- `compare_groups`
- `zero_low_counts`
- `calc_n_samples`
- `filter_ambiguous_taxa`

Parsers:

- `parse_greenegenes`
- `parse_mothur_tax_summary`
- `parse_mothur_taxonomy`
- `parse_newick`
- `parse_phyloseq`
- `parse_phylo`
- `parse_qiime_biom`
- `parse_rdp`
- `parse_silva_fasta`
- `parse_unite_general`

Writers:

- `write_greenegenes`
- `write_mothur_taxonomy`
- `write_rdp`
- `write_silva_fasta`
- `write_unite_general`

Database querying:

- `ncbi_taxon_sample`

Author(s)

Zachary Foster and Niklaus Grunwald

ncbi_taxon_sample *Download representative sequences for a taxon*

Description

Downloads a sample of sequences meant to evenly capture the diversity of a given taxon. Can be used to get a shallow sampling of vast groups. **CAUTION:** This function can make MANY queries to Genbank depending on arguments given and can take a very long time. Choose your arguments carefully to avoid long waits and needlessly stressing NCBI's servers. Use a downloaded database and a parser from the taxa package when possible.

Usage

```
ncbi_taxon_sample(name = NULL, id = NULL, target_rank,
  min_counts = NULL, max_counts = NULL, interpolate_min = TRUE,
  interpolate_max = TRUE, min_children = NULL, max_children = NULL,
  seqrange = "1:3000", getrelated = FALSE, fuzzy = TRUE,
  limit = 10, entrez_query = NULL, hypothetical = FALSE,
  verbose = TRUE)
```

Arguments

name	(character of length 1) The taxon to download a sample of sequences for.
id	(character of length 1) The taxon id to download a sample of sequences for.
target_rank	(character of length 1) The finest taxonomic rank at which to sample. The finest rank at which replication occurs. Must be a finer rank than taxon.
min_counts	(named numeric) The minimum number of sequences to download for each taxonomic rank. The names correspond to taxonomic ranks.
max_counts	(named numeric) The maximum number of sequences to download for each taxonomic rank. The names correspond to taxonomic ranks.
interpolate_min	(logical) If TRUE, values supplied to min_counts and min_children will be used to infer the values of intermediate ranks not specified. Linear interpolation between values of specified ranks will be used to determine values of unspecified ranks.
interpolate_max	(logical) If TRUE, values supplied to max_counts and max_children will be used to infer the values of intermediate ranks not specified. Linear interpolation between values of specified ranks will be used to determine values of unspecified ranks.
min_children	(named numeric) The minimum number sub-taxa of taxa for a given rank must have for its sequences to be searched. The names correspond to taxonomic ranks.
max_children	(named numeric) The maximum number sub-taxa of taxa for a given rank must have for its sequences to be searched. The names correspond to taxonomic ranks.

seqrange	(character) Sequence range, as e.g., "1:1000". This is the range of sequence lengths to search for. So "1:1000" means search for sequences from 1 to 1000 characters in length.
getrelated	(logical) If TRUE, gets the longest sequences of a species in the same genus as the one searched for. If FALSE, returns nothing if no match found.
fuzzy	(logical) Whether to do fuzzy taxonomic ID search or exact search. If TRUE, we use <code>xArbitraryXx[porgn:__txid<ID>]</code> , but if FALSE, we use <code>txid<ID></code> . Default: FALSE
limit	(numeric) Number of sequences to search for and return. Max of 10,000. If you search for 6000 records, and only 5000 are found, you will of course only get 5000 back.
entrez_query	(character; length 1) An Entrez-format query to filter results with. This is useful to search for sequences with specific characteristics. The format is the same as the one used to search genbank. (https://www.ncbi.nlm.nih.gov/books/NBK3837/#EntrezHelp.Entrez_Searching_Options)
hypothetical	(logical; length 1) If FALSE, an attempt will be made to not return hypothetical or predicted sequences judging from accession number prefixes (XM and XR). This can result in less than the <code>limit</code> being returned even if there are more sequences available, since this filtering is done after searching NCBI.
verbose	(logical) If TRUE, progress messages will be printed.

Examples

```
## Not run:

# Look up 5 ITS sequences from each fungal class
data <- ncbi_taxon_sample(name = "Fungi", target_rank = "class", limit = 5,
                        entrez_query = '"internal transcribed spacer"[All Fields]')

# Look up taxonomic information for sequences
obj <- lookup_tax_data(data, type = "seq_id", column = "gi_no")

# Plot information
filter_taxa(obj, taxon_names == "Fungi", subtaxa = TRUE) %>%
  heat_tree(node_label = taxon_names, node_color = n_obs, node_size = n_obs)

## End(Not run)
```

parse_dada2

Convert the output of dada2 to a taxmap object

Description

Convert the ASV table and taxonomy table returned by `dada2` into a `taxmap` object. An example of the input format can be found by following the `dada2` tutorial here: <https://benjjneb.github.io/dada2/tutorial.html>

Usage

```
parse_dada2(seq_table, tax_table, class_key = "taxon_name",
            class_regex = "(.*)", include_match = TRUE)
```

Arguments

seq_table	The ASV abundance matrix, with rows as samples and columns as ASV ids or sequences
tax_table	The table with taxonomic classifications for ASVs, with ASVs in rows and taxonomic ranks as columns.
class_key	(character of length 1) The identity of the capturing groups defined using class_regex. The length of class_key must be equal to the number of capturing groups specified in class_regex. Any names added to the terms will be used as column names in the output. At least one "taxon_name" must be specified. Only "info" can be used multiple times. Each term must be one of those described below: * taxon_name: The name of a taxon. Not necessarily unique, but are interpretable by a particular database. Requires an internet connection. * taxon_rank: The rank of the taxon. This will be used to add rank info into the output object that can be accessed by out\$taxon_ranks(). * info: Arbitrary taxon info you want included in the output. Can be used more than once.
class_regex	(character of length 1) A regular expression with capturing groups indicating the locations of data for each taxon in the class term in the key argument. The identity of the information must be specified using the class_key argument. The class_sep option can be used to split the classification into data for each taxon before matching. If class_sep is NULL, each match of class_regex defines a taxon in the classification.
include_match	(logical of length 1) If TRUE, include the part of the input matched by class_regex in the output object.

Value

taxmap

See Also

Other parsers: [parse_edge_list](#), [parse_greenegenes](#), [parse_mothur_tax_summary](#), [parse_mothur_taxonomy](#), [parse_newick](#), [parse_phyloseq](#), [parse_phylo](#), [parse_qiime_biom](#), [parse_rdp](#), [parse_silva_fasta](#), [parse_ubiome](#), [parse_unite_general](#)

parse_greenegenes

Parse Greengenes release

Description

Parses the greengenes database.

Usage

```
parse_greenegenes(tax_file, seq_file = NULL)
```

Arguments

`tax_file` (character of length 1) The file path to the greengenes taxonomy file.

`seq_file` (character of length 1) The file path to the greengenes sequence fasta file. This is optional.

Details

The taxonomy input file has a format like:

```
228054 k__Bacteria; p__Cyanobacteria; c__Synechococcophycideae; o__Synech...
844608 k__Bacteria; p__Cyanobacteria; c__Synechococcophycideae; o__Synech...
...
```

The optional sequence file has a format like:

```
>1111886
AACGAACGCTGGCGGCATGCCTAACACATGCAAGTCGAACGAGACCTTCGGGTCTAGTGGCGCACGGTGCGTA...
>1111885
AGAGTTTGATCCTGGCTCAGAATGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGTACGAGAAATCCCAGC...
...
```

Value

`taxmap`

See Also

Other parsers: [parse_dada2](#), [parse_edge_list](#), [parse_mothur_tax_summary](#), [parse_mothur_taxonomy](#), [parse_newick](#), [parse_phyloseq](#), [parse_phylo](#), [parse_qiime_biom](#), [parse_rdp](#), [parse_silva_fasta](#), [parse_ubiome](#), [parse_unite_general](#)

`parse_mothur_taxonomy` *Parse mothur Classify.seqs *.taxonomy output*

Description

Parse the `*.taxonomy` file that is returned by the `'Classify.seqs'` command in mothur. If confidence scores are present, they are included in the output.

