Package 'LeyLabRMisc'

March 28, 2020

Type Package

Title Ley Lab misc R functions, rmd templates, etc.

Version 0.1.3

Author Nick Youngblut

Maintainer Nick Youngblut <nyoungb2@gmail.com>

Description Ley Lab misc R functions, rmd templates, etc.

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.0.2

R topics documented:

.dist_fmt *creating a string with distance & percent explained*

Description

creating a string with distance & percent explained

Usage

```
.dist_fmt(dist, PC1_perc_exp, PC2_perc_exp, label1 = 1, label2 = 2)
```

Arguments

dist	str, distance metric
PC1_perc_exp	float, percent variance explained for PC1
PC2_perc_exp	float, percent variance explained for PC2
label1	First PC label
label2	Seconda PC label

Value

str, formatted as "metric, <PC1_perc_exp>

.estimate_rarified_richness
Helper Function for rarefaction analysis

Description

Helper Function for rarefaction analysis

Usage

```
.estimate_rarified_richness(psdata, measures, depth)
```

Arguments

psdata	phyloseq object
measures	Which diversity measures
depth	The sampling depth

Value

molten alpha diversity object

.well384_index   *making 384-well plate index*

Description

making 384-well plate index

Usage

```
.well384_index()
```

Value

named vector (Well –> location); column-wise location

.well96_index   *making a 96-well plate index*

Description

making a 96-well plate index

Usage

```
.well96_index()
```

Value

named vector (Well –> location); column-wise location

---

as.Num   *convert to numeric while avoiding factor conversion issues*

Description

convert to numeric while avoiding factor conversion issues

Usage

```
as.Num(x)
```

Arguments

x   an interable

Value

a numeric object

---

bash_job   *bash job using conda env*

Description

The conda setup is assumed to be in your ~/.bashrc If print_output == TRUE: the stdout/stderr will be printed instead of returned Else: the stdout/stderr with be returned by the function stderr/stdout is printed unless print_output==FALSE

Usage

```
bash_job(cmd, conda_env, stdout = TRUE, stderr = TRUE, print_output = TRUE)
```

Arguments

cmd	The bash command in a string format
conda_env	The conda env to use
stdout	Print the stdout from the command?
stderr	Print the stderr from the command?
quiet	No printing

---

calculate_rarefaction_curves
                    Function for rarefaction analysis

Description

Running estimate_richness_phy() at multiple subsampling depths

Usage

```
calculate_rarefaction_curves(psdata, measures, depths, parallel = FALSE)
```

Arguments

psdata	phyloseq object
measures	Which diversity measures (see vegan package)
depths	Which sequencing depths? Example: c(10, 100, 1000)

Value

A dataframe

| calc_beta_div | *vegdist + UniFrac calculation* |

Description

A wrapper around vegan::vegdist and rbiom (rbiom used for UniFrac calculations). For unifrac: "wunifrac" = weighted unifrac, "unifrac" = unweighted unifrac. The function returns a tidy dataframe of PCoA axes (PC1 & PC2), percent variance explained for each PC.

Usage

```
calc_beta_div(df, method, tree, threads = 1)
```

Arguments

df	sample x taxon dataframe. colnmaes (taxa) must match the tree tip labels if the tree is provided
method	distance method (vegdist or UniFrac)
tree	phylogeny with tips matching the df colnames
threads	threads used for UniFrac calculations with rbiom

Value

data.frame

| calc_PCoA | *Wrapper for cmdscale* |

Description

Simple wrapper for cmdscale to provide data.frame formatted table. If the distance matrices contain NAs, the samples containing NAs will be removed (with a warning).

