Package 'MMUPHin'

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Type Package

Title Meta-analysis Methods with Uniform Pipeline for Heterogeneity in Microbiome Studies

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Description MMUPHin is an R package for meta-analysis tasks of microbiome cohorts. It has function interfaces for:
a) covariate-controlled batch- and cohort effect adjustment,
b) meta-analysis differential abundance testing,
c) meta-analysis unsupervised discrete structure (clustering) discovery, and
d) meta-analysis unsupervised continuous structure discovery.

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`add_back_covariates` *Add back covariate effects to batch-corrected feature abundance data*

Description

Add back covariate effects to batch-corrected feature abundance data

Usage

```
add_back_covariates(adj_data, l_stand_feature, l_ind)
```

Arguments

`adj_data`	feature-by-sample matrix of batch-adjusted feature abundances (but without covariate effects), as returned by relocate_scale.
`l_stand_feature`	list of per-feature standardization fits, as returned by fit_stand_feature.
`l_ind`	list of indicator matrices, as returned by construct_ind.

Value

feature-by-sample matrix of batch-adjusted feature abundances with covariate effects retained.

`adjust_batch` *Zero-inflated empirical Bayes adjustment of batch effect in compositional feature abundance data*

Description

`adjust_batch` takes as input a feature-by-sample matrix of microbial abundances, and performs batch effect adjustment given provided batch and optional covariate variables. It returns the batch-adjusted abundance matrix. Additional options and parameters can be passed through the `control` parameter as a list (see details).

Usage

```
adjust_batch(feature_abd, batch, covariates = NULL, data, control)
```

Arguments

`feature_abd`	feature-by-sample matrix of abundances (proportions or counts).
`batch`	name of the batch variable. This variable in data should be a factor variable and will be converted to so with a warning if otherwise.
`covariates`	name(s) of covariates to adjust for in the batch correction model.
`data`	data frame of metadata, columns must include batch and covariates (if specified).
`control`	a named list of additional control parameters. See details.

Details

`control` should be provided as a named list of the following components (can be a subset).

zero_inflation logical. Indicates whether or not a zero-inflated model should be run. Default to TRUE (zero-inflated model). If set to FALSE then the correction will be similar to `ComBat` as provided in the `sva` package.

pseudo_count numeric. Pseudo count to add feature_abd before the methods' log transformation. Default to `NULL`, in which case `adjust_batch` will set the pseudo count automatically to half of minimal non-zero values in `feature_abd`.

diagnostic_plot character. Name for the generated diagnostic figure file. Default to `"adjust_batch_diagnostic.pdf"` Can be set to `NULL` in which case no output will be generated.

conv numeric. Convergence threshold for the method's iterative algorithm for shrinking batch effect parameters. Default to 1e-4.

maxit integer. Maximum number of iterations allowed for the method's iterative algorithm. Default to 1000.

verbose logical. Indicates whether or not verbose information will be printed.

Value

a list, with the following components:

feature_abd_adj feature-by-sample matrix of batch-adjusted abundances, normalized to the same per-sample total abundance as feature_abd.

control list of additional control parameters used in the function call.

Author(s)

Siyuan Ma, <siyuanma@g.harvard.edu>

Examples

```
data("CRC_abd", "CRC_meta")
CRC_abd_adj <- adjust_batch(feature_abd = CRC_abd,
                            batch = "studyID",
                            covariates = "study_condition",
                            data = CRC_meta)$feature_abd_adj
```

`adjust_EB` *Perform batch adjustment on standardized feature abundances, based on EB shrinked per-batch location and scale parameters*

Description

Perform batch adjustment on standardized feature abundances, based on EB shrinked per-batch location and scale parameters

Usage

```
adjust_EB(s_data, l_params_shrink, l_stand_feature, batchmod, n_batch,
  l_ind)
```

Arguments

s_data	feature-by-sample matrix of standardized abundances.
l_params_shrink	list of shrinked parameters, as returned by fit_shrink.
l_stand_feature	list of per-feature standardization fits, as returned by fit_stand_feature.
batchmod	design matrix for batch variables.
n_batch	number of batches in the data.
l_ind	list of indicator matrices, as returned by construct_ind.

Value

feature-by-sample matrix of batch-adjusted feature abundances.

---

aprior *EB prior estimation for scale parameters*

Description

EB prior estimation for scale parameters

Usage

```
aprior(delta_hat, na.rm = FALSE)
```

Arguments

delta_hat	frequentist per-batch scale estimations.
na.rm	whether or not missing values should be removed.

Value

shape hyper parameter

AST *AST transformation (modified from Maaslin2 and is different)*

Description

AST transformation (modified from Maaslin2 and is different)

Usage

```
AST(x)
```

Arguments

x	vector of abundance to be transformed.

Value

transformed vector of abundance.

back_transform_abd *Transform batch adjusted feature abundances back to the original scale in feature_abd*

Description

Transform batch adjusted feature abundances back to the original scale in feature_abd

Usage

```
back_transform_abd(adj_data, feature_abd, type_feature_abd)
```

Arguments

adj_data	feature-by-sample matrix of batch-adjusted feature abundances with covariate effects retained.
feature_abd	original feature-by-sample matrix of abundances (proportions or counts).
type_feature_abd	type of feature abundance table (counts or proportions). If counts, the final output will be rounded into counts as well.

