

# Package ‘dar’

April 8, 2025

**Title** Differential Abundance Analysis by Consensus

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**Description** Differential abundance testing in microbiome data challenges both parametric and non-parametric statistical methods, due to its sparsity, high variability and compositional nature. Microbiome-specific statistical methods often assume classical distribution models or take into account compositional specifics. These produce results that range within the specificity vs sensitivity space in such a way that type I and type II error that are difficult to ascertain in real microbiome data when a single method is used. Recently, a consensus approach based on multiple differential abundance (DA) methods was recently suggested in order to increase robustness. With dar, you can use dplyr-like pipeable sequences of DA methods and then apply different consensus strategies. In this way we can obtain more reliable results in a fast, consistent and reproducible way.

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<https://microbialgenomics-irsicaixaorg.github.io/dar/>

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'dar-package.R' 'data.R' 'deseq2.R' 'filter\_by\_abundance.R'  
'filter\_by\_prevalence.R' 'filter\_by\_rarity.R'  
'filter\_by\_variance.R' 'filter\_taxa.R' 'globals.R' 'lefse.R'  
'maaslin2.R' 'metagenomeseq.R' 'misc.R' 'phyloseq\_qc.R'  
'pkg\_check.R' 'plot\_methods.R' 'rarefaction.R' 'read\_data.R'  
'steps\_and\_checks.R' 'subset\_taxa.R' 'utils-pipe.R'  
'utils-tidy-eval.R' 'utils.R' 'wilcox.R'

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## Contents

dar-package . . . . .	4
abundance_plt . . . . .	4
add_step . . . . .	6
add_tax . . . . .	6
add_var . . . . .	7
bake . . . . .	8
contains_rarefaction . . . . .	10
cool . . . . .	11
corr_heatmap . . . . .	12
exclusion_plt . . . . .	13
export_steps . . . . .	14
find_intersections . . . . .	14

get_comparisons	15
get_phy	16
get_tax	17
get_var	17
import_steps	18
intersection_df	19
intersection_plt	20
metaHIV_phy	21
mutual_plt	22
otu_table	23
overlap_df	24
pastry_df	25
phyloseq_or_null-class	25
phy_qc	26
prep	27
PrepRecipe-class	28
prep_recipe	29
rand_id	29
read_data	30
recipe	31
recipes_pkg_check	32
required_deps	33
sample_data	34
step	34
steps_ids	35
step_aldex	36
step_ancom	38
step_corncob	42
step_deseq	45
step_filter_by_abundance	47
step_filter_by_prevalence	49
step_filter_by_rarity	50
step_filter_by_variance	52
step_filter_taxa	53
step_lefse	54
step_maaslin	57
step_metagenomeseq	59
step_rarefaction	62
step_subset_taxa	63
step_to_expr	64
step_wilcox	65
tax_table	67
test_prep_rec	67
test_rec	68
tidyeval	68
to_tibble	70
use_rarefy	71
zero_otu	72

%>% ..... 73

**Index** ..... 74

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dar-package                      *dar: Differential Abundance Analysis by Consensus*

---

### Description

To learn more about dar, start with the vignettes: `browseVignettes(package = "dar")`

### Author(s)

**Maintainer:** Francesc Catala-Moll <fcatala@irsicaixa.es> ([ORCID](#))

### See Also

Useful links:

- <https://github.com/MicrobialGenomics-IrsicaixaOrg/dar>
- <https://microbialgenomics-irsicaixaorg.github.io/dar/>
- Report bugs at <https://github.com/MicrobialGenomics-IrsicaixaOrg/dar/issues>

---

abundance\_plt                      *Abundance boxplot*

---

### Description

Abundance boxplot

### Usage

```
abundance_plt(
  rec,
  taxa_ids = NULL,
  type = "boxplot",
  transform = "compositional",
  scale = 1,
  top_n = 20
)

## S4 method for signature 'Recipe'
abundance_plt(
  rec,
  taxa_ids = NULL,
  type = "boxplot",
```

```

    transform = "compositional",
    scale = 1,
    top_n = 20
  )

## S4 method for signature 'PrepRecipe'
abundance_plt(
  rec,
  taxa_ids = NULL,
  type = "boxplot",
  transform = "compositional",
  scale = 1,
  top_n = 20
)

```

### Arguments

rec	A Recipe or Recipe step.
taxa_ids	Character vector with taxa_ids to plot. If taxa_ids is NULL the significant characteristics present in all of the executed methods will be plotted.
type	Character vector indicating the type of the result. Options: c("boxplot", "heatmap").
transform	Transformation to apply. The options include: 'compositional' (ie relative abundance), 'Z', 'log10', 'log10p', 'hellinger', 'identity', 'clr', 'alr', or any method from the <code>vegan::decostand</code> function. If the value is NULL, no normalization is applied and works with the raw counts.
scale	Scaling constant for the abundance values when transform = "scale".
top_n	Maximum number of taxa to represent. Default: 20.

### Value

ggplot2

### Examples

```

data(test_prep_rec)

## Running the function returns a boxplot,
abundance_plt(test_prep_rec)

## Giving the value "heatmap" to the type parameter, the resulting graph
## a heatmap.
# abundance_plt(test_prep_rec, type = "heatmap")

## By default, those taxa significant in all methods are plotted. If you want
## to graph some determined features, you can pass them as vector through the
## taxa_ids parameter.
# taxa_ids <- c("Otu_96", "Otu_78", "Otu_88", "Otu_35", "Otu_94", "Otu_34")
# abundance_plt(test_prep_rec, taxa_ids = taxa_ids)
# abundance_plt(test_prep_rec, taxa_ids = taxa_ids, type = "heatmap")

```

```
## abundance_plt function needs a PrepRecipe. If you pass a a non-prep
## Recipe the output is an error.
data(test_rec)
err <- testthat::expect_error(abundance_plt(test_rec))
err
```

---

add_step	<i>Add a New Operation to the Current Recipe</i>
----------	--

---

### Description

add\_step adds a step to the last location in the Recipe. add\_check does the same for checks.

### Usage

```
add_step(rec, object)

## S4 method for signature 'Recipe'
add_step(rec, object)

## S4 method for signature 'PrepRecipe'
add_step(rec, object)
```

### Arguments

rec	A <a href="#">Recipe()</a> .
object	A step or check object.

### Value

A updated [Recipe\(\)](#) with the new operation in the last slot.

---

add_tax	<i>Adds taxonomic level of interest in the Recipe.</i>
---------	--

---

### Description

Adds taxonomic level of interest in the Recipe.

### Usage

```
add_tax(rec, tax_info)

## S4 method for signature 'Recipe'
add_tax(rec, tax_info)

## S4 method for signature 'PrepRecipe'
add_tax(rec, tax_info)
```

**Arguments**

rec            A Recipe object.  
tax\_info       A character string of taxonomic levels that will be used in any context.

**Value**

A Recipe object.

**Examples**

```
data(metaHIV_phy)

## Define recipe
rec <-
  recipe(metaHIV_phy)

## add var info
rec <- add_tax(rec, tax_info = "Species")
rec

## add tax info to a prep-Recipe returns an error
data(test_prep_rec)
err <- testthat::expect_error(
  add_tax(test_prep_rec, tax_info = "Species")
)

err
```

---

add_var	<i>Adds variable of interest to the Recipe</i>
---------	--

---

**Description**

Adds variable of interest to the Recipe

**Usage**

```
add_var(rec, var_info)

## S4 method for signature 'Recipe'
add_var(rec, var_info)

## S4 method for signature 'PrepRecipe'
add_var(rec, var_info)
```

**Arguments**

<code>rec</code>	A Recipe object.
<code>var_info</code>	A character string of column names corresponding to variables that will be used in any context.

**Value**

A Recipe object.

**Examples**

```
data(metaHIV_phy)

## Define recipe
rec <- recipe(metaHIV_phy)

## add var info
rec <- add_var(rec, var_info = "RiskGroup2")
rec

## add var info to a prep-recipe returns an error
data(test_prep_rec)
err <- testthat::expect_error(
  add_var(test_prep_rec, var_info = "RiskGroup2")
)

err
```

---

bake

*Define consensus strategies from a Recipe*


---

**Description**

For a prep Recipe adds a consensus strategies to use for result extraction.

**Usage**

```
bake(
  rec,
  count_cutoff = NULL,
  weights = NULL,
  exclude = NULL,
  id = rand_id("bake")
)

## S4 method for signature 'PrepRecipe'
bake(
  rec,
```



```

    count_cutoff = NULL,
    weights = NULL,
    exclude = NULL,
    id = rand_id("bake")
  )

## S4 method for signature 'Recipe'
bake(
  rec,
  count_cutoff = NULL,
  weights = NULL,
  exclude = NULL,
  id = rand_id("bake")
)

```

### Arguments

<code>rec</code>	A Recipe object. The step will be added to the sequence of operations for this Recipe.
<code>count_cutoff</code>	Indicates the minimum number of methods in which an OTU must be present (Default: NULL). If <code>count_cutoff</code> is NULL <code>count_cutoff</code> is equal to <code>length(steps_ids(rec, "da")) - length(exclude)</code>
<code>weights</code>	Named vector with the ponderation value for each method.
<code>exclude</code>	Method ids to exclude.
<code>id</code>	A character string that is unique to this step to identify it.

### Value

An object of class `PrepRecipe`

### Examples

```

data(test_prep_rec)
rec <- test_prep_rec

## Default bake extracts common OTUs in all DA tested methods
## (In this case the Recipe contains 3 methods)
res <- bake(rec)
cool(res)

## bake and cool methods needs a PrepRecipe. If you pass a non-PrepRecipe
## the output is an error.
data(test_rec)
err <- testthat::expect_error(bake(test_rec))
err

## We can use the parameter `count_cutoff` to for example select those OTUs
## shared with at least two methods
res <- bake(rec, count_cutoff = 2)

```

```
cool(res)

## Furthermore, we can exclude methods from the consensus strategy with the
## `exclude` parameter.
res <- bake(rec, exclude = steps_ids(rec, "da")[1])
cool(res)

## Finally, we can use the `weights` parameter to weigh each method.
weights <- c(2, 1, 1)
names(weights) <- steps_ids(rec, "da")
res <- bake(rec, weights = weights)
cool(res)
```

---

contains\_rarefaction *Checks if Recipe contains a rarefaction step*

---

### Description

Checks if Recipe contains a rarefaction step

### Usage

```
contains_rarefaction(rec)
```

### Arguments

rec                    A Recipe object. The step will be added to the sequence of operations for this recipe.

### Value

boolean

### Examples

```
data(GlobalPatterns, package = "phyloseq")
rec <-
  phyloseq::subset_samples(
    GlobalPatterns, SampleType %in% c("Soil", "Skin")
  ) |>
  recipe(var_info = "SampleType", tax_info = "Genus") |>
  step_rarefaction()

contains_rarefaction(rec)
```

---

cool	<i>Extract results from defined bake</i>
------	--

---

**Description**

Extract results from defined bake

**Usage**

```
cool(rec, bake = 1)

## S4 method for signature 'Recipe'
cool(rec, bake = 1)

## S4 method for signature 'PrepRecipe'
cool(rec, bake = 1)
```

**Arguments**

rec	A Recipe object.
bake	Name or index of the bake to extract.

**Value**

tbl\_df

**Examples**

```
data(test_prep_rec)

## First we need to add bakes (extraction strategies) to the PrepRecipe.
rec <- bake(test_prep_rec)

## Finally we can extract the results with the cool method
cool(rec)

## By default cool extracts the results of the first bake. If we have more
## bakes we can extract the one that you want with the bake parameter.
rec <- bake(rec, count_cutoff = 1)
cool(rec, 2)

## bake and cool methods needs a prep-Recipe. If you pass a non-PrepRecipe
## the output is an error.
data(test_rec)
err <- testthat::expect_error(cool(test_rec))
err
```

---

 corr\_heatmap

*Plot otuput of the overlap\_df function as a heatmap.*


---

### Description

Plot otuput of the overlap\_df function as a heatmap.

### Usage

```
corr_heatmap(rec, steps = steps_ids(rec, "da"), font_size = 15, type = "all")

## S4 method for signature 'Recipe'
corr_heatmap(rec, steps = steps_ids(rec, "da"), font_size = 15, type = "all")

## S4 method for signature 'PrepRecipe'
corr_heatmap(rec, steps = steps_ids(rec, "da"), font_size = 15, type = "all")
```

### Arguments

rec	A Recipe object.
steps	Character vector with step_ids to take in account.
font_size	Size of the axis font.
type	Indicates whether to use all taxa ("all") or only those that are differentially abundant in at least one method ("da"). Default as "all".

