

# Package ‘lefser’

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**Type** Package

**Title** R implementation of the LEfSE method for microbiome biomarker discovery

**Description** lefser is the R implementation of the popular microbiome biomarker discovery tool, LEfSe. It uses the Kruskal-Wallis test, Wilcoxon-Rank Sum test, and Linear Discriminant Analysis to find biomarkers from two-level classes (and optional sub-classes).

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**License** Artistic-2.0

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**URL** <https://github.com/waldronlab/lefser>

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get_terminal_nodes	<i>Identify which elements of a string are terminal nodes</i>
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### Description

A terminal node in a taxonomy does not have any child nodes. For example, a species is a terminal node if there are no subspecies or strains that belong to that species. This function identifies which elements of a vector are terminal nodes simply by checking whether that element appears as a substring in any other element of the vector.

### Usage

```
get_terminal_nodes(string)
```

### Arguments

string	A character vector of strings to check for terminal nodes
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### Value

A logical vector indicating which elements of the string are terminal nodes

## Examples

```
# What does it do?
data("zeller14")
rownames(zeller14)[988:989]
get_terminal_nodes(rownames(zeller14)[988:989])
# How do I use it to keep only terminal nodes for a lefser analysis?
terminal_nodes <- get_terminal_nodes(rownames(zeller14))
zeller14sub <- zeller14[terminal_nodes, ]
# Then continue with your analysis!
```

---

lefser

*R implementation of the LEfSe method*


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## Description

Perform a LEfSe analysis: the function carries out differential analysis between two sample classes for multiple features and uses linear discriminant analysis to establish their effect sizes. Subclass information for each class can be incorporated into the analysis (see examples). Features with large differences between two sample classes are identified as biomarkers.

## Usage

```
lefser(
  relab,
  kruskal.threshold = 0.05,
  wilcox.threshold = 0.05,
  lda.threshold = 2,
  classCol = "CLASS",
  subclassCol = NULL,
  assay = 1L,
  trim.names = FALSE,
  checkAbundances = TRUE,
  method = "none",
  ...
)
```

## Arguments

relab	A <a href="#">SummarizedExperiment-class</a> with relative abundances in the assay
kruskal.threshold	numeric(1) The p-value for the Kruskal-Wallis Rank Sum Test (default 0.05). If multiple hypothesis testing is performed, this threshold is applied to corrected p-values.
wilcox.threshold	numeric(1) The p-value for the Wilcoxon Rank-Sum Test when 'subclassCol' is present (default 0.05). If multiple hypothesis testing is performed, this threshold is applied to corrected p-values.
lda.threshold	numeric(1) The effect size threshold (default 2.0).
classCol	character(1) Column name in colData(relab) indicating class, usually a factor with two levels (e.g., c("cases", "controls")); default "CLASS").

subclassCol	character(1) Optional column name in colData(relab) indicating the subclasses, usually a factor with two levels (e.g., c("adult", "senior")); default NULL, but can be more than two levels.
assay	The i-th assay matrix in the <a href="#">SummarizedExperiment</a> ('relab'; #' default 1).
trim.names	Default is FALSE. If TRUE, this function extracts the most specific taxonomic rank of organism.
checkAbundances	logical(1) Whether to check if the assay data in the relab input are relative abundances or counts. If counts are found, a warning will be emitted (default TRUE).
method	Default is "none" as in the original LEfSe implementation. Character string of length one, passed on to <a href="#">p.adjust</a> to set option for multiple testing. For multiple pairwise comparisons, each comparison is adjusted separately. Options are "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr" (synonym for "BH"), and "none".
...	Additional inputs to lower level functions (not used).

## Details

The LEfSe method expects relative abundances in the `expr` input. A warning will be emitted if the column sums do not result in 1. Use the `relativeAb` helper function to convert the data in the [SummarizedExperiment](#) to relative abundances. The `checkAbundances` argument enables checking the data for presence of relative abundances and can be turned off by setting the argument to FALSE.

## Value

The function returns a `data.frame` with two columns, which are names of features and their LDA scores.

