

# Package ‘microbiomeMarker’

April 10, 2023

**Title** microbiome biomarker analysis toolkit

**Version** 1.4.0

**Description** To date, a number of methods have been developed for microbiome marker discovery based on metagenomic profiles, e.g. LEfSe. However, all of these methods have its own advantages and disadvantages, and none of them is considered standard or universal. Moreover, different programs or softwares may be development using different programming languages, even in different operating systems. Here, we have developed an all-in-one R package microbiomeMarker that integrates commonly used differential analysis methods as well as three machine learning-based approaches, including Logistic regression, Random forest, and Support vector machine, to facilitate the identification of microbiome markers.

**License** GPL-3

**biocViews** Metagenomics, Microbiome, DifferentialExpression

**URL** <https://github.com/yiluheihei/microbiomeMarker>

**BugReports** <https://github.com/yiluheihei/microbiomeMarker/issues>

**Depends** R (>= 4.1.0)

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|            |                                |
|------------|--------------------------------|
| abundances | <i>Extract taxa abundances</i> |
|------------|--------------------------------|

---

**Description**

Extract taxa abundances from phyloseq objects.

**Usage**

```
abundances(object, transform = c("identity", "log10", "log10p"), norm = FALSE)
```

```
## S4 method for signature 'otu_table'
```

```
abundances(object, transform = c("identity", "log10", "log10p"), norm = FALSE)
```

```
## S4 method for signature 'phyloseq'
```

```
abundances(object, transform = c("identity", "log10", "log10p"), norm = FALSE)
```

```
## S4 method for signature 'microbiomeMarker'
```

```
abundances(object, transform = c("identity", "log10", "log10p"))
```

**Arguments**

object [otu\\_table](#), [phyloseq](#), or [microbiomeMarker](#).

transform transformation to apply, the options include:

- "identity", return the original data without any transformation.
- "log10", the transformation is  $\log_{10}(\text{object})$ , and if the data contains zeros the transformation is  $\log_{10}(1 + \text{object})$ .

- "log10p", the transformation is  $\log_{10}(1 + \text{object})$ .
- norm            logical, indicating whether or not to return the normalized taxa abundances.

**Value**

abundance matrix with taxa in rows and samples in columns.

**See Also**

[otu\\_table](#), [phyloseq](#), [microbiomeMarker](#), [transform\\_abundances](#)

**Examples**

```
data(caporaso)
abd <- abundances(caporaso)
```

---

|                |                       |
|----------------|-----------------------|
| aggregate_taxa | <i>Aggregate Taxa</i> |
|----------------|-----------------------|

---

**Description**

Summarize phyloseq data into a higher phylogenetic level.

**Usage**

```
aggregate_taxa(x, level, verbose = FALSE)
```

**Arguments**

|         |   |
|---------|---|
| x       | <a href="#">phyloseq-class</a> object                     |
| level   | Summarization level (from <code>rank_names(pseq)</code> ) |
| verbose | verbose   |

**Details**

This provides a convenient way to aggregate phyloseq OTUs (or other taxa) when the phylogenetic tree is missing. Calculates the sum of OTU abundances over all OTUs that map to the same higher-level group. Removes ambiguous levels from the taxonomy table. Returns a phyloseq object with the summarized abundances.

**Value**

Summarized phyloseq object

**Author(s)**

Contact: Leo Lahti <[microbiome-admin@googlegroups.com](mailto:microbiome-admin@googlegroups.com)>

## References

See citation('microbiome')

## Examples

```
data(caporaso)
caporaso_phylum <- aggregate_taxa(caporaso, "Phylum")
```

---

|                  |                               |
|------------------|-------------------------------|
| assign-otu_table | <i>Assign a new OTU table</i> |
|------------------|-------------------------------|

---

## Description

Assign a new OTU table in microbiomeMarker object

## Usage

```
## S4 replacement method for signature 'microbiomeMarker,otu_table'
otu_table(x) <- value

## S4 replacement method for signature 'microbiomeMarker,phyloseq'
otu_table(x) <- value

## S4 replacement method for signature 'microbiomeMarker,microbiomeMarker'
otu_table(x) <- value
```

## Arguments

|       |  |
|-------|--|
| x     | microbiomeMarker                         |
| value | otu_table, phyloseq, or microbiomeMarker |

## Value

a `microbiomeMarker` object.

---

 compare\_DA

*Comparing the results of differential analysis methods by Empirical power and False Discovery Rate*


---

## Description

Calculating power, false discovery rates, false positive rates and auc ( area under the receiver operating characteristic (ROC) curve) for various DA methods.

## Usage

```
compare_DA(
  ps,
  group,
  taxa_rank = "none",
  methods,
  args = list(),
  n_rep = 20,
  effect_size = 5,
  k = NULL,
  relative = TRUE,
  BPPARAM = BiocParallel::SnowParam(progressbar = TRUE)
)
```

## Arguments

|                      |  |
|----------------------|--|
| ps, group, taxa_rank | main arguments of all differential analysis methods. ps: a <code>phyloseq::phyloseq</code> object; group, character, the variable to set the group, must be one of the var of the sample metadata; taxa_rank: character, taxonomic rank, please not that <b>since the abundance table is spiked in the lowest level, only taxa_rank = "none" is allowed.</b>   |
| methods              | character vector, differential analysis methods to be compared, available methods are "aldex", "ancom", "ancombc", "deseq2", "edger", "lfe", "limma_voom", "metagenomeseq", "simple_stat".   |
| args                 | named list, which used to set the extra arguments of the differential analysis methods, so the names must be contained in methods. For more see details below.   |
| n_rep                | integer, number of times to run the differential analyses.   |
| effect_size          | numeric, the effect size for the spike-ins. Default 5.   |
| k                    | numeric vector of length 3, number of features to spike in each tertile (lower, mid, upper), e.g. <code>k=c(5,10,15)</code> means 5 features spiked in low abundance tertile, 10 features spiked in mid abundance tertile and 15 features spiked in high abundance tertile. Default NULL, which will spike 2 percent of the total amount of features in each tertile (a total of 6 percent), but minimum <code>c(5,5,5)</code> . |

|          |   |
|----------|---|
| relative | logical, whether rescale the total number of individuals observed for each sample to the original level after spike-in. Default TRUE. |
| BPPARAM  | <a href="#">BiocParallel::BiocParallelParam</a> instance defining the parallel back-end.  |

### Details

To make this function support for different arguments for a certain DA method `args` allows list of list of list e.g. `args = list(lefse = list(list(norm = "CPM"), list(norm = "TSS")))`, which specify to compare the different norm arguments for lefse analysis.

For `taxa_rank`, only `taxa_rank = "none"` is supported, if this argument is not "none", it will be forced to "none" internally.

### Value

an `compareDA` object, which contains a two-length list of:

- `metrics`: data.frame, FPR, AUC and spike detection rate for each run.
- `mm`: differential analysis results.

---

|            |                            |
|------------|----------------------------|
| confounder | <i>Confounder analysis</i> |
|------------|----------------------------|

---

### Description

Confounding variables may mask the actual differential features. This function utilizes constrained correspondence analysis (CCA) to measure the confounding factors.

### Usage

```
confounder(
  ps,
  target_var,
  norm = "none",
  confounders = NULL,
  permutations = 999,
  ...
)
```

### Arguments

|                           |  |
|---------------------------|--|
| <code>ps</code>           | a <a href="#">phyloseq::phyloseq</a> object.   |
| <code>target_var</code>   | character, the variable of interest  |
| <code>norm</code>         | norm the methods used to normalize the microbial abundance data. See <a href="#">normalize()</a> for more details. |
| <code>confounders</code>  | the confounding variables to be measured, if NULL, all variables in the meta data will be analyzed.                |
| <code>permutations</code> | the number of permutations, see <a href="#">vegan::anova.cca()</a> .   |
| <code>...</code>          | extra arguments passed to <a href="#">vegan::anova.cca()</a> .   |

**Value**

a `data.frame` contains three variables: `confounder`, `pseudo-F` and `p value`.

**Examples**

```
data(caporaso)
confounder(caporaso, "SampleType", confounders = "ReportedAntibioticUsage")
```

---

data-caporaso

*16S rRNA data from "Moving pictures of the human microbiome"*

---

**Description**

16S read counts and phylogenetic tree file of 34 Illumina samples derived from Moving Pictures of the Human Microbiome (Caporaso et al.) Group label: gut, left palm, right palm, and tongue - indicating different sampled body sites.

**Format**

a `phyloseq::phyloseq` object

**Author(s)**

Yang Cao

**Source**

Data was downloaded from <https://www.microbiomeanalyst.ca>

**References**

Caporaso, et al. Moving pictures of the human microbiome. *Genome Biol* 12, R50 (2011).

<https://doi.org/10.1186/gb-2011-12-5-r50>



---

data-cid\_ying

*16S rRNA data of 94 patients from CID 2012*

---

**Description**

Data from a cohort of 94 Bone Marrow Transplant patients previously published on in CID

**Format**

a `phyloseq::phyloseq` object

**Author(s)**

Yang Cao

**Source**

<https://github.com/ying14/yingtools2/tree/master/data>

**References**

Ying, et al. Intestinal Domination and the Risk of Bacteremia in Patients Undergoing Allogeneic Hematopoietic Stem Cell Transplantation, *Clinical Infectious Diseases*, Volume 55, Issue 7, 1 October 2012, Pages 905–914,

<https://academic.oup.com/cid/article/55/7/905/428203>

---

data-ecam

*Data from Early Childhood Antibiotics and the Microbiome (ECAM) study*

---

**Description**

The data from a subset of the Early Childhood Antibiotics and the Microbiome (ECAM) study, which tracked the microbiome composition and development of 43 infants in the United States from birth to 2 years of age, identifying microbiome associations with antibiotic exposure, delivery mode, and diet.

**Format**

a `phyloseq::phyloseq` object

**References**

Bokulich, Nicholas A., et al. "Antibiotics, birth mode, and diet shape microbiome maturation during early life." *Science translational medicine* 8.343 (2016): 343ra82-343ra82.

<https://github.com/FrederickHuangLin/ANCOM/tree/master/data>

---

data-enterotypes\_arumugam

*Enterotypes data of 39 samples*

---

**Description**

The data contains 22 European metagenomes from Danish, French, Italian, and Spanish individuals, and 13 Japanese and 4 American.

**Format**

a `phyloseq::phyloseq` object

**Author(s)**

Yang Cao

**References**

Arumugam, Manimozhiyan, et al. Enterotypes of the human gut microbiome. *nature* 473.7346 (2011): 174-180.

---

data-kostic\_crc

*Data from a study on colorectal cancer (kostic 2012)*

---

**Description**

The data from a study on colorectal cancer. Samples that had no DIAGNOSIS attribute assigned and with less than 500 reads (counts) were removed, and 191 samples remains (91 healthy and 86 Tumors).

**Format**

a `phyloseq::phyloseq` object

**Author(s)**

Yang Cao

**References**

Kostic et al. Genomic analysis identifies association of *Fusobacterium* with colorectal carcinoma. *Genome research*, 2012, 22(2), 292-298.

---

|             |  |
|-------------|--|
| data-oxygen | <i>Oxygen availability 16S dataset, of which taxa table has been summarized for python lefse input</i> |
|-------------|--|

---

**Description**

A small subset of the HMP 16S dataset for finding biomarkers characterizing different level of oxygen availability in different bodysites

**Format**

a `phyloseq::phyloseq` object

**Author(s)**

Yang Cao

**Source**

[http://huttenhower.sph.harvard.edu/webfm\\_send/129](http://huttenhower.sph.harvard.edu/webfm_send/129)

---

|                   |                          |
|-------------------|--------------------------|
| data-pediatic_ibd | <i>IBD stool samples</i> |
|-------------------|--------------------------|

---

**Description**

43 pediatic IBD stool samples obtained from the Integrative Human Microbiome Project Consortium (iHMP). Group label: CD and Controls.

**Format**

a `phyloseq::phyloseq` object

**Author(s)**

Yang Cao

**Source**

<https://www.microbiomeanalyst.ca/MicrobiomeAnalyst/resources>

---

data-spontaneous\_colitis

*This is a sample data from lefse python script, a 16S dataset for studying the characteristics of the fecal microbiota in a mouse model of spontaneous colitis.*

---

### Description

The dataset contains 30 abundance profiles (obtained processing the 16S reads with RDP) belonging to 10 rag2 (control) and 20 truc (case) mice.

### Format

a `phyloseq::phyloseq` object

### Author(s)

Yang Cao

### Source

[http://www.huttenhower.org/webfm\\_send/73](http://www.huttenhower.org/webfm_send/73)

---

extract\_posthoc\_res    *Extract results from a posthoc test*

---

### Description

This function extracts the results of posthoc test.