### Value

heatmap

### Examples

```
data(test_prep_rec)

## Running the function returns a UpSet plot ordered by frequency.
corr_heatmap(test_prep_rec)

## If you want to exclude a method for the plot, you can remove it with the
## step parameter. In the following example we eliminate from the graph the
## results of maaslin
corr_heatmap(test_prep_rec, steps = steps_ids(test_prep_rec, "da")[-1])

## corr_heatmap function needs a PrepRecipe. If you pass a a non-prep
## Recipe the output is an error.
data(test_rec)
err <- testthat::expect_error(corr_heatmap(test_rec))
err
```

---

exclusion_plt	<i>Plot the number of shared DA OTUs between methods.</i>
---------------	---

---

**Description**

Plot the number of shared DA OTUs between methods.

**Usage**

```
exclusion_plt(rec, steps = steps_ids(rec, "da"))

## S4 method for signature 'Recipe'
exclusion_plt(rec, steps = steps_ids(rec, "da"))

## S4 method for signature 'PrepRecipe'
exclusion_plt(rec, steps = steps_ids(rec, "da"))
```

**Arguments**

rec	A Recipe object.
steps	Character vector with step_ids to take in account.

**Value**

ggplot2-class object

**Examples**

```
data(test_prep_rec)

## Running the function returns a barplot plot,
exclusion_plt(test_prep_rec)

## If you want to exclude a method for the plot, you can remove it with the
## step parameter. In the following example we eliminate from the graph the
## results of maaslin
exclusion_plt(test_prep_rec, steps = steps_ids(test_prep_rec, "da")[-1])

## intersection_plt function needs a PrepRecipe. If you pass a a non-prep
## Recipe the output is an error.
data(test_rec)
err <- testthat::expect_error(exclusion_plt(test_rec))
err
```

---

export_steps	<i>Export step parameters as json.</i>
--------------	--

---

**Description**

Export step parameters as json.

**Usage**

```
export_steps(rec, file_name)
```

**Arguments**

rec	A Recipe object.
file_name	The path and file name of the optout file.

**Value**

invisible

**Examples**

```
data(metaHIV_phy)

## Create a Recipe with steps
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Species") |>
  step_subset_taxa(tax_level = "Kingdom", taxa = c("Bacteria", "Archaea")) |>
  step_filter_taxa(.f = "function(x) sum(x > 0) >= (0.3 * length(x))") |>
  step_filter_by_prevalence(0.4) |>
  step_maaslin()

## Prep Recipe
rec <- prep(rec, parallel = TRUE)

## Export to json file
export_steps(rec, tempfile(fileext = ".json"))
```

---

find_intersections	<i>Finds common OTU between method results</i>
--------------------	--

---

**Description**

Finds common OTU between method results

**Usage**

```
find_intersections(rec, steps = steps_ids(rec, "da"))
```

**Arguments**

rec                    A Recipe object.  
 steps                character vector with step ids to take in account

**Value**

tibble

**Examples**

```
data(test_prep_rec)

## From a PrepRecipe we can extract a tibble with all intersections
intersections <- find_intersections(test_prep_rec)
intersections

## Additionally, we can exclude some methods form the table
intersections <- find_intersections(
  test_prep_rec,
  steps = steps_ids(test_prep_rec, "da")[-1]
)

intersections
```

---

get\_comparisons                    *Generate all unique contrasts between levels of a categorical variable.*

---

**Description**

Generate all unique contrasts between levels of a categorical variable.

**Usage**

```
get_comparisons(var, phy, as_list = TRUE, n_cut = 1)
```

**Arguments**

var                    categorical variable  
 phy                    phyloseq object  
 as\_list                boolean indicating if output must be returned as a list.  
 n\_cut                 minimum of observations by level.

**Value**

tibble or list

## Examples

```
data(test_rec)
dar::get_comparisons("RiskGroup2", get_phy(test_rec))
```

---

get\_phy

*Returns phyloseq from Recipe-class object*

---

## Description

Returns phyloseq from Recipe-class object

## Usage

```
get_phy(rec)

## S4 method for signature 'Recipe'
get_phy(rec)
```

## Arguments

rec            A Recipe object

## Value

Phyloseq class object

## Examples

```
data(metaHIV_phy)

## Define recipe
rec <-
  recipe(metaHIV_phy, var_info = "RiskGroup2", tax_info = "Species")

## Extract phyloseq object
get_phy(rec)
```



---

get_tax	Returns tax_info from Recipe-class object
---------	---

---

**Description**

Returns tax\_info from Recipe-class object

**Usage**

```
get_tax(rec)

## S4 method for signature 'Recipe'
get_tax(rec)
```

**Arguments**

rec            A Recipe object

**Value**

Tibble containing tax\_info.

**Examples**

```
data(metaHIV_phy)

## Define recipe
rec <-
  recipe(metaHIV_phy, var_info = "RiskGroup2", tax_info = "Species")

## Extract taxonomic level
get_tax(rec)
```

---

get_var	Returns var_info from Recipe-class object
---------	---

---

**Description**

Returns var\_info from Recipe-class object

**Usage**

```
get_var(rec)

## S4 method for signature 'Recipe'
get_var(rec)
```

**Arguments**

rec                    A Recipe object

**Value**

Tibble containing var\_info.

**Examples**

```
data(metaHIV_phy)

## Define recipe
rec <-
  recipe(metaHIV_phy, var_info = "RiskGroup2", tax_info = "Species")

## Extract variable of interest
get_var(rec)
```

---

import\_steps

*Import steps from json file*


---

**Description**

Import steps from json file

**Usage**

```
import_steps(rec, file, parallel = TRUE, workers = future::availableCores())
```

**Arguments**

rec                    A Recipe object.

file                   Path to the input file.

parallel              if FALSE, no parallelization. if TRUE, parallel execution using future and furrr packages.

workers               Number of workers for parallelization.

**Value**

recipe-class object

**Examples**

```

data(metaHIV_phy)

## Initialize the Recipe with a phyloseq object
rec <- recipe(metaHIV_phy, "RiskGroup2", "Species")
rec

## Import steps
json_file <- system.file("extdata", "test.json", package = "dar")
rec <- import_steps(rec, json_file)
rec

## If the json file contains 'bake', the Recipe is automatically prepared.
json_file <- system.file("extdata", "test_bake.json", package = "dar")
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Species") |>
  import_steps(json_file)

rec
cool(rec)

```

---

intersection_df	<i>Returns data.frame with OTU intersection between methods</i>
-----------------	---

---

**Description**

Returns data.frame with OTU intersection between methods

**Usage**

```

intersection_df(rec, steps = steps_ids(rec, "da"), tidy = FALSE)

## S4 method for signature 'Recipe'
intersection_df(rec, steps = steps_ids(rec, "da"), tidy = FALSE)

## S4 method for signature 'PrepRecipe'
intersection_df(rec, steps = steps_ids(rec, "da"), tidy = FALSE)

```

**Arguments**

rec	A Recipe object.
steps	character vector with step_ids to take in account.
tidy	Boolean indicating if result must be in tidy format.

**Value**

data.frame class object

## Examples

```
data(test_prep_rec)

df <- intersection_df(test_prep_rec)
head(df)

## intersection_df function needs a prep-Recipe. If you pass a a non-prep
## recipe the output is an error.
data(test_rec)
err <- testthat::expect_error(intersection_df(test_rec))
err
```

---

intersection\_plt      *Plot results using UpSet plot*

---

## Description

Plot results using UpSet plot

## Usage

```
intersection_plt(
  rec,
  steps = steps_ids(rec, "da"),
  ordered_by = c("freq", "degree"),
  font_size = 2
)

## S4 method for signature 'Recipe'
intersection_plt(rec, steps, font_size)

## S4 method for signature 'PrepRecipe'
intersection_plt(
  rec,
  steps = steps_ids(rec, "da"),
  ordered_by = c("freq", "degree"),
  font_size = 2
)
```

## Arguments

rec	A Recipe object.
steps	Character vector with step_ids to take in account.
ordered_by	How the intersections in the matrix should be ordered by. Options include frequency (entered as "freq"), degree, or both in any order.
font_size	Size of the font.

**Value**

UpSet plot

**Examples**

```
data(test_prep_rec)

## Running the function returns a UpSet plot ordered by frequency.
intersection_plt(test_prep_rec)

## Alternatively, you can order the plot by degree
intersection_plt(test_prep_rec, ordered_by = "degree")

## If you want to exclude a method for the plot, you can remove it with the
## step parameter. In the following example we eliminate from the graph the
## results of maaslin
intersection_plt(test_prep_rec, steps = steps_ids(test_prep_rec, "da")[-1])

## intersection_plt function needs a PrepRecipe. If you pass a a non-prep
## Recipe the output is an error.
data(test_rec)
err <- testthat::expect_error(intersection_plt(test_rec))
err
```

---

metaHIV\_phy

*Phyloseq object from metaHIV project*

---

**Description**

A Phyloseq object containing abundance counts and sample\_data for metaHIV project. Count reads were annotated with Metaphlan3.

**Usage**

```
data("metaHIV_phy")
```

**Format**

A phyloseq object with 451 taxas, 30 samples, 3 sample variables and 7 taxonomic ranks.

**Source**

s3://fcatala-09142020-eu-west-1/cloud\_test/SpeciesQuantification/Kraken2

mutual\_plt

*Mutual finding plot***Description**

Plots number of differentially abundant features mutually found by defined number of methods, colored by the differential abundance direction and separated by comparison.

**Usage**

```
mutual_plt(
  rec,
  count_cutoff = NULL,
  comparisons = NULL,
  steps = steps_ids(rec, type = "da"),
  top_n = 20
)

## S4 method for signature 'Recipe'
mutual_plt(
  rec,
  count_cutoff = NULL,
  comparisons = NULL,
  steps = steps_ids(rec, type = "da"),
  top_n = 20
)

## S4 method for signature 'PrepRecipe'
mutual_plt(
  rec,
  count_cutoff = NULL,
  comparisons = NULL,
  steps = steps_ids(rec, type = "da"),
  top_n = 20
)
```

**Arguments**

rec	A Recipe or Recipe step.
count_cutoff	Indicates the minimum number of methods in which an OTU must be present (Default: NULL). If count_cutoff is NULL count_cutoff is equal to $\text{length}(\text{steps\_ids}(\text{rec}, \text{"da"})) * 2 / 3$ .
comparisons	By default, this function plots all comparisons. However, if the user indicates the comparison or comparisons of interest, only the selected ones will be plotted.
steps	Character vector with step_ids to take in account. Default all "da" methods.
top_n	Maximum number of taxa to represent. Default: 20.

**Value**

ggplot2

**Examples**

```
data(test_prep_rec)

## Running the function returns a tile plot,
mutual_plt(test_prep_rec)

## The count_cutoff indicates the minimum number of methods in which an OTU
## must be present. By default the value is equal to
## length(steps_ids(rec, "da")) * 2 / 3 but it is customizable.
mutual_plt(
  test_prep_rec,
  count_cutoff = length(steps_ids(test_prep_rec, "da"))
)

## A single comparisons can be plotted through the comparison parameter.
mutual_plt(test_prep_rec, comparisons = c("hts_msm"))

## If you want to exclude a method for the plot, you can remove it with the
## step parameter. In the following example we eliminate from the graph the
## results of maaslin.
mutual_plt(test_prep_rec, steps = steps_ids(test_prep_rec, "da")[-1])

## mutual_plt function needs a PrepRecipe. If you pass a a non-PrepRecipe
## the output is an error.
data(test_rec)
err <- testthat::expect_error(mutual_plt(test_rec))
err
```

---

otu\_table

*Extracts otu\_table from phyloseq inside a Recipe*

---

**Description**

Extracts otu\_table from phyloseq inside a Recipe

**Usage**

```
otu_table(rec)

## S4 method for signature 'Recipe'
otu_table(rec)
```

**Arguments**

rec                    A Recipe or Recipe step.

**Value**

A tibble

**Examples**

```
data(metaHIV_phy)

## Define recipe
rec <-
  recipe(metaHIV_phy, var_info = "RiskGroup2", tax_info = "Species")

## Extract otu_table from phyloseq object
otu_table(rec)
```

---

overlap\_df

*Overlap of significant OTUs between tested methods.*

---

**Description**

Overlap of significant OTUs between tested methods.

**Usage**

```
overlap_df(rec, steps = steps_ids(rec, "da"), type = "all")

## S4 method for signature 'Recipe'
overlap_df(rec, steps = steps_ids(rec, "da"), type = "all")

## S4 method for signature 'PrepRecipe'
overlap_df(rec, steps = steps_ids(rec, "da"), type = "all")
```

**Arguments**

rec	A Recipe object.
steps	Character vector with step_ids to take in account.
type	Indicates whether to use all taxa ("all") or only those that are differentially abundant in at least one method ("da"). Default as "all".