Usage

```
calc_PCoA(dist_mtx, k = 2)
```

Arguments

dist_mtx	distance matrix object

Value

data.frame

---

cat_file	*pretty printing of a text file via cat*

Description

This is most useful for working with IRkernl in Jupyter notebooks

Usage

```
cat_file(file_name)
```

Arguments

file_name   the name of the file to print

---

condaInfo	*"conda list" in R*

Description

This is most useful for working with IRkernl in Jupyter notebooks

Usage

```
condaInfo(conda_env)
```

Arguments

conda_env   The name of the conda env to list

---

df.dims	*Changing number of rows/columns shown when printing a data frame*

Description

This is most useful for working with IRkernl in Jupyter notebooks

Usage

```
df.dims(nrows = 4, ncols = 20)
```

Arguments

nrows   number of rows to print
ncols   number of columns to print

---

dfhead   *A simple dataframe summary*

Description

A simple dataframe summary

Usage

```
dfhead(df, n = 3)
```

Arguments

df	dataframe object
n	Number of lines to print

Value

a dataframe object

---

estimate_richness_phy   *phyloseq::estimate_richness, but includes Faith's PD*

Description

See physeq::estimate richness for full details

Usage

```
estimate_richness_phy(physeq, split = TRUE, measures = NULL)
```

Arguments

physeq	Phyloseq object
split	Splitting the OTU table
measures	Which diversity measures (Faith's PD = "FaithPD)

Value

Dataframe can calculate faith's PD (using Picante, "FaithPD")

---

extract_pltdt *Extract data from ggplot object*

Description

The data is written to files

Usage

```
extract_pltdt(plot_object, output_path)
```

Arguments

plot_object	A ggplot object
output_path	Where to write the output

---

fig_uuid *create UUID for figure file name*

Description

create UUID for figure file name

Usage

```
fig_uuid(full = FALSE)
```

Arguments

full	Full length uuid or trimmed to just 24 char?

Value

character object

---

files_to_list   *convert a vector of file paths into a named list*

Description

convert a vector of file paths into a named list

Usage

```
files_to_list(files, label_index = -1)
```

Arguments

files   Vector of file paths (eg., by using "list_files()")

label_index   Which item in the path to return? 1-indexing. If <1, samples selected from the
                 end.

Examples

```
files = c('/path/to/project/Sample1/table.txt', '/path/to/project/Sample2/table.txt')
files_to_list(files, -1)
files = c('/path/to/project/Sample1.txt', '/path/to/project/Sample2.txt')
files_to_list(files, 0)
```

Fread   *Simple wrapper around data.table::fread*

Description

Simple wrapper around data.table::fread

Usage

```
Fread(infile = NULL, cmd = NULL, sep = "\t", check.names = TRUE, ...)
```

Arguments

infile   input file name

cmd   command instead of input file (eg., "gunzip -c INFILE")

sep   value delimiter

check.names   format check column names

...   passed to data.table::fread

Value

data.table

---

hello *Hello, World!*

Description

Prints 'Hello, world!'.

Usage

```
hello()
```

Examples

```
hello()
```

---

itol_boxplot *create itol boxplot file*

Description

https://itol.embl.de/help.cgi#boxplot

Usage

```
itol_boxplot(
  df,
  dataset_label,
  out_file,
  out_dir = NULL,
  key_color = "#ff0000"
)
```

Arguments

df	Dataframe, in which the rownames should correspond with the tree labels; the columns must specify: minimum,q1,median,q3,maximum,extreme_value1,extreme_value2
dataset_label	What to label the itol dataset
out_file	Name of the output file
out_dir	Where to write the output
key_color	The color for the legend key

---

itol_colorstrip   *create itol colorstrip file*

Description

https://itol.embl.de/help.cgi#strip

Usage

```
itol_colorstrip(df, dataset_label, out_file, out_dir = NULL, legend = NULL)
```

Arguments

df	Dataframe, in which the rownames should correspond with the tree labels; the plotting parameter should be column 1
dataset_label	What to label the itol dataset
out_file	Name of the output file
out_dir	Where to write the output
legend	Specify particular legend

---

itol_externalshape   *create itol external shape file*

Description

https://itol.embl.de/help.cgi#shapes

Usage

```
itol_externalshape(
  df,
  dataset_label,
  out_file,
  out_dir = NULL,
  legend = NULL,
  WIDTH = 200
)
```

Arguments

df	Dataframe, in which the rownames should correspond with the tree labels; other columns should be values corresponding to symbol size
dataset_label	What to label the itol dataset
out_file	Name of the output file
out_dir	Where to write the output
legend	Specify particular legend