Value

feature-by-sample matrix of batch-adjusted feature abundances, with covariate effects retained and scales consistent with original abundance matrix.

bprior *EB prior estimation for scale parameters*

Description

EB prior estimation for scale parameters

Usage

```
bprior(delta_hat, na.rm = FALSE)
```

Arguments

delta_hat	frequentist per-batch location estimations.
na.rm	whether or not missing values should be removed.

Value

scale hyper parameter

catchToList *Utility for catching warning/error messages*

Description

Utility for catching warning/error messages

Usage

```
catchToList(expr)
```

Arguments

expr	an expression to run that can generate potential errors/warnings

Value

a list, capturing both the return value of the expression, as well as generated erros/warnings (NULL if no errors/warnings)

check_batch *Check batch variable*

Description

Check batch variable

Usage

```
check_batch(x, min_n_batch = 2)
```

Arguments

x	batch variable.
min_n_batch	min. number of batches (for MMUPHin functions to run).

Value

if no errors then the batch variables (factorized if not already)

check_covariates *Check covariates*

Description

Check covariates

Usage

```
check_covariates(data_covariates, batch)
```

Arguments

data_covariates	data frame of covariates.
batch	batch variable.

Value

vector of indicators per batch for if/which covariates can be fitted within the batches

check_covariates_random *Check random covariates*

Description

Check random covariates

Usage

```
check_covariates_random(data_covariates, batch)
```

Arguments

data_covariates	data frame of random covariates.
batch	batch variable.

Value

vector of indicators per batch for if/which random covariates can be fitted within the batches

check_D *Check dissimilarity object*

Description

Make sure that the input is a dissimilarity object

Usage

```
check_D(D)
```

Arguments

D	dissimilarity object.

Value

returns an error if D is not a dissimilarity. Otherwise D as a matrix.

check_exposure *Check exposure variable*

Description

Check exposure variable

Usage

```
check_exposure(exposure, batch)
```

Arguments

exposure	exposure variable.
batch	batch variable.

Value

vector of indicators per batch for whether or not the exposure can be fitted within the batches

check_feature_abd *Check feature abundance table*

Description

Given a feature abundance table, make sure that a) it has no missing values, b) all values are non-negative, c) it is either proportions (all no greater than 1) or counts (all integers).

Usage

```
check_feature_abd(feature_abd)
```

Arguments

feature_abd	feature-by-sample matrix of abundances (proportions or counts).

Value

returns an error if any of the check fails. Otherwise either "counts" or "proportions"

check_metadata *Check that metadata data frame has all the variables and not missing*

Description

Check that metadata data frame has all the variables and not missing

Usage

```
check_metadata(data, variables, no_missing = TRUE)
```

Arguments

data	data frame of metadata.
variables	name of variables (batch, covariates, etc.) to check

Value

data reduced to include only those specified in variables

check_options *Utility for checking options*

Description

Utility for checking options

Usage

```
check_options(x, x_name, options)
```

Arguments

x	the specified value
x_name	name of the specified value
options	allowed options

Value

error if x is not in options. Otherwise returns x.

check_options_continuous *Utility for checking continuous options*

Description

Utility for checking continuous options

Usage

```
check_options_continuous(x, x_name, range)
```

Arguments

x	the specified numeric value
x_name	name of the specified value
range	allowed range

Value

error if x is not within range (boundaries excluded). Otherwise returns x.

check_pseudo_count *Utility for checking pseudo count*

Description

Utility for checking pseudo count

Usage

```
check_pseudo_count(x)
```

Arguments

x	the specified pseudo count

Value

error if pseudo count is smaller than zero. Otherwise returns x.

check_rank *Check if a design matrix is full rank*

Description

Check if a design matrix is full rank

Usage

```
check_rank(design)
```

Arguments

design	design matrix.

Value

TRUE/FALSE for whether or not the design matrix is full rank.

check_samples — *Check that sample numbers and names match between a feature table and a metadata data frame*

Description

Sample names (column names of the feature table, row names of the metadata data frame) must be matching exactly. Note that this dictates that they cannot be NULL because by design data (a data frame) should have non-empty row names.

Usage

```
check_samples(feature_abd, data)
```

Arguments

feature_abd	feature-by-sample matrix of abundances (proportions or counts).
data	data frame of metadata.

Value

matched sample names

check_samples_D — *Check that sample numbers and names match between a dissimilarity matrix and a metadata data frame*

Description

Sample names (row/column names of the D matrix, row names of the metadata data frame) must be matching exactly. Note that this dictates that they cannot be NULL because by design data (a data frame) should have non-empty row names.

Usage

```
check_samples_D(D, data)
```

Arguments

D	sample-by-sample matrix of dissimilarities (proportions or counts).
data	data frame of metadata.

Value

matched sample names

`construct_design` *Construct a design model matrix given a metadata data frame, with the option to exclude the intercept.*

Description

Construct a design model matrix given a metadata data frame, with the option to exclude the intercept.