Usage

```
parse_mothur_taxonomy(file = NULL, text = NULL)
```

Arguments

file	(character of length 1) The file path to the input file. Either "file" or "text" must be used, but not both.
text	(character) An alternate input to "file". The contents of the file as a character. Either "file" or "text" must be used, but not both.

Details

The input file has a format like:

```
AY457915 Bacteria(100);Firmicutes(99);Clostridiales(99);Johnsone...
AY457914 Bacteria(100);Firmicutes(100);Clostridiales(100);Johnso...
AY457913 Bacteria(100);Firmicutes(100);Clostridiales(100);Johnso...
AY457912 Bacteria(100);Firmicutes(99);Clostridiales(99);Johnsone...
AY457911 Bacteria(100);Firmicutes(99);Clostridiales(98);Ruminoco...
```

or...

```
AY457915 Bacteria;Firmicutes;Clostridiales;Johnsonella_et_rel.;J...
AY457914 Bacteria;Firmicutes;Clostridiales;Johnsonella_et_rel.;J...
AY457913 Bacteria;Firmicutes;Clostridiales;Johnsonella_et_rel.;J...
AY457912 Bacteria;Firmicutes;Clostridiales;Johnsonella_et_rel.;J...
AY457911 Bacteria;Firmicutes;Clostridiales;Ruminococcus_et_rel.;...
```

Value

[taxmap](#)

See Also

Other parsers: [parse_dada2](#), [parse_edge_list](#), [parse_greenegenes](#), [parse_mothur_tax_summary](#), [parse_newick](#), [parse_phyloseq](#), [parse_phylo](#), [parse_qiime_biom](#), [parse_rdp](#), [parse_silva_fasta](#), [parse_ubiome](#), [parse_unite_general](#)

parse_mothur_tax_summary

*Parse mothur *.tax.summary Classify.seqs output*

Description

Parse the '*.tax.summary' file that is returned by the 'Classify.seqs' command in mothur.

Usage

```
parse_mothur_tax_summary(file = NULL, text = NULL, table = NULL)
```

Arguments

file	(character of length 1) The file path to the input file. Either "file", "text", or "table" must be used, but only one.
text	(character) An alternate input to "file". The contents of the file as a character. Either "file", "text", or "table" must be used, but only one.
table	(character of length 1) An already parsed data.frame or tibble. Either "file", "text", or "table" must be used, but only one.

Details

The input file has a format like:

```
taxlevel rankID taxon daughterlevels total A B C
0 0 Root 2 242 84 84 74
1 0.1 Bacteria 50 242 84 84 74
2 0.1.2 Actinobacteria 38 13 0 13 0
3 0.1.2.3 Actinomycetaceae-Bifidobacteriaceae 10 13 0 13 0
4 0.1.2.3.7 Bifidobacteriaceae 6 13 0 13 0
5 0.1.2.3.7.2 Bifidobacterium_choerinum_et_rel. 8 13 0 13 0
6 0.1.2.3.7.2.1 Bifidobacterium_angulatum_et_rel. 1 11 0 11 0
7 0.1.2.3.7.2.1.1 unclassified 1 11 0 11 0
8 0.1.2.3.7.2.1.1.1 unclassified 1 11 0 11 0
9 0.1.2.3.7.2.1.1.1.1 unclassified 1 11 0 11 0
10 0.1.2.3.7.2.1.1.1.1.1 unclassified 1 11 0 11 0
11 0.1.2.3.7.2.1.1.1.1.1.1 unclassified 1 11 0 11 0
12 0.1.2.3.7.2.1.1.1.1.1.1.1 unclassified 1 11 0 11 0
6 0.1.2.3.7.2.5 Bifidobacterium_longum_et_rel. 1 2 0 2 0
7 0.1.2.3.7.2.5.1 unclassified 1 2 0 2 0
8 0.1.2.3.7.2.5.1.1 unclassified 1 2 0 2 0
9 0.1.2.3.7.2.5.1.1.1 unclassified 1 2 0 2 0
```

or

```
taxon total A B C
"k__Bacteria";"p__Actinobacteria";"c__Actinobacteria";... 1 0 1 0
"k__Bacteria";"p__Actinobacteria";"c__Actinobacteria";... 1 0 1 0
"k__Bacteria";"p__Actinobacteria";"c__Actinobacteria";... 1 0 1 0
```

Value

taxmap

See Also

Other parsers: [parse_dada2](#), [parse_edge_list](#), [parse_greenegenes](#), [parse_mothur_taxonomy](#), [parse_newick](#), [parse_phyloseq](#), [parse_phylo](#), [parse_qiime_biom](#), [parse_rdp](#), [parse_silva_fasta](#), [parse_ubiome](#), [parse_unite_general](#)

parse_newick	<i>Parse a Newick file</i>
--------------	----------------------------

Description

Parse a Newick file into a taxmap object.

Usage

```
parse_newick(file = NULL, text = NULL)
```

Arguments

file	(character of length 1) The file path to the input file. Either file or text must be supplied but not both.
text	(character of length 1) The raw text to parse. Either file or text must be supplied but not both.

Details

The input file has a format like:

```
(ant:17, (bat:31, cow:22):7, dog:22, (elk:33, fox:12):40);  
(dog:20, (elephant:30, horse:60):20):50;
```

Value

[taxmap](#)

See Also

Other parsers: [parse_dada2](#), [parse_edge_list](#), [parse_greengenes](#), [parse_mothur_tax_summary](#), [parse_mothur_taxonomy](#), [parse_phyloseq](#), [parse_phylo](#), [parse_qiime_biom](#), [parse_rdp](#), [parse_silva_fasta](#), [parse_ubiome](#), [parse_unite_general](#)

parse_phylo	<i>Parse a phylo object</i>
-------------	-----------------------------

Description

Parses a phylo object from the ape package.

Usage

```
parse_phylo(obj)
```

Arguments

obj A phylo object from the ape package.

Value

taxmap

See Also

Other parsers: [parse_dada2](#), [parse_edge_list](#), [parse_greengenes](#), [parse_mothur_tax_summary](#), [parse_mothur_taxonomy](#), [parse_newick](#), [parse_phyloseq](#), [parse_qiime_biom](#), [parse_rdp](#), [parse_silva_fasta](#), [parse_ubiome](#), [parse_unite_general](#)

parse_phyloseq	<i>Convert a phyloseq to taxmap</i>
----------------	-------------------------------------

Description

Converts a phyloseq object to a taxmap object.

Usage

```
parse_phyloseq(obj, class_regex = "(.*)", class_key = "taxon_name")
```

Arguments

obj A phyloseq object

class_regex A regular expression used to parse data in the taxon names. There must be a capture group (a pair of parentheses) for each item in class_key. See [parse_tax_data](#) for examples of how this works.

class_key (character of length 1) The identity of the capturing groups defined using class_regex. The length of class_key must be equal to the number of capturing groups specified in class_regex. Any names added to the terms will be used as column names in the output. At least one "taxon_name" must be specified. Only "info" can be used multiple times. Each term must be one of those described below: * taxon_name: The name of a taxon. Not necessarily unique, but are interpretable by a particular database. Requires an internet connection. * taxon_rank: The rank of the taxon. This will be used to add rank info into the output object that can be accessed by out\$taxon_ranks(). * info: Arbitrary taxon info you want included in the output. Can be used more than once.