### Usage

```
extract_posthoc_res(object, features = NULL)
```

### Arguments

|          |  |
|----------|--|
| object   | a <code>postHocTest</code> object.   |
| features | either NULL extracts results of all features, or a character vector to specify the test results of which features are extracted. |

### Value

a `IRanges::SimpleDFrameList` object.

**Examples**

```

require(IRanges)
pht <- postHocTest(
  result = DataFrameList(
    featureA = DataFrame(
      comparisons = c("group2-group1",
        "group3-group1",
        "group3-group2"),
      diff_mean = runif(3),
      pvalue = rep(0.01, 3),
      ci_lower = rep(0.01, 3),
      ci_upper = rep(0.011, 3)
    ),
    featureB = DataFrame(
      comparisons = c("group2-group1",
        "group3-group1",
        "group3-group2"),
      diff_mean = runif(3),
      pvalue = rep(0.01, 3),
      ci_lower = rep(0.01, 3),
      ci_upper = rep(0.011, 3)
    )
  ),
  abundance = data.frame(
    featureA = runif(3),
    featureB = runif(3),
    group = c("group1", "group2", "group3")
  )
)
extract_posthoc_res(pht, "featureA")[[1]]

```

---

import\_dada2

---

*Import function to read the the output of dada2 as phyloseq object*


---

**Description**

Import the output of dada2 into phyloseq object

**Usage**

```

import_dada2(
  seq_tab,
  tax_tab = NULL,
  sam_tab = NULL,
  phy_tree = NULL,
  keep_taxa_rows = TRUE
)

```

**Arguments**

|                |   |
|----------------|---|
| seq_tab        | matrix-like, ASV table, the output of dada2::removeBimeraDenovo.  |
| tax_tab        | matrix, taxonomy table, the output of dada2::assignTaxonomy or dada2::addSpecies.                         |
| sam_tab        | data.frame or <code>phyloseq::sample_data</code> , sample data  |
| phy_tree       | <code>ape::phylo</code> class or character represents the path of the tree file                           |
| keep_taxa_rows | logical, whether keep taxa in rows or not in the otu_table of the returned phyloseq object, default TRUE. |

**Details**

The output of the dada2 pipeline is a feature table of amplicon sequence variants (an ASV table): A matrix with rows corresponding to samples and columns to ASVs, in which the value of each entry is the number of times that ASV was observed in that sample. This table is analogous to the traditional OTU table. Conveniently, taxa names are saved as ASV1, ASV2, ..., in the returned phyloseq object.

**Value**

`phyloseq::phyloseq` object hold the taxonomy info, sample metadata, number of reads per ASV.

**Examples**

```
seq_tab <- readRDS(system.file("extdata", "dada2_seqtab.rds",
  package = "microbiomeMarker"
))
tax_tab <- readRDS(system.file("extdata", "dada2_taxtab.rds",
  package = "microbiomeMarker"
))
sam_tab <- read.table(system.file("extdata", "dada2_samdata.txt",
  package = "microbiomeMarker"
), sep = "\t", header = TRUE, row.names = 1)
ps <- import_dada2(seq_tab = seq_tab, tax_tab = tax_tab, sam_tab = sam_tab)
ps
```

---

import\_picrust2

*Import function to read the output of picrust2 as phyloseq object*


---

**Description**

Import the output of picrust2 into phyloseq object

**Usage**

```
import_picrust2(
  feature_tab,
  sam_tab = NULL,
  trait = c("PATHWAY", "COG", "EC", "KO", "PFAM", "TIGRFAM", "PHENO")
)
```

**Arguments**

|             |  |
|-------------|--|
| feature_tab | character, file path of the prediction abundance table of functional feature.  |
| sam_tab     | character, file path of the sample meta data.  |
| trait       | character, options are picrust2 function traits (including "COG", "EC", "KO", "PFAM", "TIGRFAM", and "PHENO") and "PATHWAY". |

**Details**

**PICRUSt2** is a software for predicting abundances of functional profiles based on marker gene sequencing data. The functional profiles can be predicted from the taxonomic profiles using PICRUSt2. "Function" usually refers to gene families such as KEGG orthologs and Enzyme Classification numbers, but predictions can be made for any arbitrary trait.

In the phyloseq object, the predicted function abundance profile is stored in `otu_table` slot. And the functional trait is saved in `tax_table` slot, if the descriptions of function features is not added to the predicted table, `tax_table` will have only one rank `Picrust_trait` to represent the function feature id, or if the descriptions are added one more rank `Picrust_description` will be added to represent the description of function feature.

**Value**

`phyloseq::phyloseq` object.

**Examples**

```
sam_tab <- system.file(
  "extdata", "picrust2_metadata.tsv",
  package = "microbiomeMarker")
feature_tab <- system.file(
  "extdata", "path_abun_unstrat_descrip.tsv.gz",
  package = "microbiomeMarker")
ps <- import_picrust2(feature_tab, sam_tab, trait = "PATHWAY")
ps
```

---

import\_qiime2

---

*Import function to read the the output of dada2 as phyloseq object*


---

**Description**

Import the qiime2 artifacts, including feature table, taxonomic table, phylogenetic tree, representative sequence and sample metadata into phyloseq object.

## Usage

```
import_qiime2(  
  otu_qza,  
  taxa_qza = NULL,  
  sam_tab = NULL,  
  refseq_qza = NULL,  
  tree_qza = NULL  
)
```

## Arguments

|            |   |
|------------|---|
| otu_qza    | character, file path of the feature table from qiime2.                          |
| taxa_qza   | character, file path of the taxonomic table from qiime2, default NULL.          |
| sam_tab    | character, file path of the sample metadata in tsv format, default NULL.        |
| refseq_qza | character, file path of the representative sequences from qiime2, default NULL. |
| tree_qza   | character, file path of the phylogenetic tree from qiime2, default NULL.        |

## Value

`phyloseq::phyloseq` object.

## Examples

```
otuqza_file <- system.file(  
  "extdata", "table.qza",  
  package = "microbiomeMarker"  
)  
taxaqza_file <- system.file(  
  "extdata", "taxonomy.qza",  
  package = "microbiomeMarker"  
)  
sample_file <- system.file(  
  "extdata", "sample-metadata.tsv",  
  package = "microbiomeMarker"  
)  
treeqza_file <- system.file(  
  "extdata", "tree.qza",  
  package = "microbiomeMarker"  
)  
ps <- import_qiime2(  
  otu_qza = otuqza_file, taxa_qza = taxaqza_file,  
  sam_tab = sample_file, tree_qza = treeqza_file  
)  
ps
```



---

|              |   |
|--------------|---|
| marker_table | <i>Build or access the marker_table</i> |
|--------------|---|

---

## Description

This is the recommended function for both building and accessing microbiome marker table ([marker\\_table](#)).

## Usage

```
marker_table(object)

## S4 method for signature 'data.frame'
marker_table(object)

## S4 method for signature 'microbiomeMarker'
marker_table(object)
```

## Arguments

object            an object among the set of classes defined by the microbiomeMarker package that contain marker\_table

## Value

a [marker\\_table](#) object.

## Examples

```
data(enterotypes_arumugam)
mm <- run_limma_voom(
  enterotypes_arumugam,
  "Enterotype",
  contrast = c("Enterotype 3", "Enterotype 2"),
  pvalue_cutoff = 0.05,
  p_adjust = "fdr"
)
marker_table(mm)
```

---

|                    |   |
|--------------------|---|
| marker_table-class | <i>The S4 class for storing microbiome marker information</i> |
|--------------------|---|

---

## Description

This Class is inherit from data.frame. Rows represent the microbiome markers and variables represents feature of the marker.

**Fields**

names, row.names a character vector, inherited from the input data.frame  
.data a list, each element corresponding the each column of the input data.frame  
.S3Class character, the S3 class marker\_table inherited from: "data.frame"

**Author(s)**

Yang Cao

---

marker\_table<-            *Assign marker\_table to object*

---

**Description**

This function replace the marker\_table slot of object with value.

**Usage**

```
marker_table(object) <- value
```

**Arguments**

object            a [microbiomeMarker](#) object to modify.  
value            new value to replace the marker\_table slot of object. Either a marker\_table-class, a data.frame that can be coerced into marker\_table-class.

**Value**

a [microbiomeMarker](#) object.

**Examples**

```
data(enterotypes_arumugam)
mm <- run_limma_voom(
  enterotypes_arumugam,
  "Enterotype",
  contrast = c("Enterotype 3", "Enterotype 2"),
  pvalue_cutoff = 0.1,
  p_adjust = "fdr"
)
mm_marker <- marker_table(mm)
mm_marker
marker_table(mm) <- mm_marker[1:2, ]
marker_table(mm)
```

---

microbiomeMarker      *Build microbiomeMarker-class objects*

---

## Description

This the constructor to build the `microbiomeMarker` object, don't use the `new()` constructor.

## Usage

```
microbiomeMarker(  
  marker_table = NULL,  
  norm_method = NULL,  
  diff_method = NULL,  
  ...  
)
```

## Arguments

`marker_table`    a `marker_table` object differential analysis.  
`norm_method`    character, method used to normalize the input phyloseq object.  
`diff_method`    character, method used for microbiome marker identification.  
...              arguments passed to `phyloseq::phyloseq()`

## Value

a `microbiomeMarker` object.

## See Also

`phyloseq::phyloseq()`

## Examples

```
microbiomeMarker(  
  marker_table = marker_table(data.frame(  
    feature = c("speciesA", "speciesB"),  
    enrich_group = c("groupA", "groupB"),  
    ef_logFC = c(-2, 2),  
    pvalue = c(0.01, 0.01),  
    padj = c(0.01, 0.01),  
    row.names = c("marker1", "marker2")  
  )),  
  norm_method = "TSS",  
  diff_method = "DESeq2",  
  otu_table = otu_table(matrix(  
    c(4, 1, 1, 4),  
    nrow = 2, byrow = TRUE,  
    dimnames = list(c("speciesA", "speciesB"), c("sample1", "sample2"))  
  ))
```

```

),
taxa_are_rows = TRUE
),
tax_table = tax_table(matrix(
  c("speciesA", "speciesB"),
  nrow = 2,
  dimnames = list(c("speciesA", "speciesB"), "Species")
)),
sam_data = sample_data(data.frame(
  group = c("groupA", "groupB"),
  row.names = c("sample1", "sample2")
))
)

```

---

microbiomeMarker-class

*The main class for microbiomeMarker data*

---

## Description

microbiomeMarker-class is inherited from the [phyloseq::phyloseq](#) by adding a custom slot `microbiome_marker` to save the differential analysis results. And it provides a seamless interface with **phyloseq**, which makes **microbiomeMarker** simple and easy to use. For more details on see the document of [phyloseq::phyloseq](#).

## Usage

```
## S4 method for signature 'microbiomeMarker'
show(object)
```

## Arguments

object            a microbiomeMarker-class object

## Value

a `microbiomeMarker` object.

## Slots

`marker_table` a data.frame, a [marker\\_table](#) object.

`norm_method` character, method used to normalize the input phyloseq object.

`diff_method` character, method used for marker identification.

## See Also

[phyloseq::phyloseq](#), [marker\\_table](#), [summarize\\_taxa\(\)](#)

---

|         |   |
|---------|---|
| nmarker | <i>Get the number of microbiome markers</i> |
|---------|---|

---

### Description

Get the number of microbiome markers

### Usage

```
nmarker(object)

## S4 method for signature 'microbiomeMarker'
nmarker(object)

## S4 method for signature 'marker_table'
nmarker(object)
```

### Arguments

object            a [microbiomeMarker](#) or [marker\\_table](#) object

### Value

an integer, the number of microbiome markers

### Examples

```
mt <- marker_table(data.frame(
  feature = c("speciesA", "speciesB"),
  enrich_group = c("groupA", "groupB"),
  ef_logFC = c(-2, 2),
  pvalue = c(0.01, 0.01),
  padj = c(0.01, 0.01),
  row.names = c("marker1", "marker2")
))
nmarker(mt)
```

---

normalize, phyloseq-method

*Normalize the microbial abundance data*

---

## Description

It is critical to normalize the feature table to eliminate any bias due to differences in the sampling sequencing depth. This function implements six widely-used normalization methods for microbial compositional data.

For rarefying, reads in the different samples are randomly removed until the same predefined number has been reached, to assure all samples have the same library size. Rarefying normalization method is the standard in microbial ecology. Please note that the authors of phyloseq do not advocate using this rarefying a normalization procedure, despite its recent popularity

TSS simply transforms the feature table into relative abundance by dividing the number of total reads of each sample.