Usage

```
construct_design(data, with_intercept = TRUE)
```

Arguments

`data`	metadata data frame.
`with_intercept`	should intercept terms be included in the model

Value

design matrix.

`construct_ind` *Create indicator matrices for which feature/batch/samples to adjust. This is relevant for zero_inflation is TRUE and only non-zero values are adjusted.*

Description

Create indicator matrices for which feature/batch/samples to adjust. This is relevant for zero_inflation is TRUE and only non-zero values are adjusted.

Usage

```
construct_ind(feature_abd, n_batch, design, zero_inflation)
```

Arguments

`feature_abd`	feature-by-sample matrix of abundances (proportions or counts).
`n_batch`	number of batches in the data.
`design`	design matrix.
`zero_inflation`	zero inflation flag.

Value

list of indicator matrices needed by fitting in adjust_batch.

`continuous_discover` *Unsupervised meta-analytical discovery and validation of continuous structures in microbial abundance data*

Description

`continuous_discover` takes as input a feature-by-sample matrix of microbial abundances. It first performs unsupervised continuous structure discovery (PCA) within each batch. Loadings of top PCs from each batch are then mapped against each other to identify "consensus" loadings that are reproducible across batches with a network community discovery approach with **igraph**. The identified consensus loadings/scores can be viewed as continuous structures in microbial profiles that are recurrent across batches and valid in a meta-analyitical sense. `continuous_discover` returns, among other output, the identified consensus scores for continuous structures in the provided microbial abundance profiles, as well as the consensus PC loadings which can be used to assign continuous scores to any sample with the same set of microbial features.

Usage

```
continuous_discover(feature_abd, batch, data, control)
```

Arguments

`feature_abd`	feature-by-sample matrix of abundances (proportions or counts).
`batch`	name of the batch variable. This variable in data should be a factor variable and will be converted to so with a warning if otherwise.
`data`	data frame of metadata, columns must include batch.
`control`	a named list of additional control parameters. See details.

Details

`control` should be provided as a named list of the following components (can be a subset).

normalization character. Similar to the `normalization` parameter in `Maaslin2` but only `"TSS"` and `"NONE"` are allowed. Default to `"TSS"` (total sum scaling).

transform character. Similar to the `transform` parameter in `Maaslin2` but only `"AST"` and `"LOG"` are allowed. Default to `"AST"` (arcsine square root transformation).

pseudo_count numeric. Pseudo count to add feature_abd before the transformation. Default to `NULL`, in which case pseudo count will be set automatically to 0 if `transform="AST"`, and half of minimal non-zero values in `feature_abd` if `transform="LOG"`.

var_perc_cutoff numeric. A value between 0 and 1 that indicates the percentage variability explained to cut off at for selecting top PCs in each batch. Across batches, the top PCs that in total explain more than var_perc_cutoff of the total variability will be selected for meta-analytical continuous structure discovery. Default to 0.8 (PCs included need to explain at least 80 total variability).

cos_cutoff numeric. A value between 0 and 1 that indicates cutoff for absolute cosine coefficients between PC loadings to construct the method's network with. Once the top PC loadings from each batch are selected, cosine coefficients between each loading pair are calculated which indicate their similarity. Loading pairs with absolute cosine coefficients surpassing cos_cutoff are then considered as associated with each other, and represented as an edge between the

pair in a PC loading network. Network community discovery can then be performed on this network to identified densely connected "clusters" of PC loadings, which represent meta-analytically recurrent continuous structures.

cluster_function function. `cluster_function` is used to perform community structure discovery in the constructed PC loading network. This can be any of the network cluster functions provided in **igraph**. Default to `cluster_optimal`. Note that this option can be slow for larger datasets, in which case `cluster_fast_greedy` is recommended.

network_plot character. Name for the generated network figure file. Default to `"clustered_network.pdf"`. Can be set to `NULL` in which case no output will be generated.

plot_size_cutoff integer. Clusters with sizes smaller than or equal to plot_size_cutoff will be excluded in the visualized network. Defaul to 2 - visualized clusters must have at least three nodes (PC loadings).

diagnostic_plot character. Name for the generated diagnostic figure file. Default to `"continuous_diagnostic.pdf"`. Can be set to `NULL` in which case no output will be generated.

verbose logical. Indicates whether or not verbose information will be printed.

Value

a list, with the following components:

consensus_scores matrix of identified consensus continuous scores. Columns are the identified consensus scores and rows correspond to samples in feature_abd.

consensus_loadings matrix of identified consensus loadings. Columns are the identified consensus scores and rows correspond to features in feature_abd.

mat_vali matrix of validation cosine coefficients of the identified consensus loadings. Columns correspond to the identified consensus scores and rows correspond to batches.

network, communities, mat_cos components for the constructed PC loading network and community discovery results. `network` is a **igraph** `graph` object for the constructed network of associated PC loadings. `communities` is a `communities` object for the identified consensus loading clusters in `network` (output from `control$cluster_function`). `mat_cos` is the matrix of cosine coefficients between all selected top PCs from all batches.

control list of additional control parameters used in the function call.

