

Package: schtools (via r-universe)

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Title Schloss Lab Tools for Reproducible Microbiome Research

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Description A collection of useful functions and example code created and used by the Schloss Lab for reproducible microbiome research. Perform common tasks like read files created by mothur <<https://mothur.org/>>, tidy up your microbiome data, and format R Markdown documents for publication. See the website <<http://www.schlosslab.org/schtools/>> for more information, documentation, and examples.

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URL <http://www.schlosslab.org/schtools/>,
<https://github.com/SchlossLab/schtools>

BugReports <https://github.com/SchlossLab/schtools/issues>

Imports dplyr, formatR, glue, rlang, stringr, tidyr

Suggests covr, cowplot, ggplot2, ggtext, here, hexSticker, hrbthemes, knitr, purrr, readr, rmarkdown, showtext, testthat

VignetteBuilder knitr

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Repository <https://schlosslab.r-universe.dev>

RemoteUrl <https://github.com/schlosslab/schtools>

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calc_relabun	<i>Calculate OTU relative abundances from a shared file</i>
--------------	---

Description

Calculate OTU relative abundances from a shared file

Usage

```
calc_relabun(abs_abun_dat)
```

Arguments

abs_abun_dat a data frame from reading in a **shared file**. Should contain a Group column for sample names, Otu columns for absolute counts of each OTU, and rows as each sample.

Value

a new data frame with OTU relative abundances in long format.

Author(s)

Kelly Sovacool <sovacool@umich.edu>

Examples

```
shared_dat <- readr::read_tsv(system.file("extdata", "test.shared",  
  package = "schtools"  
))  
shared_dat %>% calc_relabun()
```

close_enough	<i>Check whether two numeric vectors are close enough</i>
--------------	---

Description

This is like `dplyr::near()` except with much less precision.

Usage

```
close_enough(x, y, tol = 10^-3)
```

Arguments

x	a numeric vector
y	another numeric vector
tol	tolerance (default: 10^{-3} .)

Value

TRUE if all numbers are near enough within the tolerance, otherwise FALSE

Author(s)

Kelly Sovacool <sovacool@umich.edu>

Examples

```
close_enough(0.0004, 0)  
close_enough(0.8887, 0.8884)  
close_enough(1, 2)
```

get_wildcards_tbl	<i>Get the Snakemake wildcards as a tibble</i>
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Description

Get the Snakemake wildcards as a tibble

Usage

```
get_wildcards_tbl()
```

Value

a tibble of wildcards, with columns as names and rows as values

Author(s)

Kelly Sovacool <sovacool@umich.edu>

inline_hook	<i>Inline hook for knitr to paste human-readable numbers and nice lists.</i>
-------------	--

Description

Inline hook for knitr to paste human-readable numbers and nice lists.

Usage

```
inline_hook(x)
```

Arguments

x just about anything

Value

a string where each element in x is separated by a comma and numbers are in a human-readable format.

Author(s)

Kelly Sovacool <sovacool@umich.edu>
Pat Schloss <pschloss@umich.edu>

Examples

```
inline_hook(c(1.2993992, 0.03, 1000))  
inline_hook(c("cats", "dogs"))
```

is_nearly_whole *Checks whether a number is near to a whole number*

Description

Checks whether a number is near to a whole number

Usage

```
is_nearly_whole(x)
```

Arguments

x a numeric

Value

TRUE or FALSE

Author(s)

Kelly Sovacool <sovacool@umich.edu>

Examples

```
is_nearly_whole(.Machine$double.eps^0.5)
is_nearly_whole(.Machine$double.eps^0.6)
is_nearly_whole(1)
```

is_nondesc *Check whether all elements given are sorted in non-descending order*

Description

Check whether all elements given are sorted in non-descending order

Usage

```
is_nondesc(...)
```

Arguments

... anything!

Value

TRUE if the elements are sorted in non-descending order, otherwise FALSE

Author(s)

Kelly Sovacool <sovacool@umich.edu>

Examples

```
is_nondesc(1, 2, 3)
is_nondesc(c(1, 2), 3)
is_nondesc(6, 4, 1)
is_nondesc("a", "b", "c")
is_nondesc(c("z", "y"))
```

load_deps	<i>Install & load packages</i>
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Description

Install & load packages

Usage

```
load_deps(...)
```

Arguments

... package names to install & load

Author(s)

Kelly Sovacool <sovacool@umich.edu>

log_snakemake	<i>Save output, messages, warnings, and errors to the Snakemake log file</i>
---------------	--

Description

This function checks whether a log file was specified in the Snakemake rule. If so, it directs any output, messages, warnings, or errors to the rule-specific log file. See the Snakemake documentation on [log files](#) and [R scripts](#) for more details.

Usage

```
log_snakemake(quiet = TRUE)
```

Arguments

quiet Silence messages about the status of the snakemake object and log file (default: TRUE).

