

# Package ‘LorMe’

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**Title** Lightning One-Code Resolving Microbial Ecology Solution

**Version** 1.2.0

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**Description** Provides a robust collection of functions tailored for microbial ecology analysis, encompassing both data analysis and visualization. It introduces an encapsulation feature that streamlines the process into a summary object. With the initial configuration of this summary object, users can execute a wide range of analyses with a single line of code, requiring only two essential parameters for setup. The package delivers comprehensive outputs including analysis objects, statistical outcomes, and visualization-ready data, enhancing the efficiency of research workflows. Designed with user-friendliness in mind, it caters to both novices and seasoned researchers, offering an intuitive interface coupled with adaptable customization options to meet diverse analytical needs.

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## Contents

Alpha_diversity_calculator . . . . .	3
Alpha_diversity_calculator2 . . . . .	4
anova_report . . . . .	6
auto_signif_test . . . . .	8
circulation_lm . . . . .	10
color_scheme . . . . .	11
combine_and_translate . . . . .	12
community_plot . . . . .	14
compare_plot . . . . .	16
Deseq_analysis . . . . .	17
Deseq_analysis2 . . . . .	19
differential_bar . . . . .	21
Dimension_reduction . . . . .	23
Facet_group . . . . .	24
Filter_function . . . . .	25
indicator_analysis . . . . .	26
kruskal_report . . . . .	27
LorMe . . . . .	29
manhattan . . . . .	30
Module_abundance . . . . .	32
Module_composition . . . . .	33
nc . . . . .	35
NC_remove . . . . .	36
network_analysis . . . . .	37
network_analysis2 . . . . .	39
network_stat . . . . .	42
network_visual . . . . .	42
network_visual_re . . . . .	44
network_withdiff . . . . .	45
object_config . . . . .	48
structure_plot . . . . .	50
sub_tax_summary . . . . .	52
tax_summary . . . . .	53
tbRDA_analysis . . . . .	54
testotu . . . . .	57
theme_zg . . . . .	57
Three_group . . . . .	58
Top_taxa . . . . .	58
Two_group . . . . .	60
t_test_report . . . . .	60
volcano_plot . . . . .	61
wilcox_test_report . . . . .	63

---

`Alpha_diversity_calculator`*Calculate alpha diversity based on tax summary object*

---

**Description**

Calculate alpha diversity for each sample

**Usage**

```
Alpha_diversity_calculator(taxobj, taxlevel, prefix = "")
```

**Arguments**

<code>taxobj</code>	Configured tax summary objects. See in <a href="#">object_config</a> .
<code>taxlevel</code>	taxonomy levels used for visualization. Must be one of <code>c("Domain", "Phylum", "Class", "Order", "Family", "Order")</code> .
<code>prefix</code>	A character string as prefix of diversity index. Default: ""

**Value**

'Alpha\_diversity\_calculator' returns alpha-diversity of each sample in format of column table (dataframe) combined with group information in meta file.

**Examples**

```
####data preparation####  
data("Two_group")  
require(ggplot2)  
  
###analysis###  
Alpha_results<- Alpha_diversity_calculator(taxobj = Two_group,taxlevel = "Base")  
  
#Check data frame contained alpha diversity  
head(Alpha_results$alphaframe,5)  
  
#Check contained statistics and plot list  
names(Alpha_results$plotlist)  
  
#Check statistics for Shannon  
Alpha_results$plotlist$Plotobj_Shannon$Statistics  
  
#Extract plot for Shannon  
Alpha_results$plotlist$Plotobj_Shannon$Barplot  
Alpha_results$plotlist$Plotobj_Shannon$Boxplot  
Alpha_results$plotlist$Plotobj_Shannon$Violinplot
```

---

Alpha\_diversity\_calculator2

*Calculate alpha diversity based on tax summary object or dataframe table*

---

### Description

Calculate alpha diversity of each sample

### Usage

```
Alpha_diversity_calculator2(  
  taxobj = NULL,  
  taxlevel = NULL,  
  prefix = "",  
  input,  
  inputformat,  
  reads  
)
```

### Arguments

taxobj	tax summary objects computed by <code>tax_summary</code> . Default:NULL.
taxlevel	taxonomy levels used for visualization.Must be one of c("Domain","Phylum","Class","Order","Family","O")
prefix	A character string as prefix of diversity index. Default:""
input	Reads or relative abundance of OTU/Taxa/gene data frame,see details in input-format. (Useless when taxobj is set).
inputformat	(Useless when taxobj is set) 1:data frame with first column of OTUID and last column of taxonomy 2:data frame with first column of OTUID/taxonomy 3:data frame of all numeric
reads	If the input data frame were from reads table or not(relative abundance table).(Useless when taxobj is set).

### Value

when tax taxobj is set, returns column table with group information combined with for alpha-diversity of each sample,else returns data frame for alpha-diversity of each sample

### Note

1.When input data frame is in relative abundance table,Chao and ACE are not available

### Author(s)

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**Examples**

```
### Data preparation ###
data(testotu)
groupinformation <- data.frame(
  group = c(rep("a", 10), rep("b", 10)),
  factor1 = rnorm(10),
  factor2 = rnorm(mean = 100, 10),
  subject = factor(c(1:10, 1:10))
)

# Summary OTU table into genus table and phylum table
testtax_summary <- tax_summary(
  groupfile = groupinformation,
  inputtable = testotu[, 2:21],
  reads = TRUE,
  taxonomytable = testotu[, c(1, 22)]
)

### Use taxsummary object as input ###
Alpha <- Alpha_diversity_calculator2(
  taxobj = testtax_summary,
  taxlevel = "Base"
)
head(Alpha)

# In genus level
Alpha <- Alpha_diversity_calculator2(
  taxobj = testtax_summary,
  taxlevel = "Genus",
  prefix = "Genus"
)
head(Alpha)

### Input dataframe from reads table ###
Alpha <- Alpha_diversity_calculator2(
  input = testotu,
  prefix = "Bacterial",
  inputformat = 1,
  reads = TRUE
)

### Input dataframe from relative abundance table ###
if (!require(magrittr)) install.packages("magrittr")
library(magrittr)
Alpha <- Filter_function(
  input = testotu,
  threshold = 0,
  format = 1
) %>%
Alpha_diversity_calculator2(
  input = .,
  prefix = "Bacterial",
```

```

    inputformat = 1,
    reads = FALSE
  )
  head(Alpha)

```

---

 anova\_report

*Print Analysis of Variance report*


---

## Description

Print Analysis of Variance report

## Usage

```

anova_report(
  data,
  treatment_col,
  value_col,
  prior = FALSE,
  comparison_method = "Auto",
  equally_rep = TRUE,
  report = TRUE
)

```

## Arguments

data	Data frame containing the treatment, value and other information.
treatment_col	Numeric indicating where treatment locates (column number) in data.
value_col	Numeric indicating where treatment value (column number) in data.
prior	logical. Whether conducted prior comparisons.
comparison_method	Default would automatically choose method. Method of multiple comparison, must be one of "SNK", "Tukey", "bonferroni", "LSD" or "Scheffe".
equally_rep	Logical. Whether all treatments have same number of replication.
report	Logical. If print report to console. Default:TRUE

## Value

anova\_report returns list of:

- 1)basic data description
- 2)ANOVA model
- 3)summary of ANOVA model
- 4)model of multiple comparison
- 5)difference of multiple comparison
- 6)letters of multiple comparison, which could be use for visualization.

**Examples**

```
{
  #' Data loading from 'agricolae' package
  data("cotton", package = "agricolae")

  #' ANOVA report with default settings
  anova_results <- anova_report(
    data = cotton,
    treatment_col = 3,
    value_col = 5
  )
  ## Here returns NULL because no significance among groups

  ## To conduct prior comparisons
  anova_results <- anova_report(
    data = cotton,
    treatment_col = 3,
    value_col = 5,
    prior = TRUE
  )

  ## Here found no difference among groups, thus change to a more sensitive method
  ## (maybe illegal, but only as an example)
  anova_results <- anova_report(
    data = cotton,
    treatment_col = 3,
    value_col = 5,
    prior = TRUE,
    comparison_method = "LSD"
  )

  #' Data loading 'iris' dataset
  data("iris")

  #' ANOVA report for 'iris' dataset
  anova_results <- anova_report(
    data = iris,
    treatment_col = 5,
    value_col = 2
  )

  ### Extract return

  ### Basic data description
  print(anova_results$basicdata)

  ### ANOVA model
  print(anova_results$anova_model)

  ### Summary of ANOVA model
  print(anova_results$anova_summary)
```

```

### Model of multiple comparison
print(anova_results$multiple_comparison_model)

### Difference of multiple comparison
print(anova_results$comparison_results)

### Letters of multiple comparison, which could be used for visualization
print(anova_results$comparison_letters)
}

```

---

auto\_signif\_test      *Automatic significance test*

---

## Description

Automatically conduct significance testing

## Usage

```

auto_signif_test(
  data,
  treatment_col,
  value_col,
  paired,
  subject_col,
  prior = FALSE,
  comparison_method = NULL,
  equally_rep = TRUE,
  output = "console",
  output_dir = "./",
  filename = "auto_signif_test",
  report = TRUE
)

```

## Arguments

data	Data frame containing the treatment, value and other information.
treatment_col	Numeric indicating where treatment locates (column number) in data.
value_col	Numeric indicating where treatment value (column number) in data.
paired	Logical indicating whether you want a paired t-test.
subject_col	Only meaningful when Pair is ture. Numeric indicating where subject of treatment (column number) in data.
prior	logical. Whether conducted prior comparisons.
comparison_method	Character string. Only use for more than 2 treatment. Default would automatically choose method. Method of multiple comparison,must be one of "SNK", "Tukey", "bonferroni", "LSD" or "Scheffe".



equally_rep	Logical indicating Whether all treatments have same number of replication.
output	A character string indicating output style. Default: "console", which print the report in console. And "file" is available to output report into text-file.
output_dir	Default:"./". Available only when output="file". The direction of output file.
filename	A character string indicating file name of output file. Only work when output set as 'file'.
report	Logical. If print report to console. Default:TRUE

### Value

auto\_signif\_test returns results of significant test and print report in console or file. See details in example.

See results return in [t\\_test\\_report](#), [wilcox\\_test\\_report](#), [anova\\_report](#), [kruskal\\_report](#).

### Note

1.when choose output="file", once caused error that terminate the program, use 'sink()' to end the written of exist files.