Author(s)

Siyuan Ma, <siyuanma@g.harvard.edu>

Examples

```
data("CRC_abd", "CRC_meta")
fit_continuous <- continuous_discover(feature_abd = CRC_abd,
                                      batch = "studyID",
                                      data = CRC_meta)
```

CRC_abd *Species level feature abundance data of five public CRC studies*

Description

Species level relative abundance profiles of CRC and control patients in the five public studies used in Thomas et al. (2019). These were accessed through curatedMetagenomicData.

Usage

```
data(CRC_abd)
```

Format

A feature-by-sample matrix of species-level profiles

Source

curatedMetagenomicData

References

Thomas, Andrew Maltez, Paolo Manghi, Francesco Asnicar, Edoardo Pasolli, Federica Armanini, Moreno Zolfo, Francesco Beghini et al. "Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation." Nature medicine 25, no. 4 (2019): 667.

Examples

```
data(CRC_abd)
# features included
rownames(CRC_abd)
# These are relative abundances
apply(CRC_abd, 2, sum)
# The following were used to generate the object
# library(curatedMetagenomicData)
# library(phyloseq)
# library(genefilter)
# datasets <- curatedMetagenomicData(
#   c("FengQ_2015.metaphlan_bugs_list.stool"  ,
#     "HanniganGD_2017.metaphlan_bugs_list.stool",
#     "VogtmannE_2016.metaphlan_bugs_list.stool",
#     "YuJ_2015.metaphlan_bugs_list.stool",
#     "ZellerG_2014.metaphlan_bugs_list.stool"),
#   dryrun = FALSE)
# Construct phyloseq object from the five datasets
# physeq <-
    # Aggregate the five studies into ExpressionSet
#   mergeData(datasets) %>%
    # Convert to phyloseq object
#   ExpressionSet2phyloseq() %>%
    # Subset samples to only CRC and controls
#   subset_samples(study_condition %in% c("CRC", "control")) %>%
    # Subset features to species
```

```
#   subset_taxa(!is.na(Species) & is.na(Strain)) %>%
    # Normalize abundances to relative abundance scale
#   transform_sample_counts(function(x) x / sum(x)) %>%
    # Filter features to be of at least 1e-5 relative abundance in five
    # samples
#   filter_taxa(kOverA(5, 1e-5), prune = TRUE)
# CRC_abd <- otu_table(physeq)@.Data
```

`CRC_meta` *Sample metadata of five public CRC studies*

Description

Metadata information of CRC and control patients in the five public studies used in Thomas et al. (2019). These were accessed through `curatedMetagenomicData`.

Usage

```
data(CRC_meta)
```

Format

A `data.frame` of per-sample metadata information

Source

`curatedMetagenomicData`

References

Thomas, Andrew Maltez, Paolo Manghi, Francesco Asnicar, Edoardo Pasolli, Federica Armanini, Moreno Zolfo, Francesco Beghini et al. "Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation." Nature medicine 25, no. 4 (2019): 667.

Examples

```
data(CRC_meta)
# has CRC and control samples across five studies
table(CRC_meta$studyID, CRC_meta$study_condition)
# The following were used to generate the object
# library(curatedMetagenomicData)
# library(phyloseq)
# library(genefilter)
# datasets <- curatedMetagenomicData(
#   c("FengQ_2015.metaphlan_bugs_list.stool"  ,
#     "HanniganGD_2017.metaphlan_bugs_list.stool",
#     "VogtmannE_2016.metaphlan_bugs_list.stool",
#     "YuJ_2015.metaphlan_bugs_list.stool",
#     "ZellerG_2014.metaphlan_bugs_list.stool"),
#   dryrun = FALSE)
# Construct phyloseq object from the five datasets
# physeq <-
    # Aggregate the five studies into ExpressionSet
```

```
#   mergeData(datasets) %>%
    # Convert to phyloseq object
#   ExpressionSet2phyloseq() %>%
    # Subset samples to only CRC and controls
#   subset_samples(study_condition %in% c("CRC", "control")) %>%
    # Subset features to species
#   subset_taxa(!is.na(Species) & is.na(Strain)) %>%
    # Normalize abundances to relative abundance scale
#   transform_sample_counts(function(x) x / sum(x)) %>%
    # Filter features to be of at least 1e-5 relative abundance in five
    # samples
#   filter_taxa(kOverA(5, 1e-5), prune = TRUE)
# CRC_meta <- data.frame(sample_data(physeq))
# CRC_meta$studyID <- factor(CRC_meta$studyID)
```

`create_table_maaslin` *Utility for generating empty Maaslin2 results table*

Description

Utility for generating empty Maaslin2 results table

Usage

```
create_table_maaslin(features, exposure, lvl_exposure)
```

Arguments

`features`	name of the features fitted to Maaslin2.
`exposure`	the exposure variable.
`lvl_exposure`	levels of the exposure variable, if a factor.