Value

A taxmap object

See Also

Other parsers: [parse_dada2](#), [parse_edge_list](#), [parse_greengenes](#), [parse_mothur_tax_summary](#), [parse_mothur_taxonomy](#), [parse_newick](#), [parse_phylo](#), [parse_qiime_biom](#), [parse_rdp](#), [parse_silva_fasta](#), [parse_ubioime](#), [parse_unite_general](#)

Examples

```
## Not run:

# Install phyloseq to get example data
# source('http://bioconductor.org/biocLite.R')
# biocLite('phyloseq')

# Parse example dataset
library(phyloseq)
data(GlobalPatterns)
x <- parse_phyloseq(GlobalPatterns)

# Plot data
heat_tree(x,
          node_size = n_obs,
          node_color = n_obs,
          node_label = taxon_names,
          tree_label = taxon_names)

## End(Not run)
```

parse_qiime_biom

Parse a BIOM output from QIIME

Description

Parses a file in BIOM format from QIIME into a taxmap object. This also seems to work with files from MEGAN. I have not tested if it works with other BIOM files.

Usage

```
parse_qiime_biom(file, class_regex = "(.*)", class_key = "taxon_name")
```

Arguments

file (character of length 1) The file path to the input file.

class_regex A regular expression used to parse data in the taxon names. There must be a capture group (a pair of parentheses) for each item in `class_key`. See [parse_tax_data](#) for examples of how this works.

`class_key` (character of length 1) The identity of the capturing groups defined using `class_regex`. The length of `class_key` must be equal to the number of capturing groups specified in `class_regex`. Any names added to the terms will be used as column names in the output. At least one "taxon_name" must be specified. Only "info" can be used multiple times. Each term must be one of those described below: * `taxon_name`: The name of a taxon. Not necessarily unique, but are interpretable by a particular database. Requires an internet connection. * `taxon_rank`: The rank of the taxon. This will be used to add rank info into the output object that can be accessed by `out$taxon_ranks()`. * `info`: Arbitrary taxon info you want included in the output. Can be used more than once.

Details

This function was inspired by the tutorial created by Geoffrey Zahn at <http://geoffreyzahn.com/getting-your-otu-table-into-r/>.

Value

A taxmap object

See Also

Other parsers: [parse_dada2](#), [parse_edge_list](#), [parse_greenegenes](#), [parse_mothur_tax_summary](#), [parse_mothur_taxonomy](#), [parse_newick](#), [parse_phyloseq](#), [parse_phylo](#), [parse_rdp](#), [parse_silva_fasta](#), [parse_ubiome](#), [parse_unite_general](#)

parse_rdp

Parse RDP FASTA release

Description

Parses an RDP reference FASTA file.

Usage

```
parse_rdp(input = NULL, file = NULL, include_seqs = TRUE,
          add_species = FALSE)
```

Arguments

`input` (character) One of the following:

- A character vector of sequences** See the example below for what this looks like. The parser [read_fasta](#) produces output like this.
- A list of character vectors** Each vector should have one base per element.
- A "DNABin" object** This is the result of parsers like [read.FASTA](#).
- A list of "SeqFastadna" objects** This is the result of parsers like [read.fasta](#). Either "input" or "file" must be supplied but not both.

file	The path to a FASTA file containing sequences to use. Either "input" or "file" must be supplied but not both.
include_seqs	(logical of length 1) If TRUE, include sequences in the output object.
add_species	(logical of length 1) If TRUE, add the species information to the taxonomy. In this database, the species name often contains other information as well.

Details

The input file has a format like:

```
>S000448483 Sparassis crispa; MBUH-PIRJO&ILKKA94-1587/ss5 Lineage=Root;rootrank;Fun...
ggattcccctagtaactgcgagtggaagcggaagagctcaaatttaaaatctggcggcgtcctcgtcgtccgagttgtaa
tctggagaagcgacatccgcgctggaccgtgtacaagtctcttgaaaagagcgtcgtagagggtgacaatcccgtcttt
...
```

Value

taxmap

See Also

Other parsers: [parse_dada2](#), [parse_edge_list](#), [parse_greenegenes](#), [parse_mothur_tax_summary](#), [parse_mothur_taxonomy](#), [parse_newick](#), [parse_phyloseq](#), [parse_phylo](#), [parse_qiime_biom](#), [parse_silva_fasta](#), [parse_ubiome](#), [parse_unite_general](#)

parse_silva_fasta *Parse SILVA FASTA release*

Description

Parses an SILVA FASTA file that can be found at https://www.arb-silva.de/no_cache/download/archive/release_128/Exports/.

Usage

```
parse_silva_fasta(file = NULL, input = NULL, include_seqs = TRUE)
```

Arguments

file	The path to a FASTA file containing sequences to use. Either "input" or "file" must be supplied but not both.
input	(character) One of the following: A character vector of sequences See the example below for what this looks like. The parser read_fasta produces output like this. A list of character vectors Each vector should have one base per element. A "DNAbin" object This is the result of parsers like read.FASTA .

A list of "SeqFastadna" objects This is the result of parsers like [read.fasta](#).
Either "input" or "file" must be supplied but not both.

include_seqs (logical of length 1) If TRUE, include sequences in the output object.

Details

The input file has a format like:

```
>GCVF01000431.1.2369
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospiril...
CGUGCACGGUGGAUGCCUUGGCAGCCAGAGGCGAUGAAGGACGUUGUAGCCUGCGAUAAAGCUCCGGUUAGGUGGCAAACA
ACCGUUUGACCCGGAGAUCUCCGAAUGGGGCAACCCACCCGUUGUAAGGCGGGUAUCACCGACUGAAUCCAUAGGUCGGU
...
```

Value

taxmap

See Also

Other parsers: [parse_dada2](#), [parse_edge_list](#), [parse_greengenes](#), [parse_mothur_tax_summary](#), [parse_mothur_taxonomy](#), [parse_newick](#), [parse_phyloseq](#), [parse_phylo](#), [parse_qiime_biom](#), [parse_rdp](#), [parse_ubioime](#), [parse_unite_general](#)

parse_ubioime

Converts the uBiome file format to taxmap

Description

Converts the uBiome file format to taxmap. NOTE: This is experimental and might not work if uBiome changes their format. Contact the maintainers if you encounter problems/

Usage

```
parse_ubioime(file = NULL, table = NULL)
```

Arguments

file (character of length 1) The file path to the input file. Either "file", or "table" must be used, but only one.

table (character of length 1) An already parsed data.frame or tibble. Either "file", or "table" must be used, but only one.

Details

The input file has a format like:

```
tax_name, tax_rank, count, count_norm, taxon, parent
root, root, 29393, 1011911, 1,
Bacteria, superkingdom, 29047, 1000000, 2, 131567
Campylobacter, genus, 23, 791, 194, 72294
Flavobacterium, genus, 264, 9088, 237, 49546
```

Value

`taxmap`

See Also

Other parsers: [parse_dada2](#), [parse_edge_list](#), [parse_greenegenes](#), [parse_mothur_tax_summary](#), [parse_mothur_taxonomy](#), [parse_newick](#), [parse_phyloseq](#), [parse_phylo](#), [parse_qiime_biom](#), [parse_rdp](#), [parse_silva_fasta](#), [parse_unite_general](#)

`parse_unite_general` *Parse UNITE general release FASTA*

Description

Parse the UNITE general release FASTA file

Usage

```
parse_unite_general(input = NULL, file = NULL, include_seqs = TRUE)
```

Arguments

<code>input</code>	(character) One of the following: A character vector of sequences See the example below for what this looks like. The parser read_fasta produces output like this. A list of character vectors Each vector should have one base per element. A "DNAbin" object This is the result of parsers like read.FASTA . A list of "SeqFastadna" objects This is the result of parsers like read.fasta . Either "input" or "file" must be supplied but not both.
<code>file</code>	The path to a FASTA file containing sequences to use. Either "input" or "file" must be supplied but not both.
<code>include_seqs</code>	(logical of length 1) If TRUE, include sequences in the output object.