---

itol_heatmap   *create itol heatmap file*

Description

https://itol.embl.de/help.cgi#heatmap

Usage

```
itol_heatmap(
  df,
  dataset_label,
  out_file,
  out_dir = NULL,
  tree = NULL,
  dist_method = "bray",
  color_scheme = c("color", "bw")
)
```

Arguments

df	Dataframe, in which the rownames should correspond with the tree labels; all columns should be numeric values for the heatmap
dataset_label	What to label the itol dataset
out_file	Name of the output file
out_dir	Where to write the output
tree	Tree object used for ordering the heatmap columns; if NULL, the dist_method will be used to create the tree
dist_method	vegan::vegdist method for creating the correlation dendrogram
color_scheme	Heatmap color scheme. color = blue-orange-yellow; bw=white-grey-black

---

itol_multibar   *create itol multi-bar file*

Description

https://itol.embl.de/help.cgi#multibar

Usage

```
itol_multibar(
  df,
  dataset_label,
  out_file,
  out_dir = NULL,
  legend = NULL,
  WIDTH = 200
)
```

Arguments

df	Dataframe, in which the rownames should correspond with the tree labels
dataset_label	What to label the itol dataset
out_file	Name of the output file
out_dir	Where to write the output
legend	A list that includes shapes, colors, and labels
WIDTH	Bar width

---

itol_simplebar	*create itol simple-bar file*

Description

https://itol.embl.de/help.cgi#bar

Usage

```
itol_simplebar(
  df,
  dataset_label,
  out_file,
  out_dir = NULL,
  legend = NULL,
  WIDTH = 200
)
```

Arguments

df	Dataframe, the rownames should correspond with the tree labels
dataset_label	What to label the itol dataset
out_file	Name of the output file
out_dir	Where to write the output
legend	Specify particular legend
WIDTH	Bar width

---

itol_symbol	*create itol symbol file*

Description

https://itol.embl.de/help.cgi#symbols

Usage

```
itol_symbol(df, dataset_label, out_file, out_dir = NULL, MAXIMUM_SIZE = 50)
```

Arguments

df	Dataframe, in which the rownames should correspond with the tree internal node labels, and other columns should be: symbol,size,color,fill,position,(label)
dataset_label	What to label the itol dataset
out_file	Name of the output file
out_dir	Where to write the output
MAXIMUM_SIZE	The max size of the symbols

---

list_files	*list.files with full.names=TRUE & recursive=TRUE*

Description

list.files with full.names=TRUE & recursive=TRUE

Usage

```
list_files(path, pattern = NULL, full.names = TRUE, recursive = TRUE, ...)
```

Arguments

path	a character vector of full path names; the default corresponds to the working directory,
pattern	an optional regular expression. Only file names which match the regular expression will be returned.
full.names	a logical value. If TRUE, the directory path is prepended to the file names to give a relative file path. If FALSE, the file names (rather than paths) are returned
recursive	logical. Should the listing recurse into directories?

Value

A character vector containing the names of the files in the specified directories

---

make_dir   *A helper function for creating a directory (recursively)*

Description

A helper function for creating a directory (recursively)

Usage

```
make_dir(dir, quiet = FALSE)
```

Arguments

dir	path for the new directory (will create recursively)
quite	quite output

---

overlap   *Determine counts of setdiff, intersect, & union of 2 vectors (or data.tables)*

Description

The output is printed text of intersect, each-way setdiff, and union. Data.table compatible! Just make sure to provide sel_col_x and/or sel_col_y

Usage

```
overlap(
  x,
  y,
  sel_col_x = NULL,
  sel_col_y = NULL,
  to_return = c("counts", "diff_x", "diff_y", "diff_fuzzy")
)
```

Arguments

x	vector1 or data.table. If data.table, sel_col_x must not be NULL
y	vector2 or data.table. If data.table, sel_col_y must not be NULL
sel_col_x	If x = data.table, which column to assess?
sel_col_y	If y = data.table, which column to assess?
to_return	"counts" = print overlap counts; "diff_x-or-y" = return setdiff; "diff_fuzzy" = return closest matches for those that differ (ordered best to worst)