CSS is based on the assumption that the count distributions in each sample are equivalent for low abundant genes up to a certain threshold. Only the segment of each sample's count distribution that is relatively invariant across samples is scaled by CSS

RLE assumes most features are not differential and uses the relative abundances to calculate the normalization factor.

TMM calculates the normalization factor using a robust statistics based on the assumption that most features are not differential and should, in average, be equal between the samples. The TMM scaling factor is calculated as the weighted mean of log-ratios between each pair of samples, after excluding the highest count OTUs and OTUs with the largest log-fold change.

In CLR, the log-ratios are computed relative to the geometric mean of all features.

norm\_cpm: This normalization method is from the original LefSe algorithm, recommended when very low values are present (as shown in the LefSe galaxy).

## Usage

```
## S4 method for signature 'phyloseq'
normalize(object, method = "TSS", ...)

## S4 method for signature 'otu_table'
normalize(object, method = "TSS", ...)

## S4 method for signature 'data.frame'
normalize(object, method = "TSS", ...)

## S4 method for signature 'matrix'
normalize(object, method = "TSS", ...)

norm_rarefy(
  object,
  size = min(sample_sums(object)),
  rng_seed = FALSE,
  replace = TRUE,
  trim_otus = TRUE,
  verbose = TRUE
)
```

```

norm_tss(object)

norm_css(object, sl = 1000)

norm_rle(
  object,
  locfunc = stats::median,
  type = c("poscounts", "ratio"),
  geo_means = NULL,
  control_genes = NULL
)

norm_tmm(
  object,
  ref_column = NULL,
  logratio_trim = 0.3,
  sum_trim = 0.05,
  do_weighting = TRUE,
  Acutoff = -1e+10
)

norm_clr(object)

norm_cpm(object)

```

### Arguments

|        |   |
|--------|---|
| object | a <a href="#">phyloseq::phyloseq</a> or <a href="#">phyloseq::otu_table</a>   |
| method | the methods used to normalize the microbial abundance data. Options includes: <ul style="list-style-type: none"> <li>• "none": do not normalize.</li> <li>• "rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>• "TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.</li> <li>• "TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> <li>• "RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.</li> <li>• "CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.</li> <li>• "CLR": centered log-ratio normalization.</li> <li>• "CPM": pre-sample normalization of the sum of the values to 1e+06.</li> </ul> |
| ...    | other arguments passed to the corresponding normalization methods.  |

|   |   |
|---|---|
| size, rng_seed, replace, trim_otus, verbose | extra arguments passed to <code>phyloseq::rarefy_even_depth()</code> .  |
| sl  | The value to scale.   |
| locfunc                                     | a function to compute a location for a sample. By default, the median is used.  |
| type  | method for estimation: either "ratio" or "poscounts" (recommend).   |
| geo_means                                   | default NULL, which means the geometric means of the counts are used. A vector of geometric means from another count matrix can be provided for a "frozen" size factor calculation. |
| control_genes                               | default NULL, which means all taxa are used for size factor estimation, numeric or logical index vector specifying the taxa used for size factor estimation (e.g. core taxa).       |
| ref_column                                  | column to use as reference  |
| logratio_trim                               | amount of trim to use on log-ratios   |
| sum_trim                                    | amount of trim to use on the combined absolute levels ("A" values)  |
| do_weighting                                | whether to compute the weights or not   |
| Acutoff                                     | cutoff on "A" values to use before trimming   |

**Value**

the same class with object.

**See Also**

`edgeR::calcNormFactors()`, `DESeq2::estimateSizeFactorsForMatrix()`, `metagenomeSeq::cumNorm()`  
`phyloseq::rarefy_even_depth()`  
`metagenomeSeq::calcNormFactors()`  
`DESeq2::estimateSizeFactorsForMatrix()`  
`edgeR::calcNormFactors()`

**Examples**

```
data(caporaso)
normalize(caporaso, "TSS")
```

---

phyloseq2DESeq2      *Convert phyloseq-class object to DESeqDataSet-class object*

---

**Description**

This function convert [phyloseq::phyloseq-class] to [DESeq2::DESeqDataSet-class], which can then be tested using

**Usage**

```
phyloseq2DESeq2(ps, design, ...)
```



**Arguments**

|        |   |
|--------|---|
| ps     | the [phyloseq::phyloseq-class] object to convert, which must have a [phyloseq::sample_data()] component.  |
| design | a formula or matrix, the formula expresses how the counts for each gene depend on the variables in colData. Many R formula are valid, including designs with multiple variables, e.g., ~ group + condition. This argument is passed to <a href="#">DESeq2::DESeqDataSetFromMatrix()</a> . |
| ...    | additional arguments passed to <a href="#">DESeq2::DESeqDataSetFromMatrix()</a> , Most users will not need to pass any additional arguments here.   |

**Value**

a [DESeq2::DESeqDataSet](#) object.

**See Also**

[DESeq2::DESeqDataSetFromMatrix\(\)](#), [DESeq2::DESeq\(\)](#)

**Examples**

```
data(caporaso)
phyloseq2DESeq2(caporaso, ~SampleType)
```

---

|                |  |
|----------------|--|
| phyloseq2edgeR | <i>Convert phyloseq data to edgeR DGEList object</i> |
|----------------|--|

---

**Description**

This function convert [phyloseq::phyloseq](#) object to [edgeR::DGEList](#) object, can then can be used to perform differential analysis using the methods in **edgeR**.

**Usage**

```
phyloseq2edgeR(ps, ...)
```

**Arguments**

|     |   |
|-----|---|
| ps  | a <a href="#">phyloseq::phyloseq</a> object.  |
| ... | optional, additional named arguments passed to <a href="#">edgeR::DGEList()</a> . Most users will not need to pass any additional arguments here. |

**Value**

A [edgeR::DGEList](#) object.

**Examples**

```
data(caporaso)
dge <- phyloseq2edgeR(caporaso)
```

---

```
phyloseq2metagenomeSeq
```

*Convert phyloseq data to MetagenomeSeq MRExperiment object*

---

### Description

The phyloseq data is converted to the relevant `metagenomeSeq::MRExperiment` object, which can then be tested in the zero-inflated mixture model framework in the `metagenomeSeq` package.

### Usage

```
phyloseq2metagenomeSeq(ps, ...)
```

```
otu_table2metagenomeSeq(ps, ...)
```

### Arguments

`ps` `phyloseq::phyloseq` object for `phyloseq2metagenomeSeq()`, or `phyloseq::otu_table` object for `otu_table2metagenomeSeq()`.

`...` optional, additional named arguments passed to `metagenomeSeq::newMRExperiment()`. Most users will not need to pass any additional arguments here.

### Value

A `metagenomeSeq::MRExperiment` object.

### See Also

`metagenomeSeq::fitTimeSeries()`, `metagenomeSeq::fitLogNormal()`, `metagenomeSeq::fitZig()`, `metagenomeSeq::MRtable()`, `metagenomeSeq::MRfulltable()`

### Examples

```
data(caporaso)
phyloseq2metagenomeSeq(caporaso)
```

---

```
plot.compareDA
```

*Plotting DA comparing result*

---

### Description

Plotting DA comparing result

### Usage

```
## S3 method for class 'compareDA'
plot(x, sort = c("score", "auc", "fpr", "power"), ...)
```

**Arguments**

|      |   |
|------|---|
| x    | an compareDA object, output from <code>compare_DA()</code> .  |
| sort | character string specifying sort method. Possibilities are "score" which is calculated as $(auc - 0.5) * power - fdr$ , "auc" for area under the ROC curve, "fpr" for false positive rate, "power" for empirical power. |
| ...  | extra arguments, just ignore it.  |

**Value**

a `ggplot2::ggplot` object containing 4 subplots: "auc", "fdr", "power" and "score" plot.

---

|                |                                       |
|----------------|---------------------------------------|
| plot_abundance | <i>plot the abundances of markers</i> |
|----------------|---------------------------------------|

---

**Description**

plot the abundances of markers

**Usage**

```
plot_abundance(mm, label_level = 1, max_label_len = 60, markers = NULL, group)
```

**Arguments**

|               |  |
|---------------|--|
| mm            | a <code>microbiomeMarker</code> object   |
| label_level   | integer, number of label levels to be displayed, default 1, 0 means display the full name of the feature |
| max_label_len | integer, maximum number of characters of feature label, default 60                                       |
| markers       | character vector, markers to display, default NULL, indicating plot all markers.                         |
| group         | character, the variable to set the group   |

**Value**

a `ggplot2::ggplot` object.

**Examples**

```
data(enterotypes_arumugam)
mm <- run_limma_voom(
  enterotypes_arumugam,
  "Enterotype",
  contrast = c("Enterotype 3", "Enterotype 2"),
  pvalue_cutoff = 0.01,
  p_adjust = "none"
)
plot_abundance(mm, group = "Enterotype")
```

---

plot\_cladogram      *plot cladogram of microbiomeMaker results*

---

## Description

plot cladogram of microbiomeMaker results

## Usage

```
plot_cladogram(
  mm,
  color,
  only_marker = FALSE,
  branch_size = 0.2,
  alpha = 0.2,
  node_size_scale = 1,
  node_size_offset = 1,
  clade_label_level = 4,
  clade_label_font_size = 4,
  annotation_shape = 22,
  annotation_shape_size = 5,
  group_legend_param = list(),
  marker_legend_param = list()
)
```

## Arguments

|                       |  |
|-----------------------|--|
| mm                    | a <a href="#">microbiomeMarker</a> object  |
| color                 | a color vector, used to highlight the clades of microbiome biomarker. The values will be matched in order (usually alphabetical) with the groups. If this is a named vector, then the colors will be matched based on the names instead. |
| only_marker           | logical, whether show all the features or only markers in the cladogram, default FALSE.  |
| branch_size           | numeric, size of branch, default 0.2   |
| alpha                 | alpha parameter for shading, default 0.2   |
| node_size_scale       | the parameter 'a' controlling node size: $node\_size = a * \log(\text{relative\_abundance}) + b$   |
| node_size_offset      | the parameter 'b' controlling node size: $node\_size = a * \log(\text{relative\_abundance}) + b$   |
| clade_label_level     | max level of taxa used to label the clade, other level of taxa will be shown on the side.  |
| clade_label_font_size | font size of the clade label, default 4.   |

annotation\_shape  
shape used for annotation, default 22

annotation\_shape\_size  
size used for annotation shape, default 5

group\_legend\_param, marker\_legend\_param  
a list specifying extra parameters of group legend and marker legend, such as direction ( the direction of the guide), nrow (the desired number of rows of legends). See `ggplot2::guide_legend()` for more details.

**Value**

a ggtree object

**Author(s)**

Chenhao Li, Guangchuang Yu, Chenghao Zhu, Yang Cao

**References**

This function is modified from `clada.anno` from `microbiomeViz`.

**See Also**

[ggtree::ggtree\(\)](#)

**Examples**

```
data(kostic_crc)
kostic_crc_small <- phyloseq::subset_taxa(
  kostic_crc,
  Phylum %in% c("Firmicutes")
)
mm_lefse <- run_lefse(
  kostic_crc_small,
  wilcoxon_cutoff = 0.01,
  group = "DIAGNOSIS",
  kw_cutoff = 0.01,
  multigrp_strat = TRUE,
  lda_cutoff = 4
)
plot_cladogram(mm_lefse, color = c("darkgreen", "red"))
```

---

|             |   |
|-------------|---|
| plot_ef_bar | <i>bar and dot plot of effect size of microbiomeMarker data</i> |
|-------------|---|

---

## Description

bar and dot plot of effect size microbiomeMarker data. This function returns a ggplot2 object that can be saved or further customized using **ggplot2** package.

## Usage

```
plot_ef_bar(mm, label_level = 1, max_label_len = 60, markers = NULL)
```

```
plot_ef_dot(mm, label_level = 1, max_label_len = 60, markers = NULL)
```

## Arguments

|               |  |
|---------------|--|
| mm            | a <a href="#">microbiomeMarker</a> object  |
| label_level   | integer, number of label levels to be displayed, default 1, 0 means display the full name of the feature |
| max_label_len | integer, maximum number of characters of feature label, default 60                                       |
| markers       | character vector, markers to display, default NULL, indicating plot all markers.                         |

## Value

a ggplot project

## Examples

```
data(enterotypes_arumugam)
mm <- run_limma_voom(
  enterotypes_arumugam,
  "Enterotype",
  contrast = c("Enterotype 3", "Enterotype 2"),
  pvalue_cutoff = 0.01,
  p_adjust = "none"
)
plot_ef_bar(mm)
```

---

|              |                                     |
|--------------|-------------------------------------|
| plot_heatmap | <i>Heatmap of microbiome marker</i> |
|--------------|-------------------------------------|

---

### Description

Display the microbiome marker using heatmap, in which rows represents the marker and columns represents the samples.