**Value**

df



**Examples**

```

data(test_prep_rec)

## Running the function returns a UpSet plot ordered by frequency.
df <- overlap_df(test_prep_rec, steps_ids(test_prep_rec, "da"))
head(df)

## If you want to exclude a method for the plot, you can remove it with the
## step parameter. In the following example we eliminate from the graph the
## results of maaslin
overlap_df(test_prep_rec, steps = steps_ids(test_prep_rec, "da")[-1])

## overlap_df function needs a prep-Recipe. If you pass a a non-prep
## Recipe the output is an error.
data(test_rec)
err <- testthat::expect_error(overlap_df(test_rec))
err

```

---

pastry\_df

*Pastery data for step id generation*


---

**Description**

Tibble contain

**Format**

A tbl\_df object with 228 unique pasteries.

**Value**

tibble with pastry names

**Source**

<https://raw.githubusercontent.com/prasertcbs/basic-dataset/master/pastry.csv>

---

phyloseq\_or\_null-class

*Recipe-class object*


---

**Description**

A Recipe is a description of the steps to be applied to a data set in order to prepare it for data analysis.

**Usage**

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

**Arguments**

object            A Recipe object.

**Value**

Recipe-class object

**Slots**

phyloseq Phyloseq-class object.

var\_info A tibble that contains the current set of terms in the data set. This initially defaults to the same data contained in var\_info.

tax\_info A tibble that contains the current set of taxonomic levels that will be used in the analysis.  
steps List of step-class objects that will be used by DA.

---

phy\_qc

*Phyloseq Quality Control Metrics*

---

**Description**

phy\_qc() returns a tibble. It will have information about some important metrics about the sparsity of the count matrix. The content of the table is as follows:

- var\_levels: levels of the categorical variable of interest. "all" refers to all rows of the dataset (without splitting by categorical levels).
- n: total number of values in the count matrix.
- n\_zero: number of zeros in the count matrix.
- pct\_zero: percentage of zeros in the count matrix.
- pct\_all\_zero: percentage of taxa with zero counts in all samples.
- pct\_singletons: percentage of taxa with counts in a single sample.
- pct\_doubletons: percentage of taxa with counts in two samples.
- count\_mean: average of the mean counts per sample.
- count\_min: average of the min counts per sample.
- count\_max: average of the max counts per sample.

**Usage**

```
phy_qc(rec)
```

```
## S4 method for signature 'Recipe'
phy_qc(rec)
```

**Arguments**

rec                    A Recipe or Recipe step.

**Value**

A tibble

**Examples**

```
data(metaHIV_phy)

## Define Recipe
rec <- recipe(metaHIV_phy, var_info = "RiskGroup2", tax_info = "Species")

phy_qc(rec)
```

---

prep	<i>Performs all the steps defined in a Recipe</i>
------	---

---

**Description**

For a Recipe with at least one preprocessing or DA operation run the steps in a convenient order.

**Usage**

```
prep(rec, parallel = TRUE, workers = future::availableCores(), force = FALSE)

## S4 method for signature 'Recipe'
prep(rec, parallel = TRUE, workers = future::availableCores(), force = FALSE)
```

**Arguments**

rec                    A Recipe object. and furr packages.

parallel              if FALSE, no parallelization. if TRUE, parallel execution using future and furr packages.

workers               Number of workers for parallelization.

force                  Force the reexecution of all steps. This remove previous results.

**Value**

A PrepRecipe object.

**Examples**

```

data(metaHIV_phy)

## Define Recipe
rec <-
  recipe(metaHIV_phy, var_info = "RiskGroup2", tax_info = "Class") |>
  step_subset_taxa(tax_level = "Kingdom", taxa = c("Bacteria", "Archaea")) |>
  step_filter_taxa(.f = "function(x) sum(x > 0) >= (0.03 * length(x))") |>
  step_maaslin()

## Prep Recipe
da_results <- prep(rec)

## If you try

## Consensus strategy
n_methods <- 2
da_results <- bake(da_results, count_cutoff = n_methods)
da_results

## If you try to run prep on an object of class PrepRecipe it returns an
## error.
err <- testthat::expect_error(prepare(da_results))
err

## You can force the overwrite with:
prep(rec, force = TRUE)

## This function can operate in parallel thanks to future and furrr packages.
prep(rec, parallel = TRUE, workers = 2)

```

---

PrepRecipe-class	<i>PrepRecipe-class object</i>
------------------	--------------------------------

---

**Description**

A PrepRecipe is Recipe with the results corresponding to the steps defined in the Recipe.

**Value**

PrepRecipe-class object

**Slots**

`results` Contains the results of all defined analysis in the Recipe.

`bakes` Contains the executed bakes.

---

prep_recipe	<i>Create a PrepRecipe.</i>
-------------	-----------------------------

---

**Description**

A PrepRecipe is Recipe with the results corresponding to the steps defined in the Recipe.

**Usage**

```
prep_recipe(rec, results, bakes)
```

**Arguments**

rec	A Recipe object.
results	list with the results
bakes	list with saved bakes

**Value**

An object of class PrepRecipe.

---

rand_id	<i>Make a random identification field for steps</i>
---------	---

---

**Description**

Make a random identification field for steps

**Usage**

```
rand_id(prefix = "step")
```

**Arguments**

prefix	A single character string
--------	---------------------------

**Value**

A character string with the prefix and random letters separated by and underscore.

**Examples**

```
rand_id("step")
```

---

read_data	<i>Loads Phyloseq data</i>
-----------	----------------------------

---

### Description

This function returns a validated Phyloseq object by loading it directly from a file with the .rds extension. Alternatively, this function can also take three text files as input that will be used to construct and validate the Phyloseq object: - Counts matrix with the otu\_id in the first column. - Taxonomic annotation matrix with the otu\_id in the first column. - Metadata annotation with sample\_id in the first column.

### Usage

```
read_data(data_path)

validate_otu(otu)

validate_sample_data(sample_data)

validate_tax_table(tax_table)

validate_phyloseq(phy, slots = c("sample_data", "tax_table"))

read_phyloseq(file_path)

read_file(file_path, ext = c(".txt|.csv|.tsv"))
```

### Arguments

data\_path      List of length 1 or 3, with the paths of the input files.

### Value

a phyloseq-class object

### Examples

```
# From a phyloseq object saved with .rds extension.
system.file("extdata", "metaHIV_phy.rds", package = "dar") |>
  read_data()

# From the three components of a phyloseq object saved as a plain text.
data_path <- c(
  system.file("extdata", "metaHIV_counts.txt", package = "dar"),
  system.file("extdata", "metaHIV_metadata.txt", package = "dar"),
  system.file("extdata", "metaHIV_taxas.txt", package = "dar")
)

read_data(data_path)
```

---

recipe	<i>Create a Recipe for preprocessing data</i>
--------	---

---

## Description

A Recipe is a description of the steps to be applied to a data set in order to prepare it for data analysis.

## Usage

```
recipe(
  microbiome_object = NULL,
  var_info = NULL,
  tax_info = NULL,
  steps = list()
)
```

## Arguments

microbiome_object	Phyloseq-class object or TreeSummarizedExperiment-class object.
var_info	A character string of column names corresponding to variables that will be used in any context.
tax_info	A character string of taxonomic levels that will be used in any context.
steps	list with steps.

## Value

An object of class Recipe with sub-objects:

phyloseq	object of class phyloseq with taxa abundance information.
var_info	A tibble that contains the current set of terms in the data set. This initially defaults to the same data contained in var_info.
tax_info	A tibble that contains the current set of taxonomic levels that will be used in the analysis.

## Examples

```
data(metaHIV_phy)

## Define recipe
rec <-
  recipe(metaHIV_phy, var_info = "RiskGroup2", tax_info = "Phylum") |>
  step_subset_taxa(tax_level = "Kingdom", taxa = c("Bacteria", "Archaea")) |>
  step_filter_taxa(.f = "function(x) sum(x > 0) >= (0.3 * length(x))") |>
  step_metagenomeseq(rm_zeros = 0.01) |>
  step_maaslin()
```

```

## Prep recipe
da_results <- prep(rec)

## Consensus strategy
n_methods <- 2
da_results <- bake(da_results, count_cutoff = n_methods)

## Results
cool(da_results)

## You can also crate a recipe without var and tax info
rec <- recipe(metaHIV_phy)

rec

## And define them later
rec <- rec |>
  add_var("RiskGroup2") |>
  add_tax("Genus")

rec

## When trying to add an identical step to an existing one, the system
## returns an information message.
rec <- step_aldex(rec)
rec <- step_aldex(rec)

## The same with bake
da_results <- bake(da_results)
da_results <- bake(da_results)

```

---

recipes\_pkg\_check      *Update packages*

---

### Description

This will check to see if all required packages are installed.

### Usage

```
recipes_pkg_check(pkg = NULL, step_name, ...)
```

### Arguments

pkg	A character string for the package being checked
step_name	Name of the step.
...	Extra arguments to pass to <a href="#">utils::install.packages()</a>



**Value**

Nothing is returned but a message is printed to the console about which packages (if any) should be installed along with code to do so.

---

required_deps	<i>Returns required packages for Recipe object</i>
---------------	--

---

**Description**

Returns required packages for Recipe object

**Usage**

```
required_deps(rec)

## S4 method for signature 'Recipe'
required_deps(rec)
```

**Arguments**

rec	A Recipe object
-----	-----------------

**Value**

character

**Examples**

```
data(test_rec)

## The function returns instructions to install any uninstalled dependencies
## needed to run the Recipe steps
dar::required_deps(test_rec)

## The function also works with PrepRecipe-class objects
data(test_prep_rec)
dar::required_deps(test_prep_rec)
```

---

sample_data	<i>Extracts sample_data from phyloseq inside a Recipe</i>
-------------	---

---

**Description**

Extracts sample\_data from phyloseq inside a Recipe

**Usage**

```
sample_data(rec)

## S4 method for signature 'Recipe'
sample_data(rec)
```

**Arguments**

rec                    A Recipe or Recipe step.

**Value**

A tibble

**Examples**

```
data(metaHIV_phy)

## Define recipe
rec <-
  recipe(metaHIV_phy, var_info = "RiskGroup2", tax_info = "Species")

## Extract sample_data from phyloseq object
sample_data(rec)
```

---

step	<i>Overall Wrappers to Make New step_X or check_Y Objects</i>
------	---

---

**Description**

step sets the class of the step and check is for checks.

**Usage**

```
step(subclass, ..., .prefix = "step_")

check(subclass, ..., .prefix = "check_")
```

**Arguments**

subclass	A character string for the resulting class. For example, if subclass = "blah" the step object that is returned has class step_blah or check_blah depending on the context.
...	All arguments to the operator that should be returned.
.prefix	Prefix to the subclass created.

**Value**

An updated step or check with the new class.

---

steps_ids	<i>Get step_ids from recipe</i>
-----------	---------------------------------

---

**Description**

Get step\_ids from recipe

**Usage**

```
steps_ids(rec, type = "all")
```

**Arguments**

rec	A Recipe object.
type	character vector indicating the type class. Options c("all", "da", "prepro").

**Value**

character vector

**Examples**

```
data(test_rec)

## We can extract the step identifiers from a Recipe with `step_ids`
ids <- steps_ids(test_rec)
ids

## With the `type` parameter, extract the prepro and da steps separately.
da_ids <- steps_ids(test_rec, type = "da")
da_ids

prepro_ids <- steps_ids(test_rec, type = "prepro")
prepro_ids
```

---

`step_aldex`*ALDEx2 analysis*

---

## Description

A differential abundance analysis for the comparison of two or more conditions. For example, single-organism and meta-RNA-seq high-throughput sequencing assays, or of selected and unselected values from in-vitro sequence selections. Uses a Dirichlet-multinomial model to infer abundance from counts, that has been optimized for three or more experimental replicates. Infers sampling variation and calculates the expected false discovery rate given the biological and sampling variation using the Wilcoxon rank test or Welch's t-test (`aldex.ttest`) or the glm and Kruskal Wallis tests (`aldex.glm`). Reports both P and fdr values calculated by the Benjamini Hochberg correction (Not supported in dar package).

