Package: jarbes (via r-universe)

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Title Just a Rather Bayesian Evidence Synthesis

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SystemRequirements JAGS (>= 4.3.0) (see http://mcmc-jags.sourceforge.net)

Description Provides a new class of Bayesian meta-analysis models that incorporates a model for internal and external validity bias. In this way, it is possible to combine studies of diverse quality and different types. For example, we can combine the results of randomized control trials (RCTs) with the results of observational studies (OS).

License GPL (>= 2)

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`acupuncture` *Meta-analysis: 29 randomized controlled studies (RCT) assessing the efficacy of acupuncture treatments as complementary treatment in depression patients*

Description

Meta-analysis of 29 studies on the effect of different methods of acupuncture Therapy for depression compared to usual care control groups by pooling data from RCTs.

Format

A dataframe with 29 rows and 11 columns. Each row represents study results, the columns are:

author_year Author and year.

hedges_g changes in severity between intervention and control groups calculated using Hedges´g statistic

std_err Standard Error of Hedges´g

intervention treatment administered

comparison control group treatment

country origin country of the study

sample_size total amount of patients per study

number_treatments number of treatments received per study

variation_acupuncture_points fixed: same acupuncture points used at each session; semi-fixed: some points pre-defined, some selected on the basis of the diagnosis/symptoms (location and amount); individualised: location and amount of points selected on basis of the diagnosis/symptoms

number_acupuncture_points amount of acupuncture points for fixed-points-studies

NICMAN NICMAN scale Points to evaluate the Quality of the administered acupuncture

random_sequence_generation Risk of selection bias (Random sequence generation) low risk of bias: high, high risk: low, unclear: unclear

allocation_concealment Risk of selection bias (allocation concealment) low risk of bias: high, high risk: low, unclear: unclear

blinding_participants_personnel Risk of performance bias (blinding of participants and personnel) low risk of bias: high, high risk: low, unclear: unclear

blinding_outcome_assessment Risk of detection bias (blinding oft outcome assessment) low risk of bias: high, high risk: low, unclear: unclear

incomplete_outcome_data Risk of attrition bias (incomplete outcome data) low risk of bias: high, high risk: low, unclear: unclear

selective_reporting Risk of reporting bias (selective reporting) low risk of bias: high, high risk: low, unclear: unclear

other_bias Risk of other biases; low risk of bias: high, high risk: low, unclear: unclear

Source

Armour M, Smith CA, Wang LQ, Naidoo D, Yang GY, MacPherson H, Lee MS, Hay P. Acupuncture for Depression: A Systematic Review and Meta-Analysis. J Clin Med. 2019 Jul 31;8(8):1140. doi: 10.3390/jcm8081140. PMID: 31370200; PMCID: PMC6722678.

ai_distress — *Meta-analysis of RCTs evaluating the effect of AI agents to reduce psychological distress effects*

Description

Meta-analysis of RCTs evaluating the effect of AI agents to reduce psychological distress effects

Format

A data frame with 21 RCT studies #'

study_id Study identifier.

TE Treatment effect reported; standardized mean difference with Hedges small-sample correction (Hedges' g).

seTE Standard error of `TE`, derived from the plotted 95% confidence interval using `seTE = (upper - lower) / (2 * 1.96)`. Confidence intervals are not stored.

risk_of_bias Overall Risk of Bias assessment reported in the plot (`"Low risk of bias"`, `"Some concerns"`, `"High risk of bias"`).

Source

Bleidorn, W., Schwaba, T., Zheng, A., Hopwood, C. J., Sosa, S. S., Roberts, B. W., & Briley, D. A. (2022). Personality stability and change: A meta-analysis of longitudinal studies. Psychological Bulletin, 148(7-8), 588–619. https://doi.org/10.3037/bul0000365

b3lmeta — *Bayesian Meta-Analysis for Combining Studies*

Description

This function performers a Bayesian meta-analysis

Usage

```
b3lmeta(
  data,
  mean.mu.0 = 0,
  sd.mu.0 = 10,
  scale.sigma.between = 0.5,
  df.scale.between = 1,
  scale.sigma.within = 0.5,
  df.scale.within = 1,
  nr.chains = 2,
  nr.iterations = 10000,
```

```
  nr.adapt = 1000,
  nr.burnin = 1000,
  nr.thin = 1,
  parallel = NULL
)
```

Arguments

data	A data frame with at least three columns with the following names: 1) TE = treatment effect, 2) seTE = the standard error of the treatment effect. 3) design = indicates study type or clustering subgroup.
mean.mu.0	Prior mean of the overall mean parameter mu.0 (mean across designs), default value is 0.
sd.mu.0	Prior standard deviation of mu.0 (mean across designs), the default value is 10.
scale.sigma.between	Prior scale parameter for scale gamma distribution for the precision between study types. The default value is 0.5.
df.scale.between	Degrees of freedom of the scale gamma distribution for the precision between study types. The default value is 1, which results in a Half Cauchy distribution for the standard deviation between studies. Larger values e.g. 30 corresponds to a Half Normal distribution.
scale.sigma.within	Prior scale parameter for scale gamma distribution for the precision within study types. The default value is 0.5.
df.scale.within	Degrees of freedom of the scale gamma distribution for the precision within study types. The default value is 1, which results in a Half Cauchy distribution for the standard deviation between studies. Larger values e.g. 30 corresponds to a Half Normal distribution.
nr.chains	Number of chains for the MCMC computations, default 2.
nr.iterations	Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.
nr.adapt	Number of iterations in the adaptation process, default is 1000. Some models may need more iterations during adptation.
nr.burnin	Number of iteration discard for burn-in period, default is 1000. Some models may need a longer burnin period.
nr.thin	Thinning rate, it must be a positive integer, the default value 1.
parallel	NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The results of the object of the class bcmeta can be extracted with R2jags or with rjags. In addition a summary, a print and a plot functions are implemented for this type of object.

Value

This function returns an object of the class "bmeta". This object contains the MCMC output of each parameter and hyper-parameter in the model and the data frame used for fitting the model.

References

Verde, P.E. (2021) A Bias-Corrected Meta-Analysis Model for Combining Studies of Different Types and Quality. Biometrical Journal; 1–17.

Examples

```
## Not run:
library(jarbes)



## End(Not run)
```

---

bcbnp *Bias Corrected Meta-Analysis and Meta-Regression with Dirichlet Process Mixture of normal distributions*

Description

This function performs a Bias Corrected Bayesian Nonparametric meta-analysis and meta-regression using a DPM of Normal distributions to the bias process

Usage

```
bcbnp(
  data,
  formula = ~1,
  mean.mu.theta = 0,
  sd.mu.theta = 10,
  scale.sigma.between = 0.5,
  df.scale.between = 1,
  mean.mu.k = 0,
  sd.mu.k = 10,
  g.0 = 0.5,
  g.1 = 0.5,
  a.0 = 0.5,
  a.1 = 1,
  alpha.0 = 0.5,
  alpha.1 = 2,
  K = 10,
  nr.chains = 2,
```

```
  nr.iterations = 10000,
  nr.adapt = 1000,
  nr.burnin = 1000,
  nr.thin = 1,
  parallel = NULL
)
```

Arguments

data	A data frame with at least two columns with the following names: 1) TE = treatment effect, 2) seTE = the standard error of the treatment effect.
formula	A formula for meta-regression (e.g., ~ x1 + x2). Use ~ 1 for no covariates.
mean.mu.theta	Prior mean of mu.theta, the default value is mean.mu.0 = 0.
sd.mu.theta	Prior standard deviation of mu.theta, the default value is 10^-6.
scale.sigma.between	Prior for tau.theta: Scale parameter for scale.gamma distribution for the precision 1/tau.theta^2 between studies. The default value is 0.5.
df.scale.between	Prior for tau.theta: Degrees of freedom of the scale.gamma distribution for the precision 1/tau.theta^2 between studies. The default value is 1, which results in a Half Cauchy distribution for the standard deviation between studies tau.theta. Larger values e.g. 30 corresponds to a Half Normal distribution.
mean.mu.k	Prior mean for the mean mu.k bias cluster components. The default value is 0.
sd.mu.k	Prior standard deviation for mu.k bias cluster component. The default is 10.
g.0	Shape parameter the prior of the precision tau.k. The default value is 0.5 (tau.k~ dgamma(shape, rate))
g.1	Rate parameter the prior of the precision tau.k. The default value is 0.5 (tau.k~ dgamma(shape, rate))
a.0	Parameter for the prior Beta distribution for the probability of bias. Default value is a0 = 0.5.
a.1	Parameter for the prior Beta distribution for the probability of bias. Default value is a1 = 1.
alpha.0	Lower bound of the uniform prior for the concentration parameter for the DP, the default value is 0.5.
alpha.1	Upper bound of the uniform prior for the concentration parameter for the DP, the default value depends on the sample size, see the example below. We give as working value alpha.1 = 2
K	Maximum number of clusters in the DPM, the default value depends on alpha.1, see the example below. We give as working value K = 10.
nr.chains	Number of chains for the MCMC computations, default 2.
nr.iterations	Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.
nr.adapt	Number of iterations in the adaptation process, default is 1000. Some models may need more iterations during adptation.

nr.burnin	Number of iteration discard for burn-in period, default is 1000. Some models may need a longer burnin period.
nr.thin	Thinning rate, it must be a positive integer, the default value 1.
parallel	NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The results of the object of the class bcbnp can be extracted with R2jags or with rjags. In addition a summary, a print and a plot functions are implemented for this type of object.

Value

This function returns an object of the class "bcbnp". This object contains the MCMC output of each parameter and hyper-parameter in the model and the data frame used for fitting the model.

References

Verde, P.E., and Rosner, G.L. (2025a), A Bias-Corrected Bayesian Nonparametric Model for Combining Studies With Varying Quality in Meta-Analysis. Biometrical Journal., 67: e70034. https://doi.org/10.1002/bimj.70034

Verde, P.E, and Rosner, G.L. (2025b), jarbes: an R package for bias corrected meta-analysis models

Examples

```
## Not run:
library(jarbes)


# Example: Stemcells

data("stemcells")
stemcells$TE = stemcells$effect.size
stemcells$seTE = stemcells$se.effect

# Beta(0.5, 1)
a.0 = 0.5
a.1 = 1

# alpha.max
N = dim(stemcells)[1]
alpha.max = 1/5 *((N-1)*a.0 - a.1)/(a.0 + a.1)

alpha.max

# K.max
K.max = 1 + 5*alpha.max
K.max = round(K.max)

K.max

set.seed(20233)
```

```
bcbnp.stemcell = bcbnp(stemcells
alpha.0 = 0.5,
alpha.1 = alpha.max,
a.0 = a.0,
a.1 = a.1,
K = K.max,
nr.chains = 4,
nr.iterations = 50000,
nr.adapt = 1000,
nr.burnin = 10000,
nr.thin = 4)



## End(Not run)
```

---

bcbnp_0 *Bias Corrected Meta-Analysis and Meta-Regression with Dirichlet Mixture Process of normal distributions*

Description

This function performers a Bias Corrected Bayesian Nonparametric meta-analysis and meta-regression using a DPM of Normal distributions to the bias process

Usage

```
bcbnp_0(
  data,
  mean.mu.theta = 0,
  sd.mu.theta = 10,
  scale.sigma.between = 0.5,
  df.scale.between = 1,
  mean.mu.k = 0,
  sd.mu.k = 10,
  g.0 = 0.5,
  g.1 = 0.5,
  a.0 = 0.5,
  a.1 = 1,
  alpha.0 = 0.5,
  alpha.1 = 2,
  K = 10,
  nr.chains = 2,
  nr.iterations = 10000,
  nr.adapt = 1000,
  nr.burnin = 1000,
  nr.thin = 1,
```

```
  parallel = NULL
)
```

Arguments

data	A data frame with at least two columns with the following names: 1) TE = treatment effect, 2) seTE = the standard error of the treatment effect.
mean.mu.theta	Prior mean of mu.theta, the default value is mean.mu.0 = 0.
sd.mu.theta	Prior standard deviation of mu.theta, the default value is 10^-6.
scale.sigma.between	Prior for tau.theta: Scale parameter for scale.gamma distribution for the precision 1/tau.theta^2 between studies. The default value is 0.5.
df.scale.between	Prior for tau.theta: Degrees of freedom of the scale.gamma distribution for the precision 1/tau.theta^2 between studies. The default value is 1, which results in a Half Cauchy distribution for the standard deviation between studies tau.theta. Larger values e.g. 30 corresponds to a Half Normal distribution.
mean.mu.k	Prior mean for the mean mu.k bias cluster components. The default value is 0.
sd.mu.k	Prior standard deviation for mu.k bias cluster component. The default is 10.
g.0	Shape parameter the prior of the precision tau.k. The default value is 0.5 (tau.k~ dgamma(shape, rate))
g.1	Rate parameter the prior of the precision tau.k. The default value is 0.5 (tau.k~ dgamma(shape, rate))
a.0	Parameter for the prior Beta distribution for the probability of bias. Default value is a0 = 0.5.
a.1	Parameter for the prior Beta distribution for the probability of bias. Default value is a1 = 1.
alpha.0	Lower bound of the uniform prior for the concentration parameter for the DP, the default value is 0.5.
alpha.1	Upper bound of the uniform prior for the concentration parameter for the DP, the default value depends on the sample size, see the example below. We give as working value alpha.1 = 2
K	Maximum number of clusters in the DPM, the default value depends on alpha.1, see the example below. We give as working value K = 10.
nr.chains	Number of chains for the MCMC computations, default 2.
nr.iterations	Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.
nr.adapt	Number of iterations in the adaptation process, default is 1000. Some models may need more iterations during adptation.
nr.burnin	Number of iteration discard for burn-in period, default is 1000. Some models may need a longer burnin period.
nr.thin	Thinning rate, it must be a positive integer, the default value 1.
parallel	NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The results of the object of the class bcbnp can be extracted with R2jags or with rjags. In addition a summary, a print and a plot functions are implemented for this type of object.

Value

This function returns an object of the class "bcbnp". This object contains the MCMC output of each parameter and hyper-parameter in the model and the data frame used for fitting the model.

References

Verde, P.E., and Rosner, G.L. (2025a), A Bias-Corrected Bayesian Nonparametric Model for Combining Studies With Varying Quality in Meta-Analysis. Biometrical Journal., 67: e70034. https://doi.org/10.1002/bimj.70034

Verde, P.E, and Rosner, G.L. (2025b), jarbes: an R package for bias corrected meta-analysis models

Examples

```
## Not run:
library(jarbes)


# Example: Stemcells

data("stemcells")
stemcells$TE = stemcells$effect.size
stemcells$seTE = stemcells$se.effect

# Beta(0.5, 1)
a.0 = 0.5
a.1 = 1

# alpha.max
 N = dim(stemcells)[1]
 alpha.max = 1/5 *((N-1)*a.0 - a.1)/(a.0 + a.1)

alpha.max

# K.max
K.max = 1 + 5*alpha.max
K.max = round(K.max)

K.max

set.seed(20233)

bcbnp.stemcell = bcbnp(stemcells
                           alpha.0 = 0.5,
                           alpha.1 = alpha.max,
                           a.0 = a.0,
                           a.1 = a.1,
                           K = K.max,
```

```
                              nr.chains = 4,
                              nr.iterations = 50000,
                              nr.adapt = 1000,
                              nr.burnin = 10000,
                              nr.thin = 4)


## End(Not run)
```

---

bcdpmeta *Bias Corrected Meta-Analysis with Dirichlet Process Priors*

Description

This function performers a Bayesian meta-analysis with DP as random effects

Usage

```
bcdpmeta(
  data,
  mean.mu.0 = 0,
  sd.mu.0 = 10,
  scale.sigma.between = 0.5,
  df.scale.between = 1,
  B.lower = 0,
  B.upper = 10,
  a.0 = 1,
  a.1 = 1,
  alpha.0 = 0.03,
  alpha.1 = 10,
  K = 30,
  nr.chains = 2,
  nr.iterations = 10000,
  nr.adapt = 1000,
  nr.burnin = 1000,
  nr.thin = 1,
  parallel = NULL
)
```

Arguments

data	A data frame with at least two columns with the following names: 1) TE = treatment effect, 2) seTE = the standard error of the treatment effect.
mean.mu.0	Prior mean of the mean of the base distribution default value is mean.mu.0 = 0.
sd.mu.0	Prior standard deviation of the base distribution, the default value is 10.

`scale.sigma.between`
: Prior scale parameter for scale gamma distribution for the precision between studies. The default value is 0.5.

`df.scale.between`
: Degrees of freedom of the scale gamma distribution for the precision between studies. The default value is 1, which results in a Half Cauchy distribution for the standard deviation between studies. Larger values e.g. 30 corresponds to a Half Normal distribution.

`B.lower`
: Lower bound of the bias parameter B, the default value is 0.

`B.upper`
: Upper bound of the bias parameter B, the default value is 10.

`a.0`
: Parameter for the prior Beta distribution for the probability of bias. Default value is a0 = 1.

`a.1`
: Parameter for the prior Beta distribution for the probability of bias. Default value is a1 = 1.

`alpha.0`
: Lower bound of the uniform prior for the concentration parameter for the DPM, default value is alpha.0 = 0.03.

`alpha.1`
: Upper bound of the uniform prior for the concentration parameter for the DPM, default value is alpha.1 = 10.

`K`
: Maximum number of clusters in the DPM, default value is K = 30.

`nr.chains`
: Number of chains for the MCMC computations, default 2.

`nr.iterations`
: Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.

`nr.adapt`
: Number of iterations in the adaptation process, default is 1000. Some models may need more iterations during adptation.

`nr.burnin`
: Number of iteration discard for burn-in period, default is 1000. Some models may need a longer burnin period.

`nr.thin`
: Thinning rate, it must be a positive integer, the default value 1.

`parallel`
: NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The results of the object of the class bcdpmeta can be extracted with R2jags or with rjags. In addition a summary, a print and a plot functions are implemented for this type of object.

Value

This function returns an object of the class "bcdpmeta". This object contains the MCMC output of each parameter and hyper-parameter in the model and the data frame used for fitting the model.

References

Verde, P.E. (2021) A Bias-Corrected Meta-Analysis Model for Combining Studies of Different Types and Quality. Biometrical Journal; 1–17.