Value

a table for each feature-exposure value pai; reference level of exposure, if a factor, is taken out because is absorbed into the intercept term in Maaslin2 regression

---

`diagnostic_adjust_batch`
Diagnostic visualization for adj_batch function

Description

Diagnostic visualization for adj_batch function

Usage

```
diagnostic_adjust_batch(feature_abd, feature_abd_adj, var_batch, gamma_hat,
  gamma_star, output)
```

Arguments

feature_abd	original feature-by-sample matrix of abundances (proportions or counts).
feature_abd_adj	feature-by-sample matrix of batch-adjusted feature abundances, with covariate effects retained and scales consistent with original abundance matrix.
var_batch	the batch variable (should be a factor).
gamma_hat	estimated per feature-batch gamma parameters.
gamma_star	shrinked per feature-batch gamma parameters
output	output file name

Value

(invisbly) the ggplot2 plot object

---

diagnostic_continuous_discover

Diagnostic visualization for continuous.discover function

Description

Diagnostic visualization for continuous.discover function

Usage

```
diagnostic_continuous_discover(mat_vali, lvl_batch, cos_cutoff, output)
```

Arguments

mat_vali	matrix of maximum correlations between the cluster-specific consensus loadings and top PC loadings from each batch
lvl_batch	unique batches in the data
cos_cutoff	the specified consine coefficient cutoff
output	output file name

Value

the invisble ggplot2 plot object

`diagnostic_discrete_discover` *Diagnostic visualization for discrete.discover function*

Description

Diagnostic visualization for discrete.discover function

Usage

```
diagnostic_discrete_discover(stats_internal, stats_external, lvl_batch,
  output)
```

Arguments

`stats_internal`	list of internal evaluation summary statistics
`stats_external`	list of external validation summary statistics
`lvl_batch`	unique batches in the data
`output`	

Value

the invisble ggplot2 plot object

`discrete_discover` *Unsupervised meta-analytical discovery and validation of discrete clustering structures in microbial abundance data*

Description

`discrete_discover` takes as input sample-by-sample dissimilarity measurements (generated from microbial abundance profiles), and performs unsupervised clustering within each batch across a range of cluster numbers. It then evaluates the support for each cluster number with both internal (i.e., samples within the batch) and external (i.e., samples in other batches) data. Internal evaluation is realized with `prediction.strength` and external evaluation is based on a generalized version of the same method. `discrete_discover` generates as output the evaluation statistics for each cluster number. A cluster number with good support from both internal and external evaluations provides meta-analytical evidence for discrete structures in the microbial abundance profiles.

Usage

```
discrete_discover(D, batch, data, control)
```

Arguments

`D`	sample-by-sample dissimilarity measurements. Should be provided as a `dist` object.
`batch`	name of the batch variable. This variable in data should be a factor variable and will be converted to so with a warning if otherwise.
`data`	data frame of metadata, columns must include batch.
`control`	a named list of additional control parameters. See details.

Details

`control` should be provided as a named list of the following components (can be a subset).

k_max integer. Maximum number of clusters to evaluate. `discrete_discover` will evaluate clustering structures corresponding to cluster numbers ranging from 2 to `k_max`. Default to 10.

cluster_function an interface function. This function will be used for unsupervised clustering for discrete structure evaluation. This corresponds to the `clustermethod` parameter in `prediction.strength`, and similarly, should also follow the specifications as detailed in `clusterboot`. Default to `claraCBI`

classify_method character. Classification method used to assign observations in the method's internal and external evaluation stage. Corresponds to the `classification` parameter in `prediction.strength`, and can only be either `"centroid"` or `"knn"`. Default to "centroid".

M integer. Number of random iterations to partition the batch during method's internal evaluation. Corresponds to the `M` parameter in `prediction.strength`. Default to 30.

nnk integer. Numbber of nearest neighbors if `classify_method="knn"`. Corresponds to the `nnk` parameter in `prediction.strength`. Default to 1.

diagnostic_plot character. Name for the generated diagnostic figure file. Default to `"discrete_diagnostic.pdf"`. Can be set to `NULL` in which case no output will be generated.

verbose logical. Indicates whether or not verbose information will be printed.

Value

a list, with the following components:

internal_mean, internal_se matrices of internal clustering structure evaluation measurements (prediction strengths). Columns and rows corresponds to different batches and different numbers of clusters, respectively. `internal_mean` and `internal_se`, as the names suggest, are the mean and standard error of prediction strengths for each batch/cluster number.

external_mean, external_se same structure as `internal_mean` and `internal_se`, but records external clustering structure evaluation measurements (generalized prediction strength).

control list of additional control parameters used in the function call.

Author(s)

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Examples

```
data("CRC_abd", "CRC_meta")
# Calculate Bray-Curtis dissimilarity between the samples
library(vegan)
D <- vegdist(t(CRC_abd))
fit_discrete <- discrete_discover(D = D,
                                  batch = "studyID",
                                  data = CRC_meta)
```

`fill_dimnames` *Fill in artificial row/column names to a matrix or data frame, if they are missing*

Description

Fill in artificial row/column names to a matrix or data frame, if they are missing

Usage

```
fill_dimnames(x, row_prefix, col_prefix)
```

Arguments

`x`	matrix or data frame
`row_prefix`	prefix for the artificial row names
`col_prefix`	prefix for the artificial column names

Value

x but with the missing dimension names filled in

`fit_EB` *Parametric estimation of per-batch location and scale parameters, and Empirical Bayes estimation of their priors*

Description

Parametric estimation of per-batch location and scale parameters, and Empirical Bayes estimation of their priors

Usage

```
fit_EB(s_data, l_stand_feature, batchmod, n_batch, l_ind)
```

Arguments

`s_data`	feature-by-sample matrix of standardized abundances.
`l_stand_feature`	list of per-feature standardization fits, as returned by fit_stand_feature.
`batchmod`	design matrix for batch variables.
`n_batch`	number of batches in the data.
`l_ind`	list of indicator matrices, as returned by construct_ind.