## Usage

```
step_aldex(  
  rec,  
  max_significance = 0.05,  
  mc.samples = 128,  
  denom = "all",  
  rarefy = FALSE,  
  id = rand_id("aldex")  
)  
  
## S4 method for signature 'Recipe'  
step_aldex(  
  rec,  
  max_significance = 0.05,  
  mc.samples = 128,  
  denom = "all",  
  rarefy = FALSE,  
  id = rand_id("aldex")  
)  
  
## S4 method for signature 'PrepRecipe'  
step_aldex(  
  rec,  
  max_significance = 0.05,  
  mc.samples = 128,  
  denom = "all",  
  rarefy = FALSE,  
  id = rand_id("aldex")  
)
```

**Arguments**

rec	A Recipe object. The step will be added to the sequence of operations for this Recipe.
max_significance	Benjamini-Hochberg corrected P value of Welch's t test cutoff.
mc.samples	The number of Monte Carlo instances to use to estimate the underlying distributions; since we are estimating central tendencies, 128 is usually sufficient, but larger numbers may be .
denom	An any variable (all, iqlr, zero, lvha, median, user) indicating features to use as the denominator for the Geometric Mean calculation The default "all" uses the geometric mean abundance of all features. Using "median" returns the median abundance of all features. Using "iqlr" uses the features that are between the first and third quartile of the variance of the clr values across all samples. Using "zero" uses the non-zero features in each grop as the denominator. This approach is an extreme case where there are many nonzero features in one condition but many zeros in another. Using "lvha" uses features that have low variance (bottom quartile) and high relative abundance (top quartile in every sample). It is also possible to supply a vector of row indices to use as the denominator. Here, the experimentalist is determining a-priori which rows are thought to be invariant. In the case of RNA-seq, this could include ribosomal protein genes and other house-keeping genes. This should be used with caution because the offsets may be different in the original data and in the data used by the function because features that are 0 in all samples are removed by aldex.clr.
rarefy	Boolean indicating if OTU counts must be rarefied. This rarefaction uses the standard R sample function to resample from the abundance values in the otu_table component of the first argument, physeq. Often one of the major goals of this procedure is to achieve parity in total number of counts between samples, as an alternative to other formal normalization procedures, which is why a single value for the sample.size is expected. If 'no_seed', rarefaction is performed without a set seed.
id	A character string that is unique to this step to identify it.

**Details**

The run\_aldex function is a wrapper that performs log-ratio transformation and statistical testing in a single line of code. Specifically, this function: (a) generates Monte Carlo samples of the Dirichlet distribution for each sample, (b) converts each instance using a log-ratio transform, then (c) returns test results for two sample (Welch's t, Wilcoxon) test. This function also estimates effect size for two sample analyses.

**Value**

An object of class Recipe

**See Also**

Other Diff taxa steps: [step\\_ancom\(\)](#), [step\\_corncob\(\)](#), [step\\_deseq\(\)](#), [step\\_lefse\(\)](#), [step\\_maaslin\(\)](#), [step\\_metagenomeseq\(\)](#), [step\\_wilcox\(\)](#)

**Examples**

```

data(metaHIV_phy)

## Init Recipe
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Phylum") |>
  step_subset_taxa(tax_level = "Kingdom", taxa = c("Bacteria", "Archaea")) |>
  step_filter_taxa(.f = "function(x) sum(x > 0) >= (0.4 * length(x))")

rec

## Define ALDEX step with default parameters and prep
rec <-
  step_aldex(rec) |>
  prep(parallel = FALSE)

rec

## Wearing rarefaction only for this step
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Species") |>
  step_aldex(rarefy = TRUE)

rec

```

---

step\_ancom

*ANCOM analysis*


---

**Description**

Determine taxa whose absolute abundances, per unit volume, of the ecosystem (e.g., gut) are significantly different with changes in the covariate of interest (e.g., group). The current version of `ancombc2` function implements Analysis of Compositions of Microbiomes with Bias Correction (ANCOM-BC2) in cross-sectional and repeated measurements data. In addition to the two-group comparison, ANCOM-BC2 also supports testing for continuous covariates and multi-group comparisons, including the global test, pairwise directional test, Dunnett's type of test, and trend test.

**Usage**

```

step_ancom(
  rec,
  fix_formula = get_var(rec)[[1]],
  rand_formula = NULL,
  p_adj_method = "holm",
  prv_cut = 0.1,
  lib_cut = 0,
  s0_perc = 0.05,
  group = NULL,

```

```
    struc_zero = FALSE,
    neg_lb = FALSE,
    alpha = 0.05,
    n_cl = 1,
    verbose = FALSE,
    global = FALSE,
    pairwise = FALSE,
    dunnet = FALSE,
    trend = FALSE,
    rarefy = FALSE,
    id = rand_id("ancom")
  )

## S4 method for signature 'Recipe'
step_ancom(
  rec,
  fix_formula = get_var(rec)[[1]],
  rand_formula = NULL,
  p_adj_method = "holm",
  prv_cut = 0.1,
  lib_cut = 0,
  s0_perc = 0.05,
  group = NULL,
  struc_zero = FALSE,
  neg_lb = FALSE,
  alpha = 0.05,
  n_cl = 1,
  verbose = FALSE,
  global = FALSE,
  pairwise = FALSE,
  dunnet = FALSE,
  trend = FALSE,
  rarefy = FALSE,
  id = rand_id("ancom")
)

## S4 method for signature 'PrepRecipe'
step_ancom(
  rec,
  fix_formula = get_var(rec)[[1]],
  rand_formula = NULL,
  p_adj_method = "holm",
  prv_cut = 0.1,
  lib_cut = 0,
  s0_perc = 0.05,
  group = NULL,
  struc_zero = FALSE,
  neg_lb = FALSE,
```

```

alpha = 0.05,
n_cl = 1,
verbose = FALSE,
global = FALSE,
pairwise = FALSE,
dunnet = FALSE,
trend = FALSE,
rarefy = FALSE,
id = rand_id("ancom")
)

```

## Arguments

<code>rec</code>	A Recipe object. The step will be added to the sequence of operations for this Recipe.
<code>fix_formula</code>	the character string expresses how the microbial absolute abundances for each taxon depend on the fixed effects in metadata. When specifying the <code>fix_formula</code> , make sure to include the group variable in the formula if it is not NULL.
<code>rand_formula</code>	the character string expresses how the microbial absolute abundances for each taxon depend on the random effects in metadata. ANCOM-BC2 follows the <code>lmerTest</code> package in formulating the random effects. See <code>?lmerTest::lmer</code> for more details. Default is NULL.
<code>p_adj_method</code>	character. method to adjust p-values. Default is "holm". Options include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". See <code>?stats::p.adjust</code> for more details.
<code>prv_cut</code>	a numerical fraction between 0 and 1. Taxa with prevalences less than <code>prv_cut</code> will be excluded in the analysis. For instance, suppose there are 100 samples, if a taxon has nonzero counts presented in less than 10 samples, it will not be further analyzed. Default is 0.10.
<code>lib_cut</code>	a numerical threshold for filtering samples based on library sizes. Samples with library sizes less than <code>lib_cut</code> will be excluded in the analysis. Default is 0, i.e. do not discard any sample.
<code>s0_perc</code>	a numerical fraction between 0 and 1. Inspired by Significance Analysis of Microarrays (SAM) methodology, a small positive constant is added to the denominator of ANCOM-BC2 test statistic corresponding to each taxon to avoid the significance due to extremely small standard errors, especially for rare taxa. This small positive constant is chosen as <code>s0_perc</code> -th percentile of standard error values for each fixed effect. Default is 0.05 (5th percentile).
<code>group</code>	character. The name of the group variable in metadata. <code>group</code> should be discrete. Specifying <code>group</code> is required for detecting structural zeros and performing multi-group comparisons (global test, pairwise directional test, Dunnett's type of test, and trend test). Default is NULL. If the group of interest contains only two categories, leave it as NULL.
<code>struc_zero</code>	logical. Whether to detect structural zeros based on <code>group</code> . Default is FALSE. See Details for a more comprehensive discussion on structural zeros.
<code>neg_lb</code>	logical. Whether to classify a taxon as a structural zero using its asymptotic lower bound. Default is FALSE.



alpha	numeric. Level of significance. Default is 0.05.
n_cl	numeric. The number of nodes to be forked. For details, see <code>?parallel::makeCluster</code> . Default is 1 (no parallel computing).
verbose	logical. Whether to generate verbose output during the ANCOM-BC2 fitting process. Default is FALSE.
global	logical. Whether to perform the global test. Default is FALSE.
pairwise	logical. Whether to perform the pairwise directional test. Default is FALSE.
dunnet	logical. Whether to perform the Dunnett's type of test. Default is FALSE.
trend	logical. Whether to perform trend test. Default is FALSE.
rarefy	Boolean indicating if OTU counts must be rarefied. This rarefaction uses the standard R sample function to resample from the abundance values in the <code>otu_table</code> component of the first argument, <code>physeq</code> . Often one of the major goals of this procedure is to achieve parity in total number of counts between samples, as an alternative to other formal normalization procedures, which is why a single value for the <code>sample.size</code> is expected. If <code>'no_seed'</code> , rarefaction is performed without a set seed.
id	A character string that is unique to this step to identify it.

**Value**

An object of class `Recipe`

**See Also**

Other Diff taxa steps: [step\\_aldex\(\)](#), [step\\_corncob\(\)](#), [step\\_deseq\(\)](#), [step\\_lefse\(\)](#), [step\\_maaslin\(\)](#), [step\\_metagenomeseq\(\)](#), [step\\_wilcox\(\)](#)

**Examples**

```
## Not run:
data(metaHIV_phy)

## Init Recipe
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Species") |>
  step_subset_taxa(tax_level = "Kingdom", taxa = c("Bacteria", "Archaea")) |>
  step_filter_taxa(.f = "function(x) sum(x > 0) >= (0.4 * length(x))")

rec

## Define step with default parameters and prep
rec <-
  step_ancom(rec) |>
  prep(parallel = FALSE)

rec

## Wearing rarefaction only for this step
```

```

rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Species") |>
  step_ancom(rarefy = TRUE)

rec

## End(Not run)

```

---

step\_corncob

*corncob analysis*


---

## Description

Corncob an individual taxon regression model that uses abundance tables and sample data. corn-cob is able to model differential abundance and differential variability, and addresses each of the challenges presented below:

## Usage

```

step_corncob(
  rec,
  phi.formula = stats::formula(~1),
  formula_null = stats::formula(~1),
  phi.formula_null = stats::formula(~1),
  link = "logit",
  phi.link = "logit",
  test = "Wald",
  boot = FALSE,
  B = 1000,
  filter_discriminant = TRUE,
  fdr_cutoff = 0.05,
  fdr = "fdr",
  log2FC = 0,
  rarefy = FALSE,
  id = rand_id("corncob")
)

```

```
## S4 method for signature 'Recipe'
```

```

step_corncob(
  rec,
  phi.formula = stats::formula(~1),
  formula_null = stats::formula(~1),
  phi.formula_null = stats::formula(~1),
  link = "logit",
  phi.link = "logit",
  test = "Wald",
  boot = FALSE,

```

```

    B = 1000,
    filter_discriminant = TRUE,
    fdr_cutoff = 0.05,
    fdr = "fdr",
    log2FC = 0,
    rarefy = FALSE,
    id = rand_id("corncob")
)

## S4 method for signature 'PrepRecipe'
step_corncob(
  rec,
  phi.formula = stats::formula(~1),
  formula_null = stats::formula(~1),
  phi.formula_null = stats::formula(~1),
  link = "logit",
  phi.link = "logit",
  test = "Wald",
  boot = FALSE,
  B = 1000,
  filter_discriminant = TRUE,
  fdr_cutoff = 0.05,
  fdr = "fdr",
  log2FC = 0,
  rarefy = FALSE,
  id = rand_id("corncob")
)

```

### Arguments

<code>rec</code>	A Recipe object. The step will be added to the sequence of operations for this Recipe.
<code>phi.formula</code>	An object of class formula without the response: a symbolic description of the model to be fitted to the dispersion.
<code>formula_null</code>	Formula for mean under null, without response.
<code>phi.formula_null</code>	Formula for overdispersion under null, without response.
<code>link</code>	Link function for abundance covariates, defaults to "logit".
<code>phi.link</code>	Link function for dispersion covariates, defaults to "logit".
<code>test</code>	Character. Hypothesis testing procedure to use. One of "Wald" or "LRT" (likelihood ratio test).
<code>boot</code>	Boolean. Defaults to FALSE. Indicator of whether or not to use parametric bootstrap algorithm. (See pbWald and pbLRT).
<code>B</code>	Optional integer. Number of bootstrap iterations. Ignored if boot is FALSE. Otherwise, defaults to 1000.

filter_discriminant	Boolean. Defaults to TRUE. If FALSE, discriminant taxa will not be filtered out.
fdr_cutoff	Integer. Defaults to 0.05. Desired type 1 error rate.
fdr	Character. Defaults to "fdr". False discovery rate control method, see p.adjust for more options.
log2FC	log2FC cutoff.
rarefy	Boolean indicating if OTU counts must be rarefied. This rarefaction uses the standard R sample function to resample from the abundance values in the otu_table component of the first argument, physeq. Often one of the major goals of this procedure is to achieve parity in total number of counts between samples, as an alternative to other formal normalization procedures, which is why a single value for the sample.size is expected. If 'no_seed', rarefaction is performed without a set seed.
id	A character string that is unique to this step to identify it.