### Usage

```
plot_heatmap(
  mm,
  transform = c("log10", "log10p", "identity"),
  cluster_marker = FALSE,
  cluster_sample = FALSE,
  markers = NULL,
  label_level = 1,
  max_label_len = 60,
  sample_label = FALSE,
  scale_by_row = FALSE,
  annotation_col = NULL,
  group,
  ...
)
```

### Arguments

|                                |  |
|--------------------------------|--|
| mm                             | a <a href="#">microbiomeMarker</a> object  |
| transform                      | transformation to apply, for more details see <a href="#">transform_abundances()</a> : <ul style="list-style-type: none"> <li>• "identity", return the original data without any transformation.</li> <li>• "log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>• "log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul> |
| cluster_marker, cluster_sample | logical, controls whether to perform clustering in markers (rows) and samples (cols), default FALSE.   |
| markers                        | character vector, markers to display, default NULL, indicating plot all markers.   |
| label_level                    | integer, number of label levels to be displayed, default 1, 0 means display the full name of the feature   |
| max_label_len                  | integer, maximum number of characters of feature label, default 60   |
| sample_label                   | logical, controls whether to show the sample labels in the heatmap, default FALSE.   |
| scale_by_row                   | logical, controls whether to scale the heatmap by the row (marker) values, default FALSE.  |

annotation\_col assign colors for the top annotation using a named vector, passed to col in `ComplexHeatmap::HeatmapAnnotation()`.  
 group character, the variable to set the group  
 ... extra arguments passed to `ComplexHeatmap::Heatmap()`.

**Value**

a `ComplexHeatmap::Heatmap` object.

**See Also**

`transform_abundances`, `ComplexHeatmap::Heatmap()`

**Examples**

```

data(kostic_crc)
kostic_crc_small <- phyloseq::subset_taxa(
  kostic_crc,
  Phylum %in% c("Firmicutes")
)
mm_lefse <- run_lefse(
  kostic_crc_small,
  wilcoxon_cutoff = 0.01,
  group = "DIAGNOSIS",
  kw_cutoff = 0.01,
  multigrp_strat = TRUE,
  lda_cutoff = 4
)
plot_heatmap(mm_lefse, group = "DIAGNOSIS")

```

---

|                  |                         |
|------------------|-------------------------|
| plot_postHocTest | postHocTest <i>plot</i> |
|------------------|-------------------------|

---

**Description**

Visualize the result of post-hoc test using `ggplot2`

**Usage**

```
plot_postHocTest(pht, feature, step_increase = 0.12)
```

**Arguments**

pht a `postHocTest` object  
 feature character, to plot the post-toc test result of this feature  
 step\_increase numeric vector with the increase in fraction of total height for every additional comparison to minimize overlap, default 0.12.



**Value**

a ggplot object

**Examples**

```
data(enterotypes_arumugam)
ps <- phyloseq::subset_samples(
  enterotypes_arumugam,
  Enterotype %in% c("Enterotype 3", "Enterotype 2", "Enterotype 1")
) %>%
  phyloseq::subset_taxa(Phylum == "Bacteroidetes")
pht <- run_posthoc_test(ps, group = "Enterotype")
plot_postHocTest(pht, feature = "p__Bacteroidetes|g__Alistipes")
```

---

plot\_sl\_roc

*ROC curve of microbiome marker from supervised learning methods*

---

**Description**

Show the ROC curve of the microbiome marker calculated by run\_sl.

**Usage**

```
plot_sl_roc(mm, group, nfolds = 3, nrepeats = 3, tune_length = 5, ...)
```

**Arguments**

mm a [microbiomeMarker](#) object.  
group, nfolds, nrepeats, tune\_length, ...  
same with the run\_sl().

**Value**

a `ggplot2::ggplot` object.

**See Also**

[run\\_sl\(\)](#)

**Examples**

```
data(enterotypes_arumugam)
# small example phyloseq object for test
ps_s <- phyloseq::subset_taxa(
  enterotypes_arumugam,
  Phylum %in% c("Firmicutes", "Bacteroidetes")
)

set.seed(2021)
```

```
mm <- run_sl(
  ps_s,
  group = "Gender",
  taxa_rank = "Genus",
  nfolds = 2,
  nrepeats = 1,
  top_n = 15,
  norm = "TSS",
  method = "LR",
)
plot_sl_roc(mm, group = "Gender")
```

---

postHocTest

*Build postHocTest object*


---

## Description

This function is used for create postHocTest object, and is only used for developers.

## Usage

```
postHocTest(
  result,
  abundance,
  conf_level = 0.95,
  method = "tukey",
  method_str = paste("Posthoc multiple comparisons of means: ", method)
)
```

## Arguments

|            |   |
|------------|---|
| result     | a <a href="#">IRanges::SimpleDFrameList</a> object.           |
| abundance  | data.frame.   |
| conf_level | numeric, confidence level.                                    |
| method     | character, method for posthoc test.                           |
| method_str | character, illustrates which method is used for posthoc test. |

## Value

a [postHocTest](#) object.

## Examples

```
require(IRanges)
pht <- postHocTest(
  result = DataFrameList(
    featureA = DataFrame(
      comparisons = c("group2-group1",
```

```

        "group3-group1",
        "group3-group2"),
    diff_mean = runif(3),
    pvalue = rep(0.01, 3),
    ci_lower = rep(0.01, 3),
    ci_upper = rep(0.011, 3)
  ),
  featureB = DataFrame(
    comparisons = c("group2-group1",
                  "group3-group1",
                  "group3-group2"),
    diff_mean = runif(3),
    pvalue = rep(0.01, 3),
    ci_lower = rep(0.01, 3),
    ci_upper = rep(0.011, 3)
  )
),
abundance = data.frame(
  featureA = runif(3),
  featureB = runif(3),
  group = c("group1", "group2", "grou3")
)
)
pht

```

---

|                   |   |
|-------------------|---|
| postHocTest-class | <i>The postHocTest Class, represents the result of post-hoc test result among multiple groups</i> |
|-------------------|---|

---

## Description

The postHocTest Class, represents the result of post-hoc test result among multiple groups

## Usage

```
## S4 method for signature 'postHocTest'
show(object)
```

## Arguments

object            a postHocTest-class object

## Value

a `postHocTest` object.

**Slots**

result a `IRanges::DataFrameList`, each DataFrame consists of five variables:

- comparisons: character, specify which two groups to test (the group names are separated by "\_")
- diff\_mean: numeric, difference in mean abundances
- pvalue: numeric, p values
- ci\_lower and ci\_upper: numeric, lower and upper confidence interval of difference in mean abundances

abundance abundance of each feature in each group

conf\_level confidence level

method method used for post-hoc test

method\_str method illustration

**Author(s)**

Yang Cao

---

run\_aldex

*Perform differential analysis using ALDEx2*

---

**Description**

Perform differential analysis using ALDEx2

**Usage**

```
run_aldex(
  ps,
  group,
  taxa_rank = "all",
  transform = c("identity", "log10", "log10p"),
  norm = "none",
  norm_para = list(),
  method = c("t.test", "wilcox.test", "kruskal", "glm_anova"),
  p_adjust = c("none", "fdr", "bonferroni", "holm", "hochberg", "hommel", "BH", "BY"),
  pvalue_cutoff = 0.05,
  mc_samples = 128,
  denom = c("all", "iqlr", "zero", "lvha"),
  paired = FALSE
)
```

**Arguments**

|               |  |
|---------------|--|
| ps            | a <code>phyloseq::phyloseq</code> object   |
| group         | character, the variable to set the group   |
| taxa_rank     | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(phyloseq)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(phyloseq)</code> ), e.g., OTU or ASV).  |
| transform     | character, the methods used to transform the microbial abundance. See <code>transform_abundances()</code> for more details. The options include: <ul style="list-style-type: none"> <li>"identity", return the original data without any transformation (default).</li> <li>"log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>"log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul>   |
| norm          | the methods used to normalize the microbial abundance data. See <code>normalize()</code> for more details. Options include: <ul style="list-style-type: none"> <li>"none": do not normalize.</li> <li>"rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>"TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.</li> <li>"TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> <li>"RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.</li> <li>"CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.</li> <li>"CLR": centered log-ratio normalization.</li> <li>"CPM": pre-sample normalization of the sum of the values to <math>1e+06</math>.</li> </ul> |
| norm_para     | arguments passed to specific normalization methods   |
| method        | test method, options include: "t.test" and "wilcox.test" for two groups comparison, "kruskal" and "glm_anova" for multiple groups comparison.  |
| p_adjust      | method for multiple test correction, default none, for more details see <code>stats::p.adjust</code> .   |
| pvalue_cutoff | cutoff of p value, default 0.05.   |
| mc_samples    | integer, the number of Monte Carlo samples to use for underlying distributions estimation, 128 is usually sufficient.  |
| denom         | character string, specify which features used to as the denominator for the geometric mean calculation. Options are: <ul style="list-style-type: none"> <li>"all", with all features.</li> </ul>   |

- "iqlr", accounts for data with systematic variation and centers the features on the set features that have variance that is between the lower and upper quartile of variance.
  - "zero", a more extreme case where there are many non-zero features in one condition but many zeros in another. In this case the geometric mean of each group is calculated using the set of per-group non-zero features.
  - "lvha", with house keeping features.
- paired            logical, whether to perform paired tests, only worked for method "t.test" and "wilcox.test".

### Value

a `microbiomeMarker` object.

### References

Fernandes, A.D., Reid, J.N., Macklaim, J.M. et al. Unifying the analysis of high-throughput sequencing datasets: characterizing RNA-seq, 16S rRNA gene sequencing and selective growth experiments by compositional data analysis. *Microbiome* 2, 15 (2014).

### See Also

[ALDEx2::aldex\(\)](#)

### Examples

```
data(enterotypes_arumugam)
ps <- phyloseq::subset_samples(
  enterotypes_arumugam,
  Enterotype %in% c("Enterotype 3", "Enterotype 2")
)
run_aldex(ps, group = "Enterotype")
```

---

run\_ancom

*Perform differential analysis using ANCOM*

---

### Description

Perform significant test by comparing the pairwise log ratios between all features.

### Usage

```
run_ancom(
  ps,
  group,
  confounders = character(0),
  taxa_rank = "all",
  transform = c("identity", "log10", "log10p"),
```

```

norm = "TSS",
norm_para = list(),
p_adjust = c("none", "fdr", "bonferroni", "holm", "hochberg", "hommel", "BH", "BY"),
pvalue_cutoff = 0.05,
W_cutoff = 0.75
)

```

## Arguments

|             |   |
|-------------|---|
| ps          | a <a href="#">phyloseq-class</a> object.  |
| group       | character, the variable to set the group.   |
| confounders | character vector, the confounding variables to be adjusted. default character(0), indicating no confounding variable.   |
| taxa_rank   | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(phyloseq)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(phyloseq)</code> , e.g., OTU or ASV).  |
| transform   | character, the methods used to transform the microbial abundance. See <a href="#">transform_abundances()</a> for more details. The options include: <ul style="list-style-type: none"> <li>"identity", return the original data without any transformation.</li> <li>"log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>"log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul>   |
| norm        | the methods used to normalize the microbial abundance data. See <a href="#">normalize()</a> for more details. Options include: <ul style="list-style-type: none"> <li>"none": do not normalize.</li> <li>"rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>"TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.</li> <li>"TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> <li>"RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.</li> <li>"CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.</li> <li>"CLR": centered log-ratio normalization.</li> <li>"CPM": pre-sample normalization of the sum of the values to <math>1e+06</math>.</li> </ul> |
| norm_para   | named list. other arguments passed to specific normalization methods. Most users will not need to pass any additional arguments here.   |

|               |   |
|---------------|---|
| p_adjust      | method for multiple test correction, default none, for more details see <a href="#">stats::p.adjust</a> . |
| pvalue_cutoff | significance level for each of the statistical tests, default 0.05.                                       |
| W_cutoff      | lower bound for the proportion for the W-statistic, default 0.7.  |

### Details

In an experiment with only two treatments, this tests the following hypothesis for feature  $i$ :

$$H_{0i} : E(\log(\mu_i^1)) = E(\log(\mu_i^2))$$

where  $\mu_i^1$  and  $\mu_i^2$  are the mean abundances for feature  $i$  in the two groups.

The developers of this method recommend the following significance tests if there are 2 groups, use non-parametric Wilcoxon rank sum test [stats::wilcox.test\(\)](#). If there are more than 2 groups, use nonparametric [stats::kruskal.test\(\)](#) or one-way ANOVA [stats::aov\(\)](#).

