

# Package ‘lefsr’

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**Type** Package

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

**Description** lefsr is an implementation in R of the popular “LDA Effect Size (LEfSe)” method for microbiome biomarker discovery. It uses the Kruskal-Wallis test, Wilcoxon-Rank Sum test, and Linear Discriminant Analysis to find biomarkers of groups and sub-groups.

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**License** Artistic-2.0

**Depends** SummarizedExperiment, R (>= 4.0.0)

**Imports** coin, MASS, ggplot2, S4Vectors, stats, methods, utils, dplyr

**Suggests** knitr, rmarkdown, curatedMetagenomicData, BiocStyle, phyloseq, testthat, pkgdown, covr, withr

**Encoding** UTF-8

**BugReports** <https://github.com/waldronlab/lefsr/issues>

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

**VignetteBuilder** knitr

**biocViews** Software, Sequencing, DifferentialExpression, Microbiome, StatisticalMethod, Classification

**RoxygenNote** 7.3.1

**Roxygen** list(markdown = TRUE)

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## Contents

lefser	2
lefserPlot	4
relativeAb	5
zeller14	5
<b>Index</b>	<b>7</b>

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lefser	<i>R implementation of the LEfSe method</i>
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## Description

Perform a LEfSe analysis: the function carries out differential analysis between two sample groups 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 groups are identified as biomarkers.

## Usage

```
lefser(
  relab,
  kruskal.threshold = 0.05,
  wilcox.threshold = 0.05,
  lda.threshold = 2,
  groupCol = "GROUP",
  blockCol = NULL,
  assay = 1L,
  trim.names = FALSE,
  checkAbundances = TRUE,
  ...,
  expr
)
```

## Arguments

<code>relab</code>	A <a href="#">SummarizedExperiment</a> with relative abundances in the assay
<code>kruskal.threshold</code>	numeric(1) The p-value for the Kruskal-Wallis Rank Sum Test (default 0.05).
<code>wilcox.threshold</code>	numeric(1) The p-value for the Wilcoxon Rank-Sum Test when 'blockCol' is present (default 0.05).
<code>lda.threshold</code>	numeric(1) The effect size threshold (default 2.0).
<code>groupCol</code>	character(1) Column name in <code>colData(relab)</code> indicating groups, usually a factor with two levels (e.g., <code>c("cases", "controls")</code> ); default "GROUP".
<code>blockCol</code>	character(1) Optional column name in <code>colData(relab)</code> indicating the blocks, usually a factor with two levels (e.g., <code>c("adult", "senior")</code> ); default NULL.
<code>assay</code>	The i-th assay matrix in the <code>SummarizedExperiment</code> ('relab'; default 1).
<code>trim.names</code>	Default is FALSE. If TRUE, this function extracts the most specific taxonomic rank of organism.
<code>checkAbundances</code>	logical(1) Whether to check if the assay data in the <code>relab</code> input are relative abundances or counts. If counts are found, a warning will be emitted (default TRUE).
<code>expr</code>	(deprecated) Use <code>relab</code> instead. A <a href="#">SummarizedExperiment</a> with relative abundances in the assay
<code>...</code>	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

```
# (1) Using classes only
data(zeller14)
# exclude 'adenoma'
zeller14 <- zeller14[, zeller14$study_condition != "adenoma"]
res_group <- lefser(relativeAb(zeller14),
                    groupCol = "study_condition")
head(res_group)
```

```
# (2) Using classes and subclasses
data(zeller14)
# exclude 'adenoma'
zeller14 <- zeller14[, zeller14$study_condition != "adenoma"]
res_block <- lefser(relativeAb(zeller14),
                    groupCol = "study_condition",
                    blockCol = "age_category")

head(res_block)
```

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lefserPlot

*Plots results from lefser function*


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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("red", "forestgreen"),
  trim.names = TRUE,
  title = "",
  label.font.size = 3
)
```

### Arguments

df	Data frame produced by lefser.
colors	A character(2). Colors corresponding to class 0 and 1. Defaults to c("red", "forestgreen").
trim.names	Under the default (TRUE), this function extracts the most specific taxonomic rank of organism.
title	A character(1). The title of the plot.
label.font.size	A numeric(1). 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_group)
```

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relativeAb	<i>Utility function to calculate relative abundances</i>
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**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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zeller14	<i>Example dataset for lefser</i>
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**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/>

# Index

## \* datasets

zeller14, [5](#)

lefser, [2](#)

lefserPlot, [4](#)

relativeAb, [5](#)

SummarizedExperiment, [3](#)

zeller14, [5](#)