### Details

- different sequencing depth
- excessive zeros from unobserved taxa
- high variability of empirical relative abundances (overdispersion)
- within-taxon correlation
- hypothesis testing with categorical and continuous covariates

### Value

An object of class Recipe

### See Also

Other Diff taxa steps: [step\\_aldex\(\)](#), [step\\_ancom\(\)](#), [step\\_deseq\(\)](#), [step\\_lefse\(\)](#), [step\\_maaslin\(\)](#), [step\\_metagenomeseq\(\)](#), [step\\_wilcox\(\)](#)

### Examples

```
data(metaHIV_phy)

## Init Recipe
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Phylum") |>
  step_subset_taxa(tax_level = "Kingdom", taxa = c("Bacteria", "Archaea")) |>
  step_filter_taxa(.f = "function(x) sum(x > 0) >= (0.3 * length(x))")

rec

## Define step with default parameters and prep
rec <-
  step_corncob(rec) |>
```

```
    prep(parallel = FALSE)

    rec
```

---

step\_deseq

*DESeq2 analysis*

---

## Description

Differential expression analysis based on the Negative Binomial (a.k.a. Gamma-Poisson) distribution. This function performs a default analysis through the steps: 1) estimation of size factors: `estimateSizeFactors`. 2) estimation of dispersion: `estimateDispersions`. 3) Negative Binomial GLM fitting and Wald statistics: `nbinomWaldTest`. For complete details on each step, see the manual pages of the respective functions. After the DESeq function returns a `DESeqDataSet` object, results tables (log2 fold changes and p-values) can be generated using the `results` function. Shrunken LFC can then be generated using the `lfcShrink` function.

## Usage

```
step_deseq(
  rec,
  test = "Wald",
  fitType = "local",
  betaPrior = FALSE,
  type = "ashr",
  max_significance = 0.05,
  log2FC = 0,
  rarefy = FALSE,
  id = rand_id("deseq")
)

## S4 method for signature 'Recipe'
step_deseq(
  rec,
  test = "Wald",
  fitType = "local",
  betaPrior = FALSE,
  type = "ashr",
  max_significance = 0.05,
  log2FC = 0,
  rarefy = FALSE,
  id = rand_id("deseq")
)

## S4 method for signature 'PrepRecipe'
step_deseq(
  rec,
```

```

test = "Wald",
fitType = "local",
betaPrior = FALSE,
type = "ashr",
max_significance = 0.05,
log2FC = 0,
rarefy = FALSE,
id = rand_id("deseq")
)

```

### Arguments

rec	A Recipe object. The step will be added to the sequence of operations for this Recipe.
test	Either "Wald" or "LRT", which will then use either Wald significance tests (defined by nbinomWaldTest), or the likelihood ratio test on the difference in deviance between a full and reduced model formula (defined by nbinomLRT).
fitType	either "parametric", "local", "mean", or "glmGamPoi" for the type of fitting of dispersions to the mean intensity. See estimateDispersions for description.
betaPrior	whether or not to put a zero-mean normal prior on the non-intercept coefficients. See nbinomWaldTest for description of the calculation of the beta prior. In versions $\geq 1.16$ , the default is set to FALSE, and shrunken LFCs are obtained afterwards using lfcShrink.
type	"apeglm" is the adaptive Student's t prior shrinkage estimator from the 'apeglm' package; "ashr" is the adaptive shrinkage estimator from the 'ashr' package, using a fitted mixture of normals prior - see the Stephens (2016) reference below for citation; "normal" is the 2014 DESeq2 shrinkage estimator using a Normal prior.
max_significance	The q-value threshold for significance.
log2FC	log2FC cutoff.
rarefy	Boolean indicating if OTU counts must be rarefied. This rarefaction uses the standard R sample function to resample from the abundance values in the otu_table component of the first argument, physeq. Often one of the major goals of this procedure is to achieve parity in total number of counts between samples, as an alternative to other formal normalization procedures, which is why a single value for the sample.size is expected. If 'no_seed', rarefaction is performed without a set seed.
id	A character string that is unique to this step to identify it.

### Value

An object of class Recipe

### See Also

Other Diff taxa steps: [step\\_aldex\(\)](#), [step\\_ancom\(\)](#), [step\\_corncob\(\)](#), [step\\_lefse\(\)](#), [step\\_maaslin\(\)](#), [step\\_metagenomeseq\(\)](#), [step\\_wilcox\(\)](#)

**Examples**

```

data(metaHIV_phy)

## Init Recipe
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Phylum") |>
  step_subset_taxa(tax_level = "Kingdom", taxa = c("Bacteria", "Archaea")) |>
  step_filter_taxa(.f = "function(x) sum(x > 0) >= (0.4 * length(x))")

rec

## Define step with default parameters and prep
rec <-
  step_deseq(rec) |>
  prep(parallel = FALSE)

rec

## Wearing rarefaction only for this step
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Species") |>
  step_deseq(rarefy = TRUE)

rec

```

---

step\_filter\_by\_abundance

*Filter taxa by abundance*


---

**Description**

This is a convenience wrapper around the `filter_taxa` function. It is intended to speed up filtering complex experimental objects with one function call. In the case of `filter_by_abundance`, the filtering will be based on the relative abundance of each taxon. The taxa retained in the dataset are those where the sum of their abundance is greater than the product of the total abundance and the provided threshold.

**Usage**

```

step_filter_by_abundance(
  rec,
  threshold = 0.01,
  id = rand_id("filter_by_abundance")
)

## S4 method for signature 'Recipe'
step_filter_by_abundance(
  rec,

```

```

    threshold = 0.01,
    id = rand_id("filter_by_abundance")
  )

  ## S4 method for signature 'PrepRecipe'
  step_filter_by_abundance(
    rec,
    threshold = 0.01,
    id = rand_id("filter_by_abundance")
  )

```

### Arguments

rec	A Recipe object. The step will be added to the sequence of operations for this Recipe.
threshold	The relative abundance threshold for filtering taxa, expressed as a proportion of the total abundance. For example, a threshold of 0.01 means that a taxon must make up at least 1% of the total abundance to be retained. The default value is 0.01.
id	A character string that is unique to this step to identify it.

### Details

The function calculates the total abundance of all taxa in the phyloseq object. It then compares this total abundance to the abundance of each individual taxon. If a taxon's abundance is less than the threshold times the total abundance, that taxon is removed from the phyloseq object.

### Value

A Recipe object that has been filtered based on abundance.

### Note

This function modifies `rec` in place, you might want to make a copy of `rec` before modifying it if you need to preserve the original object.

### See Also

[filter\\_taxa](#)

Other filter phy steps: [step\\_filter\\_by\\_prevalence\(\)](#), [step\\_filter\\_by\\_rarity\(\)](#), [step\\_filter\\_by\\_variance\(\)](#), [step\\_filter\\_taxa\(\)](#)

### Examples

```

data(metaHIV_phy)

## Init Recipe
rec <- recipe(metaHIV_phy, "RiskGroup2", "Phylum")
rec

```



```
## Define filter_by_abundance step with default parameters
rec <- step_filter_by_abundance(rec, threshold = 0.01)
rec
```

---

```
step_filter_by_prevalence
  Filter taxa by prevalence
```

---

## Description

This is a convenience function around the `filter_taxa` function. It is designed to speed up filtering complex experimental objects with one function call. In the case of `run_filter_by_prevalence`, the filtering will be based on the prevalence of each taxon. The taxa retained in the dataset are those where the prevalence is greater than the provided threshold.

## Usage

```
step_filter_by_prevalence(
  rec,
  threshold = 0.01,
  id = rand_id("filter_by_prevalence")
)

## S4 method for signature 'Recipe'
step_filter_by_prevalence(
  rec,
  threshold = 0.01,
  id = rand_id("filter_by_prevalence")
)

## S4 method for signature 'PrepRecipe'
step_filter_by_prevalence(
  rec,
  threshold = 0.01,
  id = rand_id("filter_by_prevalence")
)
```

## Arguments

<code>rec</code>	A Recipe object. The step will be added to the sequence of operations for this Recipe.
<code>threshold</code>	The prevalence threshold for filtering taxa, expressed as a proportion of the total number of samples. For example, a threshold of 0.01 means that a taxon must be present in at least 1% of the samples to be retained. The default value is 0.01.
<code>id</code>	A character string that is unique to this step to identify it.

## Details

The function calculates the prevalence of all taxa in the phyloseq object as the proportion of samples in which they are present. It then compares this prevalence to the threshold. If a taxon's prevalence is less than the threshold, that taxon is removed from the phyloseq object.

## Value

A Recipe object that has been filtered based on prevalence.

## Note

This function modifies `rec` in place, you might want to make a copy of `rec` before modifying it if you need to preserve the original object.

## See Also

[filter\\_taxa](#)

Other filter phy steps: [step\\_filter\\_by\\_abundance\(\)](#), [step\\_filter\\_by\\_rarity\(\)](#), [step\\_filter\\_by\\_variance\(\)](#), [step\\_filter\\_taxa\(\)](#)

## Examples

```
data(metaHIV_phy)

## Init Recipe
rec <- recipe(metaHIV_phy, "RiskGroup2", "Phylum")
rec

## Define step_filter_by_prevalence step with default parameters
rec <- step_filter_by_prevalence(rec, threshold = 0.01)
rec
```

---

`step_filter_by_rarity` *Filter taxa by rarity*

---

## Description

This is a convenience function around the `filter_taxa` function. It is designed to speed up filtering complex experimental objects with one function call. In the case of `run_filter_by_rarity`, the filtering will be based on the rarity of each taxon. The taxa retained in the dataset are those where the sum of their rarity is less than the provided threshold.

**Usage**

```
step_filter_by_rarity(rec, threshold = 0.01, id = rand_id("filter_by_rarity"))

## S4 method for signature 'Recipe'
step_filter_by_rarity(rec, threshold = 0.01, id = rand_id("filter_by_rarity"))

## S4 method for signature 'PrepRecipe'
step_filter_by_rarity(rec, threshold = 0.01, id = rand_id("filter_by_rarity"))
```

**Arguments**

rec	A Recipe object. The step will be added to the sequence of operations for this Recipe.
threshold	The rarity threshold for filtering taxa, expressed as a proportion of the total number of samples. For example, a threshold of 0.01 means that a taxon must be present in less than 1% of the samples to be retained. The default value is 0.01.
id	A character string that is unique to this step to identify it.

**Details**

The function calculates the rarity of all taxa in the phyloseq object as the proportion of samples in which they are present. It then compares this rarity to the threshold. If a taxon's rarity is greater than the threshold, that taxon is removed from the phyloseq object.

**Value**

A Recipe object that has been filtered based on rarity.

**Note**

This function modifies `rec` in place, you might want to make a copy of `rec` before modifying it if you need to preserve the original object.

**See Also**

[filter\\_taxa](#)

Other filter phy steps: [step\\_filter\\_by\\_abundance\(\)](#), [step\\_filter\\_by\\_prevalence\(\)](#), [step\\_filter\\_by\\_variance\(\)](#), [step\\_filter\\_taxa\(\)](#)

**Examples**

```
data(metaHIV_phy)

## Init Recipe
rec <- recipe(metaHIV_phy, "RiskGroup2", "Phylum")
rec

## Define step_filter_by_rarity step with default parameters
```

```
rec <- step_filter_by_rarity(rec, threshold = 0.01)
rec
```

---

```
step_filter_by_variance
```

*Filter taxa by variance*

---

## Description

This is a convenience function around the `filter_taxa` function. It is designed to speed up filtering complex experimental objects with one function call. In the case of `run_filter_by_variance`, the filtering will be based on the variance of each taxon. The taxa retained in the dataset are those where the variance of their abundance is greater than the provided threshold.

## Usage

```
step_filter_by_variance(
  rec,
  threshold = 0.01,
  id = rand_id("filter_by_variance")
)

## S4 method for signature 'Recipe'
step_filter_by_variance(
  rec,
  threshold = 0.01,
  id = rand_id("filter_by_variance")
)

## S4 method for signature 'PrepRecipe'
step_filter_by_variance(
  rec,
  threshold = 0.01,
  id = rand_id("filter_by_variance")
)
```

## Arguments

<code>rec</code>	A Recipe object. The step will be added to the sequence of operations for this Recipe.
<code>threshold</code>	The variance threshold for filtering taxa. The default value is 0.01.
<code>id</code>	A character string that is unique to this step to identify it.