### Value

a [microbiomeMarker](#) object, in which the slot of marker\_table contains four variables:

- feature, significantly different features.
- enrich\_group, the class of the differential features enriched.
- effect\_size, differential means for two groups, or F statistic for more than two groups.
- W, the W-statistic, number of features that a single feature is tested to be significantly different against.

### Author(s)

Huang Lin, Yang Cao

### References

Mandal et al. "Analysis of composition of microbiomes: a novel method for studying microbial composition", *Microbial Ecology in Health & Disease*, (2015), 26.

### Examples

```
data(enterotypes_arumugam)
ps <- phyloseq::subset_samples(
  enterotypes_arumugam,
  Enterotype %in% c("Enterotype 3", "Enterotype 2")
)
run_ancom(ps, group = "Enterotype")
```



---

|             |  |
|-------------|--|
| run_ancombc | <i>Differential analysis of compositions of microbiomes with bias correction (ANCOM-BC).</i> |
|-------------|--|

---

### Description

Differential abundance analysis for microbial absolute abundance data. This function is a wrapper of `ANCOMBC::ancombc()`.

### Usage

```
run_ancombc(
  ps,
  group,
  confounders = character(0),
  contrast = NULL,
  taxa_rank = "all",
  transform = c("identity", "log10", "log10p"),
  norm = "none",
  norm_para = list(),
  p_adjust = c("none", "fdr", "bonferroni", "holm", "hochberg", "hommel", "BH", "BY"),
  prv_cut = 0.1,
  lib_cut = 0,
  struc_zero = FALSE,
  neg_lb = FALSE,
  tol = 1e-05,
  max_iter = 100,
  conserve = FALSE,
  pvalue_cutoff = 0.05
)
```

### Arguments

|             |   |
|-------------|---|
| ps          | a <code>phyloseq::phyloseq</code> object, which consists of a feature table, a sample metadata and a taxonomy table.  |
| group       | the name of the group variable in metadata. Specifying group is required for detecting structural zeros and performing global test.   |
| confounders | character vector, the confounding variables to be adjusted. default <code>character(0)</code> , indicating no confounding variable.   |
| contrast    | this parameter only used for two groups comparison while there are multiple groups. For more please see the following details.  |
| taxa_rank   | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(phyloseq)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(phyloseq)</code> ), e.g., OTU or ASV). |

|               |   |
|---------------|---|
| transform     | character, the methods used to transform the microbial abundance. See <a href="#">transform_abundances()</a> for more details. The options include: <ul style="list-style-type: none"> <li>• "identity", return the original data without any transformation (default).</li> <li>• "log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>• "log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul>   |
| norm          | the methods used to normalize the microbial abundance data. See <a href="#">normalize()</a> for more details. Options include: <ul style="list-style-type: none"> <li>• "none": do not normalize.</li> <li>• "rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>• "TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.</li> <li>• "TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> <li>• "RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.</li> <li>• "CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.</li> <li>• "CLR": centered log-ratio normalization.</li> <li>• "CPM": pre-sample normalization of the sum of the values to <math>1e+06</math>.</li> </ul> |
| norm_para     | named list. other arguments passed to specific normalization methods. Most users will not need to pass any additional arguments here.   |
| p_adjust      | method to adjust p-values by. Default is "holm". Options include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". See <a href="#">stats::p.adjust()</a> for more details.   |
| prv_cut       | a numerical fraction between 0 and 1. Taxa with prevalences less than prv_cut will be excluded in the analysis. Default is 0.10.  |
| lib_cut       | a numerical threshold for filtering samples based on library sizes. Samples with library sizes less than lib_cut will be excluded in the analysis. Default is 0, i.e. do not filter any sample.   |
| struc_zero    | whether to detect structural zeros. Default is FALSE.   |
| neg_lb        | whether to classify a taxon as a structural zero in the corresponding study group using its asymptotic lower bound. Default is FALSE.   |
| tol           | the iteration convergence tolerance for the E-M algorithm. Default is $1e-05$ .   |
| max_iter      | the maximum number of iterations for the E-M algorithm. Default is 100.   |
| conserve      | whether to use a conservative variance estimate of the test statistic. It is recommended if the sample size is small and/or the number of differentially abundant taxa is believed to be large. Default is FALSE.   |
| pvalue_cutoff | level of significance. Default is 0.05.   |

## Details

contrast must be a two length character or NULL (default). It is only required to set manually for two groups comparison when there are multiple groups. The order determines the direction of comparison, the first element is used to specify the reference group (control). This means that, the first element is the denominator for the fold change, and the second element is used as baseline (numerator for fold change). Otherwise, users do not need to concern this parameter (set as default NULL), and if there are two groups, the first level of groups will be set as the reference group; if there are multiple groups, it will perform an ANOVA-like testing to find markers which differ in any of the groups.

## Value

a `microbiomeMarker` object.

## References

Lin, Huang, and Shyamal Das Peddada. "Analysis of compositions of microbiomes with bias correction." *Nature communications* 11.1 (2020): 1-11.

## See Also

[ANCOMBC: :ancombc](#)

## Examples

```
data(enterotypes_arumugam)
ps <- phyloseq::subset_samples(
  enterotypes_arumugam,
  Enterotype %in% c("Enterotype 3", "Enterotype 2")
)
run_ancombc(ps, group = "Enterotype")
```

---

run\_deseq2

*Perform DESeq differential analysis*

---

## Description

Differential expression analysis based on the Negative Binomial distribution using **DESeq2**.

## Usage

```
run_deseq2(
  ps,
  group,
  confounders = character(0),
  contrast = NULL,
  taxa_rank = "all",
  norm = "RLE",
```

```

norm_para = list(),
transform = c("identity", "log10", "log10p"),
fitType = c("parametric", "local", "mean", "glmGamPoi"),
sfType = "poscounts",
betaPrior = FALSE,
modelMatrixType,
useT = FALSE,
minmu = ifelse(fitType == "glmGamPoi", 1e-06, 0.5),
p_adjust = c("none", "fdr", "bonferroni", "holm", "hochberg", "hommel", "BH", "BY"),
pvalue_cutoff = 0.05,
...
)

```

## Arguments

|             |   |
|-------------|---|
| ps          | a <a href="#">phyloseq::phyloseq</a> object.  |
| group       | character, the variable to set the group, must be one of the var of the sample metadata.  |
| confounders | character vector, the confounding variables to be adjusted. default character(0), indicating no confounding variable.   |
| contrast    | this parameter only used for two groups comparison while there are multiple groups. For more please see the following details.  |
| taxa_rank   | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(phyloseq)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(phyloseq)</code> , e.g., OTU or ASV).  |
| norm        | the methods used to normalize the microbial abundance data. See <a href="#">normalize()</a> for more details. Options include: <ul style="list-style-type: none"> <li>"none": do not normalize.</li> <li>"rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>"TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> <li>"RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.</li> <li>"CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.</li> </ul> |
| norm_para   | arguments passed to specific normalization methods. Most users will not need to pass any additional arguments here.   |
| transform   | character, the methods used to transform the microbial abundance. See <a href="#">transform_abundances()</a> for more details. The options include:   |

- "identity", return the original data without any transformation (default).
- "log10", the transformation is  $\log_{10}(\text{object})$ , and if the data contains zeros the transformation is  $\log_{10}(1 + \text{object})$ .
- "log10p", the transformation is  $\log_{10}(1 + \text{object})$ .

fitType, sfType, betaPrior, modelMatrixType, useT, minmu

these seven parameters are inherited from `DESeq2::DESeq()`.

- fitType, either "parametric", "local", "mean", or "glmGamPoi" for the type of fitting of dispersions to the mean intensity.
- sfType, either "ratio", "poscounts", or "iterate" for the type of size factor estimation. We recommend to use "poscounts".
- betaPrior, whether or not to put a zero-mean normal prior on the non-intercept coefficients.
- modelMatrixType, either "standard" or "expanded", which describe how the model matrix,
- useT, logical, where Wald statistics are assumed to follow a standard Normal.
- minmu, lower bound on the estimated count for fitting gene-wise dispersion.

For more details, see `DESeq2::DESeq()`. Most users will not need to set this arguments (just use the defaults).

p\_adjust method for multiple test correction, default none, for more details see `stats::p.adjust`.  
 pvalue\_cutoff pvalue\_cutoff numeric, p value cutoff, default 0.05.  
 ... extra parameters passed to `DESeq2::DESeq()`.

## Details

**Note:** DESeq2 requires the input is raw counts (un-normalized counts), as only the counts values allow assessing the measurement precision correctly. For more details see the vignette of DESeq2 (`vignette("DESeq2")`).

Thus, this function only supports "none", "rarefy", "RLE", "CSS", and "TMM" normalization methods. We strongly recommend using the "RLE" method (default normalization method in the DESeq2 package). The other normalization methods are used for expert users and comparisons among different normalization methods.

For two groups comparison, this function utilizes the Wald test (defined by `DESeq2::nbinomWaldTest()`) for hypothesis testing. A Wald test statistic is computed along with a probability (p-value) that a test statistic at least as extreme as the observed value were selected at random. contrasts are used to specify which two groups to compare. The order of the names determines the direction of fold change that is reported.

Likelihood ratio test (LRT) is used to identify the genes that significantly changed across all the different levels for multiple groups comparisons. The LRT identified the significant features by comparing the full model to the reduced model. It is testing whether a feature removed in the reduced model explains a significant variation in the data.

contrast must be a two length character or NULL (default). It is only required to set manually for two groups comparison when there are multiple groups. The order determines the direction of comparison, the first element is used to specify the reference group (control). This means that, the first element is the denominator for the fold change, and the second element is used as baseline

(numerator for fold change). Otherwise, users do required to concern this parameter (set as default NULL), and if there are two groups, the first level of groups will set as the reference group; if there are multiple groups, it will perform an ANOVA-like testing to find markers which difference in any of the groups.

### Value

a `microbiomeMarker` object.

### References

Love, Michael I., Wolfgang Huber, and Simon Anders. "Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2." *Genome biology* 15.12 (2014): 1-21.

### See Also

`DESeq2::results()`, `DESeq2::DESeq()`

### Examples

```
data(enterotypes_arumugam)
ps <- phyloseq::subset_samples(
  enterotypes_arumugam,
  Enterotype %in% c("Enterotype 3", "Enterotype 2")) %>%
  phyloseq::subset_taxa(Phylum %in% c("Firmicutes"))
run_deseq2(ps, group = "Enterotype")
```

---

run\_edger

*Perform differential analysis using edgeR*

---

### Description

Differential expression analysis based on the Negative Binomial distribution using **edgeR**.

### Usage

```
run_edger(
  ps,
  group,
  confounders = character(0),
  contrast = NULL,
  taxa_rank = "all",
  method = c("LRT", "QLFT"),
  transform = c("identity", "log10", "log10p"),
  norm = "TMM",
  norm_para = list(),
  disp_para = list(),
  p_adjust = c("none", "fdr", "bonferroni", "holm", "hochberg", "hommel", "BH", "BY"),
```

```

    pvalue_cutoff = 0.05,
    ...
)

```

## Arguments

|             |  |
|-------------|--|
| ps          | ps a <code>phyloseq::phyloseq</code> object.   |
| group       | character, the variable to set the group, must be one of the var of the sample metadata.   |
| confounders | character vector, the confounding variables to be adjusted. default character(0), indicating no confounding variable.  |
| contrast    | this parameter only used for two groups comparison while there are multiple groups. For more please see the following details.   |
| taxa_rank   | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(phyloseq)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(phyloseq)</code> ), e.g., OTU or ASV).  |
| method      | character, used for differential analysis, please see details below for more info.   |
| transform   | character, the methods used to transform the microbial abundance. See <code>transform_abundances()</code> for more details. The options include: <ul style="list-style-type: none"> <li>"identity", return the original data without any transformation (default).</li> <li>"log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>"log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul>   |
| norm        | the methods used to normalize the microbial abundance data. See <code>normalize()</code> for more details. Options include: <ul style="list-style-type: none"> <li>"none": do not normalize.</li> <li>"rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>"TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.</li> <li>"TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> <li>"RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.</li> <li>"CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.</li> <li>"CLR": centered log-ratio normalization.</li> <li>"CPM": pre-sample normalization of the sum of the values to <math>1e+06</math>.</li> </ul> |

|               |  |
|---------------|--|
| norm_para     | arguments passed to specific normalization methods. Most users will not need to pass any additional arguments here.  |
| disp_para     | additional arguments passed to <code>edgeR::estimateDisp()</code> used for dispersions estimation. Most users will not need to pass any additional arguments here. |
| p_adjust      | method for multiple test correction, default none, for more details see <code>stats::p.adjust</code> .   |
| pvalue_cutoff | numeric, p value cutoff, default 0.05  |
| ...           | extra arguments passed to the model. See <code>edgeR::glmQLFit()</code> and <code>edgeR::glmFit()</code> for more details.   |

## Details

**Note** that edgeR is designed to work with actual counts. This means that transformation is not required in any way before inputting them to edgeR.