Examples

```
## Not run:
library(jarbes)


# Example: Stemcells

data("stemcells")
stemcells$TE = stemcells$effect.size
stemcells$seTE = stemcells$se.effect

bm1 = bcdpmeta(stemcells)
summary(bm1)


## End(Not run)
```

---

bchmr *Bias-Corrected Bayesian Nonparametric Model to combine aggregated and individual participant data for cross design synthesis.*

Description

This function performers a Bayesian cross design synthesis. The function fits a hierarchical meta-regression model based on a BC-BNP model

Usage

```
bchmr(
  data,
  two.by.two = TRUE,
  dataIPD,
  re = "normal",
  mean.mu.1 = 0,
  mean.mu.2 = 0,
  mean.mu.phi = 0,
  sd.mu.1 = 1,
  sd.mu.2 = 1,
  sd.mu.phi = 1,
  sigma.1.upper = 5,
  sigma.2.upper = 5,
  sigma.beta.upper = 5,
  mean.Fisher.rho = 0,
  sd.Fisher.rho = 1/sqrt(2),
  nr.chains = 2,
  nr.iterations = 10000,
  nr.adapt = 1000,
```

```
  nr.burnin = 1000,
  nr.thin = 1,
  parallel = NULL
)
```

Arguments

data	Aggregated data results: a data frame where the first four columns containing the number of events in the control group (yc), the number of patients in the control group (nc), the number of events in the treatment group (yt) and the number of patients in the treatment group (nt). If two.by.two = TRUE a data frame where each line contains the trial results with column names: yc, nc, yt, nt.
two.by.two	If TRUE indicates that the trial results are with names: yc, nc, yt, nt.
dataIPD	Individual participant data: a data frame where the first column is the outcome variable and the other columns represent individual participant charachteristics.
re	Random effects distribution for the resulting model. Possible values are *normal* for bivariate random effects and *sm* for scale mixtures.
mean.mu.1	Prior mean of baseline risk, default value is 0.
mean.mu.2	Prior mean of treatment effect, default value is 0.
mean.mu.phi	Prior mean of the bias parameter which measures the difference between the baseline mean mu.1 and the intercept parameter of the logistic regression of the individual participant data. The defalut vaule is 0.
sd.mu.1	Prior standard deviation of mu.1, default value is 1. The default prior of mu.1 is a logistic distribution with mean 0 and dispersion 1. The implicit prior for mu.1 in the probability scale is a uniform between 0 and 1.
sd.mu.2	Prior standard deviation of mu.2, default value is 1. The default prior of mu.2 is a logistic distribution with mean 0 and dispersion 1. The implicit prior for mu.2 in the probability scale is a uniform between 0 and 1.
sd.mu.phi	Prior standard deviation of mu.phi, default value is 1.
sigma.1.upper	Upper bound of the uniform prior of sigma.1, default value is 5.
sigma.2.upper	Upper bound of the uniform prior of sigma.2, default value is 5.
sigma.beta.upper	Upper bound of the uniform prior of sigma.beta, default value is 5.
mean.Fisher.rho	Mean of rho in the Fisher scale, default value is 0.
sd.Fisher.rho	Standard deviation of rho in the Fisher scale, default value is 1/sqrt(2).
nr.chains	Number of chains for the MCMC computations, default 5.
nr.iterations	Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.
nr.adapt	Number of iterations in the adaptation process, default is 1000. Some models may need more iterations during adptation.
nr.burnin	Number of iteration discarded for burnin period, default is 1000. Some models may need a longer burnin period.
nr.thin	Thinning rate, it must be a positive integer, the default value 1.
parallel	NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The model is experimental and under construction for the version 2.2.5 (March 2025)

Value

This function returns an object of the class "bchmr". This object contains the MCMC output of each parameter and hyper-parameter in the model, the data frame used for fitting the model, and further model outputs.

The results of the object of the class hmr can be extracted with R2jags. In addition a summary, a print and a plot function are implemented for this type of object.

References

Verde, P. E. (2019) Learning from Clinical Evidence: The Hierarchical Meta-Regression Approach. Biometrical Journal. Biometrical Journal; 1-23.

Verde, P.E., and Rosner, G.L. (2025), A Bias-Corrected Bayesian Nonparametric Model for Combining Studies With Varying Quality in Meta-Analysis. Biometrical Journal., 67: e70034. https://doi.org/10.1002/bimj.70034

Examples

```
## Not run:
library(jarbes)

data("healing")
AD <- healing[, c("y_c", "n_c", "y_t", "n_t")]

data("healingipd")

IPD <- healingipd[, c("healing.without.amp", "PAD", "neuropathy",
"first.ever.lesion", "no.continuous.care", "male", "diab.typ2",
"insulin", "HOCHD", "HOS", "CRF", "dialysis", "DNOAP", "smoking.ever",
"diabdur", "wagner.class")]

mx1 <- bchmr(AD, two.by.two = FALSE,
           dataIPD = IPD,
           re = "normal",
           sd.mu.1 = 2,
           sd.mu.2 = 2,
           sd.mu.phi = 2,
           sigma.1.upper = 5,
           sigma.2.upper = 5,
           sigma.beta.upper = 5,
           sd.Fisher.rho = 1.25,
           df.estimate = FALSE,
           df.lower = 3,
           df.upper = 10,
           nr.chains = 1,
           nr.iterations = 1500,
           nr.adapt = 100,
           nr.thin = 1)
```

```
print(mx1)


# End of the examples.


## End(Not run)
```

---

bcmeta *Bias-Corrected Meta-Analysis for Combining Studies of Different Types and Quality*

Description

This function performs a Bayesian meta-analysis to jointly combine different types of studies. The random-effects follows a finite mixture of normal distributions.

Usage

```
bcmeta(
  data,
  mean.mu.theta = 0,
  sd.mu.theta = 10,
  scale.sigma.between = 0.5,
  df.scale.between = 1,
  B.lower = 0,
  B.upper = 10,
  a.0 = 1,
  a.1 = 1,
  nu = 0.5,
  nu.estimate = FALSE,
  b.0 = 1,
  b.1 = 2,
  preclassification = "right",
  inits = NULL,
  nr.chains = 2,
  nr.iterations = 10000,
  nr.adapt = 1000,
  nr.burnin = 1000,
  nr.thin = 1,
  parallel = NULL
)
```

Arguments

`data`	A data frame with at least two columns with the following names: 1) TE = treatment effect, 2) seTE = the standard error of the treatment effect.
`mean.mu.theta`	Prior mean of the overall mean parameter mu, default value is 0.
`sd.mu.theta`	Prior standard deviation of mu, the default value is 10.
`scale.sigma.between`	Prior scale parameter for scale gamma distribution for the precision between studies. The default value is 0.5.
`df.scale.between`	Degrees of freedom of the scale gamma distribution for the precision between studies. The default value is 1, which results in a Half Cauchy distribution for the standard deviation between studies. Larger values e.g. 30 corresponds to a Half Normal distribution.
`B.lower`	Lower bound of the bias parameter B, the default value is 0.
`B.upper`	Upper bound of the bias parameter B, the default value is 10.
`a.0`	Parameter for the prior Beta distribution for the probability of bias. Default value is a0 = 1.
`a.1`	Parameter for the prior Beta distribution for the probability of bias. Default value is a1 = 1.
`nu`	Parameter for the Beta distribution for the quality weights. The default value is nu = 0.5.
`nu.estimate`	If TRUE, then we estimate nu from the data.
`b.0`	If nu.estimate = TRUE, this parameter is the shape parameter of the prior Gamma distribution for nu.
`b.1`	If nu.estimate = TRUE, this parameter is the rate parameter of the prior Gamma distribution for nu. Note that E(nu) = b.0/b.1 and we need to choose b.0 « b.1.
`preclassification`	Controls optional pre-classification of the latent bias indicators `I`. The argument can be: • `NULL`: No pre-classification. All `I[i]` are estimated. • `"right"`: Weak pre-classification to the right. The study with the largest observed effect is fixed as biased (`I = 1`) and the study with the smallest observed effect is fixed as unbiased (`I = 0`). • `"left"`: Weak pre-classification to the left. The study with the smallest observed effect is fixed as biased (`I = 1`) and the study with the largest observed effect is fixed as unbiased (`I = 0`). • A numeric vector of length `N` (number of studies including the prediction row), containing values `0`, `1`, or `NA`. Here, `1` indicates biased, `0` indicates unbiased, and `NA` indicates that the study's bias status should be estimated. If `inits` is provided, `preclassification` is ignored and all `I[i]` are treated as stochastic nodes initialized by `inits`.
`inits`	Optional initial values for MCMC chains, passed to `jags` or `jags.parallel`. Default is `NULL`.

nr.chains	Number of chains for the MCMC computations, default 2.
nr.iterations	Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.
nr.adapt	Number of iterations in the adaptation process, defualt is 1000. Some models may need more iterations during adptation.
nr.burnin	Number of iteration discared for burnin period, default is 1000. Some models may need a longer burnin period.
nr.thin	Thinning rate, it must be a positive integer, the default value 1.
parallel	NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The results of the object of the class bcmeta can be extracted with R2jags or with rjags. In addition a summary, a print and a plot functions are implemented for this type of object.

Value

This function returns an object of the class "bcmeta". This object contains the MCMC output of each parameter and hyper-parameter in the model and the data frame used for fitting the model.

References

Verde, P. E. (2017) Two Examples of Bayesian Evidence Synthesis with the Hierarchical Meta-Regression Approach. Chap.9, pag 189-206. Bayesian Inference, ed. Tejedor, Javier Prieto. InTech.

Verde, P.E. (2021) A Bias-Corrected Meta-Analysis Model for Combining Studies of Different Types and Quality. Biometrical Journal; 1–17.

Examples

```
## Not run:
library(jarbes)

# Example ppvipd data

data(ppvipd)



## End(Not run)
```

`bcmixmeta` *Bias Corrected Meta-Analysis with Dirichlet Mixture Process Priors for the biased component*

Description

This function performers a Bayesian meta-analysis with DPM as random effects

Usage

```
bcmixmeta(
  data,
  mean.mu.theta = 0,
  sd.mu.theta = 10,
  scale.sigma.between = 0.5,
  df.scale.between = 1,
  scale.sigma.beta = 0.5,
  df.scale.beta = 1,
  preclassification = "right",
  B.lower = -15,
  B.upper = 15,
  a.0 = 0.5,
  a.1 = 1,
  alpha.0 = 0.03,
  alpha.1 = 2,
  K = 10,
  nr.chains = 2,
  nr.iterations = 10000,
  nr.adapt = 1000,
  nr.burnin = 1000,
  nr.thin = 1,
  parallel = NULL
)
```

Arguments

`data`	A data frame with at least two columns with the following names: 1) TE = treatment effect, 2) seTE = the standard error of the treatment effect.
`mean.mu.theta`	Prior mean of the mean of the base distribution default value is mean.mu.theta = 0.
`sd.mu.theta`	Prior standard deviation of the base distribution, the default value is 10^-6.
`scale.sigma.between`	Prior scale parameter for scale gamma distribution for the precision between studies. The default value is 0.5.

`df.scale.between`
: Degrees of freedom of the scale gamma distribution for the precision between studies. The default value is 1, which results in a Half Cauchy distribution for the standard deviation between studies. Larger values e.g. 30 corresponds to a Half Normal distribution.

`scale.sigma.beta`
: Prior scale parameter for the scale.gamma distribution for the precision between study biases.

`df.scale.beta`
: Degrees of freedom of the scale gamma distribution for the precision between study biases. The default value is 1, which results in a Half Cauchy distribution for the standard deviation between biases.

`preclassification`
: Controls optional pre-classification of the latent bias indicators `I`. The argument can be:
  - `NULL`: No pre-classification. All `I[i]` are estimated.
  - `"right"`: Weak pre-classification to the right. The study with the largest observed effect is fixed as biased (`I = 1`) and the study with the smallest observed effect is fixed as unbiased (`I = 0`).
  - `"left"`: Weak pre-classification to the left. The study with the smallest observed effect is fixed as biased (`I = 1`) and the study with the largest observed effect is fixed as unbiased (`I = 0`).
  - A numeric vector of length `N` (number of studies including the prediction row), containing values `0`, `1`, or `NA`. Here, `1` indicates biased, `0` indicates unbiased, and `NA` indicates that the study's bias status should be estimated.

`B.lower`
: Lower bound of the bias parameter B, the default value is -15.

`B.upper`
: Upper bound of the bias parameter B, the default value is 15.

`a.0`
: Parameter for the prior Beta distribution for the probability of bias. Default value is a0 = 0.5.

`a.1`
: Parameter for the prior Beta distribution for the probability of bias. Default value is a1 = 1.

`alpha.0`
: Lower bound of the uniform prior for the concentration parameter for the DP, the default value is 0.5.

`alpha.1`
: Upper bound of the uniform prior for the concentration parameter for the DP, the default value depends on the sample size, see the example below. We give as working value alpha.1 = 2

`K`
: Maximum number of clusters in the DP, the default value depends on alpha.1, see the example below. We give as working value K = 10.

`nr.chains`
: Number of chains for the MCMC computations, default 2.

`nr.iterations`
: Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.

`nr.adapt`
: Number of iterations in the adaptation process, default is 1000. Some models may need more iterations during adptation.

`nr.burnin`
: Number of iteration discard for burn-in period, default is 1000. Some models may need a longer burnin period.

`nr.thin`
: Thinning rate, it must be a positive integer, the default value 1.

`parallel`
: NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The results of the object of the class bcmixmeta can be extracted with R2jags or with rjags. In addition a summary, a print and a plot functions are implemented for this type of object.

Value

This function returns an object of the class "bcmixmeta". This object contains the MCMC output of each parameter and hyper-parameter in the model and the data frame used for fitting the model.

References

Verde, P.E., and Rosner, G.L. (2025), A Bias-Corrected Bayesian Nonparametric Model for Combining Studies With Varying Quality in Meta-Analysis. Biometrical Journal., 67: e70034. https://doi.org/10.1002/bimj.70034

Examples

```
## Not run:
library(jarbes)


# Example: Stemcells

data("stemcells")
stemcells$TE = stemcells$effect.size
stemcells$seTE = stemcells$se.effect

# Beta(0.5, 1)
a.0 = 0.5
a.1 = 1

# alpha.max
 N = dim(stemcells)[1]
 alpha.max = 1/5 *((N-1)*a.0 - a.1)/(a.0 + a.1)

alpha.max

# K.max
K.max = 1 + 5*alpha.max
K.max = round(K.max)

K.max

set.seed(20233)

bcmix.2.stemcell = bcmixmeta(stemcells,
                             mean.mu.theta=0, sd.mu.theta=100,
                             B.lower = -15,
                             B.upper = 15,
                             alpha.0 = 0.5,
                             alpha.1 = alpha.max,
                             a.0 = a.0,
                             a.1 = a.1,
```

```
                              K = K.max,
                              df.scale.between = 1,
                              scale.sigma.between = 0.5,
                              nr.chains = 4,
                              nr.iterations = 50000,
                              nr.adapt = 1000,
                              nr.burnin = 10000,
                              nr.thin = 4)


 diagnostic(bcmix.2.stemcell, y.lim = c(-1, 15), title.plot = "Default priors")


 bcmix.2.stemcell.mcmc <- as.mcmc(bcmix.1.stemcell$BUGSoutput$sims.matrix)


theta.names <- paste(paste("theta[",1:31, sep=""),"]", sep="")
theta.b.names <- paste(paste("theta.bias[",1:31, sep=""),"]", sep="")

theta.b.greek.names <- paste(paste("theta[",1:31, sep=""),"]^B", sep="")
theta.greek.names <- paste(paste("theta[",1:31, sep=""),"]", sep="")


caterplot(bcmix.2.stemcell.mcmc,
         parms = theta.names,               # theta
         labels = theta.greek.names,
         greek = T,
         labels.loc="axis", cex =0.7,
         col = "black",
         style = "plain",
         reorder = F,
         val.lim =c(-6, 16),
         quantiles = list(outer=c(0.05,0.95),inner=c(0.16,0.84)),
         x.lab = "Effect: mean difference"
)
title( "95% posterior intervals of studies' effects")
caterplot(bcmix.2.stemcell.mcmc,
         parms = theta.b.names,             # theta.bias
         labels = theta.greek.names,
         greek = T,
         labels.loc="no",
         cex = 0.7,
         col = "grey",
         style = "plain", reorder = F,
         val.lim =c(-6, 16),
         quantiles = list(outer=c(0.025,0.975),inner=c(0.16,0.84)),
         add = TRUE,
         collapse=TRUE, cat.shift= -0.5,
)

attach.jags(bcmix.2.stemcell, overwrite = TRUE)
abline(v=mean(mu.theta), lwd =2, lty =2)
```

```
legend(9, 20, legend = c("bias corrected", "biased"),
     lty = c(1,1), lwd = c(2,2), col = c("black", "grey"))



## End(Not run)
```

---

bmeta *Bayesian Meta-Analysis for Combining Studies*

Description

This function performers a Bayesian meta-analysis

Usage

```
bmeta(
  data,
  mean.mu = 0,
  sd.mu = 10,
  scale.sigma.between = 0.5,
  df.scale.between = 1,
  df = 4,
  df.estimate = FALSE,
  df.lower = 3,
  df.upper = 30,
  re = "normal",
  nr.chains = 2,
  nr.iterations = 10000,
  nr.adapt = 1000,
  nr.burnin = 1000,
  nr.thin = 1,
  be.quiet = FALSE,
  parallel = NULL
)
```

Arguments

data	A data frame with at least two columns with the following names: 1) TE = treatment effect, 2) seTE = the standard error of the treatment effect.
mean.mu	Prior mean of the overall mean parameter mu, default value is 0.
sd.mu	Prior standard deviation of mu, the default value is 10.
scale.sigma.between	Prior scale parameter for scale gamma distribution for the precision between studies. The default value is 0.5.

`df.scale.between`
: Degrees of freedom of the scale gamma distribution for the precision between studies. The default value is 1, which results in a Half Cauchy distribution for the standard deviation between studies. Larger values e.g. 30 corresponds to a Half Normal distribution.

`df`
: Default value df = 4. When re = "sm", this parameter corresponds to the degrees of freedom of the implied Student-t random effects distribution arising from the scale mixture of normal distributions.

`df.estimate`
: Logical value indicating whether the degrees of freedom parameter of the scale mixture distribution should be estimated. If FALSE the value specified in `df` is used. Default is FALSE.

`df.lower`
: Lower bound of the prior distribution for the degrees of freedom when `df.estimate = TRUE`. Default value is 3.

`df.upper`
: Upper bound of the prior distribution for the degrees of freedom when `df.estimate = TRUE`. Default value is 30.

`re`
: Random effects distribution. Possible values are *"normal"* for Normal random effects and *"sm"* for scale mixtures of Normals (robust heavy-tailed model).

`nr.chains`
: Number of chains for the MCMC computations, default 2.

`nr.iterations`
: Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.

`nr.adapt`
: Number of iterations in the adaptation process, default is 1000. Some models may need more iterations during adptation.

`nr.burnin`
: Number of iteration discard for burn-in period, default is 1000. Some models may need a longer burnin period.

`nr.thin`
: Thinning rate, it must be a positive integer, the default value 1.

`be.quiet`
: Do not print warning message if the model does not adapt. The default value is FALSE. If you are not sure about the adaptation period choose be.quiet=TRUE.

`parallel`
: NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The results of the object of the class bcmeta can be extracted with R2jags or with rjags. In addition a summary, a print and a plot functions are implemented for this type of object.

Value

This function returns an object of the class "bmeta". This object contains the MCMC output of each parameter and hyper-parameter in the model and the data frame used for fitting the model.

References

Verde, P.E. (2021) A Bias-Corrected Meta-Analysis Model for Combining Studies of Different Types and Quality. Biometrical Journal; 1–17.

`cocluster_plot` *Co-Clustering Heatmap from a Numeric Matrix*

Description

Generates a heatmap with hierarchical clustering applied to rows and columns. It reorders the input matrix based on clustering results and visualizes the data.