## Details

The function calculates the variance of all taxa in the phyloseq object. It then compares this variance to the variance of each individual taxon. If a taxon's variance is less than the threshold, that taxon is removed from the phyloseq object.

**Value**

A Recipe object that has been filtered based on variance.

**Note**

This function modifies `rec` in place, you might want to make a copy of `rec` before modifying it if you need to preserve the original object.

**See Also**

[filter\\_taxa](#)

Other filter phy steps: [step\\_filter\\_by\\_abundance\(\)](#), [step\\_filter\\_by\\_prevalence\(\)](#), [step\\_filter\\_by\\_rarity\(\)](#), [step\\_filter\\_taxa\(\)](#)

**Examples**

```
data(metaHIV_phy)

## Init Recipe
rec <- recipe(metaHIV_phy, "RiskGroup2", "Phylum")
rec

## Define step_filter_by_variance step with default parameters
rec <- step_filter_by_variance(rec, threshold = 0.01)
rec
```

---

step_filter_taxa	<i>Filter taxa based on across-sample OTU abundance criteria</i>
------------------	--

---

**Description**

This function is directly analogous to the `genefilter` function for microarray filtering, but is used for filtering OTUs from phyloseq objects. It applies an arbitrary set of functions — as a function list, for instance, created by `filterfun` — as across-sample criteria, one OTU at a time. It takes as input a phyloseq object, and returns a logical vector indicating whether or not each OTU passed the criteria. Alternatively, if the "prune" option is set to `FALSE`, it returns the already-trimmed version of the phyloseq object.

**Usage**

```
step_filter_taxa(rec, .f, id = rand_id("filter_taxa"))

## S4 method for signature 'Recipe'
step_filter_taxa(rec, .f, id = rand_id("filter_taxa"))
```

**Arguments**

rec	A Recipe object. The step will be added to the sequence of operations for this Recipe.
.f	A function or list of functions that take a vector of abundance values and return a logical. Some canned useful function types are included in the <code>genefilter</code> package.
id	A character string that is unique to this step to identify it.

**Value**

An object of class `Recipe`

**See Also**

Other filter phy steps: [step\\_filter\\_by\\_abundance\(\)](#), [step\\_filter\\_by\\_prevalence\(\)](#), [step\\_filter\\_by\\_rarity\(\)](#), [step\\_filter\\_by\\_variance\(\)](#)

**Examples**

```
data(metaHIV_phy)

## Init Recipe
rec <- recipe(metaHIV_phy, "RiskGroup2", "Phylum")
rec

## Define filter taxa step with default parameters
rec <-
  step_filter_taxa(rec, .f = "function(x) sum(x > 0) >= (0.03 * length(x))")

rec
```

---

step\_lefse

*lefse analysis*

---

**Description**

Lefser is metagenomic biomarker discovery tool that is based on LEfSe tool and is published by Huttenhower et al. 2011. Lefser is the R implementation of the LEfSe method. Using statistical analyses, lefser compares microbial populations of healthy and diseased subjects to discover differentially expressed microorganisms. Lefser than computes effect size, which estimates magnitude of differential expression between the populations for each differentially expressed microorganism. Subclasses of classes can also be assigned and used within the analysis.

**Usage**

```
step_lefse(  
  rec,  
  kruskal.threshold = 0.05,  
  wilcox.threshold = 0.05,  
  lda.threshold = 2,  
  subclassCol = NULL,  
  assay = 1L,  
  trim.names = FALSE,  
  rarefy = TRUE,  
  id = rand_id("lefse")  
)  
  
## S4 method for signature 'Recipe'  
step_lefse(  
  rec,  
  kruskal.threshold = 0.05,  
  wilcox.threshold = 0.05,  
  lda.threshold = 2,  
  subclassCol = NULL,  
  assay = 1L,  
  trim.names = FALSE,  
  rarefy = TRUE,  
  id = rand_id("lefse")  
)  
  
## S4 method for signature 'PrepRecipe'  
step_lefse(  
  rec,  
  kruskal.threshold = 0.05,  
  wilcox.threshold = 0.05,  
  lda.threshold = 2,  
  subclassCol = NULL,  
  assay = 1L,  
  trim.names = FALSE,  
  rarefy = TRUE,  
  id = rand_id("lefse")  
)
```

**Arguments**

rec	A Recipe object. The step will be added to the sequence of operations for this Recipe.
kruskal.threshold	numeric(1) The p-value for the Kruskal-Wallis Rank Sum Test (default 0.05).
wilcox.threshold	numeric(1) The p-value for the Wilcoxon Rank-Sum Test when 'blockCol' is present (default 0.05).

lda.threshold	numeric(1) The effect size threshold (default 2.0).
subclassCol	character(1) Optional column name in 'colData(expr)' indicating the blocks, usually a factor with two levels (e.g., 'c("adult", "senior)'); default NULL).
assay	The i-th assay matrix in the 'SummarizedExperiment' ('expr'; default 1).
trim.names	If 'TRUE' extracts the most specific taxonomic rank of organism.
rarefy	Boolean indicating if OTU counts must be rarefied. This rarefaction uses the standard R sample function to resample from the abundance values in the otu_table component of the first argument, physeq. Often one of the major goals of this procedure is to achieve parity in total number of counts between samples, as an alternative to other formal normalization procedures, which is why a single value for the sample.size is expected. If 'no_seed', rarefaction is performed without a set seed.
id	A character string that is unique to this step to identify it.

**Value**

An object of class Recipe

**See Also**

Other Diff taxa steps: [step\\_aldex\(\)](#), [step\\_ancom\(\)](#), [step\\_corncob\(\)](#), [step\\_deseq\(\)](#), [step\\_maaslin\(\)](#), [step\\_metagenomeseq\(\)](#), [step\\_wilcox\(\)](#)

**Examples**

```
data(metaHIV_phy)

## Init Recipe
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Phylum") |>
  step_subset_taxa(tax_level = "Kingdom", taxa = c("Bacteria", "Archaea")) |>
  step_filter_taxa(.f = "function(x) sum(x > 0) >= (0.3 * length(x))")

rec

## Define step with default parameters
rec <- step_lefse(rec)
rec

## Running lefse without rarefaction (not recommended)
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Species") |>
  step_lefse(rarefy = FALSE)

rec
```



---

step_maaslin	<i>MaAsLin2 analysis</i>
--------------	--------------------------

---

## Description

MaAsLin2 finds associations between microbiome meta-omics features and complex metadata in population-scale epidemiological studies. The software includes multiple analysis methods (including support for multiple covariates and repeated measures), filtering, normalization, and transform options to customize analysis for your specific study.

## Usage

```
step_maaslin(  
  rec,  
  min_abundance = 0,  
  min_prevalence = 0.1,  
  min_variance = 0,  
  normalization = "TSS",  
  transform = "LOG",  
  analysis_method = "LM",  
  max_significance = 0.25,  
  random_effects = NULL,  
  correction = "BH",  
  standardize = TRUE,  
  reference = NULL,  
  rarefy = FALSE,  
  id = rand_id("maaslin")  
)  
  
## S4 method for signature 'Recipe'  
step_maaslin(  
  rec,  
  min_abundance = 0,  
  min_prevalence = 0.1,  
  min_variance = 0,  
  normalization = "TSS",  
  transform = "LOG",  
  analysis_method = "LM",  
  max_significance = 0.25,  
  random_effects = NULL,  
  correction = "BH",  
  standardize = TRUE,  
  reference = NULL,  
  rarefy = FALSE,  
  id = rand_id("maaslin")  
)
```

```
## S4 method for signature 'PrepRecipe'
step_maaslin(
  rec,
  min_abundance = 0,
  min_prevalence = 0.1,
  min_variance = 0,
  normalization = "TSS",
  transform = "LOG",
  analysis_method = "LM",
  max_significance = 0.25,
  random_effects = NULL,
  correction = "BH",
  standardize = TRUE,
  reference = NULL,
  rarefy = FALSE,
  id = rand_id("maaslin")
)
```

### Arguments

rec	A Recipe object. The step will be added to the sequence of operations for this Recipe.
min_abundance	The minimum abundance for each feature.
min_prevalence	The minimum percent of samples for which a feature is detected at minimum abundance.
min_variance	Keep features with variance greater than.
normalization	The normalization method to apply. Default: "TSS". Choices: "TSS", "CLR", "CSS", "NONE", "TMM".
transform	The transform to apply. Default: "LOG". Choices: "LOG", "LOGIT", "AST", "NONE".
analysis_method	The analysis method to apply. Default: "LM". Choices: "LM", "CPLM", "ZICP", "NEGBIN", "ZINB".
max_significance	The q-value threshold for significance.
random_effects	The random effects for the model, comma-delimited for multiple effects.
correction	The correction method for computing the q-value.
standardize	Apply z-score so continuous metadata are on the same scale.
reference	The factor to use as a reference for a variable with more than two levels provided as a string of 'variable,reference' semi-colon delimited for multiple variables.
rarefy	Boolean indicating if OTU counts must be rarefied. This rarefaction uses the standard R sample function to resample from the abundance values in the otu_table component of the first argument, physeq. Often one of the major goals of this procedure is to achieve parity in total number of counts between samples, as an alternative to other formal normalization procedures, which is why a single value for the sample.size is expected. If 'no_seed', rarefaction is performed without a set seed.

id                    A character string that is unique to this step to identify it.

### Value

An object of class Recipe

### See Also

Other Diff taxa steps: [step\\_aldex\(\)](#), [step\\_ancom\(\)](#), [step\\_corncob\(\)](#), [step\\_deseq\(\)](#), [step\\_lefse\(\)](#), [step\\_metagenomeseq\(\)](#), [step\\_wilcox\(\)](#)

### Examples

```
data(metaHIV_phy)

## Init Recipe
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Phylum") |>
  step_subset_taxa(tax_level = "Kingdom", taxa = c("Bacteria", "Archaea")) |>
  step_filter_taxa(.f = "function(x) sum(x > 0) >= (0.4 * length(x))")

rec

## Define step with default parameters and prep
rec <-
  step_maaslin(rec) |>
  prep(parallel = FALSE)

rec

## Wearing rarefaction only for this step
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Species") |>
  step_maaslin(rarefy = TRUE)

rec
```

---

step\_metagenomeseq      *MetagenomeSeq analysis*

---

### Description

metagenomeSeq is designed to determine features (be it Operational Taxonomic Unit (OTU), species, etc.) that are differentially abundant between two or more groups of multiple samples. metagenomeSeq is designed to address the effects of both normalization and under-sampling of microbial communities on disease association detection and the testing of feature correlations.

**Usage**

```

step_metagenomeseq(
  rec,
  zeroMod = NULL,
  useCSSoffset = TRUE,
  useMixedModel = FALSE,
  max_significance = 0.05,
  log2FC = 0,
  rarefy = FALSE,
  rm_zeros = 0,
  id = rand_id("metagenomeseq")
)

## S4 method for signature 'Recipe'
step_metagenomeseq(
  rec,
  zeroMod = NULL,
  useCSSoffset = TRUE,
  useMixedModel = FALSE,
  max_significance = 0.05,
  log2FC = 0,
  rarefy = FALSE,
  rm_zeros = 0,
  id = rand_id("metagenomeseq")
)

## S4 method for signature 'PrepRecipe'
step_metagenomeseq(
  rec,
  zeroMod = NULL,
  useCSSoffset = TRUE,
  useMixedModel = FALSE,
  max_significance = 0.05,
  log2FC = 0,
  rarefy = FALSE,
  rm_zeros = 0,
  id = rand_id("metagenomeseq")
)

```

**Arguments**

rec	A Recipe object. The step will be added to the sequence of operations for this Recipe.
zeroMod	The zero model, the model to account for the change in the number of OTUs observed as a linear effect of the depth of coverage.
useCSSoffset	Boolean, whether to include the default scaling parameters in the model or not.
useMixedModel	Estimate the correlation between duplicate features or replicates using duplicateCorrelation.

max_significance	The q-value threshold for significance.
log2FC	log2FC cutoff.
rarefy	Boolean indicating if OTU counts must be rarefied. This rarefaction uses the standard R sample function to resample from the abundance values in the otu_table component of the first argument, physeq. Often one of the major goals of this procedure is to achieve parity in total number of counts between samples, as an alternative to other formal normalization procedures, which is why a single value for the sample.size is expected. If 'no_seed', rarefaction is performed without a set seed.
rm_zeros	Proportion of samples of the same categorical level with more than 0 counts.
id	A character string that is unique to this step to identify it.