2.Please confirm your data is in format of dataframe, else may cause bug! (e.g. Do not use 'read.xlsx' to load data into tibble format)

### Examples

```
### Here shows different types of experimental design ###
data("cotton", package = "agricolae")
```

```
### Two randomly designed groups ###
sig_results <- auto_signif_test(
  data = cotton,
  treatment_col = 1,
  value_col = 5
)
```

```
### Two paired design groups ###
sig_results <- auto_signif_test(
  data = cotton,
  treatment_col = 1,
  value_col = 5,
  paired = TRUE,
  subject_col = 2
)
```

```
### More than two randomly designed groups ###
sig_results <- auto_signif_test(
  data = cotton,
  treatment_col = 2,
  value_col = 5
)
head(sig_results) # Check outputs
```

```

### Conduct prior comparisons ###
sig_results <- auto_signif_test(
  data = cotton,
  treatment_col = 2,
  value_col = 5,
  prior = TRUE
)
head(sig_results) # Check outputs
print(sig_results$basicdata) # Check statistical summary
print(sig_results$anova_model) # Extract ANOVA model
print(sig_results$anova_summary) # Check ANOVA summary
print(sig_results$multiple_comparison_model) # Extract multiple comparison model
print(sig_results$comparison_results) # Check between-group comparison
print(sig_results$comparison_letters) # Check letters (can be used in visualization)

## Change multiple comparison method (maybe not illegal!!)
sig_results <- auto_signif_test(
  data = cotton,
  treatment_col = 2,
  value_col = 5,
  prior = TRUE,
  comparison_method = "LSD"
)
head(sig_results) # Check outputs
print(sig_results$comparison_letters) # Note that letters become different

```

---

circulation\_lm

*Circulation of fitting Linear Models*


---

## Description

Using circulation to fit linear models between one dependent variable and series of independent variable

## Usage

```
circulation_lm(y, xframe, margin)
```

## Arguments

y	Dependent variable
xframe	Matrix or data frame of independent variable
margin	A vector of 1 or 2 indicates arrangement of xframe. 1:by rows 2:by columns

## Details

if row names(for margin 1) and column names(for margin 2) are not given, ID column of return data frame will be row/column numbers.

**Value**

Data frame contains lm statistics of all Independent Variable

**Note**

Other arguments used in function lm were set as default. See in [lm](#).

**Author(s)**

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**Examples**

```
data(testotu)

###using margin 1, arrange by rows##
dep=testotu[1,2:21]
in_dep=testotu[-1,2:21]
lm_stat<-circulation_lm(y = dep,xframe = in_dep,margin = 1)
lm_stat

###using margin 2, arrange by column##
dep=testotu[,2]
in_dep=testotu[,3:21]
lm_stat<-circulation_lm(y = dep,xframe = in_dep,margin = 2)
lm_stat
```

---

color\_scheme

*Get color scheme*

---

**Description**

color\_scheme() can generate color scheme from nine color scheme database and expand into color-Ramp

**Usage**

```
color_scheme(Plan, expand = NULL, names = NULL, show = TRUE)
```

**Arguments**

Plan	Character, 'Plan1' to 'Plan10' are optional.
expand	Numeric, default:NULL. Numeric indicating numbers to expand color scheme into colorRamp
names	Character string. Names to assign for color scheme.
show	Logical. If show assigned color in plot panel. Default:TRUE.

**Value**

If parameter 'names' is not given, 'color\_scheme' returns character string including color scheme. When 'names' is set, 'color\_scheme' returns named vector of color scheme.

**Note**

1. Parameter 'names' is strongly recommended to assign for fixed color scheme, see details in `ggplot::scale_color_manual`

**Examples**

```
### Commonly used example ###
my_color <- color_scheme(
  Plan = "Plan1",
  names = c("Treatment1", "Treatment2")
)

### Generate colorRamp still based on 'Plan1'
my_color <- color_scheme(
  Plan = "Plan1",
  expand = 4,
  names = c("Treatment1", "Treatment2", "Treatment3", "Treatment4")
)

### View color scheme from plan1 to plan10 in 'Plots' interface ###
color_scheme(Plan = "Plan1")
color_scheme(Plan = "Plan2")
color_scheme(Plan = "Plan3")
color_scheme(Plan = "Plan4")
color_scheme(Plan = "Plan5")
color_scheme(Plan = "Plan6")
color_scheme(Plan = "Plan7")
color_scheme(Plan = "Plan8")
color_scheme(Plan = "Plan9")
color_scheme(Plan = "Plan10")
```

---

combine\_and\_translate *Combine data for visualization*

---

**Description**

Combine group information and index into data frame for visualization(scatter, bar plot, alluvial, box plot etc.).

**Usage**

```
combine_and_translate(inputframe, groupframe, itemname, indexname, inputtype)
```

**Arguments**

inputframe	Data frame of index ,sample ID in column,requires all numeric(e.g. result from Alpha_diversity_calculator or Top_taxa function)
groupframe	Data frame of group information(and other abiotic/geographic factors)
itemname	A character string of your inputframe itemname
indexname	A character string of your inputframe indexname
inputtype	If sample ID were in row and index in column in inputframe.

**Value**

key-value pairs data frame

**Author(s)**

Wang Ningqi [2434066068@qq.com](mailto:2434066068@qq.com)

**Examples**

```
{
  require(magrittr)
  data(testotu)

  ## Data preparation ##
  Alpha <- Alpha_diversity_calculator2(
    input = testotu,
    prefix = "Bacterial",
    inputformat = 1,
    reads = TRUE
  )

  topotu <- data.frame(
    Top_taxa(
      input = testotu,
      n = 10,
      inputformat = 1,
      outformat = 1
    )[, -1],
    row.names = paste0(rep("otu", 11), 1:11)
  )

  groupinformation1 <- data.frame(
    group = c(rep("a", 10), rep("b", 10)),
    factor1 = rnorm(10),
    factor2 = rnorm(mean = 100, 10)
  )

  ### Use inputtype = FALSE ###
  head(Alpha)
  combine_and_translate(
    Alpha, groupinformation1,
```

```

    itemname = "Alpha", indexname = "index",
    inputtype = FALSE
  )

  ### Use inputtype = TRUE ###
  head(topotu)
  combine_and_translate(
    topotu, groupinformation1,
    itemname = "OTU", indexname = "reads",
    inputtype = TRUE
  )
}

```

---

community_plot	<i>Generate Community Composition Plot Based on Tax_summary Object</i>
----------------	--

---

## Description

Microbial community composition visualization in format of barplot, areaplot and alluvialplot

## Usage

```

community_plot(
  taxobj,
  taxlevel,
  n = 10,
  palette = "Spectral",
  nrow = NULL,
  rmprefix = NULL
)

```

## Arguments

taxobj	Configured tax summary objects. See in <a href="#">object_config</a> .
taxlevel	Character. taxonomy levels used for visualization. Must be one of c("Domain", "Phylum", "Class", "Order", "Genus", "Species").
n	Numeric. Top n taxa remained according to relative abundance. Default: 10
palette	Character. Palette for visualization, default: "Spectral", recommended to use "Paired" for more than 15 tax.
nrow	Numeric. Number of rows when wrap panels, default: NULL.
rmprefix	Numeric. Removed prefix character in taxonomy annotation. Default: NULL. See details in example.

## Value

community\_plot2 returns three ggplot objects, two data frame used in visualization and one character of filled mapping colors

**Author(s)**

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**Examples**

```
{
  require(magrittr)
  ### Data preparation ###
  data("Two_group")

  ## Use taxonomy summary objects
  phylum10 <- community_plot(
    taxobj = Two_group,
    taxlevel = "Phylum",
    n = 10,
    rmprefix = "p_"
  )

  phylum10$barplot # Check bar plot
  phylum10$areaplot # Check area plot
  phylum10$alluvialplot # Check alluvial plot

  phylum10$Top10Phylum %>% head(10) # Check top taxa data frame
  phylum10$Grouped_Top10Phylum %>% head(10) # Check grouped top taxa data frame
  print(phylum10$filled_color) # Check mapping colors

  # Double facet
  data("Facet_group")

  # Using palette by default
  phylum10 <- community_plot(
    taxobj = Facet_group,
    taxlevel = "Phylum",
    n = 10,
    rmprefix = " p_"
  )
  phylum10$barplot
  phylum10$areaplot
  phylum10$alluvialplot

  # Another example
  genus20 <- community_plot(
    taxobj = Facet_group,
    taxlevel = "Genus",
    n = 20,
    palette = "Paired",
    rmprefix = " g_"
  )
  genus20$alluvialplot
}
```

---

compare_plot	<i>Comparison plot generator This function help generate comparison plot including bar plot, box plot, and violin plot</i>
--------------	--

---

### Description

Comparison plot generator This function help generate comparison plot including bar plot, box plot, and violin plot

### Usage

```
compare_plot(
  inputframe,
  treat_location,
  value_location,
  aes_col = NULL,
  point = TRUE,
  facet_location = NULL,
  ylab_text = NULL
)
```

### Arguments

inputframe	A data frame contain information for visualization.
treat_location	Numeric. Treatment column number in inputframe.
value_location	Numeric. Value column number in inputframe.
aes_col	Named character string, default:NULL. A set of aesthetic character to map treatment to.
point	Logical. If draw point on bar, box and violin plot. Default:TRUE.
facet_location	Numeric, default:NULL. Facet column number in inputframe.
ylab_text	Character. Text for y axis.

### Value

A list contained plot and statistics

### Examples

```
data("iris")
results=compare_plot(inputframe=iris,treat_location=5,
                    value_location=1,ylab_text = "Sepal Length")

#Check statistics
results$Statistics
#Extract plot
results$Barplot
```



```
results$Boxplot
results$Violinplot

iris$Treat2=rep(c(rep("A",25),rep("B",25)),3)

results=compare_plot(inputframe=iris,treat_location=5,
                    value_location=1,facet_location = 6,
                    ylab_text = "Sepal Length")

#Check statistics
results$Statistics
#Extract plot
results$Barplot
results$Boxplot
results$Violinplot
#Extract combined plot
results$All_Barplot
results$All_Boxplot
results$All_Violinplot
```

---

Deseq\_analysis

*Deseq Analysis Function*

---

## Description

This function performs a differential expression analysis using the DESeq2 package. It is designed to work with microbiome data and can handle paired or non-paired samples.