Details

The input file has a format like:

```
>Glomeromycota_sp|KJ484724|SH523877.07FU|reps|k__Fungi;p__Glomeromycota;c__unid...
ATAATTTGCCGAACCTAGCGTTAGCGCGAGGTTCTGCGATCAACACTTATATTTAAAACCAACTCTAAATTTTGAT...
```

Value

taxmap

See Also

Other parsers: [parse_dada2](#), [parse_edge_list](#), [parse_greenegenes](#), [parse_mothur_tax_summary](#), [parse_mothur_taxonomy](#), [parse_newick](#), [parse_phyloseq](#), [parse_phylo](#), [parse_qiime_biom](#), [parse_rdp](#), [parse_silva_fasta](#), [parse_ubiome](#)

primersearch

Use EMBOSS primersearch for in silico PCR

Description

A pair of primers are aligned against a set of sequences. A [taxmap](#) object with two tables is returned: a table with information for each predicted amplicon, quality of match, and predicted amplicons, and a table with per-taxon amplification statistics. Requires the EMBOSS tool kit (<http://emboss.sourceforge.net/>) to be installed.

Usage

```
primersearch(obj, seqs, forward, reverse, mismatch = 5, clone = TRUE)
```

Arguments

obj	A taxmap object.
seqs	The sequences to do in silico PCR on. This can be any variable in <code>obj\$data</code> listed in <code>all_names(obj)</code> or an external variable. If an external variable (i.e. not in <code>obj\$data</code>), it must be named by taxon IDs or have the same length as the number of taxa in <code>obj</code> . Currently, only character vectors are accepted.
forward	(character of length 1) The forward primer sequence
reverse	(character of length 1) The reverse primer sequence
mismatch	An integer vector of length 1. The percentage of mismatches allowed.
clone	If TRUE, make a copy of the input object and add on the results (like most R functions). If FALSE, the input will be changed without saving the result, which uses less RAM.

Details

It can be confusing how the primer sequence relates to the binding sites on a reference database sequence. A simplified diagram can help. For example, if the top strand below (5' -> 3') is the database sequence, the forward primer has the same sequence as the target region, since it will bind to the other strand (3' -> 5') during PCR and extend on the 3' end. However, the reverse primer must bind to the database strand, so it will have to be the complement of the reference sequence. It also has to be reversed to make it in the standard 5' -> 3' orientation. Therefore, the reverse primer must be the reverse complement of its binding site on the reference sequence.

```
Primer 1: 5' AAGTACCTTAACGGAATTATAG 3'
Primer 2: 5' GCTCCACCTACGAAACGAAT 3'

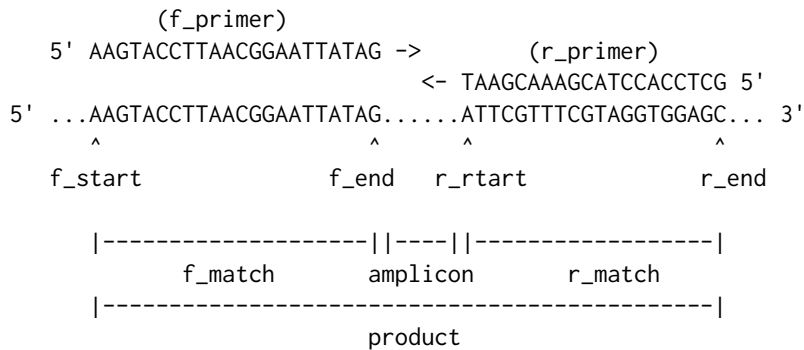
                                <- TAAGCAAAGCATCCACCTCG 5'
5' ...AAGTACCTTAACGGAATTATAG.....ATTCGTTTCGTAGGTGGAGC... 3'

3' ...TTCATGGAATTGCCTTAATATC.....TAAGCAAAGCATCCACCTCG... 5'
5' AAGTACCTTAACGGAATTATAG ->
```

However, a database might have either the top or the bottom strand as a reference sequence. Since one implies the sequence of the other, either is valid, but this is another source of confusion. If we take the diagram above and rotate it 180 degrees, it would mean the same thing, but which primer we would want to call "forward" and which we would want to call "reverse" would change. Databases of a single locus (e.g. Greengenes) will likely have a convention for which strand will be present, so relative to this convention, there is a distinct "forward" and "reverse". However, computers don't know about this convention, so the "forward" primer is whichever primer has the same sequence as its binding region in the database (as opposed to the reverse complement). For this reason, primersearch will redefine which primer is "forward" and which is "reverse" based on how it binds the reference sequence. See the example code in [primersearch_raw](#) for a demonstration of this.

Value

A copy of the input [taxmap](#) object with two tables added. One table contains amplicon information with one row per predicted amplicon with the following info:



taxon_id: The taxon IDs for the sequence.

seq_index: The index of the input sequence.
f_primer: The sequence of the forward primer.
r_primer: The sequence of the reverse primer.
f_mismatch: The number of mismatches on the forward primer.
r_mismatch: The number of mismatches on the reverse primer.
f_start: The start location of the forward primer.
f_end: The end location of the forward primer.
r_start: The start location of the reverse primer.
r_end: The end location of the reverse primer.
f_match: The sequence matched by the forward primer.
r_match: The sequence matched by the reverse primer.
amplicon: The sequence amplified by the primers, not including the primers.
product: The sequence amplified by the primers including the primers. This simulates a real PCR product.

The other table contains per-taxon information about the PCR, with one row per taxon. It has the following columns:

taxon_ids: Taxon IDs.
query_count: The number of sequences used as input.
seq_count: The number of sequences that had at least one amplicon.
amp_count: The number of amplicons. Might be more than one per sequence.
amplified: If at least one sequence of that taxon had at least one amplicon.
multiple: If at least one sequences had at least two amplicons.
prop_amplified: The proportion of sequences with at least one amplicon.
med_amp_len: The median amplicon length.
min_amp_len: The minimum amplicon length.
max_amp_len: The maximum amplicon length.
med_prod_len: The median product length.
min_prod_len: The minimum product length.
max_prod_len: The maximum product length.