**Value**

An object of class Recipe

**See Also**

Other Diff taxa steps: [step\\_aldex\(\)](#), [step\\_ancom\(\)](#), [step\\_corncob\(\)](#), [step\\_deseq\(\)](#), [step\\_lefse\(\)](#), [step\\_maaslin\(\)](#), [step\\_wilcox\(\)](#)

**Examples**

```
data(metaHIV_phy)

## Init Recipe
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Phylum") |>
  step_subset_taxa(tax_level = "Kingdom", taxa = c("Bacteria", "Archaea")) |>
  step_filter_taxa(.f = "function(x) sum(x > 0) >= (0.02 * length(x))")

rec

## Define step with default parameters and prep
rec <-
  step_metagenomeseq(rec, rm_zeros = 0.01) |>
  prep(parallel = FALSE)

rec

## Wearing rarefaction only for this step
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Species") |>
  step_metagenomeseq(rarefy = TRUE)

rec
```

---

step_rarefaction	<i>Resample an OTU table such that all samples have the same library size.</i>
------------------	--

---

## Description

Please note that the authors of phyloseq do not advocate using this as a normalization procedure, despite its recent popularity. Our justifications for using alternative approaches to address disparities in library sizes have been made available as an article in PLoS Computational Biology. See `phyloseq_to_deseq2` for a recommended alternative to rarefying directly supported in the phyloseq package, as well as the supplemental materials for the PLoS-CB article and the phyloseq extensions repository on GitHub. Nevertheless, for comparison and demonstration, the rarefying procedure is implemented here in good faith and with options we hope are useful. This function uses the standard R sample function to resample from the abundance values in the `otu_table` component of the first argument, `physeq`. Often one of the major goals of this procedure is to achieve parity in total number of counts between samples, as an alternative to other formal normalization procedures, which is why a single value for the `sample.size` is expected. This kind of resampling can be performed with and without replacement, with replacement being the more computationally-efficient, default setting. See the `replace` parameter documentation for more details. We recommend that you explicitly select a random number generator seed before invoking this function, or, alternatively, that you explicitly provide a single positive integer argument as `rngseed`.

## Usage

```
step_rarefaction(rec, id = rand_id("rarefaction"))

## S4 method for signature 'Recipe'
step_rarefaction(rec, id = rand_id("rarefaction"))

## S4 method for signature 'PrepRecipe'
step_rarefaction(rec, id = rand_id("rarefaction"))
```

## Arguments

<code>rec</code>	A Recipe object. The step will be added to the sequence of operations for this Recipe.
<code>id</code>	A character string that is unique to this step to identify it.

## Value

An object of class Recipe

## Examples

```
data(metaHIV_phy)

## Init Recipe
```

```

rec <-
  recipe(metaHIV_phy, var_info = "RiskGroup2", tax_info = "Phylum") |>
  step_subset_taxa(tax_level = "Kingdom", taxa = c("Bacteria", "Archaea")) |>
  step_filter_taxa(.f = "function(x) sum(x > 0) >= (0.03 * length(x))")

rec

## Define step with default parameters and prep
rec <- step_rarefaction(rec)

rec

```

---

step_subset_taxa	<i>Subset taxa by taxonomic level</i>
------------------	---------------------------------------

---

## Description

This is a convenience function around the `subset_taxa` function from the `phyloseq` package. It is designed to speed up subsetting complex experimental objects with one function call. In the case of `run_subset_taxa`, the subsetting will be based on the taxonomic level of each taxon. The taxa retained in the dataset are those where the taxonomic level matches the provided taxa.

## Usage

```

step_subset_taxa(rec, tax_level, taxa, id = rand_id("subset_taxa"))

## S4 method for signature 'Recipe'
step_subset_taxa(rec, tax_level, taxa, id = rand_id("subset_taxa"))

## S4 method for signature 'PrepRecipe'
step_subset_taxa(rec, tax_level, taxa, id = rand_id("subset_taxa"))

```

## Arguments

<code>rec</code>	A Recipe object. The step will be added to the sequence of operations for this Recipe.
<code>tax_level</code>	The taxonomic level for subsetting taxa.
<code>taxa</code>	The taxa to be retained in the dataset.
<code>id</code>	A character string that is unique to this step to identify it.

## Details

The function subsets the taxa in the `phyloseq` object based on the provided taxonomic level and taxa. Only the taxa that match the provided taxa at the given taxonomic level are retained in the `phyloseq` object.

**Value**

A Recipe object that has been subsetted based on taxonomic level.

**Note**

This function modifies `rec` in place, you might want to make a copy of `rec` before modifying it if you need to preserve the original object.

**See Also**

[subset\\_taxa](#)

**Examples**

```
data(metaHIV_phy)

## Init Recipe
rec <- recipe(metaHIV_phy, "RiskGroup2", "Species")
rec

## Define step_subset_taxa step with default parameters
rec <- step_subset_taxa(
  rec,
  tax_level = "Kingdom",
  taxa = c("Bacteria", "Archaea")
)
rec
```

---

step\_to\_expr

*Extracts parameters from steps and makes a character vector with the expression to evaluate*

---

**Description**

Extracts parameters from steps and makes a character vector with the expression to evaluate

**Usage**

```
step_to_expr(step)
```

**Arguments**

step                    object of class step

**Value**

character vector



---

`step_wilcox`*Wilcox analysis*

---

### Description

Performs a wilcox test to determine features (be it Operational Taxonomic Unit (OTU), species, etc.) that are differentially abundant between two or more groups of multiple samples.

### Usage

```
step_wilcox(  
  rec,  
  norm_method = "compositional",  
  max_significance = 0.05,  
  p_adj_method = "BH",  
  rarefy = FALSE,  
  id = rand_id("wilcox")  
)  
  
## S4 method for signature 'Recipe'  
step_wilcox(  
  rec,  
  norm_method = "compositional",  
  max_significance = 0.05,  
  p_adj_method = "BH",  
  rarefy = FALSE,  
  id = rand_id("wilcox")  
)  
  
## S4 method for signature 'PrepRecipe'  
step_wilcox(  
  rec,  
  norm_method = "compositional",  
  max_significance = 0.05,  
  p_adj_method = "BH",  
  rarefy = FALSE,  
  id = rand_id("wilcox")  
)
```

### Arguments

<code>rec</code>	A Recipe object. The step will be added to the sequence of operations for this Recipe.
<code>norm_method</code>	Transformation to apply. The options include: 'compositional' (ie relative abundance), 'Z', 'log10', 'log10p', 'hellinger', 'identity', 'clr', 'alr', or any method from the <code>vegan::decostand</code> function.

max_significance	The q-value threshold for significance.
p_adj_method	Character. Specifying the method to adjust p-values for multiple comparisons. Default is “BH” (Benjamini-Hochberg procedure).
rarefy	Boolean indicating if OTU counts must be rarefied. This rarefaction uses the standard R sample function to resample from the abundance values in the otu_table component of the first argument, physeq. Often one of the major goals of this procedure is to achieve parity in total number of counts between samples, as an alternative to other formal normalization procedures, which is why a single value for the sample.size is expected. If 'no_seed', rarefaction is performed without a set seed.
id	A character string that is unique to this step to identify it.

### Value

An object of class Recipe

### See Also

Other Diff taxa steps: [step\\_aldex\(\)](#), [step\\_ancom\(\)](#), [step\\_corncob\(\)](#), [step\\_deseq\(\)](#), [step\\_lefse\(\)](#), [step\\_maaslin\(\)](#), [step\\_metagenomeseq\(\)](#)

### Examples

```
data(metaHIV_phy)

## Init Recipe
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Phylum") |>
  step_subset_taxa(tax_level = "Kingdom", taxa = c("Bacteria", "Archaea")) |>
  step_filter_taxa(.f = "function(x) sum(x > 0) >= (0.4 * length(x))")

rec

## Define step with default parameters and prep
rec <-
  step_wilcox(rec) |>
  prep(parallel = FALSE)

rec

## Wearing rarefaction only for this step
rec <-
  recipe(metaHIV_phy, "RiskGroup2", "Species") |>
  step_wilcox(rarefy = TRUE)

rec
```

---

tax_table	<i>Extracts tax_table from phyloseq inside a Recipe</i>
-----------	---

---

**Description**

Extracts tax\_table from phyloseq inside a Recipe

**Usage**

```
tax_table(rec)

## S4 method for signature 'Recipe'
tax_table(rec)
```

**Arguments**

rec                    A Recipe or Recipe step.

**Value**

A tibble

**Examples**

```
data(metaHIV_phy)

## Define recipe
rec <-
  recipe(metaHIV_phy, var_info = "RiskGroup2", tax_info = "Species")

## Extract tax_table from phyloseq object
tax_table(rec)
```

---

test_prep_rec	<i>PrepRecipe for metaHIV_phy data</i>
---------------	--

---

**Description**

A Recipe created for a metaHIV\_phy object using "Riskgroup2" as a var\_info and "Genus" as a tax\_info. Also includes step\_deseq, step\_maaslin and step\_metagenomeSeq.

**Usage**

```
data("test_prep_rec")
```

**Format**

A PrepRecipe object.

---

test_rec	<i>Recipe for metaHIV_phy data</i>
----------	------------------------------------

---

**Description**

A Recipe created for a metaHIV\_phy object using "Riskgroup2" as a var\_info and "Genus" as a tax\_info.

**Usage**

```
data("test_rec")
```

**Format**

A Recipe object.

---

tidyeval	<i>Tidy eval helpers</i>
----------	--------------------------

---

**Description**

This page lists the tidy eval tools reexported in this package from rlang. To learn about using tidy eval in scripts and packages at a high level, see the [dplyr programming vignette](#) and the [ggplot2 in packages vignette](#). The [Metaprogramming section of Advanced R](#) may also be useful for a deeper dive.

- The tidy eval operators `{{`, `!!`, and `!!!` are syntactic constructs which are specially interpreted by tidy eval functions. You will mostly need `{{`, as `!!` and `!!!` are more advanced operators which you should not have to use in simple cases.

The curly-curly operator `{{` allows you to tunnel data-variables passed from function arguments inside other tidy eval functions. `{{` is designed for individual arguments. To pass multiple arguments contained in dots, use `...` in the normal way.

```
my_function <- function(data, var, ...) {
  data %>%
    group_by(...) %>%
    summarise(mean = mean({{ var }}))
}
```

- `enquo()` and `enquos()` delay the execution of one or several function arguments. The former returns a single expression, the latter returns a list of expressions. Once defused, expressions will no longer evaluate on their own. They must be injected back into an evaluation context with `!!` (for a single expression) and `!!!` (for a list of expressions).

```
my_function <- function(data, var, ...) {
  # Defuse
  var <- enquos(var)
  dots <- enquos(...)

  # Inject
  data %>%
    group_by(!!!dots) %>%
    summarise(mean = mean(!!var))
}
```

In this simple case, the code is equivalent to the usage of `{{` and `...` above. Defusing with `enquo()` or `enquos()` is only needed in more complex cases, for instance if you need to inspect or modify the expressions in some way.

- The `.data` pronoun is an object that represents the current slice of data. If you have a variable name in a string, use the `.data` pronoun to subset that variable with `[[`.

```
my_var <- "disp"
mtcars %>% summarise(mean = mean(.data[[my_var]]))
```

- Another tidy eval operator is `:=`. It makes it possible to use glue and curly-curly syntax on the LHS of `=`. For technical reasons, the R language doesn't support complex expressions on the left of `=`, so we use `:=` as a workaround.

```
my_function <- function(data, var, suffix = "foo") {
  # Use `{{` to tunnel function arguments and the usual glue
  # operator `` to interpolate plain strings.
  data %>%
    summarise("{{ var }}_mean_{suffix}" := mean({{ var }}))
}
```

- Many tidy eval functions like `dplyr::mutate()` or `dplyr::summarise()` give an automatic name to unnamed inputs. If you need to create the same sort of automatic names by yourself, use `as_label()`. For instance, the glue-tunnelling syntax above can be reproduced manually with:

```
my_function <- function(data, var, suffix = "foo") {
  var <- enquos(var)
  prefix <- as_label(var)
  data %>%
    summarise("{prefix}_mean_{suffix}" := mean(!!var))
}
```

Expressions defused with `enquo()` (or tunnelled with `{{`) need not be simple column names, they can be arbitrarily complex. `as_label()` handles those cases gracefully. If your code assumes a simple column name, use `as_name()` instead. This is safer because it throws an error if the input is not a name as expected.

## Value

The function does not return a value explicitly.

