

Package ‘microbial’

July 22, 2025

Type Package

Title Do 16s Data Analysis and Generate Figures

Version 0.0.21

Description Provides functions to enhance the available statistical analysis procedures in R by providing simple functions to analysis and visualize the 16S rRNA data. Here we present a tutorial with minimum working examples to demonstrate usage and dependencies.

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Depends R (>= 3.5.0)

Imports dplyr, plyr, magrittr, broom, phyloseq, vegan, rlang, ggplot2, ggpubr, DESeq2, SummarizedExperiment, S4Vectors, rstatix, tidyr, phangorn, randomForest, edgeR

Encoding UTF-8

LazyData true

Suggests markdown, dada2, rmarkdown, knitr, tools, Biostrings, DECIPHER, MASS, testthat

VignetteBuilder knitr

biocViews Software, GraphAndNetwork

RoxygenNote 7.2.3

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-05-15 18:20:02 UTC

Contents

.checkfile	2
.getstar	3

.lda.fun	3
betadiv	4
betatest	5
biomarker	6
buildTree	7
data-physeq	7
difftest	8
distcolor	9
do_aov	9
do_ttest	10
do_wilcox	11
glmr	11
ldamarker	12
lightcolor	13
normalize	13
otu_table	14
phy_tree	14
plotalpha	15
plotbar	16
plotbeta	17
plotdiff	18
plotLDA	19
plotmarker	20
plotquality	21
prefilter	22
preRef	23
processSeq	23
psmelt	25
richness	25
sample_data	26
subset_samples	26
subset_taxa	27
tax_table	27

Index 28

.checkfile	<i>check file format</i>
------------	--------------------------

Description

check file format

Usage

.checkfile(file)

`.getstar`

3

Arguments

<code>file</code>	<code>filename</code>
-------------------	-----------------------

<code>.getstar</code>	<i>replace p value with star</i>
-----------------------	----------------------------------

Description

replace p value with star

Usage

`.getstar(x)`

Arguments

<code>x</code>	a (non-empty) numeric data values
----------------	-----------------------------------

<code>.lda.fun</code>	<i>LEfse function</i>
-----------------------	-----------------------

Description

LEfse function

Usage

`.lda.fun(df)`

Arguments

<code>df</code>	a dataframe with groups and bacteria abundance
-----------------	--

betadiv	<i>calcaute beta diversity</i>
---------	--------------------------------

Description

calcaute beta diversity

Usage

```
betadiv(physeq, distance = "bray", method = "PCoA")
```

Arguments

physeq	A phyloseq object containing merged information of abundance, taxonomic assignment, sample data including the measured variables and categorical information of the samples, and / or phylogenetic tree if available.
distance	A string character specifying dissimilarity index to be used in calculating pairwise distances (Default index is "bray"). "unifrac", "wunifrac", "manhattan", "euclidean", "canberra", "bray", "kulczynski", "jaccard", "gower", "altGower", "morisita", "horn", "mountford", "raup", "binomial", "chao", "cao" or "mahalanobis".
method	A character string specifying ordination method. All methods available to the ordinate function of phyloseq are acceptable here as well.

Value

list with beta diversity data.frame and PCs

Author(s)

Kai Guo

Examples

```
{
  data("Physeq")
  phy<-normalize(physeq)
  res <- betadiv(phy)
}
```

betatest	<i>PERMANOVA test for phyloseq</i>
----------	------------------------------------

Description

PERMANOVA test for phyloseq

Usage

```
betatest(physeq, group, distance = "bray")
```

Arguments

physeq	A phyloseq object containing merged information of abundance, taxonomic assignment, sample data including the measured variables and categorical information of the samples, and / or phylogenetic tree if available.
group	(Required). Character string specifying name of a categorical variable that is preferred for grouping the information. information.
distance	A string character specifying dissimilarity index to be used in calculating pairwise distances (Default index is "bray"). "unifrac", "wunifrac", "manhattan", "euclidean", "canberra", "bray", "kulczynski", "jaccard", "gower", "altGower", "morisita", "horn", "mountford", "raup", "binomial", "chao", "cao" or "mahalanobis".