Usage

```
cocluster_plot(
  data,
  labels.row = NULL,
  labels.col = NULL,
  colors = "Blues",
  breaks = NULL,
  title = "Clustered Heatmap",
  border.color = "black",
  cell.ratio = 1,
  cluster.rows = TRUE,
  cluster.cols = TRUE,
  clustering.distance.rows = "euclidean",
  clustering.distance.cols = "euclidean",
  row.clustering.method = "complete",
  col.clustering.method = "complete",
  show.row.names = TRUE,
  show.col.names = TRUE,
  fontsize = 8,
  fontsize.row = NULL,
  fontsize.col = NULL,
  display.numbers = FALSE,
  round.digits = 2,
  numbers.color = "black",
  numbers.fontsize = 0.5,
  label.color = "black",
  col.name.angle = 45,
  legend = TRUE,
  legend.labels = NULL,
  show.legend.labels = TRUE,
  ...
)
```

Arguments

`data`	A numeric matrix for the heatmap.
`labels.row`	An optional character vector of new labels for the rows.

`labels.col` An optional character vector of new labels for the columns.

`colors` A character string specifying one of the predefined palettes or a custom vector of colors. Predefined options include:

- "YlOrRd", "YlOrBr", "YlGnBu", "YlGn", "Reds", "RdPu", "Purples", "PuBu", "PuBuGn", "OrRd", "Oranges", "Greys", "Greens", "GnBu", "BuPu", "BuGn", "Blues"

Defaults to "Blues".

`breaks` The number of color breaks to use for the palette. Defaults to 'NULL'.

`title` Plot title. Default: "Clustered Heatmap".

`border.color` Color of cell borders on the heatmap. Use "NA" for no border. Default: "white".

`cell.ratio` A numeric value defining the cell's height-to-width ratio. A value of 1 creates square cells. A value > 1 creates vertical rectangles, while a value < 1 creates horizontal rectangles. Default is 1.

`cluster.rows` A logical value indicating whether to cluster rows. Default: 'TRUE'.

`cluster.cols` A logical value indicating whether to cluster columns. Default: 'TRUE'.

`clustering.distance.rows`
Distance measure for row clustering. Can be a string ("euclidean", "correlation", etc.) or a pre-calculated distance object. Default: "euclidean".

`clustering.distance.cols`
Distance measure for column clustering. Can be a string ("euclidean", "correlation", etc.) or a pre-calculated distance object. Default: "euclidean".

`row.clustering.method`
Agglomeration method for row clustering (see '?hclust'). Default: "complete".

`col.clustering.method`
Agglomeration method for column clustering (see '?hclust'). Default: "complete".

`show.row.names` Logical, display row names. Default: TRUE.

`show.col.names` Logical, display column names. Default: TRUE.

`fontsize` Base font size for the plot. Default: 8.

`fontsize.row` Font size for row names. If 'NULL', defaults to 'fontsize'.

`fontsize.col` Font size for column names. If 'NULL', defaults to 'fontsize'.

`display.numbers`
Logical determining if the numeric values are also printed to the cells.

`round.digits` Numeric value. For 'display.numbers = TRUE', this sets the decimal places for all values. Default: 2.

`numbers.color` Color of the numbers. Default: "black".

`numbers.fontsize`
Font size of the numbers. Default: 'fontsize'.

`label.color` Color of the row and column labels. Default: "black".

`col.name.angle` Angle for column names. Default: 45.

`legend` A logical value indicating whether to show the color legend. Default: 'TRUE'.

`legend.labels` A character vector of custom labels for the legend.

`show.legend.labels`
Logical, display legend labels. Default: TRUE.

`...` ...

Value

A 'ggplot2' object.

`colon_cancer` *Meta-analysis: Real World Evidence in metastatic colorectal cancer, comparing antiangiogenic treatments with chemotherapy*

Description

Meta-analysis of 7 RCTs, 4 cRWE studies, and 2 matched sRWE studies evaluating progression-free survival (PFS) as a surrogate endpoint to overall survival (OS) in metastatic colorectal cancer (mCRC), comparing antiangiogenic treatments with chemotherapy.

Format

A dataframe with 13 rows and 6 columns. Each row represents study results, the columns are:

study Author and year.

study_type randomized clinical trial or comparative/single-arm real-world-evidence

pfs logarithm of hazard ratios of progression-free survival

se_pfs standard error of pfs

os logarithm of hazard ratios of overall survival

se_os standard error of os

Source

Wheaton L, Papanikos A, Thomas A, Bujkiewicz S. Using Bayesian Evidence Synthesis Methods to Incorporate Real-World Evidence in Surrogate Endpoint Evaluation. Medical Decision Making. 2023;43(5):539-552. doi:10.1177/0272989X231162852

`covid19` *Meta-analysis: Observational studies assessing the impact of risk factors on the severity and mortality of COVID-19 cases*

Description

Meta-analysis of 35 Observational Studies from PubMed, Cocharane Library and SciELO databases that assessed the impact of diabetes, hypertension, cardiovascular disease, and the use of ACEI/ARB on severity and mortality of COVID-19 cases.

Format

A dataframe with 89 rows and 12 columns. Each row represents study results, the columns are:

author Principal author and year of publication.

endpoint Endoint: severity or mortality.

risk.factor Possible risk factors: diabetes, hypertension, cardiovascular, ACE_ARB.

event.e Number of events in the group with risk factor.

n.e Number of patients in the group with risk factor.

event.c Number of events in the group without risk factor.

n.c Number of patients in the group with risk factor.

design Study design: Case Series, Cross Sectional and Retrospective Cohort.

TE Log Odds Ratio

seTE Standard Error of the Log Odds Ratio

logitPc Logit transformation of the proportion of events in the control group.

N Total number of patients.

Source

de Almeida-Pititto, B., Dualib, P.M., Zajdenverg, L. et al. Severity and mortality of COVID 19 in patients with diabetes, hypertension and cardiovascular disease: a meta-analysis. Diabetol Metab Syndr 12, 75 (2020). https://doi.org/10.1186/s13098-020-00586-4

---

diabetes_eyes *Individual Participant Data: Diabetic Eyes Data*

Description

A dataset containing detailed measurements from a study investigating the relationship between diabetes and eye health. The dataset includes patient demographics, visual acuity, and extensive macular metrics derived from optical coherence tomography (OCT) imaging.

Format

A dataframe with 270 columns and 97 rows, where each row represents a patient. The columns include:

pat Patient ID.

diabetes_type Indicator for diabetes (2 = diabetic (type 2), 0 = healthy).

sex Gender of the patient (1 = Male, 2 = Female).

age Age of the patient (years).

smoker Smoking status (1 = Smoker, 0 = Non-smoker).

weight Weight of the patient (kg).

height Height of the patient (m).

BMI Body Mass Index

VISUAL_ACUITY_RIGHT_EYE Visual acuity for the right eye.

VISUAL_ACUITY_LEFT_EYE Visual acuity for the left eye.

CONTRAST_SENSITIVITY_RIGHT_EYE Measure of contrast sensitivity for the left eye.

CONTRAST_SENSITIVITY_LEFT_EYE Measure of contrast sensitivity for the left eye.

R_PAP_RNFL_N Measurement of the right eye, Papilla, Retinal Nerve Fiber Layer, Nasal Parafovea

R_PAP_RNFL_NI Measurement of the right eye, Papilla, Retinal Nerve Fiber Layer, Nasal Inferior Parafovea

R_PAP_RNFL_TI Measurement of the right eye, Papilla, Retinal Nerve Fiber Layer, Temporal Inferior Parafovea

R_PAP_RNFL_T Measurement of the right eye, Papilla, Retinal Nerve Fiber Layer, Temporal Parafovea

R_PAP_RNFL_TS Measurement of the right eye, Papilla, Retinal Nerve Fiber Layer, Temporal Superior Parafovea

R_PAP_RNFL_G Measurement of the right eye, Papilla, Retinal Nerve Fiber Layer, Global Layer

L_PAP_RNFL_NS Measurement of the left eye, Papilla, Retinal Nerve Fiber Layer, Nasal Superior Parafovea

L_PAP_RNFL_N Measurement of the left eye, Papilla, Retinal Nerve Fiber Layer, Nasal Parafovea

L_PAP_RNFL_NI Measurement of the left eye, Papilla, Retinal Nerve Fiber Layer, Nasal Inferior Parafovea

L_PAP_RNFL_TI Measurement of the left eye, Papilla, Retinal Nerve Fiber Layer, Temporal Inferior Parafovea

L_PAP_RNFL_T Measurement of the left eye, Papilla, Retinal Nerve Fiber Layer, Temporal Parafovea

L_PAP_RNFL_TS Measurement of the left eye, Papilla, Retinal Nerve Fiber Layer, Temporal Superior Parafovea

L_PAP_RNFL_G Measurement of the left eye, Papilla, Retinal Nerve Fiber Layer, Global Layer

R_PAP_FULL_NS Measurement of the right eye, Papilla, Complete Retinal Thickness, Nasal Superior Parafovea

R_PAP_FULL_N Measurement of the right eye, Papilla, Complete Retinal Thickness, Nasal Parafovea

R_PAP_FULL_NI Measurement of the right eye, Papilla, Complete Retinal Thickness, Nasal Inferior Parafovea

R_PAP_FULL_TI Measurement of the right eye, Papilla, Complete Retinal Thickness, Temporal Inferior Parafovea

R_PAP_FULL_T Measurement of the right eye, Papilla, Complete Retinal Thickness, Temporal Parafovea

R_PAP_FULL_TS Measurement of the right eye, Papilla, Complete Retinal Thickness, Temporal Superior Parafovea

R_PAP_FULL_G Measurement of the right eye, Papilla, Complete Retinal Thickness, Global Layer

L_PAP_FULL_NS Measurement of the left eye, Papilla, Complete Retinal Thickness, Nasal Superior Parafovea

L_PAP_FULL_N Measurement of the left eye, Papilla, Complete Retinal Thickness, Nasal Parafovea

L_PAP_FULL_NI Measurement of the left eye, Papilla, Complete Retinal Thickness, Nasal Inferior Parafovea

L_PAP_FULL_TI Measurement of the left eye, Papilla, Complete Retinal Thickness, Temporal Inferior Parafovea

L_PAP_FULL_T Measurement of the left eye, Papilla, Complete Retinal Thickness, Temporal Parafovea

L_PAP_FULL_TS Measurement of the left eye, Papilla, Complete Retinal Thickness, Temporal Superior Parafovea

L_PAP_FULL_G Measurement of the left eye, Papilla, Complete Retinal Thickness, Global Layer

R_PAP_GCLIPL_NS Measurement of the right eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Nasal Superior Parafovea

R_PAP_GCLIPL_N Measurement of the right eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Nasal Parafovea

R_PAP_GCLIPL_NI Measurement of the right eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Nasal Inferior Parafovea

R_PAP_GCLIPL_TI Measurement of the right eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Temporal Inferior Parafovea

R_PAP_GCLIPL_T Measurement of the right eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Temporal Parafovea

R_PAP_GCLIPL_TS Measurement of the right eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Temporal Superior Parafovea

R_PAP_GCLIPL_G Measurement of the right eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Global Layer

L_PAP_GCLIPL_NS Measurement of the left eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Nasal Superior Parafovea

L_PAP_GCLIPL_N Measurement of the left eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Nasal Parafovea

L_PAP_GCLIPL_NI Measurement of the left eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Nasal Inferior Parafovea

L_PAP_GCLIPL_TI Measurement of the left eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Temporal Inferior Parafovea

L_PAP_GCLIPL_T Measurement of the left eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Temporal Parafovea

L_PAP_GCLIPL_TS Measurement of the left eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Temporal Superior Parafovea

L_PAP_GCLIPL_G Measurement of the left eye, Papilla, Ganglion Cell Layer and Inner Plexiform Layer combined, Global Layer

R_PAP_INLOPL_NS Measurement of the right eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Nasal Superior Parafovea

R_PAP_INLOPL_N Measurement of the right eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Nasal Parafovea

R_PAP_INLOPL_NI Measurement of the right eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Nasal Inferior Parafovea

R_PAP_INLOPL_TI Measurement of the right eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Temporal Inferior Parafovea

R_INLOPL_T Measurement of the right eye, Inner Nuclear Layer and Outer Plexiform Layer combined, Temporal Parafovea

R_PAP_INLOPL_TS Measurement of the right eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Temporal Superior Parafovea

R_PAP_INLOPL_G Measurement of the right eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Global Layer

L_PAP_INLOPL_NS Measurement of the left eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Nasal Superior Parafovea

L_PAP_INLOPL_N Measurement of the left eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Nasal Parafovea

L_PAP_INLOPL_NI Measurement of the left eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Nasal Inferior Parafovea

L_PAP_INLOPL_TI Measurement of the left eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Temporal Inferior Parafovea

L_PAP_INLOPL_T Measurement of the left eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Temporal Parafovea

L_PAP_INLOPL_TS Measurement of the left eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Temporal Superior Parafovea

L_PAP_INLOPL_G Measurement of the left eye, Papilla, Inner Nuclear Layer and Outer Plexiform Layer combined, Global Layer

R_PAP_ONLFIS_NS Measurement of the right eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Nasal Superior Parafovea

R_PAP_ONLFIS_N Measurement of the right eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Nasal Parafovea

R_PAP_ONLFIS_NI Measurement of the right eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Nasal Inferior Parafovea

R_PAP_ONLFIS_TI Measurement of the right eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Temporal Inferior Parafovea

R_PAP_ONLFIS_T Measurement of the right eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Temporal Parafovea

R_PAP_ONLFIS_TS Measurement of the right eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Temporal Superior Parafovea

R_PAP_ONLFIS_G Measurement of the right eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Global Layer

L_PAP_ONLFIS_NS Measurement of the left eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Nasal Superior Parafovea

L_PAP_ONLFIS_N Measurement of the left eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Nasal Parafovea

L_PAP_ONLFIS_NI Measurement of the left eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Nasal Inferior Parafovea

L_PAP_ONLFIS_TI Measurement of the left eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Temporal Inferior Parafovea

L_PAP_ONLFIS_T Measurement of the left eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Temporal Parafovea

L_PAP_ONLFIS_TS Measurement of the left eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Temporal Superior Parafovea

L_PAP_ONLFIS_G Measurement of the left eye, Papilla, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Global Layer

R_PAP_FBBM_NS Measurement of the right eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Nasal Superior Parafovea

R_PAP_FBBM_N Measurement of the right eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Nasal Parafovea

R_PAP_FBBM_NI Measurement of the right eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Nasal Inferior Parafovea

R_PAP_FBBM_TI Measurement of the right eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Temporal Inferior Parafovea

R_PAP_FBBM_T Measurement of the right eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Temporal Parafovea

R_PAP_FBBM_TS Measurement of the right eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Temporal Superior Parafovea

R_PAP_FBBM_G Measurement of the right eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Global Layer

L_PAP_FBBM_NS Measurement of the left eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Nasal Superior Parafovea

L_PAP_FBBM_N Measurement of the left eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Nasal Parafovea

L_PAP_FBBM_NI Measurement of the left eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Nasal Inferior Parafovea

L_PAP_FBBM_TI Measurement of the left eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Temporal Inferior Parafovea

L_PAP_FBBM_T Measurement of the left eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Temporal Parafovea

L_PAP_FBBM_TS Measurement of the left eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Temporal Superior Parafovea

L_PAP_FBBM_G Measurement of the left eye, Papilla, Photoreceptor Fiber Layer and Basal Membrane combined, Global Layer

M_R_MAC_FULL_N2 Manual measurement of the right eye, Macula, Complete Retinal Thickness, Nasal Outer Parafovea

M_R_MAC_GCLIPL_N2 Manual measurement of the right eye, Macula, Ganglion Cell Layer and Inner Plexiform Layer combined, Nasal Outer Parafovea

M_R_MAC_INLOPL_N2 Manual measurement of the right eye, Macula, Inner Nuclear Layer and Outer Plexiform Layer combined, Nasal Outer Parafovea

M_R_MAC_ONLFIS_N2 Manual measurement of the right eye, Macula, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Nasal Outer Parafovea

M_R_MAC_FBBM_N2 Manual measurement of the right eye, Macula, Photoreceptor Fiber Layer and Basal Membrane combined, Nasal Outer Parafovea

M_R_MAC_RNFL_N2 Manual measurement of the right eye, Macula, Retinal Nerve Fiber Layer, Nasal Outer Parafovea

M_L_MAC_FULL_N2 Manual measurement of the left eye, Macula, Complete Retinal Thickness, Nasal Outer Parafovea

M_L_MAC_GCLIPL_N2 Manual measurement of the left eye, Macula, Ganglion Cell Layer and Inner Plexiform Layer combined, Nasal Outer Parafovea

M_L_MAC_INLOPL_N2 Manual measurement of the left eye, Macula, Inner Nuclear Layer and Outer Plexiform Layer combined, Nasal Outer Parafovea

M_L_MAC_ONLFIS_N2 Manual measurement of the left eye, Macula, Outer Nuclear Layer and Photoreceptor Inner Segment Layer combined, Nasal Outer Parafovea

M_L_MAC_FBBM_N2 Manual measurement of the left eye, Macula, Photoreceptor Fiber Layer and Basal Membrane combined, Nasal Outer Parafovea

M_L_MAC_RNFL_N2 Manual measurement of the left eye, Macula, Retinal Nerve Fiber Layer, Nasal Outer Parafovea

R_MAC_FULL_S1 Measurement of the right eye, Macula, Complete Retinal Thickness, Superior Inner Parafovea

R_MAC_FULL_S2 Measurement of the right eye, Macula, Complete Retinal Thickness, Superior Outer Parafovea

R_MAC_FULL_N1 Measurement of the right eye, Macula, Complete Retinal Thickness, Nasal Inner Parafovea

R_MAC_FULL_N2 Measurement of the right eye, Macula, Complete Retinal Thickness, Nasal Outer Parafovea

R_MAC_FULL_I1 Measurement of the right eye, Macula, Complete Retinal Thickness, Inferior Inner Parafovea

R_MAC_FULL_I2 Measurement of the right eye, Macula, Complete Retinal Thickness, Inferior Outer Parafovea

R_MAC_FULL_T1 Measurement of the right eye, Macula, Complete Retinal Thickness, Temporal Inner Parafovea

R_MAC_FULL_T2 Measurement of the right eye, Macula, Complete Retinal Thickness, Temporal Outer Parafovea

R_MAC_FULL_C Measurement of the right eye, Macula, Complete Retinal Thickness, Center Fovea

R_MAC_RNFL_S1 Measurement of the right eye, Macula, Retinal Nerve Fiber Layer, Superior Inner Parafovea

R_MAC_RNFL_S2 Measurement of the right eye, Macula, Retinal Nerve Fiber Layer, Superior Outer Parafovea

R_MAC_RNFL_N1 Measurement of the right eye, Macula, Retinal Nerve Fiber Layer, Nasal Inner Parafovea

R_MAC_RNFL_N2 Measurement of the right eye, Macula, Retinal Nerve Fiber Layer, Nasal Outer Parafovea

R_MAC_RNFL_I1 Measurement of the right eye, Macula, Retinal Nerve Fiber Layer, Inferior Inner Parafovea

R_MAC_RNFL_I2 Measurement of the right eye, Macula, Retinal Nerve Fiber Layer, Inferior Outer Parafovea

R_MAC_RNFL_T1 Measurement of the right eye, Macula, Retinal Nerve Fiber Layer, Temporal Inner Parafovea

R_MAC_RNFL_T2 Measurement of the right eye, Macula, Retinal Nerve Fiber Layer, Temporal Outer Parafovea

R_MAC_RNFL_C Measurement of the right eye, Macula, Retinal Nerve Fiber Layer, Center Fovea

R_MAC_GCL_S1 Measurement of the right eye, Macula, Ganglion Cell Layer, Superior Inner Parafovea