## Usage

```
Deseq_analysis(  
  taxobj,  
  taxlevel,  
  comparison = NULL,  
  cutoff,  
  control_name,  
  paired = FALSE,  
  subject = NULL  
)
```

## Arguments

taxobj	Configured tax summary objects. See in <a href="#">object_config</a> .
taxlevel	The taxonomic level for the analysis. Must be one of c("Domain", "Phylum", "Class", "Order", "Family", "Genus").
comparison	A vector of conditions to compare. Default: NULL, all unique conditions are compared (only for Two groups).

cutoff	The log2 fold change cutoff for considering as differential taxon.
control_name	Character. The name of the control group for the comparison.
paired	Logical. Should the samples be treated as paired? Default: False
subject	Optional. The subject identifier for paired samples. Default: Null

**Value**

A data frame with the results of the differential expression analysis.

**Note**

1. Regulation is judged by cutoff of q-value(adjust p value).Detail see in [DESeq](#)
2. For more than two groups in taxobj, the 'comparison' must be assigned.
3. The function requires the 'DESeq2', 'S4Vectors', and 'tibble' packages.

**Author(s)**

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**See Also**

[DESeqDataSetFromMatrix](#), [DESeq](#), [DataFrame](#), [as\\_tibble](#)

**Examples**

```
if (requireNamespace("DESeq2", quietly = TRUE) &&
    requireNamespace("S4Vectors", quietly = TRUE) &&
    requireNamespace("tibble", quietly = TRUE)) {

  ### Data preparation ###
  data("Two_group")

  ### Deseq analysis ###
  deseq_results <- Deseq_analysis(
    taxobj = Two_group,
    taxlevel = "Genus",
    cutoff = 1,
    control_name = "Control"
  )

  # Visualization of volcano plot ##
  volcano_plot <- volcano_plot(
    inputframe = deseq_results,
    cutoff = 1,
    aes_col = Two_group$configuration$treat_col
  )
  volcano_plot$FC_FDR
  volcano_plot$Mean_FC

  # Visualization of Manhattan plot ##
```

```

manhattan_object <- manhattan(
  inputframe = deseq_results,
  taxlevel = "Phylum",
  control_name = "Control",
  mode = "most",
  top_n = 10,
  rmprefix = "p_"
)
manhattan_object$manhattan # Tradition manhattan plot
manhattan_object$manhattan_circle # Circular manhattan plot

# For object with more than two groups
### Data preparation ###
data("Three_group")

# Specific comparison
deseq_results_BFCF <- Deseq_analysis(
  taxobj = Three_group,
  taxlevel = "Genus",
  comparison = c("BF", "CF"),
  cutoff = 1,
  control_name = "CF"
)
volcano_plot <- volcano_plot(
  inputframe = deseq_results_BFCF,
  cutoff = 1,
  aes_col = Three_group$configuration$treat_col
)
volcano_plot$FC_FDR
} else {
  message(
    "The 'DESeq2', 'S4Vectors', and/or 'tibble' package(s) are not installed. ",
    "Please install them to use all features of Deseq_analysis."
  )
}
}

```

---

Deseq\_analysis2

*Deseq analysis*


---

## Description

Deseq analysis

## Usage

Deseq\_analysis2(inputframe, condition, cutoff, control\_name, paired, subject)

**Arguments**

inputframe	Otu/gene/taxa table with all integer numeric variables. Rownames must be Otu/gene/taxa names, colnames must be sample names with control in front and treatment behind. Reads table is recommended.
condition	A character string which indicates group of samples
cutoff	threshold of log <sub>2</sub> (Foldchange). Detail see in <a href="#">DESeq</a>
control_name	A character indicating the control group name
paired	Logical to determine if paired comparison would be used. TRUE or FALSE.
subject	A character string which indicates paired design of samples

**Value**

Statistics dataframe of all otu/gene/taxa

**Note**

1. Inputframe must be all integer numeric variables without NA/NAN/inf! In case your data is not an integer one, a practical method is to multiply them in equal proportion (eg. x 1e6) then round them into integer
2. Regulation is judged by cutoff of qvalue (adjust p value). Detail see in [DESeq](#)
3. Set cutoff as 1 is recommended. In case of too few taxa (eg. Phylum level deseql), cutoff can be set to 0.
4. If control\_name is not given, the control group will be set according to ASCII
5. The function requires the 'DESeq2', 'S4Vectors', and 'tibble' packages.

**Author(s)**

Wang Ningqi [2434066068@qq.com](mailto:2434066068@qq.com)

**See Also**

[DESeqDataSetFromMatrix](#), [DESeq](#), [DataFrame](#), [as\\_tibble](#)

**Examples**

```
{
  ### Data preparation ###
  data(testotu)
  rownames(testotu) <- testotu[, 1]
  inputotu <- testotu[, -c(1, ncol(testotu))]
  head(inputotu)
  group <- c(rep("a", 10), rep("b", 10))

  ### DESeq analysis ###
  if (requireNamespace("DESeq2", quietly = TRUE) &&
      requireNamespace("S4Vectors", quietly = TRUE) &&
      requireNamespace("tibble", quietly = TRUE)) {
```

```

Deseqresult <- Deseq_analysis2(
  inputframe = inputotu,
  condition = group,
  cutoff = 1,
  control_name = "b"
)

### Paired DESeq analysis ###
subject <- factor(c(1:10, 1:10))
Deseqresult <- Deseq_analysis2(
  inputframe = inputotu,
  condition = group,
  cutoff = 1,
  control_name = "b",
  paired = TRUE,
  subject = subject
)
}
}

```

---

differential\_bar

*Generate Differential Bar Plot and Error bar Plot*


---

## Description

Generate Differential Bar Plot and Error bar Plot

## Usage

```

differential_bar(
  taxobj,
  taxlevel,
  comparison = NULL,
  rel_threshold = 0.005,
  anno_row = "taxonomy",
  aes_col = NULL,
  limit_num = NULL
)

```

## Arguments

taxobj	Configured tax summary objects. See in <a href="#">object_config</a> .
taxlevel	Taxonomy levels used for visualization. Must be one of c("Domain", "Phylum", "Class", "Order", "Family",
comparison	A vector of conditions to compare. Default: NULL, all unique conditions are compared (only for Two groups).
rel_threshold	Threshold filtering taxa for differential analysis. Default: 0.005

anno_row	Default: 'taxonomy'. Rownames for visualization. Options are 'taxonomy' for showing taxonomic information and 'ID' for showing taxonomic ID.
aes_col	A named vector of colors to be used in the plots.
limit_num	Numeric. The maximum number of significant results to display. Default: NULL, showing all differential taxa.

**Value**

A list containing the bar plot, source data for the bar plot, difference plot, and source data for the difference plot.

**Note**

The differential analysis is performed using two-sided Welch's t-test. The p-values are adjusted using the 'BH' (i.e., FDR) method.

**Examples**

```
{
  # Data preparation
  data("Two_group")

  # Simple mode
  diff_results <- differential_bar(
    taxobj = Two_group,
    taxlevel = "Genus"
  )
  print(diff_results$Barplot) # Print Barplot
  head(diff_results$Barplot_sourcedata) # Show source data of barplot
  print(diff_results$Differenceplot) # Print Differential errorbar plot
  head(diff_results$Differenceplot_sourcedata) # Show source data of Differential errorbar plot

  require(patchwork)
  diff_results$Barplot|diff_results$Differenceplot
  # Displaying ID
  diff_results <- differential_bar(
    taxobj = Two_group,
    taxlevel = "Base",
    anno_row = "ID"
  )
  print(diff_results$Barplot)

  # Threshold adjustment
  diff_results <- differential_bar(
    taxobj = Two_group,
    taxlevel = "Base",
    rel_threshold = 0.001
  )
  print(diff_results$Barplot)

  # Limit the displaying number
```

```

diff_results <- differential_bar(
  taxobj = Two_group,
  taxlevel = "Base",
  rel_threshold = 0.001,
  limit_num = 10
)
print(diff_results$Barplot)

# For object with more than two groups
# Data preparation
data("Three_group")

# Specific comparison
Three_group_col <- Three_group$configuration$treat_col
diff_results <- differential_bar(
  taxobj = Three_group,
  taxlevel = "Genus",
  comparison = c("BF", "CF"),
  aes_col = Three_group_col
)
print(diff_results$Barplot)
}

```

---

Dimension\_reduction     *Dimension\_reduction: PCA, PCOA, and NMDS Analysis*

---

## Description

Performs dimension reduction analysis using PCA, PCOA, or NMDS.

## Usage

```
Dimension_reduction(inputframe, group, format)
```

## Arguments

inputframe	An OTU/gene/taxa table with all numeric variables and no NA/NAN/inf values.
group	Group information with the sample order the same as in inputframe.
format	The format of analysis: 1 for PCA, 2 for PCOA, 3 for NMDS.

## Value

A list containing data frames and other statistics for dimension reduction analysis.

## Note

Inputframe should be a numeric matrix without NA/NAN/inf values.

The row names of inputframe should be set as OTU/gene/taxa annotations for further analysis.

The results are combined into a list for output. Use `as.data.frame(result[[1]])` to extract the data frame, and `$result$` to extract other statistics. See examples for details.

**Author(s)**

Wang Ningqi [2434066068@qq.com](mailto:2434066068@qq.com)

**Examples**

```
### Data preparation ###
data(testotu)
rownames(testotu) <- testotu[, 1]
inputotu <- testotu[, -c(1, ncol(testotu))]
head(inputotu)

groupinformation1 <- data.frame(
  group = c(rep("a", 10), rep("b", 10)),
  factor1 = rnorm(10),
  factor2 = rnorm(mean = 100, 10)
)

### PCA ###
PCAresult <- Dimension_reduction(inputotu, groupinformation1, 1)
PCAframe <- PCAresult$outframe # Extract data for visualization
head(PCAresult$data.pca$rotation,5) # OTU coordinates

### PCOA ###
PCOAResult <- Dimension_reduction(inputotu, groupinformation1, 2)
PCOAframe <- PCOAResult$outframe # Extract data for visualization
head(PCOAResult$PCOA$values,2) # Explanation of first two axis

### NMDS ###
NMDSresult <- Dimension_reduction(inputotu, groupinformation1, 3)
NMDSframe <- NMDSresult$outframe # Extract data for visualization
# Here we got a warning of `stress is (nearly) zero: you may have insufficient data`,
# so make sure you have sufficient data for NMDS
print(NMDSresult$NMDSstat$stress) # Extract stress of NMDS
```

---

Facet\_group

*Tax summary object with Facet 2x2 Groups*

---

**Description**

Enraptured summary object with facet 2x2 Groups.Configuration has been assigned.

**Usage**

Facet\_group

**Format**

Tax summary object with configuration



---

Filter_function	<i>Filter OTU/ASV/metagenomic profile/gene profile by threshold</i>
-----------------	---

---

### Description

Sequenced data of taxonomy&gene still remains some sequencing error which we needed to be wiped off before analyzing. Here we provide function including four formats to wipe them clean.