## Examples

```
data(zeller14)
zeller14 <- zeller14[, zeller14$study_condition != "adenoma"]
tn <- get_terminal_nodes(rownames(zeller14))
zeller14tn <- zeller14[tn,]
zeller14tn_ra <- relativeAb(zeller14tn)

# (1) Using classes only
res_class <- lefser(zeller14tn_ra,
                  classCol = "study_condition")

# (2) Using classes and sub-classes
res_subclass <- lefser(zeller14tn_ra,
                      classCol = "study_condition",
                      subclassCol = "age_category")
```

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lefserClades	<i>Run lefser at different clades</i>
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### Description

lefserClades Agglomerates the features abundance at different taxonomic ranks using [mia::splitByRanks](#) and performs lefser at each rank. The analysis is run at the species, genus, family, order, class, and phylum levels.

### Usage

```
lefserClades(relab, ...)
```

### Arguments

relab	A (Tree) <a href="#">SummarizedExperiment</a> with full taxonomy in the rowData @param ... Arguments passed to the lefser function.
...	Additional arguments passed to lefser

### Details

When running lefserClades, all features with NAs in the rowData will be dropped. This is to avoid creating artificial clades with NAs.

### Value

An object of class 'lefser\_df\_clades', 'lefser\_df', and 'data.frame'.

### Examples

```
data("zeller14")
z14 <- zeller14[, zeller14$study_condition != "adenoma"]
tn <- get_terminal_nodes(rownames(z14))
z14tn <- z14[tn, ]
z14tn_ra <- relativeAb(z14tn)
z14_input <- rowNames2RowData(z14tn_ra)

resCl <- lefserClades(relab = z14_input, classCol = "study_condition")
```

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lefserPlot	<i>Plots results from lefser function</i>
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### Description

This function plots the biomarkers found by LEfSe, that are ranked according to their effect sizes and linked to their abundance in each class.

**Usage**

```
lefserPlot(
  df,
  colors = "c",
  trim.names = TRUE,
  title = "",
  label.font.size = 3
)
```

**Arguments**

<code>df</code>	Data frame produced by <code>lefser</code> . This data frame contains two columns labeled as <code>c("features", "scores")</code> .
<code>colors</code>	Colors corresponding to class 0 and 1. Options: "c" (colorblind), "l" (lefse), "g" (greyscale). Defaults to "c". This argument also accepts a <code>character(2)</code> with two color names.
<code>trim.names</code>	Under the default (TRUE), this function extracts the most specific taxonomic rank of organism.
<code>title</code>	A <code>character(1)</code> . The title of the plot.
<code>label.font.size</code>	A <code>numeric(1)</code> . The font size of the feature labels. The default is 3.

**Value**

Function returns plot of effect size scores produced by `lefser`. Positive scores represent the biomarker is more abundant in class '1'. Negative scores represent the biomarker is more abundant in class '0'.

**Examples**

```
example("lefser")
lefserPlot(res_class)
```

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<code>lefserPlotClad</code>	<i>LEfSer plot cladogram</i>
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**Description**

`lefserPlotClad` plots a cladogram from the results of `lefserClades`.

**Usage**

```
lefserPlotClad(df, colors = "c", showTipLabels = FALSE, showNodeLabels = "p")
```

**Arguments**

df	An object of class "lefser_df_clades".
colors	Colors corresponding to class 0 and 1. Options: "c" (colorblind), "l" (lefse), "g" (greyscale). Defaults to "c". This argument also accepts a character(2) with two color names.
showTipLabels	Logical. If TRUE, show tip labels. Default is FALSE.
showNodeLabels	Label's to be shown in the tree. Options: "p" = phylum, "c" = class, "o" = order, "f" = family, "g" = genus, "s" = species, "t" = strain. It can accept several options, e.g., c("p", "c").

**Value**

A ggtree object.

