

Package ‘Maaslin2’

March 30, 2021

Title Maaslin2

Version 1.4.0

Depends R (>= 3.6)

Description MaAsLin2 is comprehensive R package for efficiently determining multivariable association between clinical metadata and microbial meta'omic features. MaAsLin2 relies on general linear models to accommodate most modern epidemiological study designs, including cross-sectional and longitudinal, and offers a variety of data exploration, normalization, and transformation methods. MaAsLin2 is the next generation of MaAsLin.

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LazyData false

Imports robustbase, biglm, pcaPP, edgeR, metagenomeSeq, lpsymphony, pbapply, car, dplyr, vegan, chemometrics, ggplot2, pheatmap, logging, data.table, lmerTest, hash, optparse, MuMIn, grDevices, stats, utils, glmmTMB, MASS, cplm, pscl

Suggests knitr, testthat (>= 2.1.0)

VignetteBuilder knitr

Collate fit.R utility_scripts.R viz.R Maaslin2.R

URL <http://huttenhower.sph.harvard.edu/maaslin2>

biocViews Metagenomics, Software, Microbiome, Normalization

BugReports <https://github.com/biobakery/maaslin2/issues>

git_url <https://git.bioconductor.org/packages/Maaslin2>

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Maaslin2

MaAsLin2 is the next generation of MaAsLin, a multivariable statistical framework for finding associations between clinical metadata and potentially high-dimensional microbial multi-omics data.

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

```
Maaslin2(
  input_data,
  input_metadata,
  output,
  min_abundance = 0.0,
  min_prevalence = 0.1,
  min_variance = 0.0,
  normalization = "TSS",
  transform = "LOG",
  analysis_method = "LM",
  max_significance = 0.25,
  random_effects = NULL,
  fixed_effects = NULL,
  correction = "BH",
  standardize = TRUE,
  cores = 1,
  plot_heatmap = TRUE,
  plot_scatter = TRUE,
  heatmap_first_n = 50,
  reference = NULL
)
```

Arguments

<code>input_data</code>	The tab-delimited input file of features.
<code>input_metadata</code>	The tab-delimited input file of metadata.
<code>output</code>	The output folder to write results.
<code>min_abundance</code>	The minimum abundance for each feature.
<code>min_prevalence</code>	The minimum percent of samples for which a feature is detected at minimum abundance.
<code>min_variance</code>	Keep features with variance greater than.
<code>max_significance</code>	The q-value threshold for significance.
<code>normalization</code>	The normalization method to apply.
<code>transform</code>	The transform to apply.

analysis_method	The analysis method to apply.
random_effects	The random effects for the model, comma-delimited for multiple effects.
fixed_effects	The fixed 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.
plot_heatmap	Generate a heatmap for the significant associations.
heatmap_first_n	In heatmap, plot top N features with significant associations.
plot_scatter	Generate scatter plots for the significant associations.
cores	The number of R processes to run in parallel.
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.

Value

Data.frame containing the results from applying the model.

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Examples

```
input_data <- system.file(
  'extdata', 'HMP2_taxonomy.tsv', package="Maaslin2")
input_metadata <- system.file(
  'extdata', 'HMP2_metadata.tsv', package="Maaslin2")
fit_data <- Maaslin2(
  input_data, input_metadata, 'demo_output', transform = "AST",
  fixed_effects = c('diagnosis', 'dysbiosisnonIBD', 'dysbiosisUC', 'dysbiosisCD', 'antibiotics', 'age'),
  random_effects = c('site', 'subject'),
  normalization = 'NONE',
  reference = 'diagnosis,nonIBD',
  standardize = FALSE)
```

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