### Usage

```
Filter_function(input, threshold, format, report = TRUE)
```

### Arguments

input	Data frame of absolute abundance of standard OTU table,with the first column of OTUID and the final column of taxonomy annotation. If your data frame is gene table or not a standard OTU table, please manually transformed into a standard input data frame.
threshold	threshold of filter.Relative abundance for format 1 and 4, reads number for format 2, sample size for format 3
format	1:filter OTU/gene below overall-sample relative abundance threshold(<) 2:filter OTU/gene below overall-sample reads threshold(<) 3:filter OTU/gene reads 0 over threshold sample size(>) 4:filter OTU/gene below relative abundance threshold in each sample(<)
report	Logical. If print report to console. Default:TRUE

### Value

Dataframe of OTU/gene in format of absolute abundacne(reads) or relative abundance(%)

### Author(s)

Wang Ningqi

### Examples

```
### Data frame with absolute abundance (reads)###
### And first column of OTUID and last column of taxonomy ###
data(testotu)

#### If your data frame does not contain the OTUID column or taxonomy column,
#### you can add a simulated column to fit the input format like testotu ##

### 1. Filter OTU with total relative abundance below 0.0001###
filtered_otu <- Filter_function(
  input = testotu,
  threshold = 0.0001,
```

```
    format = 1
  )

### 2. Filter OTU with total reads below 20 ###
filtered_otu <- Filter_function(
  input = testotu,
  threshold = 20,
  format = 2
)

### 3. Filter OTU reads 0 over (>=) 11 samples ###
filtered_otu <- Filter_function(
  input = testotu,
  threshold = 11,
  format = 3
)

### 4. Filter OTU with relative abundance below 0.0001 in each sample ###
filtered_otu <- Filter_function(
  input = testotu,
  threshold = 0.0001,
  format = 4
)
```

---

indicator\_analysis      *Indicator Analysis*

---

## Description

Performs the indicator analysis based on taxonomic summary object

## Usage

```
indicator_analysis(taxobj, taxlevel, func = "r.g", reads = FALSE)
```

## Arguments

taxobj	Configured tax summary objects. See in <a href="#">object_config</a> .
taxlevel	taxonomy levels used for visualization. Must be one of c("Domain", "Phylum", "Class", "Order", "Family", "Genus", "Species").
func	Default: "r.g". The function to use for the indicator analysis, see in <a href="#">multipatt</a>
reads	A logical value indicating whether the input data is in terms of raw reads (TRUE) or relative abundance (FALSE)

## Value

A data frame with the results of the indicator analysis, including adjusted p-values, tags and taxonomic information.

**Note**

This function depends on the following packages: `indicspecies`, `permute`. These packages are not automatically loaded and should be installed before using this function.

**See Also**

[multipatt](#), [how](#)

**Examples**

```
data("Two_group")
if (requireNamespace("indicspecies", quietly = TRUE) &&
    requireNamespace("permute", quietly = TRUE)) {
  set.seed(999)
  indicator_results <- indicator_analysis(
    taxobj = Two_group,
    taxlevel = "Genus"
  )
  head(indicator_results)
}
```

---

`kruskal_report`*Print Kruskal-Wallis Rank Sum Test report*

---

**Description**

Print Kruskal-Wallis Rank Sum Test report

**Usage**

```
kruskal_report(
  data,
  treatment_col,
  value_col,
  prior = FALSE,
  comparison_method = "Auto",
  equally_rep = TRUE,
  report = TRUE
)
```

**Arguments**

<code>data</code>	Data frame containing the treatment, value and other information.
<code>treatment_col</code>	Numeric indicating where treatment locates (column number) in data.
<code>value_col</code>	Numeric indicating where treatment value (column number) in data.
<code>prior</code>	logical. Whether conducted prior comparisons.

comparison_method	Default would automatically choose method. Method of multiple comparison, must be one of "SNK" or "Tukey".
equally_rep	Logical. Whether all treatments have same number of replication.
report	Logical. If print report to console. Default:TRUE

**Value**

kruskal\_report returns list with

- 1)basic data description
- 2)summary of Kruskal-Wallis Rank Sum Test
- 3)model of multiple comparison
- 4)difference of multiple comparison
- 5)letters of multiple comparison, which could be use for visualization.

**Examples**

```
data("cotton",package ="agricolae" )
kruskal_results=kruskal_report(data = cotton,treatment_col =3,value_col = 5)
##here returns NULL because no significance among groups

##to conduct prior comparisons.
kruskal_results=kruskal_report(data = cotton,treatment_col =3,value_col = 5,prior = TRUE)

data("iris")
kruskal_results=kruskal_report(data = iris,treatment_col = 5,value_col = 2)

###extract return##

###basic data description
kruskal_results$basicdata

###summry of Kruskal-Wallis Rank Sum Test
kruskal_results$Kruskal_Wallis_summary

###model of multiple comparision
kruskal_results$muiltiple_comparision_model

###difference of multiple comparision
kruskal_results$comparision_results

###letters of multiple comparision, which could be use for visualization.
kruskal_results$comparision_letters
```

---

LorMe

*LorMe package: Lightning One-Code Resolving Microbial Ecology Program*

---

## Description

LorMe package summarizes a series of functions normally used in microbiome analysis analysis.

## Details

`_PACKAGE`

`#Basic functions####`

`auto_signif_test` Automatically conduct significance testing

`compare_plot` Comparison plot generator

`Filter_function` Filter OTU/ASV/metagenomic profile/gene profile by threshold

`tax_summary` Encapsulate meta file, feature tables and taxonomy annotation into tax summary object

`sub_tax_summary` subsets tax summary objects according to meta file

`combine_and_translate` Combine feature table with meta file and transform into a recognizable data frame for visualization.

`color_scheme` generate color scheme from nine color scheme database and expand into colorRamp

`theme_zg` A classic theme for ggplot.

`#Community features####`

`Alpha_diversity_calculator` Calculator for alpha diversity of each sample.

`Dimension_reduction` Dimension reduction analysis including PCA,PCOA and NMDS

`structure_plot` A fast view of microbial structure with PCA plot,PCOA plot and NMDS plot.

`Top_taxa` Calculate most abundant taxon

`community_plot` A fast view of microbial community with bar plot,alluvial plot and area plot.

`#Differential analysis####`

`Deseq_analysis` Performs a differential expression analysis

`indicator_analysis` Performs the indicator analysis based on taxonomic summary object

`differential_bar` Generate Differential Bar Plot and errorbar plot

`volcano_plot` Generate volcano plot base on Deseq\_analysis or indicator\_analysis results

`manhattan` Generate Manhattan Plot base on Deseq\_analysis or indicator\_analysis results

`#Network analysis####`

`network_analysis` A convenient and fast network analysis function, with output results suitable for cytoscape and gephi

`network_withdiff` Meta network analysis integrating differential taxon into a network analysis

`network_visual` Visualizes a network based on network object from `network_analysis`

[network\\_visual\\_re](#) Re-visualize or adjust network plot from [network\\_visual](#) or [network\\_withdiff](#)

[Module\\_composition](#) Pie chart for network module composition

[Module\\_abundance](#) Calculate network module abundance for each sample

[nc](#) Calculate network Natural Connectivity

[NC\\_remove](#) Conduct natural connectivity analysis

[#Correlation analysis####](#)

[circulation\\_lm](#) Quick test using circulation to fit linear models between one dependent variable and series of independent variable

[tbRDA\\_analysis](#) RDA analysis including co-linearity diagnostics and necessary statistics.

**Author(s)**

Wang Ningqi

manhattan

*Manhattan Plot Generator***Description**Generate Manhattan Plot base on [Deseq\\_analysis](#) or [indicator\\_analysis](#) results**Usage**

```
manhattan(
  inputframe,
  taxlevel = "Phylum",
  control_name,
  mode = "all",
  top_n = NULL,
  palette = "Set1",
  select_tax = NULL,
  rmprefix = NULL
)
```

**Arguments**

<code>inputframe</code>	A data frame generated from <a href="#">Deseq_analysis</a> or <a href="#">indicator_analysis</a>
<code>taxlevel</code>	Taxonomy levels used for visualization. Must be one of <code>c("Domain", "Phylum", "Class", "Order", "Family", "Genus", "Species")</code>
<code>control_name</code>	Character. The name of the control group for the comparison.
<code>mode</code>	The mode for selecting which taxa to plot: "all" for all taxa, "most" for the top N taxa, and "select" for specific taxa selection
<code>top_n</code>	The number of top taxa to plot when mode is set to "most"
<code>palette</code>	Character. Palette for visualization, default: "Set1". Optional palette same as 'RColorBrewer'. "Plan1" to "Plan10" were also optional, see in <a href="#">color_scheme</a>
<code>select_tax</code>	A vector of taxa to be selected for plotting when mode is "select".
<code>rmprefix</code>	A string prefix to be removed from the taxonomic annotation. Default: NULL.

**Value**

a list containing the Manhattan plot, circular Manhattan plot, source data, and color assignments

**Examples**

```
{
# Data preparation
data("Two_group")

# DESeq analysis
deseq_results <- Deseq_analysis(
  taxobj = Two_group,
  taxlevel = "Base",
  cutoff = 1,
  control_name = "Control"
)

# Indicator analysis
indicator_results <- indicator_analysis(
  taxobj = Two_group,
  taxlevel = "Genus"
)

# Show all with Manhattan plot
manhattan_object <- manhattan(
  inputframe = deseq_results,
  taxlevel = "Phylum",
  control_name = "Control"
)
print(manhattan_object$manhattan) # Tradition Manhattan plot
print(manhattan_object$manhattan_circle) # Circular Manhattan plot
print(manhattan_object$sourcedata) # Source data for plot
print(manhattan_object$aes_color) # Aesthetic color for plot

# Top 8 Phyla with most taxon
manhattan_object <- manhattan(
  inputframe = indicator_results,
  taxlevel = "Phylum",
  control_name = "Control",
  mode = "most",
  top_n = 8,
  palette = "Set1"
)
print(manhattan_object$manhattan)

# Specific phyla
# Top nine dominant phyla
community <- community_plot(
  taxobj = Two_group,
  taxlevel = "Phylum",
  n = 9,
  palette = "Paired",
```

```

    rmprefix = "p_"
  )

  manhattan_object <- manhattan(
    inputframe = indicator_results,
    taxlevel = "Phylum",
    control_name = "Control",
    mode = "select",
    palette = community$filled_color,
    select_tax = names(community$filled_color),
    rmprefix = "p_"
  )
  print(manhattan_object$manhattan)
  print(manhattan_object$manhattan_circle)
}

```

---

Module_abundance	<i>Calculate network module abundance for each sample</i>
------------------	---

---

### Description

Calculate network module abundance for each sample

### Usage

```
Module_abundance(network_obj, No.module)
```

### Arguments

network_obj	Network analysis results generated from <a href="#">network_analysis</a>
No.module	Numeric or numeric vector of No.module

### Value

A list containing module abundance in metafile and column table of corresponding data frame

### Examples

```

#data preparation
data("Two_group")
##network analysis
network_results<- network_analysis(taxobj = Two_group,taxlevel = "Genus",n = 10,threshold = 0.8)
require(ggplot2)
#one module
moduleframe=Module_abundance(network_obj =network_results,No.module = 3 )
moduleframe$rowframe #combine into metafile
moduleframe$columnframe #column table
#statistics

```



```

moduleframe$plotlist$Plotobj_Module3$Statistics
#extract plot
moduleframe$plotlist$Plotobj_Module3$Barplot
moduleframe$plotlist$Plotobj_Module3$Boxplot
moduleframe$plotlist$Plotobj_Module3$Violinplot

#multiple modules
moduleframe=Module_abundance(network_results,c(1,3,6))
moduleframe$rowframe
moduleframe$columnframe #column table can be used in ggplot visualization
#same as above to extract plots and statistics
moduleframe$plotlist$Plotobj_Module6$Barplot

```

---

Module\_composition      *Pie chart for network module composition*

---

## Description

This function analyzes the composition of modules within a network object, providing a visual and data summary based on taxonomic levels.