Value

PERMANOVA test result

Author(s)

Kai Guo

Examples

```
{
  data("Physeq")
  phy<-normalize(physeq)
  beta <-betatest(phy,group="SampleType")
}
```

biomarker

Identify biomarker by using randomForest method

Description

Identify biomarker by using randomForest method

Usage

```
biomarker(
  physeq,
  group,
  ntree = 500,
  pvalue = 0.05,
  normalize = TRUE,
  method = "relative"
)
```

Arguments

physeq	A phyloseq object containing merged information of abundance, taxonomic assignment, sample data including the measured variables and categorical information of the samples, and / or phylogenetic tree if available.
group	group. A character string specifying the name of a categorical variable containing grouping information.
ntree	Number of trees to grow. This should not be set to too small a number, to ensure that every input row gets predicted at least a few times.
pvalue	pvalue threshold for significant results from <code>kruskal.test</code>
normalize	to normalize the data before analysis(TRUE/FALSE)
method	A list of character strings specifying method to be used to normalize the phyloseq object Available methods are: "relative", "TMM", "vst", "log2".

Value

data frame with significant biomarker

Author(s)

Kai Guo

Examples

```
data("Physeq")
res <- biomarker(physeq, group="group")
```

buildTree	<i>contruction of plylogenetic tree (extreme slow)</i>
-----------	--

Description

contruction of plylogenetic tree (extreme slow)

Usage

buildTree(seqs)

Arguments

seqs DNA sequences

Value

tree object

Author(s)

Kai Guo

data-physeq	<i>The physeq data was modified from the (Data) Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample (2011)</i>
-------------	---

Description

Published in PNAS in early 2011. This work compared the microbial communities from 25 environmental samples and three known “mock communities” – a total of 9 sample types – at a depth averaging 3.1 million reads per sample. Authors were able to reproduce diversity patterns seen in many other published studies, while also invesitigating technical issues/bias by applying the same techniques to simulated microbial communities of known

References

Caporaso, J. G., et al. (2011). Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. PNAS, 108, 4516-4522. PMCID: PMC3063599

Examples

data(Physeq)

difftest*Calculate differential bacteria with DESeq2*

Description

Calculate differential bacteria with DESeq2

Usage

```
difftest(  
  physeq,  
  group,  
  ref = NULL,  
  pvalue = 0.05,  
  padj = NULL,  
  log2FC = 0,  
  gm_mean = TRUE,  
  fitType = "local",  
  quiet = FALSE  
)
```

Arguments

physeq	A phyloseq object containing merged information of abundance, taxonomic assignment, sample data including the measured variables and categorical information of the samples, and / or phylogenetic tree if available.
group	group (DESeq2). A character string specifying the name of a categorical variable containing grouping information.
ref	reference group
pvalue	pvalue threshold for significant results
padj	adjust p value threshold for significant results
log2FC	log2 Fold Change threshold
gm_mean	TRUE/FALSE calculate geometric means prior to estimate size factors
fitType	either "parametric", "local", or "mean" for the type of fitting of dispersions to the mean intensity.
quiet	whether to print messages at each step

Value

datafame with differential test with DESeq2

Author(s)

Kai Guo

Examples

```
data("Physeq")
res <- difftest(physeq,group="group")
```

distcolor

distinguish colors for making figures

Description

distinguish colors for making figures

Usage

```
distcolor
```

Format

An object of class character of length 41.

Author(s)

Kai Guo

do_aov

do anova test and return results as data.frame

Description

do anova test and return results as data.frame

Usage

```
do_aov(x, group, ...)
```

Arguments

x	data.frame with sample id as the column name, genes or otu as rownames
group	group factor used for comparison
...	parameters to anova_test

Author(s)

Kai Guo

Examples

```
{
  data("ToothGrowth")
  do_aov(ToothGrowth, group="supp")
}
```

do_ttest

do t.test

Description

do t.test

Usage

```
do_ttest(x, group, ref = NULL, ...)
```

Arguments

x	data.frame with sample id as the column name, genes or otu as rownames
group	group factor used for comparison
ref	reference group
...	parameters to t_test

Author(s)

Kai Guo

Examples

```
{
  data("mtcars")
  do_ttest(mtcars, group="vs")
  do_ttest(mtcars, group="cyl", ref="4")
}
```

do_wilcox

*do wilcox test***Description**

do wilcox test

Usage

do_wilcox(x, group, ref = NULL, ...)