Installing EMBOSS

The command-line tool "primersearch" from the EMBOSS tool kit is needed to use this function. How you install EMBOSS will depend on your operating system:

Linux:

Open up a terminal and type:

```
sudo apt-get install emboss
```

Mac OSX:

The easiest way to install EMBOSS on OSX is to use [homebrew](#). After installing homebrew, open up a terminal and type:

```
brew install homebrew/science/emboss
```

Windows:

There is an installer for Windows here:

<ftp://emboss.open-bio.org/pub/EMBOSS/windows/mEMBOSS-6.5.0.0-setup.exe>

Examples

```
## Not run:
# Get example FASTA file
fasta_path <- system.file(file.path("extdata", "silva_subset.fa"),
                          package = "metacoder")

# Parse the FASTA file as a taxmap object
obj <- parse_silva_fasta(file = fasta_path)

# Simulate PCR with primersearch
# Have to replace Us with Ts in sequences since primersearch
# does not understand Us.
obj <- primersearch(obj,
                   gsub(silva_seq, pattern = "U", replace = "T"),
                   forward = c("U519F" = "CAGYMGCCRCGGKAAHACC"),
                   reverse = c("Arch806R" = "GGACTACNSGGGTMTCTAAT"),
                   mismatch = 10)

# Plot what did not ampilify
obj %>%
  filter_taxa(prop_amplified < 1) %>%
  heat_tree(node_label = taxon_names,
           node_color = prop_amplified,
           node_color_range = c("grey", "red", "purple", "green"),
           node_color_trans = "linear",
           node_color_axis_label = "Proportion amplified",
           node_size = n_obs,
           node_size_axis_label = "Number of sequences",
           layout = "da",
           initial_layout = "re")

## End(Not run)
```

primersearch_raw

Use EMBOSS primersearch for in silico PCR

Description

A pair of primers are aligned against a set of sequences. The location of the best hits, quality of match, and predicted amplicons are returned. Requires the EMBOSS tool kit (<http://emboss.sourceforge.net/>) to be installed.

Usage

```
primersearch_raw(input = NULL, file = NULL, forward, reverse,
  mismatch = 5)
```

Arguments

input	(character) One of the following: A character vector of sequences See the example below for what this looks like. The parser read_fasta produces output like this. A list of character vectors Each vector should have one base per element. A "DNABin" object This is the result of parsers like read.FASTA . A list of "SeqFastadna" objects This is the result of parsers like read.fasta . Either "input" or "file" must be supplied but not both.
file	The path to a FASTA file containing sequences to use. Either "input" or "file" must be supplied but not both.
forward	(character of length 1) The forward primer sequence
reverse	(character of length 1) The reverse primer sequence
mismatch	An integer vector of length 1. The percentage of mismatches allowed.

Details

It can be confusing how the primer sequence relates to the binding sites on a reference database sequence. A simplified diagram can help. For example, if the top strand below (5' -> 3') is the database sequence, the forward primer has the same sequence as the target region, since it will bind to the other strand (3' -> 5') during PCR and extend on the 3' end. However, the reverse primer must bind to the database strand, so it will have to be the complement of the reference sequence. It also has to be reversed to make it in the standard 5' -> 3' orientation. Therefore, the reverse primer must be the reverse complement of its binding site on the reference sequence.

```
Primer 1: 5' AAGTACCTTAACGGAATTATAG 3'
Primer 2: 5' GCTCCACCTACGAAACGAAT 3'

                    <- TAAGCAAAGCATCCACCTCG 5'
5' ...AAGTACCTTAACGGAATTATAG.....ATTCGTTTCGTAGGTGGAGC... 3'

3' ...TTCATGGAATTGCCTTAATATC.....TAAGCAAAGCATCCACCTCG... 5'
5' AAGTACCTTAACGGAATTATAG ->
```

However, a database might have either the top or the bottom strand as a reference sequence. Since one implies the sequence of the other, either is valid, but this is another source of confusion. If we take the diagram above and rotate it 180 degrees, it would mean the same thing, but which primer we would want to call "forward" and which we would want to call "reverse" would change. Databases of a single locus (e.g. Greengenes) will likely have a convention for which strand will be present, so relative to this convention, there is a distinct "forward" and "reverse". However, computers don't know about this convention, so the "forward" primer is whichever primer has the same sequence as its binding region in the database (as opposed to the reverse complement). For this reason, primersearch will redefine which primer is "forward" and which is "reverse" based on how it binds the reference sequence. See the example code for a demonstration of this.

Value

A table with one row per predicted amplicon with the following info:

```

      (f_primer)
5' AAGTACCTTAACGGAATTATAG ->      (r_primer)
      <- TAAGCAAAGCATCCACCTCG 5'
5' ...AAGTACCTTAACGGAATTATAG.....ATTCGTTTCGTAGGTGGAGC... 3'
      ^           ^           ^           ^
      f_start      f_end    r_rtart      r_end

      |-----| |-----| |-----|
      f_match      amplicon      r_match
      |-----|
      product

```

f_mismatch: The number of mismatches on the forward primer

r_mismatch: The number of mismatches on the reverse primer

input: The index of the input sequence

Installing EMBOSS

The command-line tool "primersearch" from the EMBOSS tool kit is needed to use this function. How you install EMBOSS will depend on your operating system:

Linux:

Open up a terminal and type:

```
sudo apt-get install emboss
```

Mac OSX:

The easiest way to install EMBOSS on OSX is to use [homebrew](#). After installing homebrew, open up a terminal and type:

```
brew install homebrew/science/emboss
```

Windows:

There is an installer for Windows here:

<ftp://emboss.open-bio.org/pub/EMBOSS/windows/mEMBOSS-6.5.0.0-setup.exe>

Examples

```
## Not run:
```

```
### Dummy test data set ###
```

```
primer_1_site <- "AAGTACCTTAACGGAATTATAG"
primer_2_site <- "ATTCGTTTCGTAGGTGGAGC"
amplicon <- "NNNAGTGGATAGATAGGGTTCTGTGGCGTTTGGGAATTAAGATTAGAGANN"
seq_1 <- paste0("AA", primer_1_site, amplicon, primer_2_site, "AAAA")
seq_2 <- rev_comp(seq_1)
```

```

f_primer <- "ACGTACCTTAACGGAATTATAG" # Note the "C" mismatch at position 2
r_primer <- rev_comp(primer_2_site)
seqs <- c(a = seq_1, b = seq_2)

result <- primersearch_raw(seqs, forward = f_primer, reverse = r_primer)

### Real data set ###

# Get example FASTA file
fasta_path <- system.file(file.path("extdata", "silva_subset.fa"),
                          package = "metacoder")

# Parse the FASTA file as a taxmap object
obj <- parse_silva_fasta(file = fasta_path)

# Simulate PCR with primersearch
pcr_result <- primersearch_raw(obj$data$tax_data$silva_seq,
                              forward = c("U519F" = "CAGYMGCCRCGGKAAHACC"),
                              reverse = c("Arch806R" = "GGACTACNSGGGTMTCTAAT"),
                              mismatch = 10)

# Add result to input table
# NOTE: We want to add a function to handle running pcr on a
#       taxmap object directly, but we are still trying to figure out
#       the best way to implement it. For now, do the following:
obj$data$pcr <- pcr_result
obj$data$pcr$taxon_id <- obj$data$tax_data$taxon_id[pcr_result$input]

# Visualize which taxa were amplified
# This work because only amplicons are returned by `primersearch`
n_amplified <- unlist(obj$obs_apply("pcr",
                                   function(x) length(unique(x)),
                                   value = "input"))
prop_amped <- n_amplified / obj$n_obs()
heat_tree(obj,
          node_label = taxon_names,
          node_color = prop_amped,
          node_color_range = c("grey", "red", "purple", "green"),
          node_color_trans = "linear",
          node_color_axis_label = "Proportion amplified",
          node_size = n_obs,
          node_size_axis_label = "Number of sequences",
          layout = "da",
          initial_layout = "re")

## End(Not run)

```

Description

Returns the default color palette for qualitative data

Usage

`qualitative_palette()`

Value

character of hex color codes

Examples

`qualitative_palette()`

`quantative_palette` *The default quantative color palette*

Description

Returns the default color palette for quantitative data.

Usage

`quantative_palette()`

Value

character of hex color codes

Examples

`quantative_palette()`

rarefy_obs

*Calculate rarefied observation counts***Description**

For a given table in a `taxmap` object, rarefy counts to a constant total. This is a wrapper around `rrarefy` that automatically detects which columns are numeric and handles the reformatting needed to use tibbles.