R_MAC_GCL_S2 Measurement of the right eye, Macula, Ganglion Cell Layer, Superior Outer Parafovea

R_MAC_GCL_N1 Measurement of the right eye, Macula, Ganglion Cell Layer, Nasal Inner Parafovea

R_MAC_GCL_N2 Measurement of the right eye, Macula, Ganglion Cell Layer, Nasal Outer Parafovea

R_MAC_GCL_I1 Measurement of the right eye, Macula, Ganglion Cell Layer, Inferior Inner Parafovea

R_MAC_GCL_I2 Measurement of the right eye, Macula, Ganglion Cell Layer, Inferior Outer Parafovea

R_MAC_GCL_T1 Measurement of the right eye, Macula, Ganglion Cell Layer, Temporal Inner Parafovea

R_MAC_GCL_T2 Measurement of the right eye, Macula, Ganglion Cell Layer, Temporal Outer Parafovea

R_MAC_GCL_C Measurement of the right eye, Macula, Ganglion Cell Layer, Center Fovea

R_MAC_IPL_S1 Measurement of the right eye, Macula, Inner Plexiform Layer, Superior Inner Parafovea

R_MAC_IPL_S2 Measurement of the right eye, Macula, Inner Plexiform Layer, Superior Outer Parafovea

R_MAC_IPL_N1 Measurement of the right eye, Macula, Inner Plexiform Layer, Nasal Inner Parafovea

R_MAC_IPL_N2 Measurement of the right eye, Macula, Inner Plexiform Layer, Nasal Outer Parafovea

R_MAC_IPL_I1 Measurement of the right eye, Macula, Inner Plexiform Layer, Inferior Inner Parafovea

R_MAC_IPL_I2 Measurement of the right eye, Macula, Inner Plexiform Layer, Inferior Outer Parafovea

R_MAC_IPL_T1 Measurement of the right eye, Macula, Inner Plexiform Layer, Temporal Inner Parafovea

R_MAC_IPL_T2 Measurement of the right eye, Macula, Inner Plexiform Layer, Temporal Outer Parafovea

R_MAC_IPL_C Measurement of the right eye, Macula, Inner Plexiform Layer, Center Fovea

R_MAC_INL_S1 Measurement of the right eye, Macula, Inner Nuclear Layer, Superior Inner Parafovea

R_MAC_INL_S2 Measurement of the right eye, Macula, Inner Nuclear Layer, Superior Outer Parafovea

R_MAC_INL_N1 Measurement of the right eye, Macula, Inner Nuclear Layer, Nasal Inner Parafovea

R_MAC_INL_N2 Measurement of the right eye, Macula, Inner Nuclear Layer, Nasal Outer Parafovea

R_MAC_INL_I1 Measurement of the right eye, Macula, Inner Nuclear Layer, Inferior Inner Parafovea

R_MAC_INL_I2 Measurement of the right eye, Macula, Inner Nuclear Layer, Inferior Outer Parafovea

R_MAC_INL_T1 Measurement of the right eye, Macula, Inner Nuclear Layer, Temporal Inner Parafovea

R_MAC_INL_T2 Measurement of the right eye, Macula, Inner Nuclear Layer, Temporal Outer Parafovea

R_MAC_INL_C Measurement of the right eye, Macula, Inner Nuclear Layer, Center Fovea

R_MAC_OPL_S1 Measurement of the right eye, Macula, Outer Plexiform Layer, Superior Inner Parafovea

R_MAC_OPL_S2 Measurement of the right eye, Macula, Outer Plexiform Layer, Superior Outer Parafovea

R_MAC_OPL_N1 Measurement of the right eye, Macula, Outer Plexiform Layer, Nasal Inner Parafovea

R_MAC_OPL_N2 Measurement of the right eye, Macula, Outer Plexiform Layer, Nasal Outer Parafovea

R_MAC_OPL_I1 Measurement of the right eye, Macula, Outer Plexiform Layer, Inferior Inner Parafovea

R_MAC_OPL_I2 Measurement of the right eye, Macula, Outer Plexiform Layer, Inferior Outer Parafovea

R_MAC_OPL_T1 Measurement of the right eye, Macula, Outer Plexiform Layer, Temporal Inner Parafovea

R_MAC_OPL_T2 Measurement of the right eye, Macula, Outer Plexiform Layer, Temporal Outer Parafovea

R_MAC_OPL_C Measurement of the right eye, Macula, Outer Plexiform Layer, Center Fovea

R_MAC_ONL_S1 Measurement of the right eye, Macula, Outer Nuclear Layer, Superior Inner Parafovea

R_MAC_ONL_S2 Measurement of the right eye, Macula, Outer Nuclear Layer, Superior Outer Parafovea

R_MAC_ONL_N1 Measurement of the right eye, Macula, Outer Nuclear Layer, Nasal Inner Parafovea

R_MAC_ONL_N2 Measurement of the right eye, Macula, Outer Nuclear Layer, Nasal Outer Parafovea

R_MAC_ONL_I1 Measurement of the right eye, Macula, Outer Nuclear Layer, Inferior Inner Parafovea

R_MAC_ONL_I2 Measurement of the right eye, Macula, Outer Nuclear Layer, Inferior Outer Parafovea

R_MAC_ONL_T1 Measurement of the right eye, Macula, Outer Nuclear Layer, Temporal Inner Parafovea

R_MAC_ONL_T2 Measurement of the right eye, Macula, Outer Nuclear Layer, Temporal Outer Parafovea

R_MAC_ONL_C Measurement of the right eye, Macula, Outer Nuclear Layer, Center Fovea

R_MAC_RPE_S1 Measurement of the right eye, Macula, Retinal Pigment Epithelium, Superior Inner Parafovea

R_MAC_RPE_S2 Measurement of the right eye, Macula, Retinal Pigment Epithelium, Superior Outer Parafovea

R_MAC_RPE_N1 Measurement of the right eye, Macula, Retinal Pigment Epithelium, Nasal Inner Parafovea

R_MAC_RPE_N2 Measurement of the right eye, Macula, Retinal Pigment Epithelium, Nasal Outer Parafovea

R_MAC_RPE_I1 Measurement of the right eye, Macula, Retinal Pigment Epithelium, Inferior Inner Parafovea

R_MAC_RPE_I2 Measurement of the right eye, Macula, Retinal Pigment Epithelium, Inferior Outer Parafovea

R_MAC_RPE_T1 Measurement of the right eye, Macula, Retinal Pigment Epithelium, Temporal Inner Parafovea

R_MAC_RPE_T2 Measurement of the right eye, Macula, Retinal Pigment Epithelium, Temporal Outer Parafovea

R_MAC_RPE_C Measurement of the right eye, Macula, Retinal Pigment Epithelium, Center Fovea

R_MAC_PHOTO_S1 Measurement of the right eye, Macula, Unknown Layer, Superior Inner Parafovea

R_MAC_PHOTO_S2 Measurement of the right eye, Macula, Unknown Layer, Superior Outer Parafovea

R_MAC_PHOTO_N1 Measurement of the right eye, Macula, Unknown Layer, Nasal Inner Parafovea

R_MAC_PHOTO_N2 Measurement of the right eye, Macula, Unknown Layer, Nasal Outer Parafovea

R_MAC_PHOTO_I1 Measurement of the right eye, Macula, Unknown Layer, Inferior Inner Parafovea

R_MAC_PHOTO_I2 Measurement of the right eye, Macula, Unknown Layer, Inferior Outer Parafovea

R_MAC_PHOTO_T1 Measurement of the right eye, Macula, Unknown Layer, Temporal Inner Parafovea

R_MAC_PHOTO_T2 Measurement of the right eye, Macula, Unknown Layer, Temporal Outer Parafovea

R_MAC_PHOTO_C Measurement of the right eye, Macula, Unknown Layer, Center Fovea

L_MAC_FULL_S1 Measurement of the left eye, Macula, Complete Retinal Thickness, Superior Inner Parafovea

L_MAC_FULL_S2 Measurement of the left eye, Macula, Complete Retinal Thickness, Superior Outer Parafovea

L_MAC_FULL_N1 Measurement of the left eye, Macula, Complete Retinal Thickness, Nasal Inner Parafovea

L_MAC_FULL_N2 Measurement of the left eye, Macula, Complete Retinal Thickness, Nasal Outer Parafovea

L_MAC_FULL_I1 Measurement of the left eye, Macula, Complete Retinal Thickness, Inferior Inner Parafovea

L_MAC_FULL_I2 Measurement of the left eye, Macula, Complete Retinal Thickness, Inferior Outer Parafovea

L_MAC_FULL_T1 Measurement of the left eye, Macula, Complete Retinal Thickness, Temporal Inner Parafovea

L_MAC_FULL_T2 Measurement of the left eye, Macula, Complete Retinal Thickness, Temporal Outer Parafovea

L_MAC_FULL_C Measurement of the left eye, Macula, Complete Retinal Thickness, Center Fovea

L_MAC_RNFL_S1 Measurement of the left eye, Macula, Retinal Nerve Fiber Layer, Superior Inner Parafovea

L_MAC_RNFL_S2 Measurement of the left eye, Macula, Retinal Nerve Fiber Layer, Superior Outer Parafovea

L_MAC_RNFL_N1 Measurement of the left eye, Macula, Retinal Nerve Fiber Layer, Nasal Inner Parafovea

L_MAC_RNFL_N2 Measurement of the left eye, Macula, Retinal Nerve Fiber Layer, Nasal Outer Parafovea

L_MAC_RNFL_I1 Measurement of the left eye, Macula, Retinal Nerve Fiber Layer, Inferior Inner Parafovea

L_MAC_RNFL_I2 Measurement of the left eye, Macula, Retinal Nerve Fiber Layer, Inferior Outer Parafovea

L_MAC_RNFL_T1 Measurement of the left eye, Macula, Retinal Nerve Fiber Layer, Temporal Inner Parafovea

L_MAC_RNFL_T2 Measurement of the left eye, Macula, Retinal Nerve Fiber Layer, Temporal Outer Parafovea

L_MAC_RNFL_C Measurement of the left eye, Macula, Retinal Nerve Fiber Layer, Center Fovea

L_MAC_GCL_S1 Measurement of the left eye, Macula, Ganglion Cell Layer, Superior Inner Parafovea

L_MAC_GCL_S2 Measurement of the left eye, Macula, Ganglion Cell Layer, Superior Outer Parafovea

L_MAC_GCL_N1 Measurement of the left eye, Macula, Ganglion Cell Layer, Nasal Inner Parafovea

L_MAC_GCL_N2 Measurement of the left eye, Macula, Ganglion Cell Layer, Nasal Outer Parafovea

L_MAC_GCL_I1 Measurement of the left eye, Macula, Ganglion Cell Layer, Inferior Inner Parafovea

L_MAC_GCL_I2 Measurement of the left eye, Macula, Ganglion Cell Layer, Inferior Outer Parafovea

L_MAC_GCL_T1 Measurement of the left eye, Macula, Ganglion Cell Layer, Temporal Inner Parafovea

L_MAC_GCL_T2 Measurement of the left eye, Macula, Ganglion Cell Layer, Temporal Outer Parafovea

L_MAC_GCL_C Measurement of the left eye, Macula, Ganglion Cell Layer, Center Fovea

L_MAC_IPL_S1 Measurement of the left eye, Macula, Inner Plexiform Layer, Superior Inner Parafovea

L_MAC_IPL_S2 Measurement of the left eye, Macula, Inner Plexiform Layer, Superior Outer Parafovea

L_MAC_IPL_N1 Measurement of the left eye, Macula, Inner Plexiform Layer, Nasal Inner Parafovea

L_MAC_IPL_N2 Measurement of the left eye, Macula, Inner Plexiform Layer, Nasal Outer Parafovea

L_MAC_IPL_I1 Measurement of the left eye, Macula, Inner Plexiform Layer, Inferior Inner Parafovea

L_MAC_IPL_I2 Measurement of the left eye, Macula, Inner Plexiform Layer, Inferior Outer Parafovea

L_MAC_IPL_T1 Measurement of the left eye, Macula, Inner Plexiform Layer, Temporal Inner Parafovea

L_MAC_IPL_T2 Measurement of the left eye, Macula, Inner Plexiform Layer, Temporal Outer Parafovea

L_MAC_IPL_C Measurement of the left eye, Macula, Inner Plexiform Layer, Center Fovea

L_MAC_INL_S1 Measurement of the left eye, Macula, Inner Nuclear Layer, Superior Inner Parafovea

L_MAC_INL_S2 Measurement of the left eye, Macula, Inner Nuclear Layer, Superior Outer Parafovea

L_MAC_INL_N1 Measurement of the left eye, Macula, Inner Nuclear Layer, Nasal Inner Parafovea

L_MAC_INL_N2 Measurement of the left eye, Macula, Inner Nuclear Layer, Nasal Outer Parafovea

L_MAC_INL_I1 Measurement of the left eye, Macula, Inner Nuclear Layer, Inferior Inner Parafovea

L_MAC_INL_I2 Measurement of the left eye, Macula, Inner Nuclear Layer, Inferior Outer Parafovea

L_MAC_INL_T1 Measurement of the left eye, Macula, Inner Nuclear Layer, Temporal Inner Parafovea

L_MAC_INL_T2 Measurement of the left eye, Macula, Inner Nuclear Layer, Temporal Outer Parafovea

L_MAC_INL_C Measurement of the left eye, Macula, Inner Nuclear Layer, Center Fovea

L_MAC_OPL_S1 Measurement of the left eye, Macula, Outer Plexiform Layer, Superior Inner Parafovea

L_MAC_OPL_S2 Measurement of the left eye, Macula, Outer Plexiform Layer, Superior Outer Parafovea

L_MAC_OPL_N1 Measurement of the left eye, Macula, Outer Plexiform Layer, Nasal Inner Parafovea

L_MAC_OPL_N2 Measurement of the left eye, Macula, Outer Plexiform Layer, Nasal Outer Parafovea

L_MAC_OPL_I1 Measurement of the left eye, Macula, Outer Plexiform Layer, Inferior Inner Parafovea

L_MAC_OPL_I2 Measurement of the left eye, Macula, Outer Plexiform Layer, Inferior Outer Parafovea

L_MAC_OPL_T1 Measurement of the left eye, Macula, Outer Plexiform Layer, Temporal Inner Parafovea

L_MAC_OPL_T2 Measurement of the left eye, Macula, Outer Plexiform Layer, Temporal Outer Parafovea

L_MAC_OPL_C Measurement of the left eye, Macula, Outer Plexiform Layer, Center Fovea

L_MAC_ONL_S1 Measurement of the left eye, Macula, Outer Nuclear Layer, Superior Inner Parafovea

L_MAC_ONL_S2 Measurement of the left eye, Macula, Outer Nuclear Layer, Superior Outer Parafovea

L_MAC_ONL_N1 Measurement of the left eye, Macula, Outer Nuclear Layer, Nasal Inner Parafovea

L_MAC_ONL_N2 Measurement of the left eye, Macula, Outer Nuclear Layer, Nasal Outer Parafovea

L_MAC_ONL_I1 Measurement of the left eye, Macula, Outer Nuclear Layer, Inferior Inner Parafovea

L_MAC_ONL_I2 Measurement of the left eye, Macula, Outer Nuclear Layer, Inferior Outer Parafovea

L_MAC_ONL_T1 Measurement of the left eye, Macula, Outer Nuclear Layer, Temporal Inner Parafovea

L_MAC_ONL_T2 Measurement of the left eye, Macula, Outer Nuclear Layer, Temporal Outer Parafovea

L_MAC_ONL_C Measurement of the left eye, Macula, Outer Nuclear Layer, Center Fovea

L_MAC_RPE_S1 Measurement of the left eye, Macula, Retinal Pigment Epithelium, Superior Inner Parafovea

L_MAC_RPE_S2 Measurement of the left eye, Macula, Retinal Pigment Epithelium, Superior Outer Parafovea

L_MAC_RPE_N1 Measurement of the left eye, Macula, Retinal Pigment Epithelium, Nasal Inner Parafovea

L_MAC_RPE_N2 Measurement of the left eye, Macula, Retinal Pigment Epithelium, Nasal Outer Parafovea

L_MAC_RPE_I1 Measurement of the left eye, Macula, Retinal Pigment Epithelium, Inferior Inner Parafovea

L_MAC_RPE_I2 Measurement of the left eye, Macula, Retinal Pigment Epithelium, Inferior Outer Parafovea

L_MAC_RPE_T1 Measurement of the left eye, Macula, Retinal Pigment Epithelium, Temporal Inner Parafovea

L_MAC_RPE_T2 Measurement of the left eye, Macula, Retinal Pigment Epithelium, Temporal Outer Parafovea

L_MAC_RPE_C Measurement of the left eye, Macula, Retinal Pigment Epithelium, Center Fovea

L_MAC_PHOTO_S1 Measurement of the left eye, Macula, Unknown Layer, Superior Inner Parafovea

L_MAC_PHOTO_S2 Measurement of the left eye, Macula, Unknown Layer, Superior Outer Parafovea

L_MAC_PHOTO_N1 Measurement of the left eye, Macula, Unknown Layer, Nasal Inner Parafovea

L_MAC_PHOTO_N2 Measurement of the left eye, Macula, Unknown Layer, Nasal Outer Parafovea

L_MAC_PHOTO_I1 Measurement of the left eye, Macula, Unknown Layer, Inferior Inner Parafovea

L_MAC_PHOTO_I2 Measurement of the left eye, Macula, Unknown Layer, Inferior Outer Parafovea

L_MAC_PHOTO_T1 Measurement of the left eye, Macula, Unknown Layer, Temporal Inner Parafovea

L_MAC_PHOTO_T2 Measurement of the left eye, Macula, Unknown Layer, Temporal Outer Parafovea

L_MAC_PHOTO_C Measurement of the left eye, Macula, Unknown Layer, Center Fovea

Layer abbreviations include RNFL (Retinal Nerve Fiber Layer), GCL (Ganglion Cell Layer), IPL (Inner Plexiform Layer), INL (Inner Nuclear Layer), OPL (Outer Plexiform Layer), ONL (Outer Nuclear Layer), RPE (Retinal Pigment Epithelium), and IRL (Inner Retinal Layer).

Source

Steingrube, N. (2023). Analysis of early changes in the retina and their association with diabetic alterations of the corneal nerve fiber plexus in type 2 diabetes mellitus. Unpublished doctoral dissertation. Faculty of Medicine, Heinrich-Heine University Dusseldorf.

Department of Ophthalmology, University Hospital Dusseldorf, Heinrich Heine University, Germany

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`diagnostic` *Generic diagnostic function.*

Description

Generic diagnostic function.

Usage

```
diagnostic(object, ...)
```

Arguments

`object`	The object generated by the function hmr.
`...`	...

diagnostic.b3lmeta *Diagnostic function for b3lmeta object in jarbes*

Description

This function performers an approximated Bayesian cross-validation for a b3lmeta object

Usage

```
## S3 method for class 'b3lmeta'
diagnostic(
  object,
  post.p.value.cut = 0.05,
  study.names = NULL,
  size.forest = 0.4,
  lwd.forest = 0.2,
  shape.forest = 23,
  ...
)
```

Arguments

object	The object generated by the function b3lmeta.
post.p.value.cut	Posterior p-value cut point to assess outliers.
study.names	Character vector containing names of the studies used.
size.forest	Size of the center symbol mark in the forest-plot lines
lwd.forest	Thickness of the lines in the forest-plot
shape.forest	Type of symbol for the center mark in the forest-plot lines
...	...

diagnostic.bcdpmeta *Diagnostic function for bcdpmeta object in jarbes*

Description

This function performers an approximated Bayesian cross-validation for a bcmeta object and specially designed diagnostics to detect the existence of a biased component.