Arguments

x	data.frame with sample id as the column name, genes or otu as rownames
group	group factor used for comparison
ref	reference group
...	parameters to wilcox_test

Author(s)

Kai Guo

Examples

```
{
  data("mtcars")
  do_wilcox(mtcars,group="vs")
  do_wilcox(mtcars,group="cyl",ref="4")
}
```

glmr

*Do the generalized linear model regression***Description**

Do the generalized linear model regression

Usage

```
glmr(
  physeq,
  group,
  factors = NULL,
  ref = NULL,
  family = binomial(link = "logit")
)
```

Arguments

physeq	phyloseq object
group	the group factor to regression
factors	a vector to indicate adjusted factors
ref	the reference group
family	binomial() or gaussian()

Author(s)

Kai Guo

Examples

```
data("Physeq")
phy<-normalize(physeq)
fit <-glmr(phy,group="SampleType")
```

ldamarker

*Identify biomarker by using LEfSe method***Description**

Identify biomarker by using LEfSe method

Usage

```
ldamarker(physeq, group, pvalue = 0.05, normalize = TRUE, method = "relative")
```

Arguments

physeq	A phyloseq object containing merged information of abundance, taxonomic assignment, sample data including the measured variables and categorical information of the samples, and / or phylogenetic tree if available.
group	group. A character string specifying the name of a categorical variable containing grouping information.
pvalue	pvalue threshold for significant results from kruskal.test
normalize	to normalize the data before analysis(TRUE/FALSE)
method	A list of character strings specifying method to be used to normalize the phyloseq object Available methods are: "relative","TMM","vst","log2".

Author(s)

Kai Guo

Examples

```
data("Physeq")
res <- ldamarker(physeq,group="group")
```

lightcolor	<i>light colors for making figures</i>
------------	--

Description

light colors for making figures

Usage

```
lightcolor
```

Format

An object of class character of length 56.

Author(s)

Kai Guo

normalize	<i>Normalize the phyloseq object with different methods</i>
-----------	---

Description

Normalize the phyloseq object with different methods

Usage

```
normalize(physeq, group, method = "relative", table = FALSE)
```

Arguments

physeq	A phyloseq object containing merged information of abundance, taxonomic assignment, sample data including the measured variables and categorical information of the samples, and / or phylogenetic tree if available.
group	group (DESeq2). A character string specifying the name of a categorical variable containing grouping information.
method	A list of character strings specifying method to be used to normalize the phyloseq object Available methods are: "relative", "TMM", "vst", "log2".
table	return a data.frame or not

Value

phyloseq object with normalized data

Author(s)

Kai Guo

Examples

```
{
  data("Physeq")
  phy<-normalize(physeq)
}
```

otu_table	<i>extract otu table</i>
-----------	--------------------------

Description

extract otu table

Usage

```
otu_table(physeq, ...)
```

Arguments

physeq	(Required). An integer matrix, otu_table-class, or phyloseq-class.
...	parameters for the otu_table function in phyloseq package

phy_tree	<i>Retrieve phylogenetic tree (phylo-class) from object.</i>
----------	--

Description

Retrieve phylogenetic tree (phylo-class) from object.

Usage

```
phy_tree(physeq, ...)
```

Arguments

physeq	(Required). An instance of phyloseq-class that contains a phylogenetic tree. If physeq is a phylogenetic tree (a component data class), then it is returned as-is.
...	parameters for the phy_tree function in phyloseq package

plotalpha

*plot alpha diversity***Description**

plot alpha diversity

Usage

```
plotalpha(
  physeq,
  group,
  method = c("Observed", "Simpson", "Shannon"),
  color = NULL,
  geom = "boxplot",
  pvalue = 0.05,
  padj = NULL,
  sig.only = TRUE,
  wilcox = FALSE,
  show.number = FALSE
)
```

Arguments

physeq	A phyloseq object containing merged information of abundance, taxonomic assignment, sample data including the measured variables and categorical information of the samples, and / or phylogenetic tree if available.
group	group (Required). A character string specifying the name of a categorical variable containing grouping information.
method	A list of character strings specifying method to be used to calculate for alpha diversity in the data. Available methods are: "Observed", "Chao1", "ACE", "Richness", "Fisher", "Simpson", "Shannon", "Evenness", "InvSimpson".
color	A vector of character use specifying the color
geom	different geom to display("boxplot", "violin", "dotplot")
pvalue	pvalue threshold for significant dispersion results
padj	adjust p value threshold for significant dispersion results
sig.only	display the significant comparsion only(TRUE/ FALSE)
wilcox	use wilcoxon test or not
show.number	to show the pvalue instead of significant symbol(TRUE/FALSE)

Value

Returns a ggplot object. This can further be manipulated as preferred by user.