There are two test methods for differential analysis in **edgeR**, likelihood ratio test (LRT) and quasi-likelihood F-test (QLFT). The QLFT method is recommended as it allows stricter error rate control by accounting for the uncertainty in dispersion estimation.

contrast must be a two length character or NULL (default). It is only required to set manually for two groups comparison when there are multiple groups. The order determines the direction of comparison, the first element is used to specify the reference group (control). This means that, the first element is the denominator for the fold change, and the second element is used as baseline (numerator for fold change). Otherwise, users do not need to concern this parameter (set as default NULL), and if there are two groups, the first level of groups will set as the reference group; if there are multiple groups, it will perform an ANOVA-like testing to find markers which difference in any of the groups.

## Value

a `microbiomeMarker` object.

## Author(s)

Yang Cao

## References

Robinson, Mark D., and Alicia Oshlack. "A scaling normalization method for differential expression analysis of RNA-seq data." *Genome biology* 11.3 (2010): 1-9.

Robinson, Mark D., Davis J. McCarthy, and Gordon K. Smyth. "edgeR: a Bioconductor package for differential expression analysis of digital gene expression data." *Bioinformatics* 26.1 (2010): 139-140.

## See Also

`edgeR::glmFit()`, `edgeR::glmQLFit()`, `edgeR::estimateDisp()`, `normalize()`



## Examples

```
data(enterotypes_arumugam)
ps <- phyloseq::subset_samples(
  enterotypes_arumugam,
  Enterotype %in% c("Enterotype 3", "Enterotype 2")
)
run_edger(ps, group = "Enterotype")
```

---

run\_lefse

*Liner discriminant analysis (LDA) effect size (LEFSe) analysis*

---

## Description

Perform Metagenomic LEFSe analysis based on phyloseq object.

## Usage

```
run_lefse(
  ps,
  group,
  subgroup = NULL,
  taxa_rank = "all",
  transform = c("identity", "log10", "log10p"),
  norm = "CPM",
  norm_para = list(),
  kw_cutoff = 0.05,
  lda_cutoff = 2,
  bootstrap_n = 30,
  bootstrap_fraction = 2/3,
  wilcoxon_cutoff = 0.05,
  multigrp_strat = FALSE,
  strict = c("0", "1", "2"),
  sample_min = 10,
  only_same_subgrp = FALSE,
  curv = FALSE
)
```

## Arguments

|           |   |
|-----------|---|
| ps        | a <a href="#">phyloseq-class</a> object   |
| group     | character, the column name to set the group   |
| subgroup  | character, the column name to set the subgroup  |
| taxa_rank | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(phyloseq)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(phyloseq)</code> ), e.g., OTU or ASV). |

|                    |   |
|--------------------|---|
| transform          | character, the methods used to transform the microbial abundance. See <a href="#">transform_abundances()</a> for more details. The options include: <ul style="list-style-type: none"> <li>• "identity", return the original data without any transformation (default).</li> <li>• "log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>• "log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul>   |
| norm               | the methods used to normalize the microbial abundance data. See <a href="#">normalize()</a> for more details. Options include: <ul style="list-style-type: none"> <li>• "none": do not normalize.</li> <li>• "rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>• "TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.</li> <li>• "TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> <li>• "RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.</li> <li>• "CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.</li> <li>• "CLR": centered log-ratio normalization.</li> <li>• "CPM": pre-sample normalization of the sum of the values to <math>1e+06</math>.</li> </ul> |
| norm_para          | named list. other arguments passed to specific normalization methods. Most users will not need to pass any additional arguments here.   |
| kw_cutoff          | numeric, p value cutoff of kw test, default 0.05  |
| lda_cutoff         | numeric, lda score cutoff, default 2  |
| bootstrap_n        | integer, the number of bootstrap iteration for LDA, default 30  |
| bootstrap_fraction | numeric, the subsampling fraction value for each bootstrap iteration, default 2/3   |
| wilcoxon_cutoff    | numeric, p value cutoff of wilcoxon test, default 0.05  |
| multigrp_strat     | logical, for multiple group tasks, whether the test is performed in a one-against one (more strict) or in a one-against all setting, default FALSE.   |
| strict             | multiple testing options, 0 for no correction (default), 1 for independent comparisons, 2 for independent comparison.   |
| sample_min         | integer, minimum number of samples per subclass for performing wilcoxon test, default 10  |
| only_same_subgrp   | logical, whether perform the wilcoxon test only among the subgroups with the same name, default FALSE   |
| curv               | logical, whether perform the wilcoxon test using the Curtis's approach, default FALSE   |

**Value**

a [microbiomeMarker](#) object, in which the slot of marker\_table contains four variables:

- feature, significantly different features.
- enrich\_group, the class of the differential features enriched.
- lda, logarithmic LDA score (effect size)
- pvalue, p value of kw test.

**Author(s)**

Yang Cao

**References**

Segata, Nicola, et al. Metagenomic biomarker discovery and explanation. *Genome biology* 12.6 (2011): R60.

**See Also**

[normalize](#)

**Examples**

```
data(kostic_crc)
kostic_crc_small <- phyloseq::subset_taxa(
  kostic_crc,
  Phylum == "Firmicutes"
)
mm_lefse <- run_lefse(
  kostic_crc_small,
  wilcoxon_cutoff = 0.01,
  group = "DIAGNOSIS",
  kw_cutoff = 0.01,
  multigrp_strat = TRUE,
  lda_cutoff = 4
)
```

---

run\_limma\_voom

*Differential analysis using limma-voom*

---

**Description**

Differential analysis using limma-voom

**Usage**

```
run_limma_voom(
  ps,
  group,
  confounders = character(0),
  contrast = NULL,
  taxa_rank = "all",
  transform = c("identity", "log10", "log10p"),
  norm = "none",
  norm_para = list(),
  voom_span = 0.5,
  p_adjust = c("none", "fdr", "bonferroni", "holm", "hochberg", "hommel", "BH", "BY"),
  pvalue_cutoff = 0.05,
  ...
)
```

**Arguments**

|             |   |
|-------------|---|
| ps          | ps a <a href="#">phyloseq::phyloseq</a> object.   |
| group       | character, the variable to set the group, must be one of the var of the sample metadata.  |
| confounders | character vector, the confounding variables to be adjusted. default <code>character(0)</code> , indicating no confounding variable.   |
| contrast    | this parameter only used for two groups comparison while there are multiple groups. For more please see the following details.  |
| taxa_rank   | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(phyloseq)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(phyloseq)</code> ), e.g., OTU or ASV).   |
| transform   | character, the methods used to transform the microbial abundance. See <a href="#">transform_abundances()</a> for more details. The options include: <ul style="list-style-type: none"> <li>"identity", return the original data without any transformation (default).</li> <li>"log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>"log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul>               |
| norm        | the methods used to normalize the microbial abundance data. See <a href="#">normalize()</a> for more details. Options include: <ul style="list-style-type: none"> <li>"none": do not normalize.</li> <li>"rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>"TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> </ul> |

- "RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.
- "CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.

|               |   |
|---------------|---|
| norm_para     | arguments passed to specific normalization methods. Most users will not need to pass any additional arguments here.                               |
| voom_span     | width of the smoothing window used for the lowess mean-variance trend for <code>limma::voom()</code> . Expressed as a proportion between 0 and 1. |
| p_adjust      | method for multiple test correction, default none, for more details see <code>stats::p.adjust</code> .  |
| pvalue_cutoff | cutoff of p value, default 0.05.  |
| ...           | extra arguments passed to <code>limma::eBayes()</code> .  |

### Details

contrast must be a two length character or NULL (default). It is only required to set manually for two groups comparison when there are multiple groups. The order determines the direction of comparison, the first element is used to specify the reference group (control). This means that, the first element is the denominator for the fold change, and the second element is used as baseline (numerator for fold change). Otherwise, users do not need to concern this parameter (set as default NULL), and if there are two groups, the first level of groups will be set as the reference group; if there are multiple groups, it will perform an ANOVA-like testing to find markers which differ in any of the groups.

### Value

a `microbiomeMarker` object.

### References

Law, C. W., Chen, Y., Shi, W., & Smyth, G. K. (2014). voom: Precision weights unlock linear model analysis tools for RNA-seq read counts. *Genome biology*, 15(2), 1-17.

### Examples

```
data(enterotypes_arumugam)
mm <- run_limma_voom(
  enterotypes_arumugam,
  "Enterotype",
  contrast = c("Enterotype 3", "Enterotype 2"),
  pvalue_cutoff = 0.01,
  p_adjust = "none"
)
mm
```

---

|            |  |
|------------|--|
| run_marker | <i>Find makers (differentially expressed metagenomic features)</i> |
|------------|--|

---

## Description

run\_marker is a wrapper of all differential analysis functions.

## Usage

```
run_marker(
  ps,
  group,
  da_method = c("lefse", "simple_t", "simple_welch", "simple_white", "simple_kruskal",
    "simple_anova", "edger", "deseq2", "metagenomeseq", "ancom", "ancombc", "aldex",
    "limma_voom", "sl_lr", "sl_rf", "sl_svm"),
  taxa_rank = "all",
  transform = c("identity", "log10", "log10p"),
  norm = "none",
  norm_para = list(),
  p_adjust = c("none", "fdr", "bonferroni", "holm", "hochberg", "hommel", "BH", "BY"),
  pvalue_cutoff = 0.05,
  ...
)
```

## Arguments

|           |   |
|-----------|---|
| ps        | a <code>phyloseq::phyloseq</code> object  |
| group     | character, the variable to set the group  |
| da_method | character to specify the differential analysis method. The options include: <ul style="list-style-type: none"> <li>• "lefse", linear discriminant analysis (LDA) effect size (LEfSe) method, for more details see <code>run_lefse()</code>.</li> <li>• "simple_t", "simple_welch", "simple_white", "simple_kruskal", and "simple_anova", simple statistic methods; "simple_t", "simple_welch" and "simple_white" for two groups comparison; "simple_kruskal", and "simple_anova" for multiple groups comparison. For more details see <code>run_simple_stat()</code>.</li> <li>• "edger", see <code>run_edger()</code>.</li> <li>• "deseq2", see <code>run_deseq2()</code>.</li> <li>• "metagenomeseq", differential expression analysis based on the Zero-inflated Log-Normal mixture model or Zero-inflated Gaussian mixture model using metagenomeSeq, see <code>run_metagenomeseq()</code>.</li> <li>• "ancom", see <code>run_ancom()</code>.</li> <li>• "ancombc", differential analysis of compositions of microbiomes with bias correction, see <code>run_ancombc()</code>.</li> <li>• "aldex", see <code>run_aldex()</code>.</li> <li>• "limma_voom", see <code>run_limma_voom()</code>.</li> </ul> |

|               |   |
|---------------|---|
|               | <ul style="list-style-type: none"> <li>• "sl_lr", "sl_rf", and "sl_svm", three supervised learning (SL) methods: logistic regression (lr), random forest (rf), or support vector machine (svm). For more details see <a href="#">run_sl()</a>.</li> </ul>   |
| taxa_rank     | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(phyloseq)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(phyloseq)</code> ), e.g., OTU or ASV).   |
| transform     | character, the methods used to transform the microbial abundance. See <a href="#">transform_abundances()</a> for more details. The options include: <ul style="list-style-type: none"> <li>• "identity", return the original data without any transformation (default).</li> <li>• "log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>• "log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul>   |
| norm          | the methods used to normalize the microbial abundance data. See <a href="#">normalize()</a> for more details. Options include: <ul style="list-style-type: none"> <li>• "none": do not normalize.</li> <li>• "rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>• "TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.</li> <li>• "TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> <li>• "RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.</li> <li>• "CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.</li> <li>• "CLR": centered log-ratio normalization.</li> <li>• "CPM": pre-sample normalization of the sum of the values to <math>1e+06</math>.</li> </ul> |
| norm_para     | arguments passed to specific normalization methods  |
| p_adjust      | method for multiple test correction, default none, for more details see <a href="#">stats::p.adjust</a> .   |
| pvalue_cutoff | numeric, p value cutoff, default 0.05.  |
| ...           | extra arguments passed to the corresponding differential analysis functions, e.g. <a href="#">run_lefse()</a> .   |

## Details

This function is only a wrapper of all differential analysis functions, We recommend to use the corresponding function, since it has a better default arguments setting.