## Usage

```

Module_composition(
  network_obj,
  No.module,
  taxlevel = "Phylum",
  mode = "all",
  top_n = NULL,
  palette = "Set1",
  select_tax = NULL,
  rmprefix = NULL
)

```

## Arguments

network_obj	Network analysis results generated from <a href="#">network_analysis</a>
No.module	Numeric or numeric vector of No.module
taxlevel	Taxonomy levels used for visualization. Must be one of c("Domain", "Phylum", "Class", "Order", "Family", "
mode	The mode for selecting which taxa to plot: "all" for all taxa, "most" for the top N taxa, and "select" for specific taxa selection
top_n	The number of top taxa to plot when mode is set to "most"
palette	Character. Palette for visualization, default: "Set1". See optional palette in same as 'RColorBrewer'. And "Plan1" to "Plan10" were also optional, see in <a href="#">color_scheme</a>
select_tax	A vector of taxa to be selected for plotting when mode is "select".
rmprefix	A string prefix to be removed from the taxonomic annotation

**Value**

The function returns a list containing pie chart of specific module, corresponding source data and color assignments

**Examples**

```
#Data loading
data("Two_group")

# Network analysis
network_Two_group <- network_analysis(
  taxobj = Two_group,
  taxlevel = "Genus",
  reads = TRUE,
  n = 8,
  threshold = 0.7
)

# Show all taxa
module_results <- Module_composition(
  network_obj = network_Two_group,
  No.module = c(2, 5),
  taxlevel = "Phylum"
)
print(module_results$Module5$Pie)
print(module_results$Module2$Pie) # View pie chart
head(module_results$Module2$source_data_Module2) # View source data for pie chart
print(module_results$aes_color) # Check aesthetic color

# Show taxa with top five frequency
module_results <- Module_composition(
  network_obj = network_Two_group,
  No.module = c(2, 5),
  taxlevel = "Phylum",
  mode = "most",
  top_n = 5
)
print(module_results$Module2$Pie_plot_Module2)

# Show specific taxa
community <- community_plot(
  taxobj = Two_group,
  taxlevel = "Phylum",
  n = 5,
  palette = "Paired"
) # Get top 5 dominant phyla
top5_phyla <- names(community$filled_color)

module_results <- Module_composition(
  network_obj = network_Two_group,
  No.module = c(2, 5),
  taxlevel = "Phylum",
```

```

    mode = "select",
    palette = community$filled_color,
    select_tax = top5_phyla
  )
  print(module_results$Module2$Pie_plot_Module2)

  # Specific taxa with no prefix 'p__'
  module_results <- Module_composition(
    network_obj = network_Two_group,
    No.module = 2,
    taxlevel = "Phylum",
    mode = "select",
    select_tax = c("Proteobacteria", "Actinobacteria")
  )
  print(module_results$Module2$Pie_plot_Module2)

  # Remove 'p__' prefix
  module_results <- Module_composition(
    network_obj = network_Two_group,
    No.module = 2,
    taxlevel = "Phylum",
    mode = "most",
    top_n = 5,
    palette = "Set2",
    rmprefix = "p__"
  )
  print(module_results$Module2$Pie_plot_Module2)

```

---

 nc

---

*Calculate Network Natural Connectivity*


---

### Description

Calculate Network Natural Connectivity

### Usage

```
nc(adj_matrix)
```

### Arguments

`adj_matrix` Adjacency data frame or matrix. Can be calculated from [network\\_analysis](#)

### Value

Numeric value of natural connectivity

## Examples

```
{
  ### Data preparation ###
  data("Two_group")

  ### One input network analysis ###
  network_results <- network_analysis(
    taxobj = Two_group,
    taxlevel = "Base",
    reads = FALSE,
    n = 10,
    threshold = 0.6
  )

  # Convert network results to a data frame for the adjacency matrix
  network_matrix <- as.data.frame(network_results[[3]]) # Complete adjacency matrix

  # Check initial natural connectivity
  nc_initial <- nc(network_matrix)
  print(nc_initial) # Print the initial natural connectivity
}
```

---

NC\_remove

*Natural connectivity analysis*

---

## Description

Natural connectivity analysis

## Usage

```
NC_remove(input, num, seed = 1)
```

## Arguments

input	Network adjacency matrix. Can be generated by <a href="#">network_analysis</a>
num	Max number of removed nodes. Default: Automatically match max number that can be removed.
seed	Random seed Number to be set. Default: 1. See in <a href="#">set.seed</a>

## Value

NC\_remove returns data frame with removed nodes and corresponding natural connectivity

## Author(s)

Wang Ningqi [2434066068@qq.com](mailto:2434066068@qq.com)

**Examples**

```
{
  ### Data preparation ###
  data("Two_group")

  ### One input network analysis ###
  network_results <- network_analysis(
    taxobj = Two_group,
    taxlevel = "Base",
    reads = FALSE,
    n = 10,
    threshold = 0.6
  )

  network_matrix <- as.data.frame(network_results[[3]]) # Complete adjacency matrix

  # Check initial natural connectivity
  nc <- nc(network_matrix)

  # Conduct natural connectivity analysis
  nc_remove <- NC_remove(input = network_matrix)
  head(nc_remove)
  tail(nc_remove)

  # Set target number for natural connectivity analysis
  nc_remove <- NC_remove(input = network_matrix, num = 400)
}
```

---

**network\_analysis***Conduct Network analysis based on tax summary object*

---

**Description**

Conduct Network analysis based on tax summary object

**Usage**

```
network_analysis(
  taxobj,
  taxlevel,
  reads = FALSE,
  n,
  threshold,
  rel_threshold = 0,
  method = "spearman",
  display = TRUE
)
```

**Arguments**

taxobj	tax summary objects computed by <code>tax_summary</code> .
taxlevel	taxonomy levels used for analysis. Must be one of <code>c("Domain", "Phylum", "Class", "Order", "Family", "Genus")</code> .
reads	Logical, default: FALSE. Taxonomy abundance type used in analysis. FALSE for relative abundance, TRUE for absolute abundance.
n	Numeric. Number of sample size indicating kept asv/otu/gene/taxa appearing. Recommended to set more than half of total sample size.
threshold	Numeric. Threshold of absolute correlation value (r value for pearson method and rho value for spearman method).
rel_threshold	Numeric. Threshold of relative abundance included in the network analysis. Default: 0
method	Character, default: "spearman". A character indicating which correlation coefficient method to be computed. One of "pearson" or "spearman"
display	Logical, default: TRUE. If display a preview plot of network based on igraph. FALSE for the first attempt is recommended in case of too many vertices and edges.

**Details**

1. We had optimized the correlation algorithm to achieve a faster running speed. It takes less than 2 minute to calculate dataframe correlation and p value which more than 400 samples and 10000 OTUs for computer with dual Core i5 processor. However, too many vertices (>2000) or links (>10000) may slow the statistical process and visualization, so we recommend that in your first attempt, set `display` paramter as F to have a preview. Then you can adjust your `n/threshold/method` paramter to generate a suitable visualization network
2. We display a preview plot so as to adjusting your network. Generally a global figure (like we show in examples) with less than 1000 vertices and 5000 edges/links is recommended. Further more, we recommend you to output the statistics and adjacency table and use software like cytoscape or gephi for better visualization.

**Value**

One list contains nodes information table, adjacency column table, adjacency matrix and 'igraph' object.

**Note**

1. Replicates should be at least 5, more than 8 is recommend.
2. In case of too many edges/links or not a global network plot, you can stop the process immediately to prevent wasting too much time.

**Examples**

```
{
  ### Data preparation ###
  data("Two_group")
  set.seed(999)
```

```
## Analysis
network_results <- network_analysis(
  taxobj = Two_group,
  taxlevel = "Genus",
  n = 10,
  threshold = 0.8
)

# Nodes information table
network_nodes <- network_results$Nodes_info
head(network_nodes)

# Adjacency table
network_adjacency <- network_results$Adjacency_column_table
head(network_adjacency)

# Complete adjacency matrix
network_matrix <- network_results$Adjacency_matrix
print(network_matrix[1:10, 1:10])

# igraph object
igraph_object <- network_results$Igraph_object
network_stat(igraph_object) # In case you want to see statistics again
# or do other analysis based on igraph.
}
```

---

network\_analysis2      *Conduct Network analysis*

---

## Description

A convenient and fast network analysis function, with output results suitable for cytoscape and gephi

## Usage

```
network_analysis2(
  input,
  inputtype,
  n,
  threshold,
  method = "spearman",
  display = TRUE,
  input2,
  input2type
)
```

**Arguments**

input	Input dataframe with otu/gene/taxa in row and sample ID in column,at least 5 replicates(more than 8 replicates are recommended).
inputtype	Input dataframe type 1:dataframe with first column of OTUID and last column of taxonomy 2:dataframe with first column of OTUID/taxonomy 3:dataframe of all numeric
n	Only keep otu/gene/taxa appearing in n sample size
threshold	Threshold of correlation r value
method	A character string indicating which correlation coefficient is to be computed. One of "pearson" or "spearman"
display	If display a preview plot of network based on igraph. FALSE for the first attempt is recommended in case of too many vertices and edges.
input2	A second input data frame with otu/gene/taxa in row and sample ID in column. Default:NULL
input2type	The second input data frame type. Details the same as above. Default:NULL

**Details**

1. We had optimized the correlation algorithm to achieve a faster running speed. It takes less than 2 minute to calculate dataframe correlation and p value which more than 400 samples and 10000 OTUs for computer with dual Core i5 processor. However, too many vertices(>2000) or links(>10000) may slow the statistical process and visualization,so we recommend that in your first attempt,set display paramter as F to have a preview. Then you can adjust your n/threshold/method paramter to generate a suitable visualization network
2. We display a preview plot so as to adjusting your network. Generally a global figure (like we show in examples) with less than 1000 vertices and 5000 edges/links is recommended. Further more,we recommend you to output the statistics and adjacency table and use software like cytoscape or gephi for better visualization.

