Package 'Maaslin2'

November 13, 2026

Title ``Multivariable Association Discovery in Population-scale Meta-omics Studies"

Year 2021

Version 1.27.0

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, pbapply, car, dplyr, vegan, chemometrics, ggplot2, pheatmap, logging, data.table, lmerTest, hash, optparse, grDevices, stats, utils, glmmTMB, MASS, cplm, pscl, lme4, tibble

Suggests knitr, testthat (>= 2.1.0), rmarkdown, markdown

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

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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,
    heatmap_first_n = 50,
    plot_scatter = TRUE,
    max_pngs = 10,
    save_scatter = FALSE,
    save_models = FALSE,
    reference = NULL
)
```

Arguments

`input_data`	The tab-delimited input file of features.
`input_metadata`	The tab-delimited input file of metadata.
`output`	The output folder to write results.
`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.
max_significance	The q-value threshold for significance.
normalization	The normalization method to apply.
transform	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.
max_pngs	Set the maximum number of scatter plots for signficant associations to save as png files.
save_scatter	Save all scatter plot ggplot objects to an RData file.
cores	The number of R processes to run in parallel.
save_models	Return the full model outputs and save to an RData file.
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

List 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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