**Examples**

```

# `enquo()` defuses the expression supplied by your user
f <- function(arg) {
  rlang::enquo(arg)
}

f(1 + 1)

# `enquos()` works with arguments and dots. It returns a list of
# expressions
f <- function(...) {
  rlang::enquos(...)
}

f(1 + 1, 2 * 10)

# Let's create some symbols:
foo <- quote(foo)
bar <- rlang::sym("bar")

# as_name() converts symbols to strings:
foo

rlang::as_name(foo)

typeof(bar)

typeof(rlang::as_name(bar))

# as_name() unwraps quosured symbols automatically:
rlang::as_name(rlang::quo(foo))

# as_label() is useful with quoted expressions:
rlang::as_label(rlang::expr(foo(bar)))

rlang::as_label(rlang::expr(foofoo))

# It works with any R object. This is also useful for quoted
# arguments because the user might unquote constant objects:
rlang::as_label(1:3)

rlang::as_label(base::list)

```

---

to\_tibble

*Wrapper to convert phyloseq slots to tibble*


---

**Description**

Wrapper to convert phyloseq slots to tibble

**Usage**

```
to_tibble(df, id_name = "otu_id")
```

**Arguments**

**df** output of `otu_table()`, `sample_data()` or `tax_table()` phyloseq functions.  
**id\_name** Name of the new column generated from rownames

**Value**

tibble

**Examples**

```
data(test_rec)
otu_table <-
  get_phy(test_rec) |>
  phyloseq::otu_table()

dar:::to_tibble(otu_table)
```

---

use\_rarefy

*Perform Rarefaction on Phyloseq Object*

---

**Description**

This function performs rarefaction on a phyloseq object if the `rarefy` parameter is set to `TRUE`. Rarefaction is a process that randomly subsamples the data to a specified depth. This is done to account for differences in sequencing depth between samples. However, this process is not without controversy. Rarefaction can lead to loss of information and can also lead to false positives in differential abundance testing. For more information, see <https://microbiomejournal.biomedcentral.com/articles/10.1186/s40168-019-0650-2>

**Usage**

```
use_rarefy(phy, rarefy)
```

**Arguments**

**phy** A phyloseq object.  
**rarefy** A logical value indicating whether to perform rarefaction. If `'no_seed'`, rarefaction is performed without a set seed. If `FALSE`, no rarefaction is performed.

**Value**

A phyloseq object after rarefaction if `rarefy` is `TRUE` or `"no_seed"`, otherwise the original phyloseq object is returned.

## Examples

```
data(metaHIV_phy)

## With seed
# phy_rarefied <- dar:::use_rarefy(metaHIV_phy, TRUE)

## Witout seed
# phy_rarefied <- dar:::use_rarefy(metaHIV_phy, "no_seed")
```

---

zero\_otu

*Extract outs with all 0 values in at least on level of the variable*

---

## Description

Extract outs with all 0 values in at least on level of the variable

## Usage

```
zero_otu(obj, var = NULL, pct_cutoff = 0)

## S4 method for signature 'Recipe'
zero_otu(obj, var = NULL, pct_cutoff = 0)

## S4 method for signature 'phyloseq'
zero_otu(obj, var = NULL, pct_cutoff = 0)
```

## Arguments

obj	A Recipe or phyloseq object.
var	Variable of interest. Must be present in the metadata.
pct_cutoff	Minimum of pct counts samples with counts for each taxa.

## Value

character vector

## Examples

```
data(metaHIV_phy)

## Init Recipe
rec <- recipe(metaHIV_phy, "RiskGroup2", "Species")

## Extract outs with all 0 values
zero_otu(rec)
```



---

%>%

*Pipe operator*

---

**Description**

Pipe operator

**Value**

The result of calling `rhs(lhs)`.

# Index

- \* **Bake steps**
  - bake, 8
- \* **Diff taxa steps**
  - step\_aldex, 36
  - step\_ancom, 38
  - step\_corncob, 42
  - step\_deseq, 45
  - step\_lefse, 54
  - step\_maaslin, 57
  - step\_metagenomeseq, 59
  - step\_wilcox, 65
- \* **datasets**
  - metaHIV\_phy, 21
  - test\_prep\_rec, 67
  - test\_rec, 68
- \* **filter phy steps**
  - step\_filter\_by\_abundance, 47
  - step\_filter\_by\_prevalence, 49
  - step\_filter\_by\_rarity, 50
  - step\_filter\_by\_variance, 52
  - step\_filter\_taxa, 53
- \* **internal**
  - %>%, 73
  - add\_step, 6
  - dar-package, 4
  - get\_comparisons, 15
  - pastry\_df, 25
  - prep\_recipe, 29
  - read\_data, 30
  - recipes\_pkg\_check, 32
  - required\_deps, 33
  - step, 34
  - step\_ancom, 38
  - step\_to\_expr, 64
  - tidyeval, 68
  - to\_tibble, 70
  - use\_rarefy, 71
- \* **rarefaction phy steps**
  - step\_rarefaction, 62
- \* **subset phy steps**
  - step\_subset\_taxa, 63
  - .data (tidyeval), 68
  - .env (tidyeval), 68
  - := (tidyeval), 68
  - %>%, 73
  - abundance\_plt, 4
  - abundance\_plt, PrepRecipe-method (abundance\_plt), 4
  - abundance\_plt, Recipe-method (abundance\_plt), 4
  - add\_step, 6
  - add\_step, PrepRecipe-method (add\_step), 6
  - add\_step, Recipe-method (add\_step), 6
  - add\_tax, 6
  - add\_tax, PrepRecipe-method (add\_tax), 6
  - add\_tax, Recipe-method (add\_tax), 6
  - add\_var, 7
  - add\_var, PrepRecipe-method (add\_var), 7
  - add\_var, Recipe-method (add\_var), 7
  - as\_label (tidyeval), 68
  - as\_name (tidyeval), 68
  - bake, 8
  - bake, PrepRecipe-method (bake), 8
  - bake, Recipe-method (bake), 8
  - check (step), 34
  - contains\_rarefaction, 10
  - cool, 11
  - cool, PrepRecipe-method (cool), 11
  - cool, Recipe-method (cool), 11
  - corr\_heatmap, 12
  - corr\_heatmap, PrepRecipe-method (corr\_heatmap), 12
  - corr\_heatmap, Recipe-method (corr\_heatmap), 12
  - dar (dar-package), 4

- dar-package, 4
- enquo (tidyeval), 68
- enquo(), 68
- enquos (tidyeval), 68
- enquos(), 68
- exclusion\_plt, 13
- exclusion\_plt, PrepRecipe-method (exclusion\_plt), 13
- exclusion\_plt, Recipe-method (exclusion\_plt), 13
- export\_steps, 14
- filter\_taxa, 48, 50, 51, 53
- find\_intersections, 14
- get\_comparisons, 15
- get\_phy, 16
- get\_phy, Recipe-method (get\_phy), 16
- get\_tax, 17
- get\_tax, Recipe-method (get\_tax), 17
- get\_var, 17
- get\_var, Recipe-method (get\_var), 17
- import\_steps, 18
- intersection\_df, 19
- intersection\_df, PrepRecipe-method (intersection\_df), 19
- intersection\_df, Recipe-method (intersection\_df), 19
- intersection\_plt, 20
- intersection\_plt, PrepRecipe-method (intersection\_plt), 20
- intersection\_plt, Recipe-method (intersection\_plt), 20
- metaHIV\_phy, 21
- mutual\_plt, 22
- mutual\_plt, PrepRecipe-method (mutual\_plt), 22
- mutual\_plt, Recipe-method (mutual\_plt), 22
- otu\_table, 23
- otu\_table, Recipe-method (otu\_table), 23
- overlap\_df, 24
- overlap\_df, PrepRecipe-method (overlap\_df), 24
- overlap\_df, Recipe-method (overlap\_df), 24
- pastry\_df, 25
- phy\_qc, 26
- phy\_qc, Recipe-method (phy\_qc), 26
- phyloseq\_or\_null-class, 25
- prep, 27
- prep, Recipe-method (prep), 27
- prep\_recipe, 29
- PrepRecipe (prep\_recipe), 29
- PrepRecipe-class, 28
- rand\_id, 29
- read\_data, 30
- read\_file (read\_data), 30
- read\_phyloseq (read\_data), 30
- Recipe (recipe), 31
- recipe, 31
- Recipe(), 6
- Recipe-class (phyloseq\_or\_null-class), 25
- recipes\_pkg\_check, 32
- required\_deps, 33
- required\_deps, Recipe-method (required\_deps), 33
- sample\_data, 34
- sample\_data, Recipe-method (sample\_data), 34
- show, PrepRecipe-method (phyloseq\_or\_null-class), 25
- step, 34
- step\_aldex, 36, 41, 44, 46, 56, 59, 61, 66
- step\_aldex, PrepRecipe-method (step\_aldex), 36
- step\_aldex, Recipe-method (step\_aldex), 36
- step\_ancom, 37, 38, 44, 46, 56, 59, 61, 66
- step\_ancom, PrepRecipe-method (step\_ancom), 38
- step\_ancom, Recipe-method (step\_ancom), 38
- step\_corncob, 37, 41, 42, 46, 56, 59, 61, 66
- step\_corncob, PrepRecipe-method (step\_corncob), 42
- step\_corncob, Recipe-method (step\_corncob), 42
- step\_deseq, 37, 41, 44, 45, 56, 59, 61, 66
- step\_deseq, PrepRecipe-method (step\_deseq), 45

- step\_deseq, Recipe-method (step\_deseq),  
45
- step\_filter\_by\_abundance, 47, 50, 51, 53,  
54
- step\_filter\_by\_abundance, PrepRecipe-method  
(step\_filter\_by\_abundance), 47
- step\_filter\_by\_abundance, Recipe-method  
(step\_filter\_by\_abundance), 47
- step\_filter\_by\_prevalence, 48, 49, 51, 53,  
54
- step\_filter\_by\_prevalence, PrepRecipe-method  
(step\_filter\_by\_prevalence), 49
- step\_filter\_by\_prevalence, Recipe-method  
(step\_filter\_by\_prevalence), 49
- step\_filter\_by\_rarity, 48, 50, 50, 53, 54
- step\_filter\_by\_rarity, PrepRecipe-method  
(step\_filter\_by\_rarity), 50
- step\_filter\_by\_rarity, Recipe-method  
(step\_filter\_by\_rarity), 50
- step\_filter\_by\_variance, 48, 50, 51, 52,  
54
- step\_filter\_by\_variance, PrepRecipe-method  
(step\_filter\_by\_variance), 52
- step\_filter\_by\_variance, Recipe-method  
(step\_filter\_by\_variance), 52
- step\_filter\_taxa, 48, 50, 51, 53, 53
- step\_filter\_taxa, Recipe-method  
(step\_filter\_taxa), 53
- step\_lefse, 37, 41, 44, 46, 54, 59, 61, 66
- step\_lefse, PrepRecipe-method  
(step\_lefse), 54
- step\_lefse, Recipe-method (step\_lefse),  
54
- step\_maaslin, 37, 41, 44, 46, 56, 57, 61, 66
- step\_maaslin, PrepRecipe-method  
(step\_maaslin), 57
- step\_maaslin, Recipe-method  
(step\_maaslin), 57
- step\_metagenomeseq, 37, 41, 44, 46, 56, 59,  
59, 66
- step\_metagenomeseq, PrepRecipe-method  
(step\_metagenomeseq), 59
- step\_metagenomeseq, Recipe-method  
(step\_metagenomeseq), 59
- step\_rarefaction, 62
- step\_rarefaction, PrepRecipe-method  
(step\_rarefaction), 62
- step\_rarefaction, Recipe-method  
(step\_rarefaction), 62
- step\_subset\_taxa, 63
- step\_subset\_taxa, PrepRecipe-method  
(step\_subset\_taxa), 63
- step\_subset\_taxa, Recipe-method  
(step\_subset\_taxa), 63
- step\_to\_expr, 64
- step\_wilcox, 37, 41, 44, 46, 56, 59, 61, 65
- step\_wilcox, PrepRecipe-method  
(step\_wilcox), 65
- step\_wilcox, Recipe-method  
(step\_wilcox), 65
- steps\_ids, 35
- subset\_taxa, 64
- tax\_table, 67
- tax\_table, Recipe-method (tax\_table), 67
- test\_prep\_rec, 67
- test\_rec, 68
- tibble\_or\_NULL-class  
(phyloseq\_or\_null-class), 25
- tidyeval, 68
- to\_tibble, 70
- use\_rarefy, 71
- utils::install.packages(), 32
- validate\_otu (read\_data), 30
- validate\_phyloseq (read\_data), 30
- validate\_sample\_data (read\_data), 30
- validate\_tax\_table (read\_data), 30
- zero\_otu, 72
- zero\_otu, phyloseq-method (zero\_otu), 72
- zero\_otu, Recipe-method (zero\_otu), 72