Author(s)

Kai Guo

Examples

```
{
  data("Physeq")
  plotalpha(physeq,group="SampleType")
}
```

plotbar	<i>plot bar for relative abundance for bacteria</i>
---------	---

Description

plot bar for relative abundance for bacteria

Usage

```
plotbar(
  physeq,
  level = "Phylum",
  color = NULL,
  group = NULL,
  top = 5,
  return = FALSE,
  fontsize.x = 5,
  fontsize.y = 12
)
```

Arguments

physeq	A phyloseq object containing merged information of abundance, taxonomic assignment, sample data including the measured variables and categorical information of the samples, and / or phylogenetic tree if available.
level	the level to plot
color	A vector of character use specifying the color
group	group (Optional). A character string specifying the name of a categorical variable containing grouping information.
top	the number of most abundance bacteria to display
return	return the data with the relative abundance
fontsize.x	the size of x axis label
fontsize.y	the size of y axis label

Value

Returns a ggplot object. This can further be manipulated as preferred by user.

Author(s)

Kai Guo

Examples

```
data("Physeq")
phy<-normalize(physeq)
plotbar(phy,level="Phylum")
```

plotbeta

plot beta diversity

Description

plot beta diversity

Usage

```
plotbeta(
  physeq,
  group,
  shape = NULL,
  distance = "bray",
  method = "PCoA",
  color = NULL,
  size = 3,
  ellipse = FALSE
)
```

Arguments

physeq	A phyloseq object containing merged information of abundance, taxonomic assignment, sample data including the measured variables and categorical information of the samples, and / or phylogenetic tree if available.
group	(Required). Character string specifying name of a categorical variable that is preferred for grouping the information. information.
shape	shape(Optional) Character string specifying shape of a categorical variable
distance	A string character specifying dissimilarity index to be used in calculating pairwise distances (Default index is "bray"). "unifrac","wunifrac","manhattan", "euclidean", "canberra", "bray", "kulczynski", "jaccard", "gower", "altGower", "morisita", "horn", "mountford", "raup" , "binomial", "chao", "cao" or "mahalanobis".

method	A character string specifying ordination method. All methods available to the ordinate function of phyloseq are acceptable here as well.
color	user defined color for group
size	the point size
ellipse	draw ellipse or not

Value

ggplot2 object

Author(s)

Kai Guo

Examples

```
{
  data("Physeq")
  phy<-normalize(physeq)
  plotbeta(phy,group="SampleType")
}
```

plotdiff	<i>plot differential results</i>
----------	----------------------------------

Description

plot differential results

Usage

```
plotdiff(
  res,
  level = "Genus",
  color = NULL,
  pvalue = 0.05,
  padj = NULL,
  log2FC = 0,
  size = 3,
  fontsize.x = 5,
  fontsize.y = 10,
  horiz = TRUE
)
```

Arguments

res	differential test results from diff_test
level	the level to plot
color	A vector of character use specifying the color
pvalue	pvalue threshold for significant results
padj	adjust p value threshold for significant results
log2FC	log2 Fold Change threshold
size	size for the point
fontsize.x	the size of x axis label
fontsize.y	the size of y axis label
horiz	horizontal or not (TRUE/FALSE)

Value

ggplot object

Author(s)

Kai Guo

Examples

```
data("Physeq")
res <- difftest(physeq,group="group")
plotdiff(res,level="Genus",padj=0.001)
```

plotLDA

plot LEfSe results from ldamarker function

Description

plot LEfSe results from ldamarker function

Usage

```
plotLDA(
  x,
  group,
  lda = 2,
  pvalue = 0.05,
  padj = NULL,
  color = NULL,
  fontsize.x = 4,
  fontsize.y = 5
)
```