Usage

```
rarefy_obs(obj, data, sample_size = NULL, cols = NULL,
           other_cols = FALSE, out_names = NULL, dataset = NULL)
```

Arguments

<code>obj</code>	A <code>taxmap</code> object
<code>data</code>	The name of a table in <code>obj\$data</code> .
<code>sample_size</code>	The sample size counts will be rarefied to. This can be either a single integer or a vector of integers of equal length to the number of columns.
<code>cols</code>	The columns in <code>data</code> to use. By default, all numeric columns are used. Takes one of the following inputs: TRUE/FALSE: All/No columns will be used. Character vector: The names of columns to use Numeric vector: The indexes of columns to use Vector of TRUE/FALSE of length equal to the number of columns: Use the columns corresponding to TRUE values.
<code>other_cols</code>	Preserve in the output non-target columns present in the input data. New columns will always be on the end. The "taxon_id" column will be preserved in the front. Takes one of the following inputs: NULL: No columns will be added back, not even the taxon id column. TRUE/FALSE: All/None of the non-target columns will be preserved. Character vector: The names of columns to preserve Numeric vector: The indexes of columns to preserve Vector of TRUE/FALSE of length equal to the number of columns: Preserve the columns corresponding to TRUE values.
<code>out_names</code>	The names of count columns in the output. Must be the same length as <code>cols</code> (or <code>unique(groups)</code> , if <code>groups</code> is used).
<code>dataset</code>	DEPRECATED. use "data" instead.

Value

A tibble

See Also

Other calculations: [calc_group_mean](#), [calc_group_median](#), [calc_group_rsd](#), [calc_group_stat](#), [calc_n_samples](#), [calc_obs_props](#), [calc_prop_samples](#), [calc_taxon_abund](#), [compare_groups](#), [counts_to_presence](#), [zero_low_counts](#)

Examples

```
## Not run:
# Parse data for examples
x = parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
                  class_key = c(tax_rank = "info", tax_name = "taxon_name"),
                  class_regex = "^(.+)_(.+)$")

# Rarefy all numeric columns
rarefy_obs(x, "tax_data")

# Rarefy a subset of columns
rarefy_obs(x, "tax_data", cols = c("700035949", "700097855", "700100489"))
rarefy_obs(x, "tax_data", cols = 4:6)
rarefy_obs(x, "tax_data", cols = startsWith(colnames(x$data$tax_data), "70001"))

# Including all other columns in output
rarefy_obs(x, "tax_data", other_cols = TRUE)

# Including specific columns in output
rarefy_obs(x, "tax_data", cols = c("700035949", "700097855", "700100489"),
          other_cols = 2:3)

# Rename output columns
rarefy_obs(x, "tax_data", cols = c("700035949", "700097855", "700100489"),
          out_names = c("a", "b", "c"))

## End(Not run)
```

read_fasta

Read a FASTA file

Description

Reads a FASTA file. This is the FASTA parser for metacoder. It simply tries to read a FASTA file into a named character vector with minimal fuss. It does not do any checks for valid characters etc. Other FASTA parsers you might want to consider include [read.FASTA](#) or [read.fasta](#).

Usage

```
read_fasta(file_path)
```

Arguments

file_path (character of length 1) The path to a file to read.

Value

named character vector

Examples

```
# Get example FASTA file
fasta_path <- system.file(file.path("extdata", "silva_subset.fa"),
                          package = "metacoder")

# Read fasta file
my_seqs <- read_fasta(fasta_path)
```

reverse

Reverse sequences

Description

Find the reverse of one or more sequences stored as a character vector. This is a wrapper for [rev](#) for character vectors instead of lists of character vectors with one value per letter.

Usage

```
reverse(seqs)
```

Arguments

seqs A character vector with one element per sequence.

See Also

Other sequence transformations: [complement](#), [rev_comp](#)

Examples

```
reverse(c("aagtGGTGaa", "AAGTGGT"))
```

rev_comp	<i>Reverse complement sequences</i>
----------	-------------------------------------

Description

Make the reverse complement of one or more sequences stored as a character vector. This is a wrapper for [comp](#) for character vectors instead of lists of character vectors with one value per letter. IUPAC ambiguity codes are handled and the upper/lower case is preserved.

Usage

```
rev_comp(seqs)
```

Arguments

seqs A character vector with one element per sequence.

See Also

Other sequence transformations: [complement](#), [reverse](#)

Examples

```
rev_comp(c("aagtGGTGaa", "AAGTGGT"))
```

write_greenegenes	<i>Write an imitation of the Greengenes database</i>
-------------------	--

Description

Attempts to save taxonomic and sequence information of a taxmap object in the Greengenes output format. If the taxmap object was created using [parse_greenegenes](#), then it should be able to replicate the format exactly with the default settings.

Usage

```
write_greenegenes(obj, tax_file = NULL, seq_file = NULL,  
  tax_names = obj$get_data("taxon_names")[[1]],  
  ranks = obj$get_data("gg_rank")[[1]],  
  ids = obj$get_data("gg_id")[[1]],  
  sequences = obj$get_data("gg_seq")[[1]])
```

Arguments

obj	A taxmap object
tax_file	(character of length 1) The file path to save the taxonomy file.
seq_file	(character of length 1) The file path to save the sequence fasta file. This is optional.
tax_names	(character named by taxon ids) The names of taxa
ranks	(character named by taxon ids) The ranks of taxa
ids	(character named by taxon ids) Sequence ids
sequences	(character named by taxon ids) Sequences

Details

The taxonomy output file has a format like:

```
228054 k__Bacteria; p__Cyanobacteria; c__Synechococcophycideae; o__Synech...
844608 k__Bacteria; p__Cyanobacteria; c__Synechococcophycideae; o__Synech...
...
```

The optional sequence file has a format like:

```
>1111886
AACGAACGCTGGCGGCATGCCTAACACATGCAAGTCGAACGAGACCTTCGGGTCTAGTGGCGCACGGGTGCGTA...
>1111885
AGAGTTTGATCCTGGCTCAGAAATGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGTACGAGAAATCCCAGC...
...
```

See Also

Other writers: [make_dada2_asv_table](#), [make_dada2_tax_table](#), [write_mothur_taxonomy](#), [write_rdp](#), [write_silva_fasta](#), [write_unite_general](#)

write_mothur_taxonomy *Write an imitation of the Mothur taxonomy file*

Description

Attempts to save taxonomic information of a taxmap object in the mothur ‘*.taxonomy’ format. If the taxmap object was created using [parse_mothur_taxonomy](#), then it should be able to replicate the format exactly with the default settings.

Usage

```
write_mothur_taxonomy(obj, file,
  tax_names = obj$get_data("taxon_names")[[1]],
  ids = obj$get_data("sequence_id")[[1]], scores = NULL)
```


Arguments

obj	A taxmap object
file	(character of length 1) The file path to save the sequence fasta file. This is optional.
tax_names	(character named by taxon ids) The names of taxa
ids	(character named by taxon ids) Sequence ids
scores	(numeric named by taxon ids)

Details

The output file has a format like:

```
AY457915 Bacteria(100);Firmicutes(99);Clostridiales(99);Johnsone...
AY457914 Bacteria(100);Firmicutes(100);Clostridiales(100);Johnso...
AY457913 Bacteria(100);Firmicutes(100);Clostridiales(100);Johnso...
AY457912 Bacteria(100);Firmicutes(99);Clostridiales(99);Johnsone...
AY457911 Bacteria(100);Firmicutes(99);Clostridiales(98);Ruminoco...
```

or...

```
AY457915 Bacteria;Firmicutes;Clostridiales;Johnsonella_et_rel.;J...
AY457914 Bacteria;Firmicutes;Clostridiales;Johnsonella_et_rel.;J...
AY457913 Bacteria;Firmicutes;Clostridiales;Johnsonella_et_rel.;J...
AY457912 Bacteria;Firmicutes;Clostridiales;Johnsonella_et_rel.;J...
AY457911 Bacteria;Firmicutes;Clostridiales;Ruminococcus_et_rel.;...
```

See Also

Other writers: [make_dada2_asv_table](#), [make_dada2_tax_table](#), [write_greenegenes](#), [write_rdp](#), [write_silva_fasta](#), [write_unite_general](#)

write_rdp

Write an imitation of the RDP FASTA database

Description

Attempts to save taxonomic and sequence information of a taxmap object in the RDP FASTA format. If the taxmap object was created using [parse_rdp](#), then it should be able to replicate the format exactly with the default settings.