**Value**

a `microbiomeMarker` object.

**See Also**

`run_lefse()`, `run_simple_stat()`, `run_test_two_groups()`, `run_test_multiple_groups()`, `run_edger()`, `run_deseq2`, `run_metagenomeseq`, `run_ancom()`, `run_ancombc()`, `run_aldex()`, `run_limma_voom()`, `run_sl()`

---

run\_metagenomeseq      *metagenomeSeq differential analysis*

---

**Description**

Differential expression analysis based on the Zero-inflated Log-Normal mixture model or Zero-inflated Gaussian mixture model using `metagenomeSeq`.

**Usage**

```
run_metagenomeseq(
  ps,
  group,
  confounders = character(0),
  contrast = NULL,
  taxa_rank = "all",
  transform = c("identity", "log10", "log10p"),
  norm = "CSS",
  norm_para = list(),
  method = c("ZILN", "ZIG"),
  p_adjust = c("none", "fdr", "bonferroni", "holm", "hochberg", "hommel", "BH", "BY"),
  pvalue_cutoff = 0.05,
  ...
)
```

**Arguments**

|                          |   |
|--------------------------|---|
| <code>ps</code>          | a <code>phyloseq::phyloseq</code> object.   |
| <code>group</code>       | character, the variable to set the group, must be one of the var of the sample metadata.  |
| <code>confounders</code> | character vector, the confounding variables to be adjusted. default <code>character(0)</code> , indicating no confounding variable.   |
| <code>contrast</code>    | this parameter only used for two groups comparison while there are multiple groups. For more please see the following details.  |
| <code>taxa_rank</code>   | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(ps)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(ps)</code> ), e.g., OTU or ASV). |



|               |   |
|---------------|---|
| transform     | character, the methods used to transform the microbial abundance. See <a href="#">transform_abundances()</a> for more details. The options include: <ul style="list-style-type: none"> <li>• "identity", return the original data without any transformation (default).</li> <li>• "log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>• "log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul>   |
| norm          | the methods used to normalize the microbial abundance data. See <a href="#">normalize()</a> for more details. Options include: <ul style="list-style-type: none"> <li>• "none": do not normalize.</li> <li>• "rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>• "TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.</li> <li>• "TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> <li>• "RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.</li> <li>• "CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.</li> <li>• "CLR": centered log-ratio normalization.</li> <li>• "CPM": pre-sample normalization of the sum of the values to <math>1e+06</math>.</li> </ul> |
| norm_para     | arguments passed to specific normalization methods.   |
| method        | character, which model used for differential analysis, "ZILN" (Zero-inflated Log-Normal mixture model) or "ZIG" (Zero-inflated Gaussian mixture model). And the zero-inflated log-normal model is preferred due to the high sensitivity and low FDR.  |
| p_adjust      | method for multiple test correction, default none, for more details see <a href="#">stats::p.adjust</a> .   |
| pvalue_cutoff | numeric, p value cutoff, default 0.05   |
| ...           | extra arguments passed to the model. more details see <a href="#">metagenomeSeq::fitFeatureModel()</a> and <a href="#">metagenomeSeq::fitZig()</a> , e.g. control (can be setted using <a href="#">metagenomeSeq::zigControl()</a> ) for <a href="#">metagenomeSeq::fitZig()</a> .  |

## Details

metagenomeSeq provides two differential analysis methods, zero-inflated log-normal mixture model (implemented in [metagenomeSeq::fitFeatureModel\(\)](#)) and zero-inflated Gaussian mixture model (implemented in [metagenomeSeq::fitZig\(\)](#)). We recommend fitFeatureModel over fitZig due to high sensitivity and low FDR. Both [metagenomeSeq::fitFeatureModel\(\)](#) and [metagenomeSeq::fitZig\(\)](#) require the abundance profiles before normalization.

For [metagenomeSeq::fitZig\(\)](#), the output column is the coefficient of interest, and logFC column in the output of [metagenomeSeq::fitFeatureModel\(\)](#) is analogous to coefficient. Thus, logFC

is really just the estimate the coefficient of interest in `metagenomeSeq::fitFeatureModel()`. For more details see these question [Difference between fitFeatureModel and fitZIG in metagenomeSeq](#).

`contrast` must be a two length character or NULL (default). It is only required to set manually for two groups comparison when there are multiple groups. The order determines the direction of comparison, the first element is used to specify the reference group (control). This means that, the first element is the denominator for the fold change, and the second element is used as baseline (numerator for fold change). Otherwise, users do required to concern this parameter (set as default NULL), and if there are two groups, the first level of groups will set as the reference group; if there are multiple groups, it will perform an ANOVA-like testing to find markers which difference in any of the groups.

Of note, `metagenomeSeq::fitFeatureModel()` is not allows for multiple groups comparison.

### Value

a `microbiomeMarker` object.

### Author(s)

Yang Cao

### References

Paulson, Joseph N., et al. "Differential abundance analysis for microbial marker-gene surveys." *Nature methods* 10.12 (2013): 1200-1202.

### Examples

```
data(enterotypes_arumugam)
ps <- phyloseq::subset_samples(
  enterotypes_arumugam,
  Enterotype %in% c("Enterotype 3", "Enterotype 2")
)
run_metagenomeseq(ps, group = "Enterotype")
```

---

run\_posthoc\_test

*Post hoc pairwise comparisons for multiple groups test.*

---

### Description

Multiple group test, such as anova and Kruskal-Wallis rank sum test, can be used to uncover the significant feature among all groups. Post hoc tests are used to uncover specific mean differences between pair of groups.

**Usage**

```
run_posthoc_test(
  ps,
  group,
  transform = c("identity", "log10", "log10p"),
  norm = "TSS",
  norm_para = list(),
  conf_level = 0.95,
  method = c("tukey", "games_howell", "scheffe", "welch_uncorrected")
)
```

**Arguments**

|            |   |
|------------|---|
| ps         | a <a href="#">phyloseq::phyloseq</a> object   |
| group      | character, the variable to set the group  |
| transform  | character, the methods used to transform the microbial abundance. See <a href="#">transform_abundances()</a> for more details. The options include: <ul style="list-style-type: none"> <li>• "identity", return the original data without any transformation (default).</li> <li>• "log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>• "log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul>   |
| norm       | the methods used to normalize the microbial abundance data. See <a href="#">normalize()</a> for more details. Options include: <ul style="list-style-type: none"> <li>• a integer, e.g. 1e6 (default), indicating pre-sample normalization of the sum of the values to 1e6.</li> <li>• "none": do not normalize.</li> <li>• "rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>• "TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.</li> <li>• "TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> <li>• "RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.</li> <li>• "CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.</li> <li>• "CLR": centered log-ratio normalization.</li> </ul> |
| norm_para  | arguments passed to specific normalization methods  |
| conf_level | confidence level, default 0.95  |
| method     | one of "tukey", "games_howell", "scheffe", "welch_uncorrected", defining the method for the pairwise comparisons. See details for more information.   |

**Value**

a `postHocTest` object

**See Also**

`postHocTest`, `run_test_multiple_groups()`

**Examples**

```
data(enterotypes_arumugam)
ps <- phyloseq::subset_samples(
  enterotypes_arumugam,
  Enterotype %in% c("Enterotype 3", "Enterotype 2", "Enterotype 1")
) %>%
  phyloseq::subset_taxa(Phylum == "Bacteroidetes")
pht <- run_posthoc_test(ps, group = "Enterotype")
pht
```

---

`run_simple_stat`*Simple statistical analysis of metagenomic profiles*

---

**Description**

Perform simple statistical analysis of metagenomic profiles. This function is a wrapper of `run_test_two_groups` and `run_test_multiple_groups`.

**Usage**

```
run_simple_stat(
  ps,
  group,
  taxa_rank = "all",
  transform = c("identity", "log10", "log10p"),
  norm = "TSS",
  norm_para = list(),
  method = c("welch.test", "t.test", "white.test", "anova", "kruskal"),
  p_adjust = c("none", "fdr", "bonferroni", "holm", "hochberg", "hommel", "BH", "BY"),
  pvalue_cutoff = 0.05,
  diff_mean_cutoff = NULL,
  ratio_cutoff = NULL,
  eta_squared_cutoff = NULL,
  conf_level = 0.95,
  nperm = 1000,
  ...
)
```

**Arguments**

|                                |  |
|--------------------------------|--|
| ps                             | a <code>phyloseq::phyloseq</code> object   |
| group                          | character, the variable to set the group   |
| taxa_rank                      | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(phyloseq)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(phyloseq)</code> ), e.g., OTU or ASV).  |
| transform                      | character, the methods used to transform the microbial abundance. See <code>transform_abundances()</code> for more details. The options include: <ul style="list-style-type: none"> <li>"identity", return the original data without any transformation (default).</li> <li>"log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>"log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul>   |
| norm                           | the methods used to normalize the microbial abundance data. See <code>normalize()</code> for more details. Options include: <ul style="list-style-type: none"> <li>"none": do not normalize.</li> <li>"rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>"TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.</li> <li>"TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> <li>"RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.</li> <li>"CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.</li> <li>"CLR": centered log-ratio normalization.</li> <li>"CPM": pre-sample normalization of the sum of the values to <math>1e+06</math>.</li> </ul> |
| norm_para                      | arguments passed to specific normalization methods   |
| method                         | test method, options include: "welch.test", "t.test" and "white.test" for two groups comparison, "anova" and "kruskal" for multiple groups comparison.   |
| p_adjust                       | method for multiple test correction, default none, for more details see <code>stats::p.adjust</code> .   |
| pvalue_cutoff                  | numeric, p value cutoff, default 0.05  |
| diff_mean_cutoff, ratio_cutoff | only used for two groups comparison, cutoff of different means and ratios, default NULL which means no effect size filter.   |
| eta_squared_cutoff             | only used for multiple groups comparison, numeric, cutoff of effect size (eta squared) default NULL which means no effect size filter.   |

`conf_level` only used for two groups comparison, numeric, confidence level of interval.  
`nperm` integer, only used for two groups comparison, number of permutations for white non parametric t test estimation  
`...` only used for two groups comparison, extra arguments passed to `t.test()` or `fisher.test()`.

**Value**

a `microbiomeMarker` object.

**See Also**

`run_test_two_groups()`, `run_test_multiple_groups()`

**Examples**

```

data(enterotypes_arumugam)
ps <- phyloseq::subset_samples(
  enterotypes_arumugam,
  Enterotype %in% c("Enterotype 3", "Enterotype 2")
)
run_simple_stat(ps, group = "Enterotype")

```

---

run\_sl

*Identify biomarkers using supervised learning (SL) methods*


---

**Description**

Identify biomarkers using logistic regression, random forest, or support vector machine.

**Usage**

```

run_sl(
  ps,
  group,
  taxa_rank = "all",
  transform = c("identity", "log10", "log10p"),
  norm = "none",
  norm_para = list(),
  nfolds = 3,
  nrepeats = 3,
  sampling = NULL,
  tune_length = 5,
  top_n = 10,
  method = c("LR", "RF", "SVM"),
  ...
)

```

**Arguments**

|             |   |
|-------------|---|
| ps          | a <a href="#">phyloseq-class</a> object.  |
| group       | character, the variable to set the group.   |
| taxa_rank   | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(phyloseq)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(phyloseq)</code> ), e.g., OTU or ASV).   |
| transform   | character, the methods used to transform the microbial abundance. See <a href="#">transform_abundances()</a> for more details. The options include: <ul style="list-style-type: none"> <li>• "identity", return the original data without any transformation (default).</li> <li>• "log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>• "log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul>   |
| norm        | the methods used to normalize the microbial abundance data. See <a href="#">normalize()</a> for more details. Options include: <ul style="list-style-type: none"> <li>• "none": do not normalize.</li> <li>• "rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>• "TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.</li> <li>• "TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.</li> <li>• "RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.</li> <li>• "CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.</li> <li>• "CLR": centered log-ratio normalization.</li> <li>• "CPM": pre-sample normalization of the sum of the values to <math>1e+06</math>.</li> </ul> |
| norm_para   | named list. other arguments passed to specific normalization methods. Most users will not need to pass any additional arguments here.   |
| nfolds      | the number of splits in CV.   |
| nrepeats    | the number of complete sets of folds to compute.  |
| sampling    | a single character value describing the type of additional sampling that is conducted after resampling (usually to resolve class imbalances). Values are "none", "down", "up", "smote", or "rose". For more details see <a href="#">caret::trainControl()</a> .   |
| tune_length | an integer denoting the amount of granularity in the tuning parameter grid. For more details see <a href="#">caret::train()</a> .   |

|        |  |
|--------|--|
| top_n  | an integer denoting the top n features as the biomarker according the importance score.                                      |
| method | supervised learning method, options are "LR" (logistic regression), "RF" (random forest), or "SVM" (support vector machine). |
| ...    | extra arguments passed to the classification. e.g., importance for randomForest::randomForest.                               |

### Details

Only support two groups comparison in the current version. And the marker was selected based on its importance score. Moreover, The hyper-parameters are selected automatically by a grid-search based method in the N-time K-fold cross-validation. Thus, the identified biomarker based can be biased due to model overfitting for small datasets (e.g., with less than 100 samples).