Value

list of parameter estimations.

fit_shrink — *A posteriori shrink per-batch location and scale parameters towards their EB priors*

Description

A posteriori shrink per-batch location and scale parameters towards their EB priors

Usage

```
fit_shrink(s_data, l_params, batchmod, n_batch, l_ind, control)
```

Arguments

s_data	feature-by-sample matrix of standardized abundances.
l_params	list of parameter fits, as returned by fit_EB.
batchmod	design matrix for batch variables.
n_batch	number of batches in the data.
l_ind	list of indicator matrices, as returned by construct_ind.
control	list of control parameters (passed on to it_sol)

Value

list of shrinked per-batch location and scale parameters.

fit_stand_feature — *Fit lm and standardize all features*

Description

Fit lm and standardize all features

Usage

```
fit_stand_feature(s_data, design, l_ind)
```

Arguments

s_data	feature-by-sample matrix of abundances (proportions or counts).
design	design matrix.
l_ind	list of indicator matrices, as returned by construct_ind.

Value

list of two componet: the standardized feature abundance matrix, and a list of per-feature standardization fits.

it_sol — *Iteratively solve for one feature's shrinked location and scale parameters*

Description

Iteratively solve for one feature's shrinked location and scale parameters

Usage

```
it_sol(s_data, g_hat, d_hat, g_bar, t2, a, b, control)
```

Arguments

s_data	the feature's standardized abundances.
g_hat	the feature's location parameter frequentist estimations.
d_hat	the feature's scale parameter frequentist estimations.
g_bar	EB estimation of location hyper parameters.
t2	EB estimation of location hyper parameters.
a	EB estimation of scale hyper parameters.
b	EB estimation of scale hyper parameters.
control	list of control parameters

Value

matrix of shrinked location and scale parameters.

lm_meta — *Covariate adjusted meta-analytical differential abundance testing*

Description

`lm_meta` runs differential abundance models on microbial profiles within individual studies/batches, and aggregates per-batch effect sizes with a meta-analysis fixed/random effects model. It takes as input a feature-by-sample microbial abundance table and the accompanying meta data data frame which should includes the batch indicator variable, the main exposure variable for differential abundance testing, and optional covariates and random covariates. The function first runs `Maaslin2` models on the exposure with optional covariates/random covariates in each batch. The per-batch effect sizes are then aggregated with `rma.uni` and reported as output. Additional parameters, including those for both `Maaslin2` and `rma.uni` can be provided through `control` (see details).

Usage

```
lm_meta(
  feature_abd,
  batch,
  exposure,
  covariates = NULL,
  covariates_random = NULL,
  data,
  control
)
```

Arguments

feature_abd	feature-by-sample matrix of abundances (proportions or counts).
batch	name of the batch variable. This variable in data should be a factor variable and will be converted to so with a warning if otherwise.
exposure	name of the exposure variable for differential abundance testing.
covariates	names of covariates to adjust for in Maaslin2 differential abundance testing models.
covariates_random	names of random effects grouping covariates to adjust for in Maaslin2 differential abundance testing models.
data	data frame of metadata, columns must include exposure, batch, and covariates and covariates_random (if specified).
control	a named list of additional control parameters. See details.

Details

control should be provided as a named list of the following components (can be a subset).

normalization character. normalization parameter for Maaslin2. See Maaslin2 for details and allowed values. Default to "TSS" (total sum scaling).

transform character. transform parameter for Maaslin2. See Maaslin2 for details and allowed values. Default to "AST" (arcsine square root transformation).

analysis_method character. analysis_method parameter for Maaslin2. See Maaslin2 for details and allowed values. Default to "LM" (linear modeling).

rma_method character. method parameter for rma.uni. See rma.uni for details and allowed values. Default to "REML" (estricted maximum-likelihood estimator).

output character. Output directory for intermediate Maaslin2 output and the optional forest plots. Default to "MMUPHin_lm_meta".

forest_plot character. Suffix in the name for the generated forest plots visualizing significant meta-analyitical differential abundance effects. Default to "forest.pdf". Can be set to NULL in which case no output will be generated.

rma_conv numeric. Convergence threshold for rma.uni (corresponds to control$threshold. See rma.uni for details. Default to 1e-4.

rma_maxit integer. Maximum number of iterations allowed for rma.uni (corresponds to control$maxiter. See rma.uni for details. Default to 1000.

verbose logical. Indicates whether or not verbose information will be printed.

Value

a list, with the following components:

meta_fits data frame of per-feature meta-analyitical differential abundance results, including columns for effect sizes, p-values and q-values, heterogeneity statistics such as τ^2 and I^2, as well as weights for individual batches. Many of these statistics are explained in detail in `rma.uni`.

maaslin_fits list of data frames, each one corresponding to the fitted results of Maaslin2 in a individual batch. See `Maaslin2` on details of these output.

control list of additional control parameters used in the function call.