Usage

```
## S3 method for class 'bcdpmeta'
diagnostic(
  object,
  post.p.value.cut = 0.05,
  study.names = NULL,
  size.forest = 0.4,
  lwd.forest = 0.2,
  shape.forest = 23,
  bias.plot = TRUE,
  cross.val.plot = FALSE,
  level = c(0.5, 0.75, 0.95),
  x.lim = c(0, 1),
  y.lim = c(0, 10),
  x.lab = "P(Bias)",
  y.lab = "Mean Bias",
  title.plot = paste("Bias Diagnostics Contours (50%, 75% and 95%)"),
  kde2d.n = 25,
  marginals = TRUE,
  bin.hist = 30,
  color.line = "black",
  color.hist = "white",
  color.data.points = "black",
  alpha.data.points = 0.1,
  S = 5000,
  ...
)
```

Arguments

object	The object generated by the function b3lmeta.
post.p.value.cut	Posterior p-value cut point to assess outliers.
study.names	Character vector containing names of the studies used.
size.forest	Size of the center symbol mark in the forest-plot lines
lwd.forest	Thickness of the lines in the forest-plot
shape.forest	Type of symbol for the center mark in the forest-plot lines
bias.plot	Display the bias plot. The default is TRUE.
cross.val.plot	Display the cross validation plot. The default is FALSE.
level	Vector with the probability levels of the contour plot. The default values are: 0.5, 0.75, and 0.95.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.

title.plot	Text for setting a title in the bias plot.
kde2d.n	The number of grid points in each direction for the non-parametric density estimation. The default is 25.
marginals	If TRUE the marginal histograms of the posteriors are added to the plot.
bin.hist	The number of bins in for the histograms. The default value is 30.
color.line	The color of the contour lines. The default is "black.
color.hist	The color of the histogram bars. The default is "white".
color.data.points	The color of the data points. The default is "black".
alpha.data.points	Transparency of the data points.
S	The number of sample values from the joint posterior distribution used to approximate the contours. The default is S=5000.
...	...

`diagnostic.bcmeta` *Diagnostic function for bcmeta object in jarbes*

Description

This function performers an approximated Bayesian cross-validation for a bcmeta object and specially designed diagnostics to detect the existence of a biased component.

Usage

```
## S3 method for class 'bcmeta'
diagnostic(
  object,
  post.p.value.cut = 0.05,
  study.names = NULL,
  size.forest = 0.4,
  lwd.forest = 0.2,
  shape.forest = 23,
  bias.plot = TRUE,
  level = c(0.5, 0.75, 0.95),
  x.lim = c(0, 1),
  y.lim = c(0, 10),
  x.lab = expression(pi^{
     B
 }),
  y.lab = expression(mu[beta]),
  title.plot = paste("Bias Diagnostics Contours (50%, 75% and 95%)"),
  kde2d.n = 25,
  marginals = TRUE,
```

```
  bin.hist = 30,
  color.line = "black",
  color.hist = "white",
  color.data.points = "black",
  alpha.data.points = 0.1,
  S = 5000,
  ...
)
```

Arguments

object	The object generated by the function b3lmeta.
post.p.value.cut	Posterior p-value cut point to assess outliers.
study.names	Character vector containing names of the studies used.
size.forest	Size of the center symbol mark in the forest-plot lines
lwd.forest	Thickness of the lines in the forest-plot
shape.forest	Type of symbol for the center mark in the forest-plot lines
bias.plot	Display the bias plot. The default is TRUE.
level	Vector with the probability levels of the contour plot. The default values are: 0.5, 0.75, and 0.95.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot	Text for setting a title in the bias plot.
kde2d.n	The number of grid points in each direction for the non-parametric density estimation. The default is 25.
marginals	If TRUE the marginal histograms of the posteriors are added to the plot.
bin.hist	The number of bins in for the histograms. The default value is 30.
color.line	The color of the contour lines. The default is "black.
color.hist	The color of the histogram bars. The default is "white".
color.data.points	The color of the data points. The default is "black".
alpha.data.points	Transparency of the data points.
S	The number of sample values from the joint posterior distribution used to approximate the contours. The default is S=5000.
...	...

`diagnostic.bcmixmeta` *Diagnostic function for bcmixmeta object in jarbes*

Description

This function performers an approximated Bayesian cross-validation for a bcmeta object and specially designed diagnostics to detect the existence of a biased component.

Usage

```
## S3 method for class 'bcmixmeta'
diagnostic(
  object,
  post.p.value.cut = 0.05,
  study.names = NULL,
  size.forest = 0.4,
  lwd.forest = 0.2,
  shape.forest = 23,
  bias.plot = TRUE,
  cross.val.plot = FALSE,
  level = c(0.5, 0.75, 0.95),
  cut.point = 0,
  x.lim = c(0, 1),
  y.lim = c(0, 10),
  x.lab = "P(Bias|Data)",
  y.lab = expression(beta^new),
  title.plot = paste("Bias Diagnostics Contours (50%, 75% and 95%)"),
  kde2d.n = 25,
  marginals = TRUE,
  bin.hist = 30,
  color.line = "black",
  color.hist = "white",
  color.data.points = "black",
  alpha.data.points = 0.1,
  S = 5000,
  ...
)
```

Arguments

`object`	The object generated by the function b3lmeta.
`post.p.value.cut`	Posterior p-value cut point to assess outliers.
`study.names`	Character vector containing names of the studies used.
`size.forest`	Size of the center symbol mark in the forest-plot lines
`lwd.forest`	Thickness of the lines in the forest-plot

shape.forest	Type of symbol for the center mark in the forest-plot lines
bias.plot	Display the bias plot. The default is TRUE.
cross.val.plot	Display the cross validation plot. The default is FALSE.
level	Vector with the probability levels of the contour plot. The default values are: 0.5, 0.75, and 0.95.
cut.point	This is a reference point for the bias distribution. The default value is cut.point = 0 to understand if we can learn bias from the data
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot	Text for setting a title in the bias plot.
kde2d.n	The number of grid points in each direction for the non-parametric density estimation. The default is 25.
marginals	If TRUE the marginal histograms of the posteriors are added to the plot.
bin.hist	The number of bins in for the histograms. The default value is 30.
color.line	The color of the contour lines. The default is "black.
color.hist	The color of the histogram bars. The default is "white".
color.data.points	The color of the data points. The default is "black".
alpha.data.points	Transparency of the data points.
S	The number of sample values from the joint posterior distribution used to approximate the contours. The default is S=5000.
...	...

`diagnostic.bmeta` *Diagnostic function for bmeta object in jarbes*

Description

This function performers an approximated Bayesian cross-validation for a b3lmeta object

Usage

```
## S3 method for class 'bmeta'
diagnostic(
  object,
  post.p.value.cut = 0.05,
  median.w = 1.5,
  study.names = NULL,
  size.forest = 0.4,
```

```
  lwd.forest = 0.2,
  shape.forest = 23,
  ...
)
```

Arguments

object	The object generated by the function bmeta.
post.p.value.cut	Posterior p-value cut point to assess outliers.
median.w	Change color if median of a weight > median.w. The default value is 1.5.
study.names	Character vector containing names of the studies used.
size.forest	Size of the center symbol mark in the forest-plot lines
lwd.forest	Thickness of the lines in the forest-plot
shape.forest	Type of symbol for the center mark in the forest-plot lines
...	...

---

diagnostic.hmr *Diagnostic function for hmr object in jarbes*

Description

This function performers a specially designed diagnostic for a hmr object

Usage

```
## S3 method for class 'hmr'
diagnostic(
  object,
  median.w = 1.5,
  study.names,
  size.forest = 0.4,
  lwd.forest = 0.2,
  shape.forest = 23,
  mu.phi = TRUE,
  mu.phi.x.lim.low = -10,
  mu.phi.x.lim.up = 10,
  colour.hist.mu.phi = "royalblue",
  colour.prior.mu.phi = "black",
  colour.posterior.mu.phi = "blue",
  title.plot.mu.phi = "Prior-to-Posterior Sensitivity",
  title.plot.weights = "Outlier Detection",
  ...
)
```

Arguments

object	The object generated by the function hmr.
median.w	Change colour if median of a weight > median.w. The default value is 1.5.
study.names	Character vector containing names of the studies used.
size.forest	Size of the center symbol mark in the forest-plot lines
lwd.forest	Thickness of the lines in the forest-plot
shape.forest	Type of symbol for the center mark in the forest-plot lines
mu.phi	Prior-to-posterior sensitivity analysis of mu.phi. Default value is TRUE.
mu.phi.x.lim.low	Lower limit of the prior to posterior plot for mu.phi
mu.phi.x.lim.up	Upper limit of the prior to posterior plot for mu.phi
colour.hist.mu.phi	colour of the posterior mu.phi histogram
colour.prior.mu.phi	colour of the prior of mu.phi
colour.posterior.mu.phi	colour of the posterior of mu.phi
title.plot.mu.phi	Text for the title in the mu phi plot.
title.plot.weights	Text for the title of the posterior weights.
...	...

---

diagnostic.metarisk *Diagnostic function for metarisk object in jarbes*

Description

This function performers a specially designed diagnostic for a metarisk object

Usage

```
## S3 method for class 'metarisk'
diagnostic(
  object,
  median.w = 1.5,
  study.names,
  size.forest = 0.4,
  lwd.forest = 0.2,
  shape.forest = 23,
  ...
)
```

Arguments

object	The object generated by the function hmr.
median.w	Change color if median of a weight > median.w. The default value is 1.5.
study.names	Character vector containing names of the studies used.
size.forest	Size of the center symbol mark in the forest-plot lines
lwd.forest	Thickness of the lines in the forest-plot
shape.forest	Type of symbol for the center mark in the forest-plot lines
...	...

---

dpmeta *Bayesian Meta-Analysis with Dirichlet Process Priors*

Description

This function performers a Bayesian meta-analysis with DP as random effects

Usage

```
dpmeta(
  data,
  mean.mu.0 = 0,
  sd.mu.0 = 10,
  scale.sigma.between = 0.5,
  df.scale.between = 1,
  alpha.0 = 0.03,
  alpha.1 = 10,
  K = 30,
  nr.chains = 2,
  nr.iterations = 10000,
  nr.adapt = 1000,
  nr.burnin = 1000,
  nr.thin = 1,
  parallel = NULL
)
```

Arguments

data	A data frame with at least two columns with the following names: 1) TE = treatment effect, 2) seTE = the standard error of the treatment effect.
mean.mu.0	Prior mean of the mean of the base distribution default value is mean.mu.0 = 0.
sd.mu.0	Prior standard deviation of the base distribution, the default value is 10.
scale.sigma.between	Prior scale parameter for scale gamma distribution for the precision between studies. The default value is 0.5.

`df.scale.between`
: Degrees of freedom of the scale gamma distribution for the precision between studies. The default value is 1, which results in a Half Cauchy distribution for the standard deviation between studies. Larger values e.g. 30 corresponds to a Half Normal distribution.

`alpha.0`
: Lower bound of the uniform prior for the concentration parameter for the DPM, default value is alpha.0 = 0.03.

`alpha.1`
: Upper bound of the uniform prior for the concentration parameter for the DPM, default value is alpha.1 = 10.

`K`
: Maximum number of clusters in the DP, default value is K = 30.

`nr.chains`
: Number of chains for the MCMC computations, default 2.

`nr.iterations`
: Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.

`nr.adapt`
: Number of iterations in the adaptation process, default is 1000. Some models may need more iterations during adptation.

`nr.burnin`
: Number of iteration discard for burn-in period, default is 1000. Some models may need a longer burnin period.

`nr.thin`
: Thinning rate, it must be a positive integer, the default value 1

`parallel`
: NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The results of the object of the class bcmeta can be extracted with R2jags or with rjags. In addition a summary, a print and a plot functions are implemented for this type of object.

Value

This function returns an object of the class "dpmeta". This object contains the MCMC output of each parameter and hyper-parameter in the model and the data frame used for fitting the model.

References

Verde, P.E. (2021) A Bias-Corrected Meta-Analysis Model for Combining Studies of Different Types and Quality. Biometrical Journal; 1–17.

Examples

```
## Not run:
library(jarbes)


# Example: Stemcells

data("stemcells")
stemcells$TE = stemcells$effect.size
stemcells$seTE = stemcells$se.effect

bm1 = dpmmeta(stemcells)
```

```
summary(bm1)
plot(bm1, x.lim = c(-1, 7), y.lim = c(0, 1))

diagnostic(bm1, study.names = stemcells$trial,
           post.p.value.cut = 0.05,
           lwd.forest = 0.5, shape.forest = 4)

diagnostic(bm1, post.p.value.cut = 0.05,
           lwd.forest = 0.5, shape.forest = 4)

## End(Not run)
```

`dpmetareg` *Bayesian Meta-Analysis with Dirichlet Process Priors*

Description

This function performers a Bayesian meta-analysis with DP as random effects

Usage

```
dpmetareg(
  data,
  x,
  mean.mu.0 = 0,
  sd.mu.0 = 10,
  scale.sigma.between = 0.5,
  df.scale.between = 1,
  alpha.0 = 0.03,
  alpha.1 = 10,
  K = 30,
  nr.chains = 2,
  nr.iterations = 10000,
  nr.adapt = 1000,
  nr.burnin = 1000,
  nr.thin = 1,
  parallel = NULL
)
```

Arguments

`data`	A data frame with at least two columns with the following names: 1) TE = treatment effect, 2) seTE = the standard error of the treatment effect.
`x`	a covariate to perform meta-regression.
`mean.mu.0`	Prior mean of the mean of the base distribution default value is mean.mu.0 = 0.
`sd.mu.0`	Prior standard deviation of the base distribution, the default value is 10.

`scale.sigma.between`
: Prior scale parameter for scale gamma distribution for the precision between studies. The default value is 0.5.

`df.scale.between`
: Degrees of freedom of the scale gamma distribution for the precision between studies. The default value is 1, which results in a Half Cauchy distribution for the standard deviation between studies. Larger values e.g. 30 corresponds to a Half Normal distribution.

`alpha.0`
: Lower bound of the uniform prior for the concentration parameter for the DPM, default value is alpha.0 = 0.03.

`alpha.1`
: Upper bound of the uniform prior for the concentration parameter for the DPM, default value is alpha.1 = 10.

`K`
: Maximum number of clusters in the DPM, default value is K = 30.

`nr.chains`
: Number of chains for the MCMC computations, default 2.

`nr.iterations`
: Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.

`nr.adapt`
: Number of iterations in the adaptation process, default is 1000. Some models may need more iterations during adptation.

`nr.burnin`
: Number of iteration discard for burn-in period, default is 1000. Some models may need a longer burnin period.

`nr.thin`
: Thinning rate, it must be a positive integer, the default value 1.

`parallel`
: NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The results of the object of the class bcmeta can be extracted with R2jags or with rjags. In addition a summary, a print and a plot functions are implemented for this type of object.

Value

This function returns an object of the class "dpmetareg". This object contains the MCMC output of each parameter and hyper-parameter in the model and the data frame used for fitting the model.

References

Verde, P.E. (2021) A Bias-Corrected Meta-Analysis Model for Combining Studies of Different Types and Quality. Biometrical Journal; 1–17.

Examples

```
## Not run:
library(jarbes)



## End(Not run)
```

dpmmeta *Bayesian Meta-Analysis with Dirichlet Process Mixtures Priors*

Description

This function performers a Bayesian meta-analysis with DPM as random effects

Usage

```
dpmmeta(
  data,
  mean.mu.0 = 0,
  sd.mu.0 = 10,
  scale.sigma.between = 0.5,
  df.scale.between = 1,
  alpha.0 = 0.03,
  alpha.1 = 10,
  K = 5,
  nr.chains = 2,
  nr.iterations = 10000,
  nr.adapt = 1000,
  nr.burnin = 1000,
  nr.thin = 1,
  parallel = NULL
)
```

Arguments

`data`	A data frame with at least two columns with the following names: 1) TE = treatment effect, 2) seTE = the standard error of the treatment effect.
`mean.mu.0`	Prior mean of the mean of the base distribution default value is mean.mu.0 = 0.
`sd.mu.0`	Prior standard deviation of the base distribution, the default value is 10.
`scale.sigma.between`	Prior scale parameter for scale gamma distribution for the precision between studies. The default value is 0.5.
`df.scale.between`	Degrees of freedom of the scale gamma distribution for the precision between studies. The default value is 1, which results in a Half Cauchy distribution for the standard deviation between studies. Larger values e.g. 30 corresponds to a Half Normal distribution.
`alpha.0`	Lower bound of the uniform prior for the concentration parameter for the DPM, default value is alpha.0 = 0.03.
`alpha.1`	Upper bound of the uniform prior for the concentration parameter for the DPM, default value is alpha.1 = 10.
`K`	Maximum number of clusters in the DPM, default value is K = 5.

nr.chains	Number of chains for the MCMC computations, default 2.
nr.iterations	Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.
nr.adapt	Number of iterations in the adaptation process, default is 1000. Some models may need more iterations during adptation.
nr.burnin	Number of iteration discard for burn-in period, default is 1000. Some models may need a longer burnin period.
nr.thin	Thinning rate, it must be a positive integer, the default value 1.
parallel	NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The results of the object of the class bcmeta can be extracted with R2jags or with rjags. In addition a summary, a print and a plot functions are implemented for this type of object.

Value

This function returns an object of the class "bmeta". This object contains the MCMC output of each parameter and hyper-parameter in the model and the data frame used for fitting the model.

References

Verde, P.E. (2021) A Bias-Corrected Meta-Analysis Model for Combining Studies of Different Types and Quality. Biometrical Journal; 1–17.

Examples

```
## Not run:
library(jarbes)


# Example: Stemcells

data("stemcells")
stemcells$TE = stemcells$effect.size
stemcells$seTE = stemcells$se.effect

bm1 = dpmmeta(stemcells)
summary(bm1)
plot(bm1, x.lim = c(-1, 7), y.lim = c(0, 1))

diagnostic(bm1, study.names = stemcells$trial,
           post.p.value.cut = 0.05,
           lwd.forest = 0.5, shape.forest = 4)

diagnostic(bm1, post.p.value.cut = 0.05,
           lwd.forest = 0.5, shape.forest = 4)

## End(Not run)
```

effect *Generic effect function.*

Description

Generic effect function.

Usage

```
effect(object, ...)
```

Arguments

object	The object generated by the function hmr.
...	...

effect.hmr *Posterior distribution of Effectiveness for a subgroup of patients*

Description

This function estimates the posterior distribution for a subgroup of patients identified with the function hmr (Hierarchical Meta-Regression).