Arguments

x	LEfse results from ldamarker
group	a vector include two character to show the group comparsion
lda	LDA threshold for significant biomarker
pvalue	pvalue threshold for significant results
padj	adjust p value threshold for significant results
color	A vector of character use specifying the color
fontsize.x	the size of x axis label
fontsize.y	the size of y axis label

Value

ggplot2 object

Author(s)

Kai Guo

Examples

```
data("Physeq")
res <- ldamarker(physeq,group="group")
plotLDA(res,group=c("A","B"),lda=5,pvalue=0.05)
```

plotmarker

plot the biomarker from the biomarker function with randomForest

Description

plot the biomarker from the biomarker function with randomForest

Usage

```
plotmarker(
  x,
  level = "Genus",
  top = 30,
  rotate = FALSE,
  dot.size = 8,
  label.color = "black",
  label.size = 6
)
```

Arguments

x	biomarker results from randomForest
level	the bacteria level to display
top	the number of important biomarker to draw
rotate	TRUE/FALSE
dot.size	size for the dot
label.color	label color
label.size	label size

Value

ggplot2 object

Author(s)

Kai Guo

Examples

```
data("Physeq")
res <- biomarker(physeq,group="group")
plotmarker(res,level="Genus")
```

plotquality	<i>plot the quality for the fastq file</i>
-------------	--

Description

plot the quality for the fastq file

Usage

```
plotquality(file, n = 5e+05, aggregate = FALSE)
```

Arguments

file	(Required). character. File path(s) to fastq or fastq.gz file(s).
n	(Optional). Default 500,000. The number of records to sample from the fastq file.
aggregate	(Optional). Default FALSE. If TRUE, compute an aggregate quality profile for all fastq files provided.

Value

figure

Examples

```
plotquality(system.file("extdata", "sam1F.fastq.gz", package="dada2"))
```

prefilter

filter the phyloseq

Description

filter the phyloseq

Usage

```
prefilter(physeq, min = 10, perc = 0.05)
```

Arguments

physeq	A phyloseq object containing merged information of abundance, taxonomic assignment, sample data including the measured variables and categorical information of the samples, and / or phylogenetic tree if available.
min	Numeric, the threshold for minimal Phylum shown in samples
perc	Numeric, input the percentage of samples for which to filter low counts.

Value

filter phyloseq object

Author(s)

Kai Guo

Examples

```
data("Physeq")  
physeqs<-prefilter(physeq)
```

preRef	<i>Download the reference database</i>
--------	--

Description

Download the reference database

Usage

```
preRef(ref_db, path = ".")
```

Arguments

ref_db	the reference database
path	path for the database

Value

the path of the database

Author(s)

Kai Guo

Examples

```
preRef(ref_db="silva",path=tempdir())
```

processSeq	<i>Perform dada2 analysis</i>
------------	-------------------------------

Description

Perform dada2 analysis

Usage

```
processSeq(  
  path = ".",  
  truncLen = c(0, 0),  
  trimLeft = 0,  
  trimRight = 0,  
  minLen = 20,  
  maxLen = Inf,  
  sample_info = NULL,
```

```

train_data = "silva_nr99_v138_train_set.fa.gz",
train_species = "silva_species_assignment_v138.fa.gz",
outpath = NULL,
saveobj = FALSE,
buildtree = FALSE,
verbose = TRUE
)

```

Arguments

path	working dir for the input reads
truncLen	(Optional). Default 0 (no truncation). Truncate reads after truncLen bases. Reads shorter than this are discarded.
trimLeft	(Optional). The number of nucleotides to remove from the start of each read.
trimRight	(Optional). Default 0. The number of nucleotides to remove from the end of each read. If both truncLen and trimRight are provided, truncation will be performed after trimRight is enforced.
minLen	(Optional). Default 20. Remove reads with length less than minLen. minLen is enforced after trimming and truncation.
maxLen	(Optional). Default Inf (no maximum). Remove reads with length greater than maxLen. maxLen is enforced before trimming and truncation.
sample_info	(Optional).sample information for the sequence
train_data	(Required).training database
train_species	(Required). species database
outpath	(Optional).the path for the filtered reads and th out table
saveobj	(Optional).Default FALSE. save the phyloseq object output.
buildtree	build phylogenetic tree or not(default: FALSE)
verbose	(Optional). Default TRUE. Print verbose text output.