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Examples

```
data("CRC_abd", "CRC_meta")
fit_meta <- lm_meta(feature_abd = CRC_abd,
                    exposure = "study_condition",
                    batch = "studyID",
                    covariates = c("gender", "age"),
                    data = CRC_meta)$meta_fits
```

LOG *LOG transformation (modified from Maaslin2 and is different)*

Description

LOG transformation (modified from Maaslin2 and is different)

Usage

```
LOG(x)
```

Arguments

x	vector of abundance to be transformed.

Value

transformed vector of abundance.

Maaslin2_wrapper *Wrapper function for Maaslin2*

Description

Wrapper function for Maaslin2

Usage

```
Maaslin2_wrapper(feature_abd, data, exposure, covariates = NULL,
  covariates_random = NULL, output = tempdir(),
  normalization = "TSS", transform = "AST", analysis_method = "LM")
```

Arguments

feature_abd	feature*sample matrix of feature abundance.
data	data frame of metadata.
exposure	name of exposure variable.
covariates	name of covariates.
covariates_random	name of random covariates.
output	directory for Maaslin2.
normalization	normalization parameter for Maaslin2.
transform	transformation parameter for Maaslin2.
analysis_method	analysis method parameter for Maaslin2.

Value

a data frame recording per-feature coefficients, p-values, etc. from running Maaslin2.

match_control *Match user-specified control parameters with default, and modify if needed*

Description

Match user-specified control parameters with default, and modify if needed

Usage

```
match_control(default, control)
```

Arguments

default	list of default control parameters
control	list of user-provided control parameters

Value

list of control parameters, set to user provided values if specified and default other wise

normalize_features *Normalize feature abundance table (modified from Maaslin2)*

Description

Normalize feature abundance table (modified from Maaslin2)

Usage

```
normalize_features(features, normalization = "NONE", pseudo_count = 0)
```

Arguments

features	feature-by-sample matrix of abundances (proportions or counts).
normalization	normalization method.
pseudo_count	pseudo count to be added to feature_abd.

Value

normalized abundance table.

relocate_scale *Relocate and scale feature abundances to correct for batch effects, given shrinked per-batch location and scale parameters*

Description

Relocate and scale feature abundances to correct for batch effects, given shrinked per-batch location and scale parameters

Usage

```
relocate_scale(s_data, l_params_shrink, batchmod, n_batch, l_ind)
```

Arguments

s_data	feature-by-sample matrix of standardized abundances.
l_params_shrink	list of shrinked parameters, as returned by fit_shrink.
batchmod	design matrix for batch variables.
n_batch	number of batches in the data.
l_ind	list of indicator matrices, as returned by construct_ind.

Value

feature-by-sample matrix of batch-adjusted feature abundances (but without covariate effects).

rename_maaslin — *Utility for temporarily renaming samples/features for Maaslin2 run to bypass the rare cases where unconventional names can cause exceptions*

Description

Utility for temporarily renaming samples/features for Maaslin2 run to bypass the rare cases where unconventional names can cause exceptions

Usage

```
rename_maaslin(old_names, prefix)
```

Arguments

old_names	vector of names.
prefix	prefix for the replacement (new numbered names).

Value

vector of new names - numbered vector with same length as old names and with the specified prefix

rma_wrapper — *Wrapper for fitting fixed/random effects meta-analysis model using metafor*

Description

Wrapper for fitting fixed/random effects meta-analysis model using metafor

Usage

```
rma_wrapper(maaslin_fits, method = "REML", output = tempdir(),
  forest_plot = NULL, rma_conv = 1e-06, rma_maxit = 1000,
  verbose = TRUE)
```

Arguments

maaslin_fits	list of Maaslin2 result data frames, outputted from Maaslin2_wrapper.
method	meta-analysis model to run, options provided in metafor::rma.
output	directory for the output forest plots.
forest_plot	logical. should forest plots be generated for the significant associations.
rma_conv	rma threshold control.
rma_maxit	rma maximum iteration control.
verbose	should verbose information be printed.

Value

a data frame recording per-feature meta-analysis association results. (coefficients, p-values, etc.)

`set_pseudo` *Set pseudo count for an abundance matrix. Pseudo count is currently set to half of minimum non-zero values*

Description

Set pseudo count for an abundance matrix. Pseudo count is currently set to half of minimum non-zero values

Usage

```
set_pseudo(features)
```

Arguments

`features`	feature-by-sample matrix of abundances (proportions or counts).

Value

the pseudo count

`shorten_name` *Utility for shorter names Useful when plotting per-feature figures where feature names could be cutoff*

Description

Utility for shorter names Useful when plotting per-feature figures where feature names could be cutoff

Usage

```
shorten_name(x, cutoff = 3, replacement = "..")
```

Arguments

`x`	vector of names
`cutoff`	number of maximum string length before start cutting off the middle

Value

vector of new names with .. replacing the middle part if name is longer than cutoff

standardize_feature *Centralize (by design matrix) and standardize (by pooled variance across all batches) feature abundances for empirical Bayes fit*

Description

Centralize (by design matrix) and standardize (by pooled variance across all batches) feature abundances for empirical Bayes fit

Usage

```
standardize_feature(y, i_design, n_batch)
```

Arguments

y	vector of non-zero abundance of a single feature (if zero-inflated is true).
i_design	design matrix for the feature; samples with zeros are taken out (if zero-inflated is true).
n_batch	number of batches in the data.