Usage

```
write_rdp(obj, file, tax_names = obj$get_data("taxon_names")[[1]],
          ranks = obj$get_data("rdp_rank")[[1]],
          ids = obj$get_data("rdp_id")[[1]],
          info = obj$get_data("seq_name")[[1]],
          sequences = obj$get_data("rdp_seq")[[1]])
```

Arguments

obj	A taxmap object
file	(character of length 1) The file path to save the sequence fasta file. This is optional.
tax_names	(character named by taxon ids) The names of taxa
ranks	(character named by taxon ids) The ranks of taxa
ids	(character named by taxon ids) Sequence ids
info	(character named by taxon ids) Info associated with sequences. In the example output shown here, this field corresponds to "Sparassis crispa; MBUH-PIRJO&ILKKA94-1587/ss5"
sequences	(character named by taxon ids) Sequences

Details

The output file has a format like:

```
>S000448483 Sparassis crispa; MBUH-PIRJO&ILKKA94-1587/ss5 Lineage=Root;rootrank;Fun...
ggattcccctagtaactgcgagtgaagcgggaagagctcaaatttaaaatctggcggcgtcctcgtcgtccgagttgtaa
tctggagaagcgacatccgcgctggaccgtgtacaagtctcttgaaaagagcgtcgtagagggtgacaatcccgtcttt
...
```

See Also

Other writers: [make_dada2_asv_table](#), [make_dada2_tax_table](#), [write_greenegenes](#), [write_mothur_taxonomy](#), [write_silva_fasta](#), [write_unite_general](#)

write_silva_fasta *Write an imitation of the SILVA FASTA database*

Description

Attempts to save taxonomic and sequence information of a taxmap object in the SILVA FASTA format. If the taxmap object was created using [parse_silva_fasta](#), then it should be able to replicate the format exactly with the default settings.

Usage

```
write_silva_fasta(obj, file,
  tax_names = obj$get_data("taxon_names")[[1]],
  other_names = obj$get_data("other_name")[[1]],
  ids = obj$get_data("ncbi_id")[[1]],
  start = obj$get_data("start_pos")[[1]],
  end = obj$get_data("end_pos")[[1]],
  sequences = obj$get_data("silva_seq")[[1]])
```

Arguments

obj	A taxmap object
file	(character of length 1) The file path to save the sequence fasta file. This is optional.
tax_names	(character named by taxon ids) The names of taxa
other_names	(character named by taxon ids) Alternate names of taxa. Will be added after the primary name.
ids	(character named by taxon ids) Sequence ids
start	(character) The start position of the sequence.
end	(character) The end position of the sequence.
sequences	(character named by taxon ids) Sequences

Details

The output file has a format like:

```
>GCVF01000431.1.2369 Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospiril...
CGUGCACGGUGGAUGCCUUGGCAGCCAGAGGCGAUGAAGGACGUUGUAGCCUGCGAUAAGCUCCGGUUAGGUGGCAAACA
ACCGUUUGACCCGGAGAUCCGAAUGGGCAACCCACCCGUUGUAAGGCGGGUAUCACCGACUGAAUCCAUAGGUCGGU
...
```

See Also

Other writers: [make_dada2_asv_table](#), [make_dada2_tax_table](#), [write_greenegenes](#), [write_mothur_taxonomy](#), [write_rdp](#), [write_unite_general](#)

write_unite_general *Write an imitation of the UNITE general FASTA database*

Description

Attempts to save taxonomic and sequence information of a taxmap object in the UNITE general FASTA format. If the taxmap object was created using [parse_unite_general](#), then it should be able to replicate the format exactly with the default settings.

Usage

```
write_unite_general(obj, file,
  tax_names = obj$get_data("taxon_names")[[1]],
  ranks = obj$get_data("unite_rank")[[1]],
  sequences = obj$get_data("unite_seq")[[1]],
  seq_name = obj$get_data("organism")[[1]],
  ids = obj$get_data("unite_id")[[1]],
  gb_acc = obj$get_data("acc_num")[[1]],
  type = obj$get_data("unite_type")[[1]])
```

Arguments

obj	A taxmap object
file	(character of length 1) The file path to save the sequence fasta file. This is optional.
tax_names	(character named by taxon ids) The names of taxa
ranks	(character named by taxon ids) The ranks of taxa
sequences	(character named by taxon ids) Sequences
seq_name	(character named by taxon ids) Name of sequences. Usually a taxon name.
ids	(character named by taxon ids) UNITE sequence ids
gb_acc	(character named by taxon ids) Genbank accession numbers
type	(character named by taxon ids) What type of sequence it is. Usually "rep" or "ref".

Details

The output file has a format like:

```
>Glomeromycota_sp|KJ484724|SH523877.07FU|reps|k__Fungi;p__Glomeromycota;c__unid...
ATAATTTGCCGAACCTAGCGTTAGCGCGAGGTTCTGCGATCAACACTTATATTTAAAACCCAACCTTAAATTTTGTAT...
...
```

See Also

Other writers: [make_dada2_asv_table](#), [make_dada2_tax_table](#), [write_greenes](#), [write_mothur_taxonomy](#), [write_rdp](#), [write_silva_fasta](#)

zero_low_counts	<i>Replace low counts with zero</i>
-----------------	-------------------------------------

Description

For a given table in a [taxmap](#) object, convert all counts below a minimum number to zero. This is useful for effectively removing "singletons", "doubletons", or other low abundance counts.

Usage

```
zero_low_counts(obj, data, min_count = 2, use_total = FALSE,
  cols = NULL, other_cols = FALSE, out_names = NULL,
  dataset = NULL)
```

Arguments

obj	A taxmap object
data	The name of a table in obj\$data.
min_count	The minimum number of counts needed for a count to remain unchanged. Any count less than this will be converted to a zero. For example, min_count = 2 would remove singletons.
use_total	If TRUE, the min_count applies to the total count for each row (e.g. OTU counts for all samples), rather than each cell in the table. For example use_total = TRUE, min_count = 10 would convert all counts of any row to zero if the total for all counts in that row was less than 10.
cols	The columns in data to use. By default, all numeric columns are used. Takes one of the following inputs: TRUE/FALSE: All/No columns will be used. Character vector: The names of columns to use Numeric vector: The indexes of columns to use Vector of TRUE/FALSE of length equal to the number of columns: Use the columns corresponding to TRUE values.
other_cols	Preserve in the output non-target columns present in the input data. New columns will always be on the end. The "taxon_id" column will be preserved in the front. Takes one of the following inputs: NULL: No columns will be added back, not even the taxon id column. TRUE/FALSE: All/None of the non-target columns will be preserved. Character vector: The names of columns to preserve Numeric vector: The indexes of columns to preserve Vector of TRUE/FALSE of length equal to the number of columns: Preserve the columns corresponding to TRUE values.
out_names	The names of count columns in the output. Must be the same length as cols (or unique(groups), if groups is used).
dataset	DEPRECATED. use "data" instead.