---

p.dims   *Global change of plot size options*

Description

This is most useful for working with IRkernl in Jupyter notebooks

Usage

```
p.dims(w = 5, h = 5, res = 200)
```

Arguments

w	figure width
h	figure height
res	figure resolution (DPI)

---

path_get_label   *splitting path and returning just one item in the vector*

Description

splitting path and returning just one item in the vector

Usage

```
path_get_label(file_path, index)
```

Arguments

file_path	File path
index	Which item in the path to return? 1-indexing. If <1, samples selected from the end.

Value

string

---

phyloseq2df   *Convert a sub-object of a phyloseq object to a dataframe*

Description

A helper function for converting OTU, taxonomy, and metadata to dataframes

Usage

```
phyloseq2df(physeq_obj, physeq_func, long = FALSE)
```

Arguments

physeq_obj	The phyloseq object
physeq_func	Which object do you want ('otu_table', 'tax_table', or 'sample_data')
long	Do you want the table in "long" format ("gathered")

Value

A tibble

---

pipelineInfo   *pipeline sessionInfo*

Description

sessionInfo for LeyLab snakemake pipelines

Usage

```
pipelineInfo(pipeline_path, head_n = 10)
```

Arguments

pipeline_path	The path to the pipeline directory
head_n	The number of lines to print from the readme

| Plot | *plot figure and save the figure grob object to a file at the same time* |

Description

This is most useful for working with IRkernl in Jupyter notebooks

Usage

```
Plot(
  p,
  file = NULL,
  path = NULL,
  suffix = "",
  saveObj = TRUE,
  saveImg = FALSE,
  width = NA,
  height = NA,
  ...
)
```

Arguments

p	Plot object (ggplot2, base, etc)
file	File name to write
path	Path to write to
suffix	File name suffix (eg., '.png')
saveObj	Write the Robj to a file?
saveImg	Write the image to a file?
width	Figure width. If NA, uses global options
height	Figure height. If NA, uses global options

| qsave_obj | *Simple function for serializing a distance matrix or list of distance matrices* |

Description

Serializing done with the "qs" R package.

Usage

```
qsave_obj(x, file, msg = "Writing file to: ", threads = 1)
```

Arguments

x	a distance matrix or list of distance matrices
file	file name to save to
threads	number of threads used for serializing

Value

the input distance matrix or list of distance matrices

---

read_bracken   *Function for reading in a bracken taxonomy table*

Description

The table will be converted to long form (sample ~ abundance). Only "_frac" or "_num" columns will be kept (see "keep_frac"). Taxonomy will be split into separate levels (see "tax_levs").

Usage

```
read_bracken(
  infile,
  is_gzip = FALSE,
  n_lines = 0,
  keep_frac = TRUE,
  tax_levs = c("Domain", "Phylum", "Class", "Order", "Family", "Genus", "Species")
)
```

Arguments

infile	Path to bracken table file
is_gzip	Is the table file gzip'ed?
n_lines	Number of lines to read. If < 1, all lines will be read.
keep_frac	If TRUE, keep all columns ending in "_frac"; otherwise, keep "_num" columns.
tax_levs	Taxonomic levels to separate the taxonomy column into.

Value

data.table

Robj_md5sum   *Dump an R object as text to a temp file and get the md5sum of the file*

Description

Dump an R object as text to a temp file and get the md5sum of the file

Usage

```
Robj_md5sum(Robj)
```

Arguments

Robj   Any R object

Value

md5sum

---

row_means   *rowMeans that works inside a dplyr::mutate() call*

Description

rowMeans that works inside a dplyr::mutate() call

Usage

```
row_means(..., na.rm = TRUE)
```

---

row_sums   *rowSums that works inside a dplyr::mutate() call*

Description

rowSums that works inside a dplyr::mutate() call

Usage

```
row_sums(..., na.rm = TRUE)
```

---

send_email   *A helper function to send an email via the mail bash cmd*

Description

A helper function to send an email via the mail bash cmd

Usage

```
send_email(
  body,
  subject = "R job complete",
  email = NULL,
  email_ext = "tuebingen.mpg.de"
)
```