Value

a list with component: y_stand for vector of centralized and standardized feature abundance, and stand_mean/varpooled for the location and scale factor (these are used later to back transform the batch-shrinked feature abundance).

transform_features *Transform feature abunadnce table (modified from Maaslin2)*

Description

Transform feature abunadnce table (modified from Maaslin2)

Usage

```
transform_features(features, transform = "NONE", pseudo_count = 0)
```

Arguments

features	feature-by-sample matrix of abundances (proportions or counts).
transform	transformation method.
pseudo_count	pseudo count to be added to feature_abd..

Value

transformed abundance table.

TSS *TSS normalization (modified from Maaslin2)*

Description

TSS normalization (modified from Maaslin2)

Usage

```
TSS(x)
```

Arguments

x	vector of abundance to be normalized.

Value

normalized vector of abundance.

vaginal_abd *Species level feature abundance data of two public vaginal studies*

Description

Species level relative abundance profiles of vaginal samples in the two public studies provided in curatedMetagenomicData.

Usage

```
data(vaginal_abd)
```

Format

A feature-by-sample matrix of species-level profiles

Source

curatedMetagenomicData

References

Pasolli, Edoardo, Lucas Schiffer, Paolo Manghi, Audrey Renson, Valerie Obenchain, Duy Tin Truong, Francesco Beghini et al. "Accessible, curated metagenomic data through ExperimentHub." Nature methods 14, no. 11 (2017): 1023.

Examples

```
data(vaginal_abd)
# features included
rownames(vaginal_abd)
# These are relative abundances
apply(vaginal_abd, 2, sum)
# The following were used to generate the object
# library(curatedMetagenomicData)
# library(phyloseq)
# datasets <- curatedMetagenomicData(
#   "*metaphlan_bugs_list.vagina*",
#   dryrun = FALSE)
# Construct phyloseq object from the five datasets
# physeq <-
  # Aggregate the five studies into ExpressionSet
#   mergeData(datasets) %>%
  # Convert to phyloseq object
#   ExpressionSet2phyloseq() %>%
  # Subset features to species
#   subset_taxa(!is.na(Species) & is.na(Strain)) %>%
  # Normalize abundances to relative abundance scale
#   transform_sample_counts(function(x) x / sum(x)) %>%
  # Filter features to be of at least 1e-5 relative abundance in two samples
#   filter_taxa(kOverA(2, 1e-5), prune = TRUE)
# vaginal_abd <- otu_table(physeq)@.Data
```

---

vaginal_meta *Sample metadata of two public vaginal studies*

Description

Metadata information of vaginal samples in the two public studies provided in curatedMetagenomicData.

Usage

```
data(vaginal_meta)
```

Format

A data.frame of per-sample metadata information

Source

curatedMetagenomicData

References

Pasolli, Edoardo, Lucas Schiffer, Paolo Manghi, Audrey Renson, Valerie Obenchain, Duy Tin Truong, Francesco Beghini et al. "Accessible, curated metagenomic data through ExperimentHub." Nature methods 14, no. 11 (2017): 1023.

Examples

```
data(vaginal_meta)
# has vaginal samples across two studies
table(vaginal_meta$studyID, vaginal_meta$body_site)
# The following were used to generate the object
# library(curatedMetagenomicData)
# library(phyloseq)
# datasets <- curatedMetagenomicData(
#   "*metaphlan_bugs_list.vagina*",
#   dryrun = FALSE)
# Construct phyloseq object from the five datasets
# physeq <-
  # Aggregate the five studies into ExpressionSet
#   mergeData(datasets) %>%
  # Convert to phyloseq object
#   ExpressionSet2phyloseq() %>%
  # Subset features to species
#   subset_taxa(!is.na(Species) & is.na(Strain)) %>%
  # Normalize abundances to relative abundance scale
#   transform_sample_counts(function(x) x / sum(x)) %>%
  # Filter features to be of at least 1e-5 relative abundance in two samples
#   filter_taxa(kOverA(2, 1e-5), prune = TRUE)
# vaginal_meta <- data.frame(sample_data(physeq))
# vaginal_meta$studyID <- factor(vaginal_meta$studyID)
```

---

visualize_continuous_discover

Visualization of the clustered network for the continuous.discover function

---

Description

Visualization of the clustered network for the continuous.discover function

Usage

```
visualize_continuous_discover(graph_pc, membership_loading,
  size_communities, plot_size_cutoff, short_names, output)
```

Arguments

graph_pc	the full pc network constructed from correlated PCs
membership_loading	membership of PC loadings from community discovery
size_communities	ordered (largest to smallest) size of the identified communities
plot_size_cutoff	cluster size cutoff (for cluster to be included in the visualized PC network)
short_names	shorter names of the loadings
output	output file name

Value

an invisible list of the subsetted network and memberships (to reproduce the plot)

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