The argument top\_n is used to denote the number of markers based on the importance score. There is no rule or principle on how to select top\_n, however, usually it is very useful to try a different top\_n and compare the performance of the marker predictions for the testing data.

### Value

a [microbiomeMarker](#) object.

### Author(s)

Yang Cao

### See Also

[caret::train\(\)](#), [caret::trainControl\(\)](#)

### Examples

```
data(enterotypes_arumugam)
# small example phyloseq object for test
ps_small <- phyloseq::subset_taxa(
  enterotypes_arumugam,
  Phylum %in% c("Firmicutes", "Bacteroidetes")
)

set.seed(2021)
mm <- run_sl(
  ps_small,
  group = "Gender",
  taxa_rank = "Genus",
  nfolds = 2,
  nrepeats = 1,
  top_n = 15,
  norm = "TSS",
  method = "LR",
)
mm
```



---

```
run_test_multiple_groups
```

*Statistical test for multiple groups*

---

**Description**

Statistical test for multiple groups

**Usage**

```
run_test_multiple_groups(
  ps,
  group,
  taxa_rank = "all",
  transform = c("identity", "log10", "log10p"),
  norm = "TSS",
  norm_para = list(),
  method = c("anova", "kruskal"),
  p_adjust = c("none", "fdr", "bonferroni", "holm", "hochberg", "hommel", "BH", "BY"),
  pvalue_cutoff = 0.05,
  effect_size_cutoff = NULL
)
```

**Arguments**

|           |   |
|-----------|---|
| ps        | a <a href="#">phyloseq::phyloseq</a> object   |
| group     | character, the variable to set the group  |
| taxa_rank | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(phyloseq)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(phyloseq)</code> ), e.g., OTU or ASV).   |
| transform | character, the methods used to transform the microbial abundance. See <a href="#">transform_abundances()</a> for more details. The options include: <ul style="list-style-type: none"> <li>"identity", return the original data without any transformation (default).</li> <li>"log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>"log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul> |
| norm      | the methods used to normalize the microbial abundance data. See <a href="#">normalize()</a> for more details. Options include: <ul style="list-style-type: none"> <li>"none": do not normalize.</li> <li>"rarefy": random subsampling counts to the smallest library size in the data set.</li> <li>"TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.</li> </ul>  |

- "TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.
- "RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.
- "CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.
- "CLR": centered log-ratio normalization.
- "CPM": pre-sample normalization of the sum of the values to 1e+06.

|                    |   |
|--------------------|---|
| norm_para          | arguments passed to specific normalization methods  |
| method             | test method, must be one of "anova" or "kruskal"  |
| p_adjust           | method for multiple test correction, default none, for more details see <a href="#">stats::p.adjust</a> .   |
| pvalue_cutoff      | numeric, p value cutoff, default 0.05.  |
| effect_size_cutoff | numeric, cutoff of effect size default NULL which means no effect size filter. The eta squared is used to measure the effect size for anova/kruskal test. |

### Value

a `microbiomeMarker` object.

### See Also

[run\\_posthoc\\_test\(\)](#), [run\\_test\\_two\\_groups\(\)](#), [run\\_simple\\_stat\(\)](#)

### Examples

```
data(enterotypes_arumugam)
ps <- phyloseq::subset_samples(
  enterotypes_arumugam,
  Enterotype %in% c("Enterotype 3", "Enterotype 2", "Enterotype 1")
)
mm_anova <- run_test_multiple_groups(
  ps,
  group = "Enterotype",
  method = "anova"
)
```

---

run\_test\_two\_groups     *Statistical test between two groups*

---

## Description

Statistical test between two groups

## Usage

```
run_test_two_groups(
  ps,
  group,
  taxa_rank = "all",
  transform = c("identity", "log10", "log10p"),
  norm = "TSS",
  norm_para = list(),
  method = c("welch.test", "t.test", "white.test"),
  p_adjust = c("none", "fdr", "bonferroni", "holm", "hochberg", "hommel", "BH", "BY"),
  pvalue_cutoff = 0.05,
  diff_mean_cutoff = NULL,
  ratio_cutoff = NULL,
  conf_level = 0.95,
  nperm = 1000,
  ...
)
```

## Arguments

|           |   |
|-----------|---|
| ps        | a <a href="#">phyloseq::phyloseq</a> object   |
| group     | character, the variable to set the group  |
| taxa_rank | character to specify taxonomic rank to perform differential analysis on. Should be one of <code>phyloseq::rank_names(phyloseq)</code> , or "all" means to summarize the taxa by the top taxa ranks ( <code>summarize_taxa(ps, level = rank_names(ps)[1])</code> ), or "none" means perform differential analysis on the original taxa ( <code>taxa_names(phyloseq)</code> ), e.g., OTU or ASV.  |
| transform | character, the methods used to transform the microbial abundance. See <a href="#">transform_abundances()</a> for more details. The options include: <ul style="list-style-type: none"> <li>"identity", return the original data without any transformation (default).</li> <li>"log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>"log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul> |
| norm      | the methods used to normalize the microbial abundance data. See <a href="#">normalize()</a> for more details. Options include: <ul style="list-style-type: none"> <li>"none": do not normalize.</li> </ul>  |

- "rarefy": random subsampling counts to the smallest library size in the data set.
- "TSS": total sum scaling, also referred to as "relative abundance", the abundances were normalized by dividing the corresponding sample library size.
- "TMM": trimmed mean of m-values. First, a sample is chosen as reference. The scaling factor is then derived using a weighted trimmed mean over the differences of the log-transformed gene-count fold-change between the sample and the reference.
- "RLE", relative log expression, RLE uses a pseudo-reference calculated using the geometric mean of the gene-specific abundances over all samples. The scaling factors are then calculated as the median of the gene counts ratios between the samples and the reference.
- "CSS": cumulative sum scaling, calculates scaling factors as the cumulative sum of gene abundances up to a data-derived threshold.
- "CLR": centered log-ratio normalization.
- "CPM": pre-sample normalization of the sum of the values to 1e+06.

norm\_para arguments passed to specific normalization methods  
 method test method, must be one of "welch.test", "t.test" or "white.test"  
 p\_adjust method for multiple test correction, default none, for more details see [stats::p.adjust](#).  
 pvalue\_cutoff numeric, p value cutoff, default 0.05  
 diff\_mean\_cutoff, ratio\_cutoff  
 cutoff of different means and ratios, default NULL which means no effect size filter.  
 conf\_level numeric, confidence level of interval.  
 nperm integer, number of permutations for white non parametric t test estimation  
 ... extra arguments passed to [t.test\(\)](#) or [fisher.test\(\)](#)

### Value

a [microbiomeMarker](#) object.

### Author(s)

Yang Cao

### See Also

[run\\_test\\_multiple\\_groups\(\)](#), [run\\_simple\\_stat](#)

### Examples

```
data(enterotypes_arumugam)
mm_welch <- run_test_two_groups(
  enterotypes_arumugam,
  group = "Gender",
  method = "welch.test"
)
mm_welch
```

---

|               |                                  |
|---------------|----------------------------------|
| subset_marker | <i>Subset microbiome markers</i> |
|---------------|----------------------------------|

---

**Description**

Subset markers based on an expression related to the columns and values within the `marker_table` slot of `mm`.

**Usage**

```
subset_marker(mm, ...)
```

**Arguments**

`mm` a `microbiomeMarker` or `marker_table` object.  
`...` the subsetting expression passed to `base::subset()`.

**Value**

a subset object in the same class with `mm`.

**Examples**

```
data(enterotypes_arumugam)
mm <- run_limma_voom(
  enterotypes_arumugam,
  "Enterotype",
  contrast = c("Enterotype 3", "Enterotype 2"),
  pvalue_cutoff = 0.01,
  p_adjust = "none"
)
subset_marker(mm, pvalue < 0.005)
```

---

|                |   |
|----------------|---|
| summarize_taxa | <i>Summarize taxa into a taxonomic level within each sample</i> |
|----------------|---|

---

**Description**

Provides summary information of the representation of a taxonomic levels within each sample.

**Usage**

```
summarize_taxa(ps, level = rank_names(ps)[1], absolute = TRUE, sep = "|")
```

**Arguments**

|          |  |
|----------|--|
| ps       | a <a href="#">phyloseq-class</a> object.   |
| level    | taxonomic level to summarize, default the top level rank of the ps.                  |
| absolute | logical, whether return the absolute abundance or relative abundance, default FALSE. |
| sep      | a character string to separate the taxonomic levels.                                 |

**Value**

a [phyloseq::phyloseq](#) object, where each row represents a taxa, and each col represents the taxa abundance of each sample.

**Examples**

```
data(enterotypes_arumugam)
summarize_taxa(enterotypes_arumugam)
```

---

|                   |   |
|-------------------|---|
| summary.compareDA | <i>Summary differential analysis methods comparison results</i> |
|-------------------|---|

---

**Description**

Summary differential analysis methods comparison results

**Usage**

```
## S3 method for class 'compareDA'
summary(
  object,
  sort = c("score", "auc", "fpr", "power"),
  boot = TRUE,
  boot_n = 1000L,
  prob = c(0.05, 0.95),
  ...
)
```

**Arguments**

|        |   |
|--------|---|
| object | an compareDA object, output from <a href="#">compare_DA()</a> .   |
| sort   | character string specifying sort method. Possibilities are "score" which is calculated as $(auc - 0.5) * power - fdr$ , "auc" for area under the ROC curve, "fpr" for false positive rate, "power" for empirical power. |
| boot   | logical, whether use bootstrap for confidence limites of the score, default TRUE. Recommended to be TRUE unless n_rep is larger then 100 in <a href="#">compare_DA()</a> .  |
| boot_n | integer, number of bootstraps, default 1000L.   |
| prob   | two length numeric vector, confidence limits for score, default <code>c(0.05, 0.95)</code> .  |
| ...    | extra arguments affecting the summary produced.   |

**Value**

a data.frame containing measurements for differential analysis methods:

- call: differential analysis commands.
- auc: area under curve of ROC.
- fpr: false positive rate
- power: empirical power.
- fdr: false discover7y rate.
- score: score which is calculated as  $(auc - 0.5) * power - fdr$ .
- score\_\*: confidence limits of score.

---

transform\_abundances *Transform the taxa abundances in otu\_table sample by sample*

---

**Description**

Transform the taxa abundances in otu\_table sample by sample, which means the counts of each sample will be transformed individually.

**Usage**

```
transform_abundances(object, transform = c("identity", "log10", "log10p"))
```

**Arguments**

- |           |   |
|-----------|---|
| object    | <a href="#">otu_table</a> , <a href="#">phyloseq</a> , or <a href="#">microbiomeMarker</a> .  |
| transform | transformation to apply, the options include: <ul style="list-style-type: none"> <li>• "identity", return the original data without any transformation.</li> <li>• "log10", the transformation is <math>\log_{10}(\text{object})</math>, and if the data contains zeros the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> <li>• "log10p", the transformation is <math>\log_{10}(1 + \text{object})</math>.</li> </ul> |

**Value**

A object matches the class of argument object with the transformed otu\_table.

**See Also**

[abundances\(\)](#)

## Examples

```
data(oxygen)
x1 <- transform_abundances(oxygen)
head(otu_table(x1), 10)
x2 <- transform_abundances(oxygen, "log10")
head(otu_table(x2), 10)
x3 <- transform_abundances(oxygen, "log10p")
head(otu_table(x3), 10)
```

---

[ *Extract marker\_table object* ]

---

## Description

Operators acting on `marker_table` to extract parts.

## Usage

```
## S4 method for signature 'marker_table,ANY,ANY,ANY'
x[i, j, ..., drop = TRUE]
```

## Arguments

|                   |                                     |
|-------------------|-------------------------------------|
| <code>x</code>    | a <code>marker_table</code> object. |
| <code>i, j</code> | elements to extract.                |
| <code>...</code>  | see <code>base::Extract()</code> .  |
| <code>drop</code> | ignored now.                        |

## Value

a `marker_table` object.

## See Also

[base::Extract\(\)](#)



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