Arguments

body	The email body
subject	The email subject line
email	The email address. If NULL, then username used
email_ext	The part after the "at" symbol

Value

The output of the system() call

---

snakemakeInfo   *snakemake conda info*

Description

snakemake conda info

Usage

```
snakemakeInfo(config_file, pipeline_dir, conda_env)
```

Arguments

config_file	The path to the config file
pipeline_dir	The path to the pipeline_directory
conda_env	The conda env that has snakemake installed

Value

The environment info

---

summary_x   *Summary for numeric vectors that includes sd and stderr*

Description

sd = standard deviation stderr = standard error of the mean (sd(x) / sqrt(length(x)))

Usage

```
summary_x(x, label = NULL, sel_col = NULL, rnd = 3)
```

Arguments

x	a numeric vector
label	row name label for the output. If NULL, then the label will be the input object label.
sel_col	If "x" is data.table or data.frame, which column to assess?
rnd	number of digits to round sd and stderr to

Value

a matrix

---

tidy_pcoa   *PCoA on a 'long' (tidy) tibble, and a long tibble is returned*

Description

Perform PCoA in a "tidy" way. If multiple diversity metrics are provided (eg., "bray" and "jaccard"), all PCoA results will be combined into one data.frame.

Usage

```
tidy_pcoa(
  df,
  taxon_col,
  sample_col,
  abundance_col,
  dists = c("bray", "jaccard"),
  tree = NULL,
  threads = 1,
  threads_unifrac = 1,
  k = 2,
  dist_mtx_file = NULL,
  pcoa_file = NULL
)
```

Arguments

df	data.frame or tibble
taxon_col	the column specifying taxa or OTUs (no quotes needed)
sample_col	the column specifying sample names (no quotes needed)
abundance_col	the column specifying the taxon abundances in each sample (no quotes needed)
dists	vector of beta-diversity distances ('wunifrac' = weighted UniFrac, 'unifrac' = unweighted Unifrac; see vegan::vegsist for others)
tree	phylogeny for UniFrac calculations. It can have more tips that what is in the data.frame
threads	number of parallel calculations of each distance metric (1 thread per distance)
threads_unifrac	
	number of threads to use for wunifrac & unifrac calculations
k	passed to cmdscale
dist_mtx_file	file name for saving the distance matrices (qs serialization; use ".qs" for the file extension)
pcoa_file	file name for saving the raw pcoa results

Details

Weighted/Unweighted UniFrac is calculated via the rbiom R package. All other beta-diversity metrics are calculated via the vegan R package.

Value

data.frame

---

unique_n	*Pretty print number of unique elements in a vector*

Description

The result will be cat'ed to the screen. tidytable compatable. Maje

Usage

```
unique_n(x, label = "items", sel_col = NULL)
```

Arguments

x	a vector or data.table. If data.table, sel_col must not be NULL
label	what to call the items in the vector (eg., "samples")
sel_col	If x is data.table or data.frame, which column to assess?

---

well2index   *Convert between wellID and column-num*

Description

Useful for converting between WellIDs (eg., "A2") and well position in a plate (eg., 9)

Usage

```
well2index(x, plate_type = "96-well")
```

Arguments

x	A vector of well IDs
plate_type	Either 96-well or 384-well

Value

A vector of plate positions

---

write_table   *writing table convience function*

Description

This is most useful for working with IRkernl in Jupyter notebooks

Usage

```
write_table(df, file, sep = "\t", quote = FALSE, row.names = FALSE, ...)
```

Arguments

df	Data.frame to write out
file	Output file path
sep	the field separator string. Values within each row of x are separated by this string
quote	a logical value (TRUE or FALSE) or a numeric vector. If TRUE, any character or factor columns will be surrounded by double quotes.
row.names	either a logical value indicating whether the row names of x are to be written along with x, or a character vector of row names to be written.
...	Passed to write.table

Index