Value

A tibble

See Also

Other calculations: [calc_group_mean](#), [calc_group_median](#), [calc_group_rsd](#), [calc_group_stat](#), [calc_n_samples](#), [calc_obs_props](#), [calc_prop_samples](#), [calc_taxon_abund](#), [compare_groups](#), [counts_to_presence](#), [rarefy_obs](#)

Examples

```
## Not run:
# Parse data for examples
x = parse_tax_data(hmp_otus, class_cols = "lineage", class_sep = ";",
```

```
class_key = c(tax_rank = "info", tax_name = "taxon_name"),
class_regex = "^(.+)_(.+) $"

# Default use
zero_low_counts(x, "tax_data")

# Use only a subset of columns
zero_low_counts(x, "tax_data", cols = c("700035949", "700097855", "700100489"))
zero_low_counts(x, "tax_data", cols = 4:6)
zero_low_counts(x, "tax_data", cols = startsWith(colnames(x$data$tax_data), "70001"))

# Including all other columns in output
zero_low_counts(x, "tax_data", other_cols = TRUE)

# Including specific columns in output
zero_low_counts(x, "tax_data", cols = c("700035949", "700097855", "700100489"),
  other_cols = 2:3)

# Rename output columns
zero_low_counts(x, "tax_data", cols = c("700035949", "700097855", "700100489"),
  out_names = c("a", "b", "c"))

## End(Not run)
```

Index

*Topic **data**

- hmp_otus, [32](#)
 - hmp_samples, [33](#)
- ape, [3](#)
- as_phyloseq, [3](#)
- as_tree, [28](#)
-
- calc_group_mean, [4](#), [7](#), [8](#), [10](#), [12](#), [14](#), [16](#), [18](#),
[21](#), [61](#), [69](#)
- calc_group_median, [5](#), [6](#), [8](#), [10](#), [12](#), [14](#), [16](#),
[18](#), [21](#), [61](#), [69](#)
- calc_group_rsd, [5](#), [7](#), [7](#), [10](#), [12](#), [14](#), [16](#), [18](#),
[21](#), [61](#), [69](#)
- calc_group_stat, [5](#), [7](#), [8](#), [9](#), [12](#), [14](#), [16](#), [18](#),
[21](#), [61](#), [69](#)
- calc_n_samples, [5](#), [7](#), [8](#), [10](#), [11](#), [14](#), [16](#), [18](#),
[21](#), [38](#), [61](#), [69](#)
- calc_obs_props, [5](#), [7](#), [8](#), [10](#), [12](#), [13](#), [16](#), [18](#),
[21](#), [38](#), [61](#), [69](#)
- calc_prop_samples, [5](#), [7](#), [8](#), [10](#), [12](#), [14](#), [15](#),
[18](#), [21](#), [61](#), [69](#)
- calc_taxon_abund, [5](#), [7](#), [8](#), [10](#), [12](#), [14](#), [16](#), [18](#),
[21](#), [37](#), [61](#), [69](#)
- comp, [19](#), [63](#)
- compare_groups, [5](#), [7](#), [8](#), [10](#), [12](#), [14](#), [16](#), [17](#),
[21](#), [31](#), [38](#), [61](#), [69](#)
- complement, [19](#), [62](#), [63](#)
- counts_to_presence, [5](#), [7](#), [8](#), [10](#), [12](#), [14](#), [16](#),
[18](#), [20](#), [61](#), [69](#)
-
- diverging_palette, [21](#)
-
- filter_ambiguous_taxa, [22](#), [38](#)
- filter_taxa, [22](#)
-
- ggsave, [27](#), [31](#)
- graph, [35](#)
-
- heat_tree, [23](#), [31](#), [37](#)
- heat_tree_matrix, [17](#), [31](#), [37](#)
-
- hmp_otus, [32](#), [33](#)
- hmp_samples, [32](#), [33](#), [33](#)
-
- igraph, [24](#), [28](#)
- is_ambiguous, [34](#)
-
- layout_functions, [35](#)
-
- make_dada2_asv_table, [36](#), [37](#), [64](#)–[68](#)
- make_dada2_tax_table, [36](#), [36](#), [64](#)–[68](#)
- max, [10](#)
- mean, [10](#)
- metacoder, [37](#)
- metacoder-package (metacoder), [37](#)
-
- ncbi_taxon_sample, [38](#), [39](#)
- nicely, [28](#)
-
- parse_dada2, [36](#), [40](#), [42](#)–[52](#)
- parse_edge_list, [41](#)–[52](#)
- parse_greenegenes, [38](#), [41](#), [41](#), [43](#)–[52](#), [63](#)
- parse_mothur_tax_summary, [38](#), [41](#)–[43](#), [43](#),
[45](#)–[52](#)
- parse_mothur_taxonomy, [38](#), [41](#), [42](#), [42](#),
[44](#)–[52](#), [64](#)
- parse_newick, [38](#), [41](#)–[44](#), [45](#), [46](#)–[52](#)
- parse_phylo, [38](#), [41](#)–[45](#), [45](#), [47](#)–[52](#)
- parse_phyloseq, [38](#), [41](#)–[46](#), [46](#), [48](#)–[52](#)
- parse_qiime_biom, [38](#), [41](#)–[47](#), [47](#), [49](#)–[52](#)
- parse_rdp, [38](#), [41](#)–[48](#), [48](#), [50](#)–[52](#), [65](#)
- parse_silva_fasta, [38](#), [41](#)–[49](#), [49](#), [51](#), [52](#), [66](#)
- parse_tax_data, [46](#), [47](#)
- parse_ubiome, [41](#)–[50](#), [50](#), [52](#)
- parse_unite_general, [38](#), [41](#)–[51](#), [51](#), [67](#)
- phylo, [3](#)
- primersearch, [37](#), [52](#)
- primersearch_raw, [53](#), [55](#)
-
- qualitative_palette, [58](#)
- quantative_palette, [59](#)

rarefy_obs, [5](#), [7](#), [8](#), [10](#), [12](#), [14](#), [16](#), [18](#), [21](#), [38](#),
[60](#), [69](#)
read.FASTA, [48](#), [49](#), [51](#), [56](#), [61](#)
read.fasta, [48](#), [50](#), [51](#), [56](#), [61](#)
read_fasta, [48](#), [49](#), [51](#), [56](#), [61](#)
rev, [62](#)
rev_comp, [19](#), [62](#), [63](#)
reverse, [19](#), [62](#), [63](#)
rrarefy, [60](#)

taxmap, [4](#), [6–9](#), [11](#), [13](#), [15](#), [17](#), [20](#), [22–24](#), [31](#),
[34](#), [41–46](#), [49–53](#), [60](#), [68](#), [69](#)
taxmap(), [22](#)

with_dh, [28](#)
with_dr1, [28](#)
with_fr, [28](#)
with_gem, [28](#)
with_graphopt, [28](#)
with_kk, [28](#)
with_lgl, [28](#)
with_mds, [28](#)
write_greengenes, [36–38](#), [63](#), [65–68](#)
write_mothur_taxonomy, [36–38](#), [64](#), [64](#),
[66–68](#)
write_rdp, [36–38](#), [64](#), [65](#), [65](#), [67](#), [68](#)
write_silva_fasta, [36–38](#), [64–66](#), [66](#), [68](#)
write_unite_general, [36–38](#), [64–67](#), [67](#)

zero_low_counts, [5](#), [7](#), [8](#), [10](#), [12](#), [14](#), [16](#), [18](#),
[21](#), [38](#), [61](#), [68](#)