Usage

```
## S3 method for class 'hmr'
effect(
  object,
  B.lower = 0,
  B.upper = 3,
  k = 1,
  level = c(0.5, 0.75, 0.95),
  x.lim = c(-9, 5),
  y.lim = c(-1, 5),
  x.lab = "Baseline risk",
  y.lab = "Effectiveness",
 title.plot = paste("Posterior Effectiveness for a subgroup (50%, 75% and 95%)"),
  kde2d.n = 25,
  marginals = TRUE,
  bin.hist = 30,
  color.line = "black",
  color.hist = "white",
  color.data.points = "black",
  alpha.data.points = 0.1,
```

```
  S = 5000,
  display.probability = FALSE,
  line.no.effect = 0,
  font.size.title = 20,
  ...
)
```

Arguments

object	The object generated by the function hmr.
B.lower	Lower limit of bias correction. The default is 0 meaning no bias correction.
B.upper	Upper limit of bias correction. The default is 3 meaning three times bias correction.
k	Covariable number indicating the subgroup.
level	Vector with the probability levels of the contour plot. The default values are: 0.5, 0.75, and 0.95.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot	Text for setting a title in the bias plot.
kde2d.n	The number of grid points in each direction for the non-parametric density estimation. The default is 25.
marginals	If TRUE the marginal histograms of the posteriors are added to the plot.
bin.hist	The number of bins in for the histograms. The default value is 30.
color.line	The color of the contour lines. The default is "black.
color.hist	The color of the histogram bars. The default is "white".
color.data.points	The color of the data points. The default is "black".
alpha.data.points	Transparency of the data points.
S	The number of sample values from the joint posterior distribution used to approximate the contours. The default is S=5000.
display.probability	Logical, if TRUE the figure display probabilities.
line.no.effect	Horizontal line used as reference for no effect.
font.size.title	Font size of the title.
...	...

fnrpcr *Meta-Analysis: Variation in False-Negative Rate of Reverse Transcriptase Polymerase Chain Reaction–Based SARS-CoV-2 Tests by Time Since Exposure*

Description

A dataset summarizing the variation in false-negative rates of reverse transcriptase polymerase chain reaction (RT-PCR)–based SARS-CoV-2 tests as a function of time since exposure.

Format

A data frame with 410 rows and 11 columns. Each row represents the results from a study. The columns include:

study Name of the author conducting the study.

test Type of testing performed.

day Number of days since symptom onset.

day_min Minimum number of days since symptom onset. Applicable for studies by Guo et al. and Kim et al.

day_max Maximum number of days since symptom onset. Applicable for studies by Guo et al. and Kim et al.

n Total number of tests conducted on a given day.

test_pos Number of positive test results.

inconclusive Number of inconclusive test results. Applicable for studies by Kujawski et al. and Danis et al.

nqp Number of positive but non-quantifiable test results, where the viral load is below the quantification threshold of log10(1) copies/1000 cells.

pct_pos Proportion of positive tests expressed as a percentage.

Source

Kucirka LM, Lauer SA, Laeyendecker O, Boon D, Lessler J. Variation in False-Negative Rate of Reverse Transcriptase Polymerase Chain Reaction-Based SARS-CoV-2 Tests by Time Since Exposure. Ann Intern Med. 2020 Aug 18;173(4):262-267. doi: 10.7326/M20-1495. Epub 2020 May 13. PMID: 32422057; PMCID: PMC7240870.

forestplot_compare *Forest Plot Comparison for One or Two Models*

Description

Creates a forest plot comparing parameter estimates from either: - a single model with one parameter set. - a single model with two different parameter sets. - two different models with matching parameters.

Usage

```
forestplot_compare(
  model1,
  model2 = NULL,
  pars,
  pars2 = NULL,
  plotmath.labels = NULL,
  plotmath.labels2 = NULL,
  study.labels = NULL,
  consolidate.param.labels = FALSE,
  model1.name = "Model 1",
  model2.name = "Model 2",
  model.legend.title = "Model",
  ref.lines = c(0),
  colors = c("blue", "red"),
  point.size = 3,
  point.shapes = c(16, 17),
  prob = 0.5,
  prob.outer = 0.9,
  point.est = "median",
  x.lab = "Estimate",
  y.lab = NULL,
  inner.line.thickness = 1.5,
  outer.line.thickness = 0.5,
  x.lim = NULL,
  param.distance = 0.3,
  group.spacing = 1,
  flip.coords = FALSE,
  x.label.angle = 0,
  study.label.size = 11,
  ...
)
```

Arguments

model1	First model object. Can be an 'mcmc.list' object, a model with BUGS output, a matrix, or a data frame of MCMC draws.

`model2` Optional second model object. If omitted, the function can compare two parameter sets within model1. Accepted types are the same as ‘model1‘.

`pars` Character vector of parameter names for the first model or first parameter set

`pars2` Optional character vector of parameter names for the second parameter set in model1. Ignored if model2 is provided.

`plotmath.labels` Optional vector of plotmath expressions as strings to label parameters in the first model or set.

`plotmath.labels2` Optional vector of plotmath expressions for parameters in the second parameter set in model1.

`study.labels` Optional character vector of labels to use for studies on the y-axis. If provided, these labels will replace parameter names, and each study label will correspond to a pair of estimates.

`consolidate.param.labels` Logical. If ‘TRUE‘ and ‘study.labels‘ is ‘NULL‘ for comparison plots, displays a single consolidated label for the parameter pair. If ‘FALSE‘ (default), displays a label for each individual parameter. Ignored for single model plots.

`model1.name` Label for the first model in the plot legend.

`model2.name` Label for the second model or parameter set in the legend.

`model.legend.title` Title for the model legend.

`ref.lines` Numeric vector of vertical reference lines to display.

`colors` Vector of colors for each model or parameter set.

`point.size` Size of point estimate markers.

`point.shapes` Shapes used for points corresponding to each model or set

`prob` Width of the inner credible interval (e.g. 0.5 for 50 % interval).

`prob.outer` Width of the outer credible interval (e.g. 0.9 for 90% interval).

`point.est` Which point estimate to use: "median" or "mean", default is "median".

`x.lab` Label for the x-axis.

`y.lab` Label for the y-axis.

`inner.line.thickness` Thickness of inner credible interval lines.

`outer.line.thickness` Thickness of outer credible interval lines.

`x.lim` Optional numeric vector of length two to fix x-axis limits.

`param.distance` Numeric, controls the vertical distance between points for different models/parameter sets within the same study. Default is 0.3.

`group.spacing` Numeric, controls the vertical spacing between different studies/group of parameters. Default is 1.

`flip.coords` Logical, if TRUE, flips the x and y axes, creating a horizontal plot. Default is FALSE.

`x.label.angle` Numeric. Angle for x-axis labels when 'flip.coords = TRUE'. Default is 0.

`study.label.size` Numeric. Text size for study or parameter labels on the y-axis (or x-axis if flipped).

`...` ...

`ganzfeld` *Meta-Analysis of Free-Response Studies, 1992–2008: Assessing the Noise Reduction Model in Parapsychology*

Description

This dataset contains the results of 30 studies on the ganzfeld procedure, a technique used in parapsychology to test for extrasensory perception (ESP). Each row represents a study, with columns for the study ID, author, year of publication, number of hits (successful ESP trials), and total number of trials conducted.

Format

A data frame with 30 rows and 5 columns.

study Study ID

author First author

year Year of publication

n Number of trials

y Number of hits

Source

Storm, Lance, Patrizio E. Tressoldi, and Lorenzo Di Risio. "Meta-analysis of free-response studies, 1992–2008: Assessing the noise reduction model in parapsychology." Psychological bulletin 136.4 (2010): 471.

`healing` *Efficacy of diabetic foot healing using adjuvant treatments*

Description

Meta-analysis of 35 randomized controlled trials investigating the effectiveness in the application of adjuvant therapies for diabetic patients compared to medical routine care, where the endpoint was healing without amputations within a period less than or equal to one year.

Format

A matrix with 35 rows and 9 columns. Each row represents study results, the columns are:

Study Name of the first author and year.

n_t Number of patients in the treatment group.

n_c Number of patients in the control group.

y_t Number of heal patients in the treatment group.

y_c Number of heal patients in the control group.

ndrop Total number of drop out patients.

fup_weeks Length of followup in weeks.

PAD Inclusion of patients with peripheral arterial disease.

wagner_4 Inclusion of patients with Wagner score 3 and 4.

Source

The data were obtainded from: Centre for Clinical Practice at NICE (UK and others) (2011), Clinical guideline 119. Diabetic foot problems: Inpatient Management of Diabetic Foot Problems. Tech. rep., National Institute for Health and Clinical Excellence.

References

Verde, P.E. (2018) The Hierarchical Meta-Regression Approach and Learning from Clinical Evidence. Technical Report.

`healingipd` *Individual participant data for diabetic patients*

Description

Prospective cohort study.

Format

A dataframe with 260 rows and 18 columns. Each row represents a patient, the columns are:

healing.without.amp Outcome variable: Healing without amputation with in one year.

duration_lesion_days Duration of leasions in days at baseline.

PAD Peripheral arterial disease yes/no.

neuropathy Neuropathy yes/no.

first.ever.lesion First ever lesion yes/no.

no.continuous.care No continuous care yes/no.

male yes/no.

diab.typ2 Diabetes type 2 yes/no.

insulin Insulin dependent yes/no.

HOCHD HOCHD yes/no.

HOS HOCHD yes/no.

CRF CRF yes/no.

dialysis Dialysis yes/no.

DNOAP DNOAP yes/no.

smoking.ever Ever smoke yes/no.

age Age at baseline in years.

diabdur Diabetes duration at baseline.

wagner.class Wagner score 1-2 vs. 3-4-5.

Source

Morbach, S, et al. (2012). Long-Term Prognosis of Diabetic Foot Patients and Their Limbs: Amputation and death over the course of a decade,Diabetes Care, 35, 10, 2012-2017.

References

Verde, P.E. (2018) The Hierarchical Meta-Regression Approach and Learning from Clinical Evidence. Technical Report.

`hips` *Meta-analysis: generalized evidence synthesis of total hip replacement*

Description

Meta-analysis of 15 studies investigating total hip replacement to compare the risk of revision of cemented and uncemented implantfixation modalities, by pooling treatment effectestimates from OS and RCTs.

Format

A dataframe with 15 rows and 12 columns. Each row represents study results, the columns are:

Study Author and year.

Study_type Study desing.

N_of_revisions Number of revisions.

Total_cemented Total number of cemmented cases.

N_of_revisions_uncemented Number of uncemented revisions.

Total_uncemented Total number of uncemmented cases.

Relative_risks_computed RR calculated from the two by two table.

L95CI Lower 95prc CI

U95CI Upper 95prc CI

mean_age Mean age of the study

proportion_of_women Proportion of women in the study.

Follow_up Time to follow-up in years.

Source

Schnell-Inderst P, Iglesias CP, Arvandi M, Ciani O, Matteucci Gothe R, Peters J, Blom AW, Taylor RS and Siebert U (2017). A bias-adjusted evidence synthesis of RCT and observational data: the case of total hip replacement. Health Econ. 26(Suppl. 1): 46–69.

`hmr` *Bayesian meta-analysis to combine aggregated and individual participant data for cross design synthesis.*

Description

This function performers a Bayesian cross design synthesis. The function fits a hierarchical meta-regression model based on a bivariate random effects model.

Usage

```
hmr(
  data,
  two.by.two = TRUE,
  dataIPD,
  re = "normal",
  link = "logit",
  mean.mu.1 = 0,
  mean.mu.2 = 0,
  mean.mu.phi = 0,
  sd.mu.1 = 1,
  sd.mu.2 = 1,
  sd.mu.phi = 1,
  sigma.1.upper = 5,
  sigma.2.upper = 5,
  sigma.beta.upper = 5,
  mean.Fisher.rho = 0,
  sd.Fisher.rho = 1/sqrt(2),
  df = 4,
  df.estimate = FALSE,
  df.lower = 3,
  df.upper = 20,
  split.w = FALSE,
  nr.chains = 2,
  nr.iterations = 10000,
```

```
  nr.adapt = 1000,
  nr.burnin = 1000,
  nr.thin = 1,
  parallel = NULL
)
```

Arguments

data	Aggregated data results: a data frame where the first four columns containing the number of events in the control group (yc), the number of patients in the control group (nc), the number of events in the treatment group (yt) and the number of patients in the treatment group (nt). If two.by.two = TRUE a data frame where each line contains the trial results with column names: yc, nc, yt, nt.
two.by.two	If TRUE indicates that the trial results are with names: yc, nc, yt, nt.
dataIPD	Individual participant data: a data frame where the first column is the outcome variable and the other columns represent individual participant charachteristics.
re	Random effects distribution for the resulting model. Possible values are *normal* for bivariate random effects and *sm* for scale mixtures.
link	The link function used in the model. Possible values are *logit*, *cloglog probit*.
mean.mu.1	Prior mean of baseline risk, default value is 0.
mean.mu.2	Prior mean of treatment effect, default value is 0.
mean.mu.phi	Prior mean of the bias parameter which measures the difference between the baseline mean mu.1 and the intercept parameter of the logistic regression of the individual participant data. The defalut vaule is 0.
sd.mu.1	Prior standard deviation of mu.1, default value is 1. The default prior of mu.1 is a logistic distribution with mean 0 and dispersion 1. The implicit prior for mu.1 in the probability scale is a uniform between 0 and 1.
sd.mu.2	Prior standard deviation of mu.2, default value is 1. The default prior of mu.2 is a logistic distribution with mean 0 and dispersion 1. The implicit prior for mu.2 in the probability scale is a uniform between 0 and 1.
sd.mu.phi	Prior standard deviation of mu.phi, default value is 1.
sigma.1.upper	Upper bound of the uniform prior of sigma.1, default value is 5.
sigma.2.upper	Upper bound of the uniform prior of sigma.2, default value is 5.
sigma.beta.upper	Upper bound of the uniform prior of sigma.beta, default value is 5.
mean.Fisher.rho	Mean of rho in the Fisher scale, default value is 0.
sd.Fisher.rho	Standard deviation of rho in the Fisher scale, default value is 1/sqrt(2).
df	If de.estimate = FALSE, then df is the degrees of freedom for the scale mixture distribution, default value is 4.
df.estimate	Estimate the posterior of df. The default value is FALSE.
df.lower	Lower bound of the prior of df. The default value is 3.
df.upper	Upper bound of the prior of df. The default value is 30.

split.w	Split the w parameter in two independent weights one for each random effect. The default value is FALSE.
nr.chains	Number of chains for the MCMC computations, default 5.
nr.iterations	Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.
nr.adapt	Number of iterations in the adaptation process, default is 1000. Some models may need more iterations during adptation.
nr.burnin	Number of iteration discarded for burnin period, default is 1000. Some models may need a longer burnin period.
nr.thin	Thinning rate, it must be a positive integer, the default value 1.
parallel	NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The number of events in the control and treated group are modeled with two conditional Binomial distributions and the random-effects are based on a bivariate scale mixture of Normals.

The individual participant data is modeled as a Bayesian logistic regression for participants in the control group. Coefficients in the regression are modeled as exchangeables.

The function calculates the implicit hierarchical meta-regression, where the treatment effect is regressed to the baseline risk (rate of events in the control group). The scale mixture weights are used to adjust for internal validity and structural outliers identification.

The implicit hierarchical meta-regression is used to predict the treatment effect for subgroups of individual participant data.

Computations are done by calling JAGS (Just Another Gibbs Sampler) to perform MCMC (Markov Chain Monte Carlo) sampling and returning an object of the class *mcmc.list*.

Installation of JAGS: It is important to note that R 3.3.0 introduced a major change in the use of toolchain for Windows. This new toolchain is incompatible with older packages written in C++. As a consequence, if the installed version of JAGS does not match the R installation, then the rjags package will spontaneously crash. Therefore, if a user works with R version >= 3.3.0, then JAGS must be installed with the installation program JAGS-4.2.0-Rtools33.exe. For users who continue using R 3.2.4 or an earlier version, the installation program for JAGS is the default installer JAGS-4.2.0.exe.

Value

This function returns an object of the class "hmr". This object contains the MCMC output of each parameter and hyper-parameter in the model, the data frame used for fitting the model, the link function, type of random effects distribution and the splitting information for conflict of evidence analysis.

The results of the object of the class hmr can be extracted with R2jags. In addition a summary, a print and a plot function are implemented for this type of object.

References

Verde, P.E, Ohmann, C., Icks, A. and Morbach, S. (2016) Bayesian evidence synthesis and combining randomized and nonrandomized results: a case study in diabetes. Statistics in Medicine. Volume 35, Issue 10, 10 May 2016, Pages: 1654 to 1675.

Verde, P. E. (2019) Learning from Clinical Evidence: The Hierarchical Meta-Regression Approach. Biometrical Journal. Biometrical Journal; 1-23.

