

# Package ‘LeyLabRMisc’

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**Type** Package

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

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

**License** GPL-3

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.well384_index	<i>making 384-well plate index</i>
----------------	------------------------------------

---

### Description

making 384-well plate index

### Usage

```
.well384_index()
```

### Value

named vector (Well → location); column-wise location

---

.well96_index	<i>making a 96-well plate index</i>
---------------	-------------------------------------

---

### Description

making a 96-well plate index

### Usage

```
.well96_index()
```

### Value

named vector (Well → location); column-wise location

---

as.Num	<i>convert to numeric while avoiding factor conversion issues</i>
--------	---

---

### Description

convert to numeric while avoiding factor conversion issues

### Usage

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

### Arguments

x                      an interable

### Value

a numeric object

---

bash_job	<i>bash job using conda env</i>
----------	---------------------------------

---

### 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 will 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	<i>Function for rarefaction analysis</i>
------------------------------	--

---

### 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_alpha_div	<i>Calculate common alpha-diversity metrics</i>
----------------	---

---

**Description**

Faith's Phylogenetic Diversity ("PD") can be calculated only if a tree is provided. The tree can have extra tips, but there must be tip labels for all taxa in the provided table.

**Usage**

```
calc_alpha_div(df, tree = NULL, index = c("nobs", "shannon", "PD"))
```

**Arguments**

df	sample x taxon abundance table (usual format for vegan)
tree	tree with tips matching taxa in the abundance table (only needed for PD)
index	which of the indices to calculate? (nobs = no. of observations, shannon = Shannon Index, PD = Faith's PD)

**Value**

a data.frame of alpha diversity values (and sample names)

---

calc_beta_div	<i>vegdist + UniFrac calculation</i>
---------------	--------------------------------------

---

**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. colnames (taxa) must match the tree tip labels if the tree is provided
method	distance method ( <code>vegdist</code> or <code>UniFrac</code> )
tree	phylogeny with tips matching the df colnames
threads	threads used for UniFrac calculations with <code>rbiom</code>

**Value**

data.frame

---

calc_PCoA	<i>Wrapper for cmdscale</i>
-----------	-----------------------------

---

**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	<i>pretty printing of a text file via cat</i>
----------	---

---

**Description**

This is most useful for working with IRkernel in Jupyter notebooks

**Usage**

```
cat_file(file_name)
```

**Arguments**

file_name	the name of the file to print
-----------	-------------------------------

---

condaInfo	<i>"conda list" in R</i>
-----------	--------------------------

---

**Description**

This is most useful for working with IRkernel in Jupyter notebooks

**Usage**

```
condaInfo(conda_env)
```

**Arguments**

conda_env	The name of the conda env to list
-----------	-----------------------------------

---

df.dims	<i>Changing number of rows/columns shown when printing a data frame</i>
---------	---

---

**Description**

This is most useful for working with IRkernel in Jupyter notebooks

**Usage**

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

**Arguments**

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

---

dfhead	<i>A simple dataframe summary</i>
--------	-----------------------------------

---

**Description**

A simple dataframe summary

**Usage**

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

Arguments

df	dataframe object
n	Number of lines to print

Value

a dataframe object

---

dist_format	<i>creating a string with distance &amp; percent explained</i>
-------------	--

---

Description

creating a string with distance & percent explained

Usage

```
dist_format(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	<i>Helper Function for rarefaction analysis</i>
----------------------------	---

---

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

---

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	<i>create UUID for figure file name</i>
----------	---

---

**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	<i>convert a vector of file paths into a named list</i>
---------------	---

---

**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	<i>Simple wrapper around data.table::fread</i>
-------	--

---

**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	<i>Hello, World!</i>
-------	----------------------

---

**Description**

Prints 'Hello, world!'.

**Usage**

```
hello()
```

**Examples**

```
hello()
```

---

itol_boxplot	<i>create itol boxplot file</i>
--------------	---------------------------------

---

### 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	<i>create itol colorstrip file</i>
-----------------	------------------------------------

---

### 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	<i>create itol external shape file</i>
--------------------	--

---

**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	<i>create itol heatmap file</i>
--------------	---------------------------------

---

**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	<i>create itol multi-bar file</i>
---------------	-----------------------------------

---

**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	<i>create itol simple-bar file</i>
----------------	------------------------------------

---

**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	<i>create itol symbol file</i>
-------------	--------------------------------

---

**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	<i>list.files with full.names=TRUE &amp; recursive=TRUE</i>
------------	---

---

**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	<i>A helper function for creating a directory (recursively)</i>
----------	---

---

**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	<i>Determine counts of setdiff, intersect, &amp; union of 2 vectors (or data.tables)</i>
---------	--

---

### 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	<i>Global change of plot size options</i>
--------	---

---

### Description

This is most useful for working with IRkernel 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	<i>splitting path and returning just one item in the vector</i>
----------------	---

---

**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	<i>Convert a sub-object of a phyloseq object to a dataframe</i>
-------------	---

---

**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	<i>pipeline sessionInfo</i>
--------------	-----------------------------

---

**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	<i>plot figure and save the figure grob object to a file at the same time</i>
------	---

---

**Description**

This is most useful for working with IRkernel 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	<i>Simple function for serializing a distance matrix or list of distance matrices</i>
-----------	---

---

### 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	<i>Function for reading in a bracken taxonomy table</i>
--------------	---

---

### 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"). tidytable (w/ data.table) used to speed the process up.

### 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	<i>Dump an R object as text to a temp file and get the md5sum of the file</i>
-------------	---

---

**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	<i>rowMeans that works inside a dplyr::mutate() call</i>
-----------	--

---

**Description**

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

**Usage**

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

---

row_sums	<i>rowSums that works inside a dplyr::mutate() call</i>
----------	---

---

**Description**

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

**Usage**

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

---

send_email	<i>A helper function to send an email via the mail bash cmd</i>
------------	---

---

**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

---

size_objects	Returns the sizes of R objects
--------------	--------------------------------

---

**Description**

Returns the sizes of R objects

**Usage**

```
size_objects(Robj)
```

**Arguments**

Robj	Vector with the names of R objects as characters
------	--

**Value**

A list with the name of R objects as names and the formatted size of the objects

---

snakemakeInfo	<i>snakemake conda info</i>
---------------	-----------------------------

---

**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 ( $\text{sd}(x) / \sqrt{\text{length}(x)}$ )

**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 <code>vegan::vegdist</code> for others)
tree	phylogeny for UniFrac calculations. It can have more tips than 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 <code>cmdscale</code>
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	<i>Pretty print number of unique elements in a vector</i>
----------	---

---

**Description**

The result will be cat'ed to the screen. tidytable compatible. Major

**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	<i>Convert between wellID and column-num</i>
------------	--

---

**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	<i>writing table convience function</i>
-------------	---

---

**Description**

This is most useful for working with IRkernel 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

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