**Value**

One list contains a statistics table of network vertices/nodes and an adjacency table. One preview plot of network in the plot interface and an igraph object(named igraph1) in global environment.

**Note**

1. Replicates should be at least 5,more than 8 is recommend.
2. In case of too many edges/links or not a global network plot, you can stop the process immediately to prevent wasting too much time.

**Author(s)**

Wang Ningqi [2434066068@qq.com](mailto:2434066068@qq.com)



**Examples**

```

{
  ### Data preparation ###
  data(testotu)
  rownames(testotu) <- testotu[, 1]
  inputotu <- testotu[, -c(1, ncol(testotu))]
  head(inputotu)
  set.seed(999)
  ### One input network analysis ###
  network_result <- network_analysis2(
    inputotu,
    3,
    10,
    0.9,
    "spearman",
    TRUE
  )

  # Nodes information table
  network_nodes <- network_result$Nodes_info
  head(network_nodes)

  # Adjacency table
  network_adjacency <- network_result$Adjacency_column_table
  head(network_adjacency)

  # Complete adjacency matrix
  network_matrix <- network_result$Adjacency_matrix
  print(network_matrix[1:10, 1:10])

  # igraph object
  igraph_object <- network_result$Igraph_object
  network_stat(igraph_object) # In case you want to see statistics again
  # or do other analysis based on igraph.

  ### Two inputs network analysis ###
  inputotu1 <- inputotu[1:456, ]
  inputotu2 <- inputotu[524:975, ]
  network_result <- network_analysis2(
    input = inputotu1,
    inputtype = 3,
    input2 = inputotu2,
    input2type = 3,
    n = 10,
    threshold = 0.85,
    method = "spearman",
    display = TRUE
  )

  #### Incorrect demonstration !! ####
  {
    network_result <- network_analysis2(inputotu, 3, 3, 0.8, "spearman", TRUE)
  }

```

```
}  
# Total edges/links: 10199  
# Total vertices: 826  
# Too many edges and not a global network  
}
```

---

network_stat	<i>Igraph network statistics</i>
--------------	----------------------------------

---

### Description

Igraph network statistics

### Usage

```
network_stat(input, report = TRUE)
```

### Arguments

input	An igraph object.
report	Logical. If print report to console. Default:TRUE

### Value

network statistics

### Author(s)

Wang Ningqi [2434066068@qq.com](mailto:2434066068@qq.com)

---

network_visual	<i>Network Visualization</i>
----------------	------------------------------

---

### Description

Visualizes a network based on a network object from [network\\_analysis](#).

**Usage**

```
network_visual(
  network_obj,
  mode = "major_module",
  major_num = 5,
  taxlevel = NULL,
  select_tax = NULL,
  palette = "Set1",
  vertex.size = 6
)
```

**Arguments**

network_obj	A network analysis results object generated from <a href="#">network_analysis</a> .
mode	The visualization mode, optionally "major_module" or "major_tax".
major_num	The number of major modules to display in the network.
taxlevel	Taxonomy levels used for visualization when mode is "major_tax".
select_tax	A vector of taxa to be selected for displaying in "major_tax" mode.
palette	Character. Palette for visualization.
vertex.size	Numeric. The size of the vertices.

**Value**

A list containing the configured igraph object and the coordinates of the vertices, with network visualization displayed in the plots panel.

**Examples**

```
{
# Data preparation
data("Two_group")
set.seed(999)
# Analysis
network_results <- network_analysis(
  taxobj = Two_group,
  taxlevel = "Species",
  n = 10,
  threshold = 0.6
)

# Default mode
network_visual_obj <- network_visual(network_obj = network_results)

# View again
network_visual_re(network_visual_obj)

# More modules
network_visual_obj <- network_visual(
```



**Arguments**

network_visual_obj	Network object from <a href="#">network_visual</a> or <a href="#">network_withdiff</a>
module_paint	Logical. If network module should be painted. Only work for network object from <a href="#">network_withdiff</a> .
module_num	Numeric indicating which module to be painted.
module_palette	Character string with at least two elements. Palette for painting modules.
vertex.size	Numeric. The size of the vertices, default:6. Only for network object from <a href="#">network_visual</a>
vertex.shape	Character. The shape of vertices, default: "circle"

**Value**

NULL but visualization in plot panel.

---

network\_withdiff      *Network Analysis with Differential Species*

---

**Description**

Meta network analysis integrating differential taxon into a network analysis

**Usage**

```
network_withdiff(network_obj, diff_frame, aes_col = NULL, tag_threshold = 5)
```

**Arguments**

network_obj	Network analysis results generated from <a href="#">network_analysis</a>
diff_frame	Differential analysis results generated from <a href="#">indicator_analysis</a> or <a href="#">Deseq_analysis</a> .
aes_col	A named vector of colors to be used to highlight differential taxon vertices
tag_threshold	Numeric. A threshold for the minimum number of differential taxon to display.

**Value**

A list containing the configured igraph object, vertices coordinates, parameters, and tag statistics.

**Examples**

```

{
  # Data preparation
  data("Two_group")
  set.seed(999)
  # Analysis
  network_results <- network_analysis(
    taxobj = Two_group,
    taxlevel = "Genus",
    n = 10,
    threshold = 0.8
  )
  indicator_results <- indicator_analysis(
    taxobj = Two_group,
    taxlevel = "Genus"
  )
  deseq_results <- Deseq_analysis(
    taxobj = Two_group,
    taxlevel = "Genus",
    cutoff = 1,
    control_name = "Control"
  )

  # Visualize
  network_diff_obj <- network_withdiff(
    network_obj = network_results,
    diff_frame = indicator_results
  )
  # Check contained tags for each model
  print(network_diff_obj$tag_statistics$sum_of_tags)
  # Check contained different tags for each model
  print(network_diff_obj$tag_statistics$detailed_tags)

  # Re-visualize
  network_visual_re(
    network_visual_obj = network_diff_obj,
    module_paint = TRUE,
    module_num = c(1, 4)
  ) # Show module with most Treatment indicators

  my_module_palette <- color_scheme(
    c("#83BA9E", "#F49128"),
    5
  )
  network_visual_re(
    network_visual_obj = network_diff_obj,
    module_paint = TRUE,
    module_num = c(1, 4, 6, 3, 8),
    module_palette = my_module_palette
  ) # Show module with most Treatment indicators

  # Available also for DESeq analysis results

```

```
network_diff_obj <- network_withdiff(  
  network_obj = network_results,  
  diff_frame = deseq_results  
)  
  
# Parameter adjustment  
network_diff_obj <- network_withdiff(  
  network_obj = network_results,  
  diff_frame = indicator_results,  
  tag_threshold = 20  
) # The 'tag_threshold' set too high  
  
network_diff_obj <- network_withdiff(  
  network_obj = network_results,  
  diff_frame = indicator_results,  
  tag_threshold = 10  
) # Set lower  
# Check contained tags for each model  
print(network_diff_obj$tag_statistics$sum_of_tags)  
# Check contained different tags for each model  
print(network_diff_obj$tag_statistics$detailed_tags)  
  
network_diff_obj <- network_withdiff(  
  network_obj = network_results,  
  diff_frame = indicator_results,  
  tag_threshold = 1  
) # Set too low  
  
# Another example  
data("Three_group")  
network_results <- network_analysis(  
  taxobj = Three_group,  
  taxlevel = "Genus",  
  n = 15,  
  threshold = 0.9  
)  
indicator_results <- indicator_analysis(  
  taxobj = Three_group,  
  taxlevel = "Genus"  
)  
  
tag_color <- c(  
  "CF" = "#F8766D",  
  "CF_OF" = "#FFFF00",  
  "OF" = "#00BA38",  
  "OF_BF" = "#800080",  
  "BF" = "#619CFF",  
  "CF_BF" = "#00FFFF"  
)  
network_diff_obj <- network_withdiff(  
  network_obj = network_results,  
  diff_frame = indicator_results,  
  aes_col = tag_color,
```

```

    tag_threshold = 10
  )

  # Re-visualize
  print(network_diff_obj$tag_statistics$detailed_tags)
  network_visual_re(
    network_visual_obj = network_diff_obj,
    module_paint = TRUE,
    module_num = c(8, 10, 11)
  ) # Show module with most BF indicators
  network_visual_re(
    network_visual_obj = network_diff_obj,
    module_paint = TRUE,
    module_num = c(1, 6, 8)
  ) # Show module with most BF and OF_BF indicators
}

```

---

object\_config

*Set taxonomy summary configuration*


---

### Description

This function set taxonomy summary configuration by assigning treatment column number, facet column number, replication column number, treatment mapping color, treatment order and facet order.

### Usage

```

object_config(
  taxobj,
  treat_location,
  facet_location = NULL,
  rep_location,
  subject_location = NULL,
  treat_col = NULL,
  treat_order = NULL,
  facet_order = NULL
)

```

### Arguments

taxobj            Taxonomic summary object generated by [tax\\_summary](#)

treat\_location   Numeric. Treatment column number in metafile/groupinformation.

facet\_location   Numeric, default:NULL. Facet column number in metafile/groupinformation.

rep\_location     Numeric. Replication column number in metafile/groupinformation.



subject_location	Numeric, default:NULL. Subject column number in metafile/group information (used for pairwise experiment).
treat_col	Named character string, default:NULL. A set of aesthetic character to map treatment to.
treat_order	Character string, default:NULL. The character string indicating treatment displaying order.
facet_order	Character string, default:NULL. The character string indicating facet displaying order.

**Value**

object\_config returns taxonomy summary object with configuration.