Examples

```
## Not run:
library(jarbes)

data("healing")
AD <- healing[, c("y_c", "n_c", "y_t", "n_t")]

data("healingipd")

IPD <- healingipd[, c("healing.without.amp", "PAD", "neuropathy",
"first.ever.lesion", "no.continuous.care", "male", "diab.typ2",
"insulin", "HOCHD", "HOS", "CRF", "dialysis", "DNOAP", "smoking.ever",
"diabdur", "wagner.class")]

mx2 <- hmr(AD, two.by.two = FALSE,
           dataIPD = IPD,
           re = "sm",
           link = "logit",
           sd.mu.1 = 2,
           sd.mu.2 = 2,
           sd.mu.phi = 2,
           sigma.1.upper = 5,
           sigma.2.upper = 5,
           sigma.beta.upper = 5,
           sd.Fisher.rho = 1.25,
           df.estimate = FALSE,
           df.lower = 3,
           df.upper = 10,
           nr.chains = 1,
           nr.iterations = 1500,
           nr.adapt = 100,
           nr.thin = 1)

print(mx2)




# This experiment corresponds to Section 4 in Verde (2018).
#
# Experiment: Combining aggretated data from RCTs and a single
# observational study with individual participant data.
#
```

```
# In this experiment we assess conflict of evidence between the RCTs
# and the observational study with a partially identified parameter
# mu.phi.
#
# We run two simulated data: 1) mu.phi = 0.5 which is diffucult to
# identify. 2) mu.phi = 2 which can be identify. The simulations are
# used to see if the hmr() function can recover mu.phi.
#


library(MASS)
library(ggplot2)
library(jarbes)
library(gridExtra)
library(mcmcplots)
library(R2jags)

# Simulation of the IPD data

invlogit <- function (x)
{
 1/(1 + exp(-x))
}


 #Experiment 1: External validity bias

set.seed(2018)
 # mean control
 pc <- 0.7
 # mean treatment
pt <- 0.4
 # reduction of "amputations" odds ratio
OR <- (pt/(1-pt)) /(pc/(1-pc))
OR

# mu_2
log(OR)
mu.2.true <- log(OR)
 #sigma_2
 sigma.2.true <- 0.5
 # mu_1
mu.1.true <- log(pc/(1-pc))
mu.1.true
#sigma_1
sigma.1.true <- 1
# rho
rho.true <- -0.5
Sigma <- matrix(c(sigma.1.true^2, sigma.1.true*sigma.2.true*rho.true,
                  sigma.1.true*sigma.2.true*rho.true, sigma.2.true^2),
                  byrow = TRUE, ncol = 2)
Sigma
```

```
theta <- mvrnorm(35, mu = c(mu.1.true, mu.2.true),
                 Sigma = Sigma )


plot(theta, xlim = c(-2,3))
abline(v=mu.1.true, lty = 2)
abline(h=mu.2.true, lty = 2)
abline(a = mu.2.true, b=sigma.2.true/sigma.1.true * rho.true, col = "red")
abline(lm(theta[,2]~theta[,1]), col = "blue")

# Target group
mu.T <- mu.1.true + 2 * sigma.1.true
abline(v=mu.T, lwd = 3, col = "blue")
eta.true <- mu.2.true + sigma.2.true/sigma.1.true*rho.true* mu.T
eta.true
exp(eta.true)
abline(h = eta.true, lty =3, col = "blue")
# Simulation of each primary study:
n.c <- round(runif(35, min = 30, max = 60),0)
n.t <- round(runif(35, min = 30, max = 60),0)
y.c <- y.t <- rep(0, 35)
p.c <- exp(theta[,1])/(1+exp(theta[,1]))
p.t <- exp(theta[,2]+theta[,1])/(1+exp(theta[,2]+theta[,1]))
for(i in 1:35)
{
  y.c[i] <- rbinom(1, n.c[i], prob = p.c[i])
  y.t[i] <- rbinom(1, n.t[i], prob = p.t[i])
}

AD.s1 <- data.frame(yc=y.c, nc=n.c, yt=y.t, nt=n.t)

# Data set for mu.phi = 0.5 ......................................

# Parameters values
mu.phi.true <- 0.5
pc = 0.7
mu.1.true= log(pc/(1-pc))

beta0 <- mu.1.true + mu.phi.true
beta1 <- 2.5
beta2 <- 2

# Regression variables

x1 <- rnorm(200)
x2 <- rbinom(200, 1, 0.5)

# Binary outcome as a function of "b0 + b1 * x1 + b2 * x2"

y <- rbinom(200, 1,
         invlogit(beta0 + beta1 * x1 + beta2 * x2))
```

```
# Preparing the plot to visualize the data
jitter.binary <- function(a, jitt = 0.05)

 ifelse(a==0, runif(length(a), 0, jitt),
        runif(length(a), 1-jitt, 1))


plot(x1, jitter.binary(y), xlab = "x1",
    ylab = "Success probability")

curve(invlogit(beta0 + beta1*x),
     from = -2.5, to = 2.5, add = TRUE, col ="blue", lwd = 2)
curve(invlogit(beta0 + beta1*x + beta2),
     from = -2.5, to = 2.5, add = TRUE, col ="red", lwd =2)
legend("bottomright", c("b2 = 0", "b2 = 2"),
      col = c("blue", "red"), lwd = 2, lty = 1)

noise <- rnorm(100*20)
dim(noise) <- c(100, 20)
n.names <- paste(rep("x", 20), seq(3, 22), sep="")
colnames(noise) <- n.names

data.IPD <- data.frame(y, x1, x2, noise)


# Application of HMR ......................................

res.s2 <- hmr(AD.s1, two.by.two = FALSE,
             dataIPD = data.IPD,
             sd.mu.1 = 2,
             sd.mu.2 = 2,
             sd.mu.phi = 2,
             sigma.1.upper = 5,
             sigma.2.upper = 5,
             sd.Fisher.rho = 1.5,
             parallel="jags.parallel")


print(res.s2)

# Data set for mu.phi = 2 .................................
# Parameters values

mu.phi.true <- 2
beta0 <- mu.1.true + mu.phi.true
beta1 <- 2.5
beta2 <- 2

# Regression variables
x1 <- rnorm(200)
x2 <- rbinom(200, 1, 0.5)
# Binary outcome as a function of "b0 + b1 * x1 + b2 * x2"
y <- rbinom(200, 1,
```

```
           invlogit(beta0 + beta1 * x1 + beta2 * x2))

# Preparing the plot to visualize the data
jitter.binary <- function(a, jitt = 0.05)

 ifelse(a==0, runif(length(a), 0, jitt),
        runif(length(a), 1-jitt, 1))

plot(x1, jitter.binary(y), xlab = "x1",
    ylab = "Success probability")

curve(invlogit(beta0 + beta1*x),
     from = -2.5, to = 2.5, add = TRUE, col ="blue", lwd = 2)
curve(invlogit(beta0 + beta1*x + beta2),
     from = -2.5, to = 2.5, add = TRUE, col ="red", lwd =2)
legend("bottomright", c("b2 = 0", "b2 = 2"),
      col = c("blue", "red"), lwd = 2, lty = 1)

noise <- rnorm(100*20)
dim(noise) <- c(100, 20)
n.names <- paste(rep("x", 20), seq(3, 22), sep="")
colnames(noise) <- n.names

data.IPD <- data.frame(y, x1, x2, noise)

# Application of HMR ........................................


res.s3 <- hmr(AD.s1, two.by.two = FALSE,
             dataIPD = data.IPD,
             sd.mu.1 = 2,
             sd.mu.2 = 2,
             sd.mu.phi = 2,
             sigma.1.upper = 5,
             sigma.2.upper = 5,
             sd.Fisher.rho = 1.5,
             parallel="jags.parallel"
)

print(res.s3)

# Posteriors for mu.phi ........................
attach.jags(res.s2)
mu.phi.0.5 <- mu.phi
df.phi.05 <- data.frame(x = mu.phi.0.5)

attach.jags(res.s3)
mu.phi.1 <- mu.phi
df.phi.1 <- data.frame(x = mu.phi.1)


p1 <- ggplot(df.phi.05, aes(x=x))+
 xlab(expression(mu[phi])) +
```

```
 ylab("Posterior distribution")+
 xlim(c(-7,7))+
 geom_histogram(aes(y=..density..),fill = "royalblue",
             colour = "black", alpha= 0.4, bins=60) +
 geom_vline(xintercept = 0.64, colour = "black", size = 1.7, lty = 2)+
 geom_vline(xintercept = 0.5, colour = "black", size = 1.7, lty = 1)+
 stat_function(fun = dlogis,
               n = 101,
               args = list(location = 0, scale = 1), size = 1.5) + theme_bw()

p2 <- ggplot(df.phi.1, aes(x=x))+
 xlab(expression(mu[phi])) +
 ylab("Posterior distribution")+
 xlim(c(-7,7))+
 geom_histogram(aes(y=..density..),fill = "royalblue",
                colour = "black", alpha= 0.4, bins=60) +
 geom_vline(xintercept = 2.2, colour = "black", size = 1.7, lty = 2)+
 geom_vline(xintercept = 2, colour = "black", size = 1.7, lty = 1)+
 stat_function(fun = dlogis,
               n = 101,
               args = list(location = 0, scale = 1), size = 1.5) + theme_bw()

grid.arrange(p1, p2, ncol = 2, nrow = 1)


# Cater plots for regression coefficients ........................

var.names <- names(data.IPD[-1])
v <- paste("beta", names(data.IPD[-1]), sep = ".")

mcmc.x.2 <- as.mcmc.rjags(res.s2)
mcmc.x.3 <- as.mcmc.rjags(res.s3)

greek.names <- paste(paste("beta[",1:22, sep=""),"]", sep="")
par.names <- paste(paste("beta.IPD[",1:22, sep=""),"]", sep="")

caterplot_compare(mcmc.x.2, mcmc.x.3, par.names,
                  plotmath_labels = greek.names,
                  ref_lines = c(0, 2, 2.5))

# End of the examples.


## End(Not run)
```

---

longcovid *Meta-analysis: Long-COVID Health Outcomes*

Description

This dataset is based on a comprehensive meta-analysis of 33 studies, sourced from various databases, including the Cochrane COVID-19 Study Register (comprising the Cochrane Central Register of Controlled Trials, Medline, Embase, clinicaltrials.gov, the World Health Organization's International Clinical Trials Registry Platform, and medRxiv) and the World Health Organization's COVID-19 research database. The analysis focused on evaluating health outcomes related to Long-COVID in controlled studies. Specifically, it examines the health outcomes in terms of incident medicinal diagnoses.

The dataset includes the assessment of risk of bias based on the Joanna Briggs Institute (JBI) tool for cohort studies, along with various participant and study details such as sample size, effect type, follow-up time, and disease severity.

Format

A data frame with 271 rows and 27 columns. Each row represents the results of a single study. The columns include:

study Name of the first author and publication year.

category Category of the health outcome.

outcome_disease Definition of the health outcome or disease.

data_source Type of data source: Administrative data, Health records, Patients claims, Survey, Combination of health records and claims.

sample_size Total number of participants.

effect_type Type of effect reported: RR (Relative Risk), HR (Hazard Ratio), or OR (Odds Ratio).

effect Estimated effect based on the effect type.

TE Logarithm of the estimated effect.

seTE Standard error of the logarithm of the estimated effect.

rate_control Event rate in the control group.

follow_up_time Follow-up time in weeks.

mean_age Mean age of the participants.

disease_severity Indicator for inclusion of severe or critical disease participants ("no" or "yes").

reinfection Indicator for inclusion of reinfected participants ("no" or "yes").

no_of_confounders Number of confounders for which adjustments were made in the study.

uncertainty_of_confounders high if ROB4 OR ROB5 is high or unclear or low otherwise.

list_of_confounders List of confounders considered in the study.

ROB1 Were the two groups similar and recruited from the same population?

ROB2 Were the exposures measured similarly to assign participants to exposed and unexposed groups?

ROB3 Was the exposure measured in a valid and reliable way?

ROB4 Were confounding factors identified?

ROB5 Were strategies to address confounding factors stated?

ROB6 Were the groups/participants free of the outcome at the start of the study (or at the moment of exposure)?

ROB7 Were the outcomes measured in a valid and reliable way?

ROB8 Was the follow-up time reported and sufficient to allow outcomes to occur?

ROB9 Was follow-up complete, and if not, were the reasons for loss to follow-up described and explored?

ROB10 Were strategies to address incomplete follow-up utilized?

ROB11 Was appropriate statistical analysis used?

Source

Franco JVA, Garegnani LI, Metzendorf MI, Heldt K, Mumm R, Scheidt-Nave C. Post-COVID-19 conditions in adults: systematic review and meta-analysis of health outcomes in controlled studies. BMJ Medicine. 2024;3:e000723.

`macula_rwe` *Meta-analysis: 83 observational studies assessing the effectiveness of intravitreal therapy for diabetic maculaedema*

Description

Meta-analysis of 82 studies comparing 12-month visual acuity change results in routine clinical practices of intravitreal therapy for diabetic maculaedema (DME) to the change in RCTs by pooling data published in the last decade on treated eyes of treatment effect from OS.

Format

A dataframe with 83 rows and 24 columns. Each row represents study results, the columns are:

therapy Used Medication

author_year Author and year.

study_design Study type/Design

eyes Number of tested eyes.

TE Mean Change in Visual Acuity after 12-Months. Where Visual Acuity is measured in VAR (Visual Acuity Rating) score

seTE Standard Error of the Treatment Effect

lower_95pct_ci Lower 95prc CI for TE

upper_95pct_ci Upper 95prc CI for TE

number_of_patients_at_baseline Number of Patients in Study at Baseline

mean_age The mean age of patients per study

sd_age The standard deviation of age of patients per study

se_age The standard error of age of patients per study

baseline_va Mean Visual Acuity at Baseline. Where Visual Acuity is measured in VAR (Visual Acuity Rating) score

sd_baseline_va The standard deviation of Visual Acuity at Baseline. Where Visual Acuity is measured in VAR (Visual Acuity Rating) score

se_baseline_va The standard error of Visual Acuity at Baseline. Where Visual Acuity is measured in VAR (Visual Acuity Rating) score

12_month_va Mean Visual Acuity after 12 months. Where Visual Acuity is measured in VAR (Visual Acuity Rating) score

sd_12_month_va The standard deviation of Visual Acuity after 12 months. Where Visual Acuity is measured in VAR (Visual Acuity Rating) score

se_12_month_va The standard error of Visual Acuity after 12 months. Where Visual Acuity is measured in VAR (Visual Acuity Rating) score

baseline_cst Mean Central Subfield Thickness at Baseline

sd_baseline_cst The standard deviation of Central Subfield Thickness at Baseline

se_baseline_cst The standard error of Central Subfield Thickness at Baseline

12_month_cst Mean Central Subfield Thickness after 12 months

sd_12_month_cst The standard deviation of Central Subfield Thickness after 12 months

se_12_month_cst The standard error of Central Subfield Thickness after 12 months

Source

Mehta H, Nguyen V, Barthelmes D, Pershing S, Chi GC, Dopart P, Gillies MC. Outcomes of Over 40,000 Eyes Treated for Diabetic Macula Edema in Routine Clinical Practice: A Systematic Review and Meta-analysis. Adv Ther. 2022 Dec;39(12):5376-5390. doi: 10.1007/s12325-022-02326-8. Epub 2022 Oct 15. PMID: 36241963; PMCID: PMC9618488.

`metarisk` *Bayesian meta-analysis for using baseline risk adjustment*

Description

This function performers a Bayesian meta-analysis to analyse heterogeneity of the treatment effect as a function of the baseline risk. The function fits a hierarchical meta-regression model based on a bivariate random effects model.

Usage

```
metarisk(
  data,
  two.by.two = TRUE,
  re = "normal",
  link = "logit",
  mean.mu.1 = 0,
  mean.mu.2 = 0,
```

```
  sd.mu.1 = 1,
  sd.mu.2 = 1,
  sigma.1.upper = 5,
  sigma.2.upper = 5,
  mean.Fisher.rho = 0,
  sd.Fisher.rho = 1/sqrt(2),
  df = 4,
  df.estimate = FALSE,
  df.lower = 3,
  df.upper = 20,
  split.w = FALSE,
  nr.chains = 2,
  nr.iterations = 10000,
  nr.adapt = 1000,
  nr.burnin = 1000,
  nr.thin = 1,
  parallel = NULL
)
```

Arguments

`data`	A data frame where the first four columns containing the number of events in the control group (yc), the number of patients in the control group (nc), the number of events in the treatment group (yt) and the number of patients in the treatment group (nt). If two.by.two = TRUE a data frame where each line contains the trial results with column names: yc, nc, yt, nt.
`two.by.two`	If TRUE indicates that the trial results are with names: yc, nc, yt, nt.
`re`	Random effects distribution for the resulting model. Possible values are *normal* for bivariate random effects and *sm* for scale mixtures.
`link`	The link function used in the model. Possible values are *logit*, *cloglog probit*.
`mean.mu.1`	Prior mean of baseline risk, default value is 0.
`mean.mu.2`	Prior mean of the relative treatment effect, default value is 0.
`sd.mu.1`	Prior standard deviation of mu.1, default value is 1. The default prior of mu.1 is a logistic distribution with mean 0 and dispersion 1. The implicit prior for mu.1 in the probability scale is a uniform between 0 and 1.
`sd.mu.2`	Prior standard deviation of mu.2, default value is 1. The default prior of mu.2 is a logistic distribution with mean 0 and dispersion 1. The implicit prior for mu.2 in the probability scale is a uniform between 0 and 1.
`sigma.1.upper`	Upper bound of the uniform prior of sigma.1, default value is 5.
`sigma.2.upper`	Upper bound of the uniform prior of sigma.2, default value is 5.
`mean.Fisher.rho`	Mean of rho in the Fisher scale default value is 0.
`sd.Fisher.rho`	Standard deviation of rho in the Fisher scale, default value is 1/sqrt(2).
`df`	If de.estimate = FALSE, then df is the degrees of freedom for the scale mixture distribution, default value is 4.

df.estimate	Estimate the posterior of df. The default value is FALSE.
df.lower	Lower bound of the prior of df. The default value is 3.
df.upper	Upper bound of the prior of df. The default value is 30.
split.w	Split the w parameter in two independent weights one for each random effect. The default value is FALSE.
nr.chains	Number of chains for the MCMC computations, default 5.
nr.iterations	Number of iterations after adapting the MCMC, default is 10000. Some models may need more iterations.
nr.adapt	Number of iterations in the adaptation process, defualt is 1000. Some models may need more iterations during adptation.
nr.burnin	Number of iteration discared for burnin period, default is 1000. Some models may need a longer burnin period.
nr.thin	Thinning rate, it must be a positive integer, the default value is 1.
parallel	NULL -> jags, 'jags.parallel' -> jags.parallel execution

Details

The number of events in the control and treated group are modeled with two conditional Binomial distributions and the random-effects are based on a bivariate scale mixture of Normals.

The function calculates the implicit hierarchical meta-regression, where the treatment effect is regressed to the baseline risk (rate of events in the control group). The scale mixture weights are used to adjust for internal validity and structural outliers identification.

Computations are done by calling JAGS (Just Another Gibbs Sampler) to perform MCMC (Markov Chain Monte Carlo) sampling and returning an object of the class *mcmc.list*.

Value

This function returns an object of the class "metarisk". This object contains the MCMC output of each parameter and hyper-parameter in the model, the data frame used for fitting the model, the link function, type of random effects distribution and the splitting information for conflict of evidence analysis.

The results of the object of the class metadiag can be extracted with R2jags or with rjags. In addition a summary, a print and a plot functions are implemented for this type of object.

References

Verde, P.E. (2019) The hierarchical meta-regression approach and learning from clinical evidence. Biometrical Journal. 1 - 23.

Verde, P. E. (2017) Two Examples of Bayesian Evidence Synthesis with the Hierarchical Meta-Regression Approach. Chap.9, pag 189-206. Bayesian Inference, ed. Tejedor, Javier Prieto. InTech.