Author(s)

Kelly Sovacool <sovacool@umich.edu>

Examples

```
# The Snakemake object doesn't exist, so nothing happens
log_snakemake(quiet = FALSE)
```

parse_tax	<i>Convert taxonomy strings into dataframe of labels based on taxonomic classification</i>
-----------	--

Description

Convert taxonomy strings into dataframe of labels based on taxonomic classification

Usage

```
parse_tax(dat)
```

Arguments

dat dataframe from mothur taxonomy file with columns OTU, Size, and Taxonomy

Value

a wide dataframe with taxonomic labels

Author(s)

Nick Lesniak, <nlesniak@umich.edu>

Examples

```
taxonomy_filepath <- system.file("extdata",
  "test.taxonomy",
  package = "schtools"
)
taxonomy_tbl <- read_tax(taxonomy_filepath)
head(taxonomy_tbl)
```

paste_oxford_list *Create a prose string from a list or vector*

Description

The word 'and' is inserted before the last element and an Oxford comma is used.

Usage

```
paste_oxford_list(x)
```

Arguments

x a list or vector

Value

a string where each element in x is separated by a comma

Author(s)

Pat Schloss <pschloss@umich.edu>

Kelly Sovacool <sovacool@umich.edu>

Examples

```
paste_oxford_list(1:3)
paste_oxford_list(c("cats", "dogs", "turtles"))
```

pool_taxon_counts *Pool OTU counts at a particular taxonomic level*

Description

Enables comparing analyses at different taxonomic resolutions, as seen in [doi:10.1128/mbio.03161-21](https://doi.org/10.1128/mbio.03161-21). Implementation adapted from [here](#).

Usage

```
pool_taxon_counts(otu_shared_dat, otu_tax_dat, taxon_level)
```

Arguments

otu_shared_dat data frame created from a **shared file** at the OTU level.

otu_tax_dat data frame created from a **taxonomy file** at the OTU level. Must be from the same dataset as the shared file.

taxon_level taxonomic level to pool OTUs into. Options: "kingdom", "phylum", "class", "order", "family", "genus". This should be the name of a column in otu_tax_dat as a character string.

Value

a shared data frame with the OTUs at the specified taxon_level and a corresponding taxonomy dataframe with new OTU numbers.

Author(s)

Kelly Sovacool, <sovacool@umich.edu>
Pat Schloss <pschloss@umich.edu>

Examples

```
tax_dat <- read_tax(system.file("extdata", "test.taxonomy",
  package = "schtools"
))
shared_dat <- readr::read_tsv(system.file("extdata", "test.shared",
  package = "schtools"
))
pool_taxon_counts(shared_dat, tax_dat, "genus")
pool_taxon_counts(shared_dat, tax_dat, "family")
pool_taxon_counts(shared_dat, tax_dat, "phylum")
```

read_dist	<i>Read in lower left triangular matrix from file</i>
-----------	---

Description

Read in lower left triangular matrix from file

Usage

```
read_dist(dist_filename)
```

Arguments

dist_filename filename of lower left triangular matrix (.dist)

Value

distance matrix as a tibble

Author(s)

Nick Lesniak, <nlesniak@umich.edu>

Examples

```
dist_filepath <- system.file("extdata",
  "sample.final.thetayc.0.03.lt.ave.dist",
  package = "schtools"
)
dist_tbl <- read_dist(dist_filepath)
head(dist_tbl)
```

read_tax	<i>Read in a taxonomy file and parse it to a wide dataframe</i>
----------	---

Description

Read in a taxonomy file and parse it to a wide dataframe

Usage

```
read_tax(taxonomy_filename, sep = "\t")
```

Arguments

taxonomy_filename
filename of taxonomy file

sep
Character that separates fields of the taxonomy file. (Default: \t).

Value

dataframe of taxonomic labels, formatted by parse_tax()

Author(s)

Nick Lesniak, <nlesniak@umich.edu>

Kelly Sovacool, <sovacool@umich.edu>

Examples

```
taxonomy_filepath <- system.file("extdata",
  "test.taxonomy",
  package = "schtools"
)
taxonomy_tbl <- read_tax(taxonomy_filepath)
head(taxonomy_tbl)
```

set_knitr_opts	<i>Set knitr chunk options & inline hook</i>
----------------	--

Description

Call this function in the setup chunk of your R Markdown files.

Usage

```
set_knitr_opts()
```

Author(s)

Pat Schloss <pschloss@umich.edu>

Kelly Sovacool <sovacool@umich.edu>

theme_lucas	<i>Sarah's go-to theme for ggplot2</i>
-------------	--

Description

Requires the hrbrthemes package and the PT Sans and PT Sans Narrow fonts from Google Fonts.

Usage

```
theme_lucas()
```

Value

list of ggproto objects

Author(s)

Sarah Lucas <salucas@umich.edu>

Examples

```
library(ggplot2)
library(showtext)

# run once to download the PT Sans fonts
font_add_google(name = "PT Sans", family = "PT Sans")
font_add_google(name = "PT Sans Narrow", family = "PT Sans Narrow")
showtext_auto()

# make a plot with theme_lucas()
```

```
ggplot(mtcars) +  
  aes(x = mpg, y = wt, color = cyl) +  
  geom_point() +  
  theme_lucas()
```

theme_sovacool	<i>Kelly's go-to theme for ggplot2</i>
----------------	--

Description

Uses `ggplot2::theme_bw()` and removes margins.

Usage

```
theme_sovacool()
```

Value

list of ggproto objects

Author(s)

Kelly Sovacool <sovacool@umich.edu>

Examples

```
library(ggplot2)  
ggplot(mtcars) +  
  aes(x = mpg, y = wt, color = cyl) +  
  geom_point() +  
  theme_sovacool()
```

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