**Author(s)**

Wang Ningqi [2434066068@qq.com](mailto:2434066068@qq.com)

**Examples**

```
{
  ### Data preparation ###
  data(testotu)
  groupinformation <- data.frame(
    group = c(rep("a", 10), rep("b", 10)),
    factor1 = rnorm(10),
    factor2 = rnorm(mean = 100, 10),
    subject = factor(c(1:10, 1:10)),
    group2 = c(rep("e", 5), rep("f", 5), rep("e", 5), rep("f", 5))
  )

  ### Packaging metafile, community data, and taxonomy table ###
  test_object <- tax_summary(
    groupfile = groupinformation,
    inputtable = testotu[, 2:21],
    reads = TRUE,
    taxonomytable = testotu[, c(1, 22)]
  )

  ### Object configuration ###
  test_object_plan1 <- object_config(
    taxobj = test_object,
    treat_location = 1,
    rep_location = 4
  )

  ### Facet configuration ###
  test_object_plan2 <- object_config(
    taxobj = test_object,
    treat_location = 1,
    rep_location = 4,
```



**Examples**

```

####data preparation####
data("Two_group")

####analysis####
set.seed(999)
community_structure<- structure_plot(taxobj = Two_group,taxlevel = "Base")
#check output list in console (not run)
#####Output list##
#####Plot#
####PCApplot:named as('PCA_Plot')(1/3)
####PCoAplot:named as('PCoA_Plot')(2/3)
####NMDSplot:named as('NMDS_Plot')(3/3)
#####Analysis object#
####PCA object:named as('PCA_object')
####PCoA object:named as('PCoA_object')
####NMDS object:named as ('NMDS_object')
#####Coordinates dataframe#
####PCA Coordinates dataframe:named as('PCA_coordinates')
####PCoA Coordinates dataframe:named as('PCoA_coordinates')
####NMDS Coordinates dataframe:named as('NMDS_coordinates')
#####Done##
#check PERMANOVA results
community_structure$PERMANOVA_statistics

#extract plot
community_structure$PCA_Plot
community_structure$PCoA_Plot
community_structure$NMDS_Plot

#extract object
PCA_obj<- community_structure$PCA_object
print(PCA_obj)

#extract coordinates frame
PCA_coord<- community_structure$PCA_coordinates
head(PCA_coord)

#stick plot
set.seed(999)
community_structure<- structure_plot(taxobj = Two_group,taxlevel = "Base",diagram = "stick")
community_structure$PCoA_Plot

#faced form
data("Facet_group")
set.seed(999)
community_structure<- structure_plot(taxobj = Facet_group,taxlevel = "Genus",diagram = "stick")
community_structure$PERMANOVA_statistics
community_structure$PCA_Plot
community_structure$PCoA_Plot
community_structure$NMDS_Plot

```

---

sub_tax_summary	<i>Subsetting tax summary objects</i>
-----------------	---------------------------------------

---

**Description**

Subsetting tax summary objects

**Usage**

```
sub_tax_summary(taxobj, ..., specificnum = NULL, taxnum = NULL)
```

**Arguments**

taxobj	tax summary objects computed by <a href="#">tax_summary</a> .
...	logical expression that are defined in terms of the variables in Groupfile of tax summary objects. See details in <a href="#">subset</a> .
specificnum	specific numbers indicating samples to keep based on Groupfile of tax summary objects.
taxnum	specific numbers indicating taxonomy to keep based on Base file

**Value**

Subset of tax summary objects. Same as [tax\\_summary](#).

**Author(s)**

Wang Ningqi [2434066068@qq.com](mailto:2434066068@qq.com)

**Examples**

```
data("Three_group")

# Check meta file
print(Three_group$Groupfile)

# Subsetting tax summary objects

# Select BF and OF groups
sub_testtax_summary <- sub_tax_summary(Three_group, Group %in% c("BF", "OF"))
print(sub_testtax_summary$Groupfile)

# Subsetting according to taxonomy

Proteo <- sub_tax_summary(
  Three_group,
  taxnum = which(Three_group$Base_taxonomy$Phylum == "p__Proteobacteria")
)
print(Proteo$Phylum_percent) # Check phylum table
print(Proteo$Genus_percent) # Check genus table
```

---

tax_summary	<i>Encapsulate meta file, feature tables and taxonomy annotation into tax summary object</i>
-------------	--

---

### Description

The function packages meta file, feature tables and taxonomy annotation into tax summary object

### Usage

```
tax_summary(
  groupfile,
  inputtable,
  reads = TRUE,
  taxonomytable,
  into = "standard",
  sep = ";",
  outputtax = c("Phylum", "Genus")
)
```

### Arguments

groupfile	A data frame containing treatment information
inputtable	OTU/ASV/species data frame with all numeric. Samples ID should be in column names.
reads	Logical.True for reads table and FALSE for percentage table. Default: TRUE
taxonomytable	Taxonomy annotation data frame,with first column OTU/ASV/TAX number ID and second column taxonomy annotation. See details in example.
into	Names of separated taxonomy to create as character vector. Must select from c("Domain","Phylum","Class","Order","Family","Genus","Species"). Shortcut input: 1)By default."standard":c("Domain","Phylum","Class","Order","Family","Genus","Species"). Used for standard taxonomy annotation to OTU/ASV table. 2)"complete":c("Domain","Kingdom","Phylum","Class","Order","Family","Genus","Species"). Used for complete taxonomy annotation to meta genomic table.
sep	Separator of taxonomy table.Default: ";"
outputtax	Names of output taxonomy level table. Default:c("Phylum","Genus"). Shortcut input is available with 'standard' and 'complete' same as above.

### Value

One list containing taxonomy table data frame,containing reads and percentage table for each specified output. Full taxonomy annotation data frame is output in global environment.

### Note

For taxonomy annotation with 'Kingdom' level, please set 'into' parameter as 'complete'!!!

**Author(s)**

Wang Ningqi [2434066068@qq.com](mailto:2434066068@qq.com)

**Examples**

```
{
  # Load data
  data(testotu)

  # Create group information data frame
  groupinformation <- data.frame(
    group = c(rep("a", 10), rep("b", 10)),
    factor1 = rnorm(10),
    factor2 = rnorm(mean = 100, 10),
    subject = factor(c(1:10, 1:10))
  )

  # Packaging data into a taxonomy summary object
  test_object <- tax_summary(
    groupfile = groupinformation,
    inputtable = testotu[, 2:21],
    reads = TRUE,
    taxonomytable = testotu[, c(1, 22)]
  )

  # Check integrated object
  print(test_object)

  # Extract genus relative abundance table
  test_Genus <- test_object$Genus_percent
  head(test_Genus)

  # Check corresponding taxonomy information of genus table
  test_Genus_tax <- test_object$Genus_taxonomy
  head(test_Genus_tax)

  # Summary base table into all taxonomy levels with standard output
  test_object <- tax_summary(
    groupfile = groupinformation,
    inputtable = testotu[, 2:21],
    reads = TRUE,
    taxonomytable = testotu[, c(1, 22)],
    outputtax = "standard"
  )
  head(test_object$Species_percent) # View first 10 rows of species percentage
  head(test_object$Genus) # View first 10 rows of genus table
}
```

**Description**

RDA analysis including co-linearity diagnostics and necessary statistics.

**Usage**

```
tbRDA_analysis(otudata, envdata, collinearity, perm.test = TRUE)
```

**Arguments**

otudata	Feature table of all numeric variable, with annotation in row names
envdata	Environmental factor of all numeric variable, with sample-ID in row names and environmental factor in column names
collinearity	If done collinearity diagnostics. Default, TRUE.
perm.test	Logical. If conduct permutation test. Default: TRUE.

**Value**

Three permutation test result print ,one preview plot ,a RDA object(default name:otu.tab.1) and a summary of RDA object

**Note**

1. When Axis length in first axis more than 4, you should choose CCA instead of RDA.

**Author(s)**

Wang Ningqi [2434066068@qq.com](mailto:2434066068@qq.com)

**Examples**

```
### Data preparation ###
library(vegan)
data(varechem)
head(varechem)
data(testotu)
require(tidyr); require(magrittr) ## Or use pipe command in "dplyr"

sep_testotu <- Filter_function(
  input = testotu,
  threshold = 0.0001,
  format = 1
) %>%
separate(
  ., col = taxonomy,
  into = c("Domain", "Phylum", "Order", "Family", "Class", "Genus", "Species"),
  sep = ";"
)

top10phylum <- aggregate(
  sep_testotu[, 2:21],
```

```

    by = list(sep_testotu$Phylum),
    FUN = sum
  ) %>%
  Top_taxa(
    input = .,
    n = 10,
    inputformat = 2,
    outformat = 1
  )
rownames(top10phylum) <- top10phylum[, 1]
top10phylum <- top10phylum[, -1]

group <- data.frame(
  group = c(rep("a", 10), rep("b", 10)),
  factor1 = rnorm(10),
  factor2 = rnorm(mean = 100, 10)
)

### RDA analysis ###
set.seed(999)
RDAResult <- tbRDA_analysis(
  top10phylum,
  varechem[1:20, ],
  TRUE
)

# Environmental statistics
print(RDAResult$factor_statistics)

# Visualization using ggplot
rda_object <- RDAResult$rda_object
rda_summary <- RDAResult$rdasummary
rda_scores <- RDAResult$rdascores
rda_env <- as.data.frame(rda_scores$biplot)
rda_sample <- as.data.frame(rda_scores$sites)
rda_otu <- as.data.frame(rda_scores$species)

xlab <- paste0("RDA1:", round(RDAResult$rdasummary$concont$importance[2, 1], 4) * 100, "%")
ylab <- paste0("RDA2:", round(RDAResult$rdasummary$concont$importance[2, 2], 4) * 100, "%")

library(ggplot2)
# Create a sample RDA plot
RDAPlot <- ggplot(data = rda_sample, aes(RDA1, RDA2)) +
  geom_point(aes(color = group$group), size = 2) +
  geom_point(data = rda_otu, pch = "+", color = "orange", size = 4) +
  geom_hline(yintercept = 0) +
  geom_vline(xintercept = 0) +
  geom_segment(data = rda_env, aes(x = 0, y = 0, xend = RDA1 * 0.8, yend = RDA2 * 0.8),
    arrow = arrow(angle = 22.5, length = unit(0.35, "cm")),
    linetype = 1, size = 0.6, colour = "red") +
  geom_text_repel(color = "red", data = rda_env,
    aes(RDA1, RDA2, label = row.names(rda_env))) +
  labs(x = xlab, y = ylab, color = "Treatment",

```



```

    title = paste0("p = ", anova.cca(rda_object)["Model", "Pr(>F)"]) +
    stat_ellipse(aes(color = group$group), level = 0.95) +
    geom_text_repel(size = 3, color = "orange",
                    data = subset(rda_otu, RDA1 > 0.1 | RDA1 < (-0.1)),
                    aes(RDA1, RDA2, label = rownames(subset(rda_otu, RDA1>0.1|RDA1<(-0.1)))))) +
    theme_zg()

# Print the RDA plot
print(RDAplot)

```

---

testotu

*test otudata*


---

### Description

A dataset containing 20 samples and 1000 OTUs from soil to test,taxonomy information is covered randomly(not actual)

### Usage

```
testotu
```

### Format

A data frame with 1000 rows and 22 variables.