Value

list include count table, summary table, taxonomy information and phyloseq object

Author(s)

Kai Guo

psmelt	<i>Melt phyloseq data object into large data.frame</i>
--------	--

Description

Melt phyloseq data object into large data.frame

Usage

```
psmelt(physeq, ...)
```

Arguments

physeq	A sample_data-class, or a phyloseq-class object with a sample_data. If the sample_data slot is missing in physeq, then physeq will be returned as-is, and a warning will be printed to screen.
...	parameters for the subset_samples function in phyloseq package

richness	<i>calculat the richness for the phyloseq object</i>
----------	--

Description

calculat the richness for the phyloseq object

Usage

```
richness(physeq, method = c("Observed", "Simpson", "Shannon"))
```

Arguments

physeq	A phyloseq object containing merged information of abundance, taxonomic assignment, sample data including the measured variables and categorical information of the samples, and / or phylogenetic tree if available.
method	A list of character strings specifying method to be used to calculate for alpha diversity in the data. Available methods are: "Observed", "Chao1", "ACE", "Richness", "Fisher", "Simpson", "Shannon", "Evenness", "InvSimpson".

Value

data.frame of alpha diversity

Author(s)

Kai Guo

Examples

```
{
  data("Physeq")
  rich <-richness(physeq,method=c("Simpson", "Shannon"))
}
```

sample_data	<i>extract sample information</i>
-------------	-----------------------------------

Description

extract sample information

Usage

```
sample_data(physeq, ...)
```

Arguments

- physeq (Required). A data.frame-class, or a phyloseq-class object.
- ... parameters for the sample_data function in phyloseq package

subset_samples	<i>Subset the phyloseq based on sample</i>
----------------	--

Description

Subset the phyloseq based on sample

Usage

```
subset_samples(physeq, ...)
```

Arguments

- physeq A sample_data-class, or a phyloseq-class object with a sample_data. If the sample_data slot is missing in physeq, then physeq will be returned as-is, and a warning will be printed to screen.
- ... parameters for the subset_samples function in phyloseq package

subset_taxa	<i>Subset species by taxonomic expression</i>
-------------	---

Description

Subset species by taxonomic expression

Usage

```
subset_taxa(physeq, ...)
```

Arguments

physeq	A sample_data-class, or a phyloseq-class object with a sample_data. If the sample_data slot is missing in physeq, then physeq will be returned as-is, and a warning will be printed to screen.
...	parameters for the subset_taxa function in phyloseq package

tax_table	<i>extract taxonomy table</i>
-----------	-------------------------------

Description

extract taxonomy table

Usage

```
tax_table(physeq, ...)
```

Arguments

physeq	An object among the set of classes defined by the phyloseq package that contain taxonomyTable.
...	parameters for the tax_table function in phyloseq package

Index

- * **datasets**
 - distcolor, [9](#)
 - lightcolor, [13](#)
- * **data**
 - data-physeq, [7](#)
 - .checkfile, [2](#)
 - .getstar, [3](#)
 - .lda.fun, [3](#)
- betadiv, [4](#)
- betatest, [5](#)
- biomarker, [6](#)
- buildTree, [7](#)
- data-physeq, [7](#)
- difftest, [8](#)
- distcolor, [9](#)
- do_aov, [9](#)
- do_ttest, [10](#)
- do_wilcox, [11](#)
- glmr, [11](#)
- ldamarker, [12](#)
- lightcolor, [13](#)
- normalize, [13](#)
- otu_table, [14](#)
- phy_tree, [14](#)
- physeq (data-physeq), [7](#)
- plotalpha, [15](#)
- plotbar, [16](#)
- plotbeta, [17](#)
- plotdiff, [18](#)
- plotLDA, [19](#)
- plotmarker, [20](#)
- plotquality, [21](#)
- prefilter, [22](#)
- preRef, [23](#)
- processSeq, [23](#)
- psmelt, [25](#)
- richness, [25](#)
- sample_data, [26](#)
- subset_samples, [26](#)
- subset_taxa, [27](#)
- tax_table, [27](#)