

Package: MetaHD (via r-universe)

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Type Package

Title A Multivariate Meta-Analysis Model for Metabolomics Data

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Description Performs multivariate meta-analysis for high-dimensional metabolomics data for integrating and collectively analysing individual-level metabolomics data generated from multiple studies as well as for combining summary estimates. This approach accounts for correlation between metabolites, considers variability within and between studies, handles missing values and uses shrinkage estimation to allow for high dimensionality. A detailed vignette with example datasets and code to prepare data and analyses are available on <<https://bookdown.org/a2delivera/MetaHD/>>.

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Depends R (>= 3.5.0)

LazyData true

RoxygenNote 7.3.2

Imports dplyr, tidyr, metafor, corpcor, Matrix, matrixcalc, Rcpp (>= 1.0.0)

LinkingTo Rcpp, RcppArmadillo

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MetaHD	<i>A Multivariate Meta-Analysis Model for Metabolomics Data</i>
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Description

The MetaHD function performs a multivariate meta-analysis for combining summary estimates obtained from multiple metabolomic studies by using restricted maximum likelihood estimation. Assuming a meta-analysis is based on N outcomes/metabolites and K studies:

Usage

```
MetaHD(
  Y, Slist,
  Psi = NULL,
  method = c("reml", "fixed"),
  bscov = c("unstructured", "diag"),
  rigls.maxiter = 1,
  est.wscor = FALSE,
  shrinkCor = TRUE,
  impute.na = FALSE,
  impute.var = 10^4
)
```

Arguments

<code>Y</code>	: treatment effect sizes of the outcomes. This should be in the form of a $K \times N$ matrix
<code>Slist</code>	: K -dimensional list of $N \times N$ matrices representing within-study variances and covariances of the treatment effects. If within-study correlations are not available, input associated variances of treatment effects in the form of a $K \times N$ matrix and set <code>est.wscor = TRUE</code> .
<code>Psi</code>	: $N \times N$ matrix representing between-study variances and covariances of the treatment effects. (optional, if not specified this will be estimated internally by "MetaHD" using "estimateBSvar" and "estimateCorMat" functions in "MetaHD" package)
<code>method</code>	: estimation method: "fixed" for fixed-effects models, "reml" for random-effects models fitted through restricted maximum likelihood
<code>bscov</code>	: a character vector defining the structure of the random-effects covariance matrix. Among available covariance structures, the user can select "unstructured" to obtain between-study covariance matrix with diagonal elements (variances)

estimated using restricted maximum likelihood and off-diagonal elements (covariances) reflecting the correlations estimated via shrinkage and "diag" (diagonal) for between-study variances as diagonal elements and zero covariances

`rigls.maxiter` : maximum number of iterations of the restricted iterative generalized least square algorithm. Default is set to 1

`est.wscor` : a logical value indicating whether the within-study correlation matrix needs to be estimated or not. Default is FALSE

`shrinkCor` : a logical value indicating whether a shrinkage estimator should be used to estimate within- or between-study correlation matrix. Default is TRUE

`impute.na` : a logical value indicating whether missing values need to be imputed or not. Default is FALSE

`impute.var` : multiplier for replacing the missing variances in `Slist`. (a large value, default is 10^4)

Value

A list of objects containing `estimate` : a N-dimensional vector of the combined estimates, `std.err` : a N-dimensional vector of the associated standard errors, `pVal` : a N-dimensional vector of the p-values, `I2.stat` : I2 statistic

MetaHDInput	<i>Creating Input Data for MetaHD When Individual-Level Data are Available</i>
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Description

The `MetaHDInput` function creates input data `Y` (treatment effects) and `Slist` (within-study covariance matrices) for MetaHD when individual-level data are available. Assuming that the individual-level data are in the following format, with 'study' in column 1, 'group' in column 2 and outcomes in rest of the columns, with samples in rows.

Usage

```
MetaHDInput(data)
```

Arguments

`data` a dataframe consisting of individual-level data in the format, where 'study' in column 1, 'group' in column 2 and outcomes in rest of the columns and samples in rows.

Value

A list of objects containing :

`Y` treatment effect sizes of the outcomes in the form of a $K \times N$ matrix, where K is the number of studies and N is the number of outcomes.

`Slist` K -dimensional list of $N \times N$ matrices representing within-study variances and covariances of the treatment effects

Examples

```
input_data <- MetaHDInput(realdata)

Y <- input_data$Y
Slist <- input_data$Slist

## MULTIVARIATE RANDOM-EFFECTS META-ANALYSIS, ESTIMATED WITH REML
model <- MetaHD(Y, Slist, method = "reml", bscov = "unstructured")
model$estimate
model$pVal
```

realdata	<i>An Individual-Level Metabolomics Dataset</i>
----------	---

Description

This is a subset of data, publicly available on MetaboAnalyst example datasets.

Usage

```
realdata
```

Format

A data frame with 172 observations on 14 metabolites.

Examples

```
head(realdata)
```

simdata.1	<i>Simulated Dataset 1 : With Complete Data</i>
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Description

This dataset consists of a list of two data frames containing treatment effect-sizes and within-study covariance matrices

Usage

```
simdata.1
```

Format

A list of data frames as follows:

Y treatment effect sizes of the metabolites in the form of a 12 x 30 matrix, where 12 is the number of studies and 30 is the number of metabolites.

Slist 12-dimensional list of 30 x 30 matrices representing within-study variances and covariances of the treatment effects

Examples

```
Y <- simdata.1$Y
Slist <- simdata.1$Slist

head(Y)
head(Slist[[1]])
head(Slist[[12]])
```

simdata.2

Simulated Dataset 2 : With Data Missing-At-Random

Description

This dataset consists of a list of two data frames containing treatment effect-sizes and within-study covariance matrices with missing values

Usage

```
simdata.2
```

Format

A list of data frames as follows:

Y treatment effect sizes of the metabolites in the form of a 12 x 30 matrix, where 12 is the number of studies and 30 is the number of metabolites.

Slist 12-dimensional list of 30 x 30 matrices representing within-study variances and covariances of the treatment effects

Examples

```
Y <- simdata.2$Y
Slist <- simdata.2$Slist

head(Y)
head(Slist[[1]])
head(Slist[[12]])
```

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