---

theme\_zg

*A classic theme for ggplot*


---

### Description

A classic theme for ggplot

### Usage

```
theme_zg()
```

### Value

ggplot theme

### Note

Build inside the LorMe package, Please use theme\_zg() as a theme directly

---

Three_group	<i>Tax summary object with three groups</i>
-------------	---

---

**Description**

Enraptured summary object with three groups.Configuration has been assigned.

**Usage**

Three\_group

**Format**

Tax summary object with configuration

---

Top_taxa	<i>Calculate top taxa and others</i>
----------	--------------------------------------

---

**Description**

Top taxa is widely used in data analysis,here we provide a simple function to calculate which simplify your R script.

**Usage**

Top\_taxa(input, n, inputformat, outformat)

**Arguments**

input	Reads or relative abundance(recommended) of OTU/Taxa/gene data frame,see details in inputformat
n	Top n taxa remained according to relative abundance
inputformat	1:data frame with first column of OTUID and last column of taxonomy 2:data frame with first column of OTUID/taxonomy (recommended!!!) 3:data frame of all numeric,with row names of OTUID/taxonomy
outformat	1. return outformat the same as inputformat 2. return data frame of all numeric with OTU/gene/taxa ID in row names(not available for inputformat 1).

**Value**

Data frame with top n taxa

**Author(s)**

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**Examples**

```
### Data preparation ###
data(testotu)
require(tidyr); require(magrittr) ## Or use pipe command in "dplyr"

testotu.pct <- data.frame(
  OTU.ID = testotu[, 1],
  sweep(testotu[, -c(1, 22)], 2, colSums(testotu[, -c(1, 22)]), "/"),
  taxonomy = testotu[, 22]
)

sep_testotu <- Filter_function(
  input = testotu,
  threshold = 0.0001,
  format = 1
) %>%
  separate(
    ., col = taxonomy,
    into = c("Domain", "Phylum", "Order", "Family", "Class", "Genus", "Species"),
    sep = ";"
  )

phylum <- aggregate(
  sep_testotu[, 2:21], by = list(sep_testotu$Phylum), FUN = sum
)

phylum1 <- data.frame(row.names = phylum[, 1], phylum[, -1])

##### Input format 1, top 100 OTU #####
top100otu <- Top_taxa(
  input = testotu.pct,
  n = 100,
  inputformat = 1,
  outformat = 1
)

##### Input format 2, top 15 phylum #####
head(phylum)
top15phylum <- Top_taxa(
  input = phylum,
  n = 15,
  inputformat = 2,
  outformat = 1
)

##### Input format 3, top 15 phylum #####
head(phylum1)
top15phylum <- Top_taxa(
```

```

input = phylum1,
n = 15,
inputformat = 3,
outformat = 1
)

```

---

Two\_group                      *Tax summary object with two groups*

---

### Description

Enraptured summary object with two groups. Configuration has been assigned.

### Usage

Two\_group

### Format

Tax summary object with configuration

---

t\_test\_report                      *Print Student's t-Test report*

---

### Description

Print Student's t-Test report

### Usage

```

t_test_report(
  data,
  treatment_col,
  value_col,
  paired,
  subject_col,
  report = TRUE
)

```

### Arguments

data	Data frame containing the treatment, value and other information.
treatment_col	Numeric indicating where treatment locates (column number) in data.
value_col	Numeric indicating where treatment value (column number) in data.
paired	Logical indicating whether you want a paired t-test.
subject_col	Only meaningful when Pair is ture. Numeric indicating where subject of treatment (column number) in data.
report	Logical. If print report to console. Default:TRUE

**Value**

t\_test\_report returns list containing:

1. data frame of basic data description
2. results of student's t-Test

**Examples**

```
{
  ### Data preparation ###
  testdata <- data.frame(
    treatment = c(rep("A", 6), rep("B", 6)),
    subject = rep(c(1:6), 2),
    value = c(rnorm(6, 2), rnorm(6, 1))
  )

  # Perform t-test (unpaired)
  t_test_result <- t_test_report(
    data = testdata,
    treatment_col = 1,
    value_col = 3
  )

  # Perform paired t-test
  t_test_result <- t_test_report(
    data = testdata,
    treatment_col = 1,
    value_col = 3,
    paired = TRUE,
    subject_col = 2
  )

  ### Basic data description ###
  print(t_test_result[[1]])
  print(t_test_result$basicdata)

  ### T-test results ###
  print(t_test_result[[2]])
  print(t_test_result$t.test_results)
}
```

---

 volcano\_plot

*Generate Volcano plot base on Deseq\_analysis or indicator\_analysis results*

---

**Description**

Generate Volcano plot base on Deseq\_analysis or indicator\_analysis results

**Usage**

```
volcano_plot(inputframe, cutoff = NULL, aes_col = c("#FE5C5C", "#75ABDE"))
```

**Arguments**

inputframe	A data frame containing the results based on <a href="#">Deseq_analysis</a> or <a href="#">indicator_analysis</a> (only two group indicators)
cutoff	A numeric value specifying the fold change cutoff, should be the same as in <a href="#">Deseq_analysis</a>
aes_col	A named vector of colors to be used in the plots

**Value**

A list of two ggplot objects, one for the fold change versus adjusted p-value plot and another for the mean abundance versus fold change or enrichment factor plot.

**Author(s)**

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**Examples**

```
###data prepration###

{
  # Load data
  data("Two_group")

  # Define color based on treatment column
  mycolor <- Two_group$configuration$treat_col

  ### DESeq analysis ###
  deseq_results <- Deseq_analysis(
    taxobj = Two_group,
    taxlevel = "Genus",
    cutoff = 1,
    control_name = "Control"
  )

  ### Or indicator analysis ###
  indicator_results <- indicator_analysis(
    taxobj = Two_group,
    taxlevel = "Genus"
  )

  # Create volcano plot for DESeq results
  volcano_plot <- volcano_plot(
    inputframe = deseq_results,
    cutoff = 1,
    aes_col = mycolor
  )
}
```

```

print(volcano_plot$FC_FDR) # Fold Change and FDR values
print(volcano_plot$Mean_FC) # Mean Fold Change values

# Create volcano plot for indicator results
volcano_plot <- volcano_plot(
  inputframe = indicator_results,
  cutoff = 1,
  aes_col = mycolor
)
print(volcano_plot$FC_FDR) # Fold Change and FDR values
print(volcano_plot$Mean_FC) # Mean Fold Change values
}

```

---

wilcox\_test\_report      *Print Wilcoxon Rank Sum and Signed Rank Tests report*

---

## Description

Print Wilcoxon Rank Sum and Signed Rank Tests report

## Usage

```

wilcox_test_report(
  data,
  treatment_col,
  value_col,
  paired = FALSE,
  subject_col = NULL,
  report = TRUE
)

```

## Arguments

data	Data frame containing the treatment, value and other information.
treatment_col	Numeric indicating where treatment locates (column number) in data.
value_col	Numeric indicating where treatment value (column number) in data.
paired	Logical indicating whether you want a paired test.
subject_col	Only meaningful when Pair is ture. Numeric indicating where subject of treatment (column number) in data.
report	Logical. If print report to console. Default:TRUE

## Value

wilcox\_test\_report returns data frame of basic data description.

**Examples**

```
{
  # Data preparation
  testdata <- data.frame(
    treatment = c(rep("A", 6), rep("B", 6)),
    subject = rep(1:6, 2),
    value = c(rnorm(6, 2), rnorm(6, 1))
  )

  # Wilcoxon test (unpaired)
  wilcox_result <- wilcox_test_report(
    data = testdata,
    treatment_col = 1,
    value_col = 3
  )

  # Wilcoxon signed rank test (paired)
  wilcox_result <- wilcox_test_report(
    data = testdata,
    treatment_col = 1,
    value_col = 3,
    paired = TRUE,
    subject_col = 2
  )

  ### Basic data description ###
  print(wilcox_result)
}
```



# Index

## \* datasets

- Facet\_group, 24
  - testotu, 57
  - Three\_group, 58
  - Two\_group, 60
- Alpha\_diversity\_calculator, 3, 29
- Alpha\_diversity\_calculator2, 4
- anova\_report, 6, 9
- as\_tibble, 18, 20
- auto\_signif\_test, 8, 29
- circulation\_lm, 10, 30
- color\_scheme, 11, 29, 30, 33
- combine\_and\_translate, 12, 29
- community\_plot, 14, 29
- compare\_plot, 16, 29
- DataFrame, 18, 20
- DESeq, 18, 20
- Deseq\_analysis, 17, 29, 30, 45, 62
- Deseq\_analysis2, 19
- DESeqDataSetFromMatrix, 18, 20
- differential\_bar, 21, 29
- Dimension\_reduction, 23, 29
- Facet\_group, 24
- facet\_wrap, 50
- Filter\_function, 25, 29
- geom\_point, 50
- how, 27
- indicator\_analysis, 26, 29, 30, 45, 62
- kruskal\_report, 9, 27
- lm, 11
- LorMe, 29
- manhattan, 29, 30
- Module\_abundance, 30, 32
- Module\_composition, 30, 33
- multipatt, 26, 27
- nc, 30, 35
- NC\_remove, 30, 36
- network\_analysis, 29, 32, 33, 35, 36, 37, 42, 43, 45
- network\_analysis2, 39
- network\_stat, 42
- network\_visual, 29, 30, 42, 44, 45
- network\_visual\_re, 30, 44
- network\_withdiff, 29, 30, 44, 45, 45
- object\_config, 3, 14, 17, 21, 26, 48, 50
- set.seed, 36
- stat\_ellipse, 50
- structure\_plot, 29, 50
- sub\_tax\_summary, 29, 52
- subset, 52
- t\_test\_report, 9, 60
- tax\_summary, 4, 29, 38, 48, 52, 53
- tbRDA\_analysis, 30, 54
- testotu, 57
- theme\_zg, 29, 57
- Three\_group, 58
- Top\_taxa, 29, 58
- Two\_group, 60
- volcano\_plot, 29, 61
- wilcox\_test\_report, 9, 63