**Examples**

```
data("zeller14")
z14 <- zeller14[, zeller14$study_condition != "adenoma"]
tn <- get_terminal_nodes(rownames(z14))
z14tn <- z14[tn, ]
z14tn_ra <- relativeAb(z14tn)
z14_input <- rowNames2RowData(z14tn_ra)

resCl <- lefserClades(relab = z14_input, classCol = "study_condition")
ggt <- lefserPlotClad(df = resCl)
```

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lefserPlotFeat	<i>Plot Feature</i>
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**Description**

lefserPlotFeat plots the abundance data of a DA feature across all samples.

**Usage**

```
lefserPlotFeat(res, fName, colors = "colorblind")
```

**Arguments**

res	An object of class lefser_df, output of the lefser function.
fName	A character string. The name of a feature in the lefser_df object.
colors	Colors corresponding to class 0 and 1. Options: "c" (colorblind), "l" (lefse), "g" (greyscale). Defaults to "c". This argument also accepts a character(2) with two color names.

**Details**

The solid lines represent the mean by class or by class+subclass (if the subclass variable is present). The dashed lines represent the median by class or by class+subclass (if the subclass variable is present).

**Value**

A ggplot object.

**Examples**

```
data(zeller14)
zeller14 <- zeller14[, zeller14$study_condition != "adenoma"]
tn <- get_terminal_nodes(rownames(zeller14))
zeller14tn <- zeller14[tn,]
zeller14tn_ra <- relativeAb(zeller14tn)

# (1) Using classes only
res_class <- lefser(zeller14tn_ra,
  classCol = "study_condition")
# (2) Using classes and sub-classes
res_subclass <- lefser(zeller14tn_ra,
  classCol = "study_condition",
  subclassCol = "age_category")
plot_class <- lefserPlotFeat(res_class, res_class$features[[1]])
plot_subclass <- lefserPlotFeat(res_subclass, res_subclass$features[[2]])
```

---

relativeAb

*Utility function to calculate relative abundances*

---

**Description**

The function calculates the column totals and divides each value within the column by the respective column total.

This function calculates the relative abundance of each feature in the [SummarizedExperiment](#) object containing count data, expressed as counts per million (CPM)

**Usage**

```
relativeAb(se, assay = 1L)
```

**Arguments**

`se` A [SummarizedExperiment](#) object with counts

`assay` The *i*-th assay matrix in the [SummarizedExperiment](#) ('relab'; #' default 1).

**Value**

returns a new [SummarizedExperiment](#) object with counts per million calculated and added as a new assay named `rel_abs`.



## Examples

```
se <- SummarizedExperiment(  
  assays = list(  
    counts = matrix(  
      rep(1, 4), ncol = 1, dimnames = list(LETTERS[1:4], "SAMP")  
    )  
  )  
)  
assay(se)  
assay(relativeAb(se))
```

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rowNames2RowData	<i>RowNames to RowData</i>
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## Description

rowNames2RowData transforms the taxonomy stored in the row names to the rowData in a [SummarizedExperiment](#).

## Usage

```
rowNames2RowData(x)
```

## Arguments

x                    A [SummarizedExperiment](#) with the features taxonomy in the rownames.

## Value

The same [SummarizedExperiment](#) with the taxonomy now in the rowData.

## Examples

```
data("zeller14")  
  
## Keep only "CRC" and "control" (dichotomous variable)  
z14 <- zeller14[, zeller14$study_condition %in% c("control", "CRC")]  
  
## Get terminal nodes  
tn <- get_terminal_nodes(rownames(z14))  
z14_tn <- z14[tn, ]  
  
## Normalize to relative abundance (also known as Total Sum Scaling)  
z14_tn_ra <- relativeAb(z14_tn)  
  
## Add the taxonomy to the rowData  
input_se <- rowNames2RowData(z14_tn_ra)
```

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zeller14

*Example dataset for lefser*

---

### **Description**

The ZellerG\_2014 dataset contains microbiome count data for CRC patients and controls. It was for curatedMetagenomicData using the script in the package directory "data-raw".

### **Usage**

```
data("zeller14")
```

### **Format**

A [SummarizedExperiment](#) with 1585 features, 199 samples

**study\_condition** adenoma, control, CRC

**age\_category** adult, senior

### **Source**

<https://pubmed.ncbi.nlm.nih.gov/25432777/>

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