Examples

```
## Not run:
library(jarbes)

# This example is used to test the function and it runs in about 5 seconds.
# In a real application you must increase the number of MCMC interations.
# For example use: nr.burnin = 5000 and nr.iterations = 20000




# The following examples corresponds to Section 4 in Verde (2019).
# These are simulated examples to investigate internal and
# external validity bias in meta-analysis.


library(MASS)
library(ggplot2)
library(jarbes)
library(gridExtra)


#Experiment 1: External validity bias

set.seed(2018)
# mean control
pc <- 0.7
# mean treatment
pt <- 0.4
# reduction of "amputations" odds ratio
OR <- (pt/(1-pt)) /(pc/(1-pc))
OR

# mu_2
log(OR)
mu.2.true <- log(OR)
#sigma_2
sigma.2.true <- 0.5
# mu_1
mu.1.true <- log(pc/(1-pc))
mu.1.true
#sigma_1
sigma.1.true <- 1
# rho
rho.true <- -0.5
Sigma <- matrix(c(sigma.1.true^2, sigma.1.true*sigma.2.true*rho.true,
                  sigma.1.true*sigma.2.true*rho.true, sigma.2.true^2),
                  byrow = TRUE, ncol = 2)
Sigma

theta <- mvrnorm(35, mu = c(mu.1.true, mu.2.true),
```

```
                Sigma = Sigma )


plot(theta, xlim = c(-2,3))
abline(v=mu.1.true, lty = 2)
abline(h=mu.2.true, lty = 2)
abline(a = mu.2.true, b=sigma.2.true/sigma.1.true * rho.true, col = "red")
abline(lm(theta[,2]~theta[,1]), col = "blue")

# Target group
mu.T <- mu.1.true + 2 * sigma.1.true
abline(v=mu.T, lwd = 3, col = "blue")
eta.true <- mu.2.true + sigma.2.true/sigma.1.true*rho.true* mu.T
eta.true
exp(eta.true)
abline(h = eta.true, lty =3, col = "blue")
# Simulation of each primary study:
n.c <- round(runif(35, min = 30, max = 60),0)
n.t <- round(runif(35, min = 30, max = 60),0)
y.c <- y.t <- rep(0, 35)
p.c <- exp(theta[,1])/(1+exp(theta[,1]))
p.t <- exp(theta[,2]+theta[,1])/(1+exp(theta[,2]+theta[,1]))
for(i in 1:35)
{
 y.c[i] <- rbinom(1, n.c[i], prob = p.c[i])
 y.t[i] <- rbinom(1, n.t[i], prob = p.t[i])
}

AD.s1 <- data.frame(yc=y.c, nc=n.c, yt=y.t, nt=n.t)

############################################################
incr.e <- 0.05
incr.c <- 0.05
n11 <- AD.s1$yt
n12 <- AD.s1$yc
n21 <- AD.s1$nt - AD.s1$yt
n22 <- AD.s1$nc - AD.s1$yc
AD.s1$TE <- log(((n11 + incr.e)*(n22 + incr.c))/((n12 + incr.e) * (n21 + incr.c)))
AD.s1$seTE <- sqrt((1/(n11 + incr.e) + 1/(n12 + incr.e) +
                     1/(n21 + incr.c) + 1/(n22 + incr.c)))

Pc <- ((n12 + incr.c)/(AD.s1$nc + 2*incr.c))

AD.s1$logitPc <- log(Pc/(1-Pc))

AD.s1$Ntotal <- AD.s1$nc + AD.s1$nt
rm(list=c("Pc", "n11","n12","n21","n22","incr.c", "incr.e"))


dat.points <- data.frame(TE = AD.s1$TE, logitPc = AD.s1$logitPc, N.total = AD.s1$Ntotal)
#####################################################################

res.s1 <- metarisk(AD.s1, two.by.two = FALSE, sigma.1.upper = 5,
```

```
                  sigma.2.upper = 5,
                  sd.Fisher.rho = 1.5)

print(res.s1, digits = 4)


library(R2jags)
attach.jags(res.s1)
eta.hat <- mu.2 + rho*sigma.2/sigma.1*(mu.T - mu.1)
mean(eta.hat)
sd(eta.hat)

OR.eta.hat <- exp(eta.hat)
mean(OR.eta.hat)
sd(OR.eta.hat)
quantile(OR.eta.hat, probs = c(0.025, 0.5, 0.975))

ind.random <- sample(1:18000, size = 80, replace = FALSE)

#############################################################
p1 <- ggplot(dat.points, aes(x = logitPc, y = TE, size = N.total)) +
      xlab("logit Baseline Risk")+
      ylab("log(Odds Ratio)")+
      geom_point(shape = 21, colour = "blue") + scale_size_area(max_size=10)+
      scale_x_continuous(name= "Rate of The Control Group (logit scale)",
                         limits=c(-2, 5)) +
     geom_vline(xintercept = mu.T, colour = "blue", size = 1, lty = 1) +
       geom_hline(yintercept = eta.true, colour = "blue", size = 1, lty = 1)+
         geom_abline(intercept=beta.0[ind.random],
                     slope=beta.1[ind.random],alpha=0.3,
                     colour = "grey", size = 1.3, lty = 2)+
         geom_abline(intercept = mean(beta.0[ind.random]),
         slope = mean(beta.1[ind.random]),
         colour = "black", size = 1.3, lty = 2)+
     geom_abline(intercept = mu.2.true, slope = sigma.2.true/sigma.1.true * rho.true,
     colour = "blue", size = 1.2)+ theme_bw()


# Posterior of eta.hat

eta.df <- data.frame(x = OR.eta.hat)


p2 <- ggplot(eta.df, aes(x = x)) +
 xlab("Odds Ratio") +
 ylab("Posterior distribution")+
 geom_histogram(fill = "royalblue", colour = "black", alpha= 0.4, bins=80) +
 geom_vline(xintercept = exp(eta.true), colour = "black", size = 1.7, lty = 1)+
 geom_vline(xintercept = c(0.28, 0.22, 0.35), colour = "black", size = 1, lty = 2)+
 theme_bw()


grid.arrange(p1, p2, ncol = 2, nrow = 1)
```

```
#Experiment 2: Internal validity bias and assesing conflict of evidence between the RCTs.


set.seed(2018)
ind <- sample(1:35, size=5, replace = FALSE)
ind
AD.s4.contaminated <- AD.s1[ind,1:4]
AD.s4.contaminated$yc <- AD.s1$yt[ind]
AD.s4.contaminated$yt <- AD.s1$yc[ind]
AD.s4.contaminated$nc <- AD.s1$nt[ind]
AD.s4.contaminated$nt <- AD.s1$nc[ind]
AD.s4.contaminated <- rbind(AD.s4.contaminated,
                         AD.s1[-ind,1:4])

res.s4 <- metarisk(AD.s4.contaminated,
                   two.by.two = FALSE,
                   re = "sm",
                   sigma.1.upper = 3,
                   sigma.2.upper = 3,
                   sd.Fisher.rho = 1.5,
                   df.estimate = TRUE)

print(res.s4, digits = 4)

attach.jags(res.s4)

w.s <- apply(w, 2, median)
w.u <- apply(w, 2, quantile, prob = 0.75)
w.l <- apply(w, 2, quantile, prob = 0.25)

studies <- c(ind,c(1,3,4,5,6,8,9,10,11,13,14,17,18,19,20:35))


dat.weights <- data.frame(x = studies,
                          y = w.s,
                         ylo  = w.l,
                         yhi  = w.u)

# Outliers:
w.col <- studies %in% ind
w.col.plot <- ifelse(w.col, "black", "grey")
w.col.plot[c(9,17, 19,27,34,35)] <- "black"

w.plot <- function(d){
  # d is a data frame with 4 columns
  # d$x gives variable names
  # d$y gives center point
  # d$ylo gives lower limits
  # d$yhi gives upper limits

  p <- ggplot(d, aes(x=x, y=y, ymin=ylo, ymax=yhi) )+
       geom_pointrange( colour=w.col.plot, lwd =0.8)+
```

```
        coord_flip() + geom_hline(yintercept = 1, lty=2)+
        xlab("Study ID") +
        ylab("Scale mixture weights") + theme_bw()
        return(p)}

w.plot(dat.weights)

#List of other possible statistical models:
#    1) Different link functions: logit, cloglog and probit

#    2) Different random effects distributions:
#       "normal" or "sm = scale mixtures".

#    3) For the scale mixture random effects:
#       split.w = TRUE => "split the weights".

#    4) For the scale mixture random effects:
#       df.estimate = TRUE => "estimate the degrees of freedom".

#    5) For the scale mixture random effects:
#       df.estimate = TRUE => "estimate the degrees of freedom".

#    6) For the scale mixture random effects:
#       df = 4 => "fix the degrees of freedom to a particual value".
#       Note that df = 1 fits a Cauchy bivariate distribution to
#       the random effects.
#End of the examples


## End(Not run)
```

`personality` *Meta-Analysis: Evolution of Personality Traits over time*

Description

Meta-Analysis: Evolution of Personality Traits over time

Format

A data frame with 52 studies reporting 18 variables:

authoryear First author and publication year.

country Country where the study was performed.

female Proportion of females in the study.

nameMeasure Instrument used to measure the personality trait.

old Whether the study is "newly coded data" or not.

trait Personality trait measured.

N_T1 Number of participants at T1.

N_T2 Number of participants at T2.

age1 Mean age at T1.

age2 Mean age at T2.

lag Difference in years between T1 and T2.

Mean_T1 Mean score at T1.

SD_T1 SD at T1.

Mean_T2 Mean score at T2.

SD_T2 SD at T2.

r12 Correlation coefficient between T1 and T2.

TE Fisher z-transformed correlation.

seTE Standard error of TE.

Source

Bleidorn, Wiebke, et al. (2022). Personality stability and change: A meta-analysis of longitudinal studies. Psychological Bulletin, 148(7-8), 588–619. doi:10.1037/bul0000365

`plot.b3lmeta` *Generic plot function for b3lmeta object in jarbes.*

Description

Generic plot function for b3lmeta object in jarbes.

Generic plot function for b3lmeta object in jarbes.

Usage

```
## S3 method for class 'b3lmeta'
plot(
  x,
  x.lim = c(-3, 3),
  y.lim = c(0, 2.7),
  x.lab = "Treatment Effect: log(OR)",
  y.lab = "Posterior",
  title.plot.1 = "Mean Design Components",
  title.plot.2 = "Three Levels Bayesian Meta-Analysis",
  ...
)

## S3 method for class 'b3lmeta'
plot(
```

```
  x,
  x.lim = c(-3, 3),
  y.lim = c(0, 2.7),
  x.lab = "Treatment Effect: log(OR)",
  y.lab = "Posterior",
  title.plot.1 = "Mean Design Components",
  title.plot.2 = "Three Levels Bayesian Meta-Analysis",
  ...
)
```

Arguments

x	The object generated by the b3lmeta function.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot.1	Text for the posterior means by design.
title.plot.2	Text for the posterior pooled mean.
...	...

---

plot.bcbnp *Generic plot function for bcbnp object.*

Description

This function is built with ‘ggplot2‘. Parameters such as ‘binwidth‘, ‘adjust‘, ‘density.color‘, ‘density.lwd‘, and ‘density.lty‘ correspond directly to arguments in the ‘ggplot2‘ geoms.

Usage

```
## S3 method for class 'bcbnp'
plot(
  x,
  plot.type = "predictive",
  n.samples = NULL,
  x.lim = NULL,
  y.lim = NULL,
  x.lab = NULL,
  y.lab = "Posterior Predictive Distribution",
  title.plot = NULL,
  show.histogram = TRUE,
  show.rug = NULL,
  binwidth = 0.08,
  adjust = 1,
```

```
  density.color = "blue",
  hist.color = "black",
  hist.fill = "grey95",
  rug.color = "green",
  rug.alpha = 1,
  density.alpha = 0.2,
  density.lwd = 1,
  density.lty = 1,
  ...
)
```

Arguments

x	The object generated by the bcbnp function (the BC-BNP model output).
plot.type	A character string specifying the type of plot: - "predictive": Plots the posterior predictive distribution of a new study. - "mu_posterior": Plots the posterior of the overall mean (mu.theta). - "tau_posterior": Plots the posterior of the between-study standard deviation (tau.theta).
n.samples	The number of posterior samples to plot. If NULL, all samples are used.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot	Text for setting a title in the plot.
show.histogram	A logical value indicating whether to show the histogram.
show.rug	A logical value indicating whether to show the rug plot. Defaults to TRUE for predictive and mu plots, FALSE for tau.
binwidth	A numeric value specifying the bin width for the histogram.
adjust	A numeric value for the density bandwidth adjustment.
density.color	A character value for the density curve color.
hist.color	A character value for the histogram border color.
hist.fill	A character value for the histogram fill color.
rug.color	A character value for the rug plot color.
rug.alpha	A numeric value between 0 and 1 for the rug plot transparency.
density.alpha	A numeric value for the density curve transparency.
density.lwd	A numeric value for the density curve line width.
density.lty	A numeric value for the density curve line type.
...	...

plot.bcbnp_0 *Generic plot function for bcbnp_0 object.*

Description

This function is built with 'ggplot2'. Parameters such as 'binwidth', 'adjust', 'density.color', 'density.lwd', and 'density.lty' correspond directly to arguments in the 'ggplot2' geoms.

Usage

```
## S3 method for class 'bcbnp_0'
plot(
  x,
  plot.type = "predictive",
  n.samples = NULL,
  x.lim = NULL,
  y.lim = NULL,
  x.lab = NULL,
  y.lab = "Density",
  title.plot = NULL,
  show.histogram = TRUE,
  show.rug = NULL,
  binwidth = 0.08,
  adjust = 1,
  density.color = "blue",
  hist.color = "black",
  hist.fill = "grey95",
  rug.color = "green",
  rug.alpha = 1,
  density.alpha = 0.2,
  density.lwd = 1,
  density.lty = 1,
  ...
)
```

Arguments

x	The object generated by the bcbnp_0 function (the BC-BNP model output).
plot.type	A character string specifying the type of plot: - "predictive": Plots the posterior predictive distribution of a new study (unbiased density vs potentially biased histogram). - "mu_posterior": Plots the posterior of the overall mean (mu.theta). - "tau_posterior": Plots the posterior of the between-study standard deviation (tau.theta).
n.samples	The number of posterior samples to plot. If NULL, all samples are used.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.

x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot	Text for setting a title in the plot.
show.histogram	A logical value indicating whether to show the histogram.
show.rug	A logical value indicating whether to show the rug plot. Defaults to TRUE for predictive and mu plots, FALSE for tau.
binwidth	A numeric value specifying the bin width for the histogram.
adjust	A numeric value for the density bandwidth adjustment.
density.color	A character value for the density curve color.
hist.color	A character value for the histogram border color.
hist.fill	A character value for the histogram fill color.
rug.color	A character value for the rug plot color.
rug.alpha	A numeric value between 0 and 1 for the rug plot transparency.
density.alpha	A numeric value for the density curve transparency.
density.lwd	A numeric value for the density curve line width.
density.lty	A numeric value for the density curve line type.
...	...

`plot.bcdpmeta` *Generic plot function for bcdpmeta object in jarbes.*

Description

Generic plot function for bcdpmeta object in jarbes.

Usage

```
## S3 method for class 'bcdpmeta'
plot(
  x,
  x.lim = c(-3, 3),
  y.lim = c(0, 2),
  x.lab = "Treatment Effect: log(OR)",
  y.lab = "Posterior",
  title.plot.1 = "Model Components",
  title.plot.2 = "Bias Corrected Meta-Analysis",
  ...
)
```

Arguments

x	The object generated by the bcmeta function.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot.1	Text for the posterior means by component (biased and bias corrected).
title.plot.2	Text for the posterior mean (pooled and predictive).
...	...

---

plot.bcmeta *Generic plot function for bcmeta object.*

Description

This function is built with 'ggplot2'. Parameters such as 'binwidth', 'adjust', 'density.color', 'density.lwd', 'density.lty', and 'density.alpha' correspond directly to arguments in the 'ggplot2' geoms.

Usage

```
## S3 method for class 'bcmeta'
plot(
  x,
  plot.type = "predictive_with_bias",
  n.samples = NULL,
  x.lim = NULL,
  y.lim = NULL,
  x.lab = expression(theta^{
     new
 }),
  y.lab = "Posterior Predictive Distribution",
  title.plot = "Bias-Corrected Meta-Analysis",
  show.histogram = TRUE,
  show.rug = TRUE,
  show.legend.lines = FALSE,
  binwidth = 0.08,
  adjust = 1,
  density.color = "blue",
  density.lty = "solid",
  density.lwd = 1,
  density.alpha = 0.2,
  hist.color = "black",
  hist.fill = "grey95",
  rug.color = "green",
```

```
  rug.alpha = 0.5,
  predictive.color = "blue",
  mu.color = "black",
  bias.color = "red",
  ...
)
```

Arguments

x	The object generated by the bcmeta function.
plot.type	A character string specifying the type of plot: "predictive_with_bias" (default), "predictive", "tau_posterior".
n.samples	The number of posterior samples to plot.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis. Defaults to θ^{new}.
y.lab	Text with the label of the y-axis. Defaults to "Posterior Predictive Distribution".
title.plot	Text for setting a title in the plot. Defaults to "Bias-Corrected Meta-Analysis".
show.histogram	A logical value indicating whether to show the histogram.
show.rug	A logical value indicating whether to show the rug plot.
show.legend.lines	A logical value indicating whether to show the legend for the density curves in the "predictive_with_bias" plot.
binwidth	A numeric value specifying the bin width for the histogram.
adjust	A numeric value to adjust the bandwidth of the density curves.
density.color	A character value for the density curve color (used for non-comparison plots).
density.lty	A character value for the density curve line type.
density.lwd	A numeric value for the density curve line width.
density.alpha	A numeric value between 0 and 1 for the density curve transparency.
hist.color	A character value for the histogram border color.
hist.fill	A character value for the histogram fill color.
rug.color	A character value for the rug plot color.
rug.alpha	A numeric value between 0 and 1 for the rug plot transparency.
predictive.color	A character value specifying the color of the posterior predictive density curve in "predictive_with_bias".
mu.color	A character value specifying the color of the posterior mean density curve in "predictive_with_bias".
bias.color	A character value specifying the color of the bias-inflated mean density curve in "predictive_with_bias".
...	...

plot.bcmixmeta *Generic plot function for bcmixmeta object.*

Description

This function is built with ‘ggplot2‘. Parameters such as ‘binwidth‘, ‘adjust‘, ‘density.color‘, ‘density.lwd‘, and ‘density.lty‘ correspond directly to arguments in the ‘ggplot2‘ geoms.

Usage

```
## S3 method for class 'bcmixmeta'
plot(
  x,
  plot.type = "predictive_with_bias",
  n.samples = NULL,
  x.lim = NULL,
  y.lim = NULL,
  x.lab = NULL,
  y.lab = "Posterior Predictive Distribution",
  title.plot = NULL,
  show.histogram = TRUE,
  show.rug = TRUE,
  show.legend = FALSE,
  binwidth = 0.08,
  adjust = 1,
  predictive.color = "blue",
  mu.color = "black",
  bias.color = "red",
  hist.color = "black",
  hist.fill = "grey95",
  rug.color = "green",
  rug.alpha = 1,
  density.alpha = 0.4,
  density.lwd = 1,
  density.lty = 1,
  ...
)
```

Arguments

x	The object generated by the bcmixmeta function (the BC-BNP model output).
plot.type	A character string specifying the type of plot: "predictive_with_bias" (default), "predictive", "mu_posterior", "tau_posterior".
n.samples	The number of posterior samples to plot. If NULL, all posterior samples are used.
x.lim	Numeric vector of length 2 specifying the x-axis limits.

y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot	Text for setting a title in the plot.
show.histogram	A logical value indicating whether to show the histogram.
show.rug	A logical value indicating whether to show the rug plot.
show.legend	A logical value indicating whether to display the legend.
binwidth	A numeric value specifying the bin width for the histogram.
adjust	A numeric value to adjust the bandwidth of the density curves.
predictive.color	A character value specifying the color of the posterior predictive density curve.
mu.color	A character value specifying the color of the posterior mean density curve.
bias.color	A character value specifying the color of the bias-adjusted mean density curve.
hist.color	A character value for the histogram border color.
hist.fill	A character value for the histogram fill color.
rug.color	A character value for the rug plot color.
rug.alpha	A numeric value between 0 and 1 specifying the rug plot transparency.
density.alpha	A numeric value between 0 and 1 specifying density transparency.
density.lwd	A numeric value specifying density line width.
density.lty	A numeric value specifying density line type.
...	...

`plot.bmeta` *Generic plot function for bmeta object in jarbes.*

Description

This function is built with 'ggplot2'. Parameters such as 'binwidth', 'adjust', 'density.colors', 'density.lwd', 'density.lty', and 'density.alpha' correspond directly to arguments in the 'ggplot2' geoms.

Usage

```
## S3 method for class 'bmeta'
plot(
  x,
  n.samples = NULL,
  x.lim = NULL,
  y.lim = NULL,
  x.lab = expression(mu[theta]),
  y.lab = "Posterior Distribution",
  title.plot = NULL,
```

```
  show.legend = TRUE,
  legend.labels = c("Posterior of the difference in means",
    "Posterior Predictive Distribution"),
  legend.title = "Distribution",
  show.histogram = TRUE,
  show.rug = TRUE,
  show.vlines = TRUE,
  binwidth = 0.08,
  adjust = 1,
  density.colors = c("black", "blue"),
  density.lwd = c(1, 1),
  density.lty = c("solid", "dashed"),
  density.alpha = c(0.2, 0.2),
  hist.color = "black",
  hist.fill = "grey95",
  rug.color = "green",
  rug.alpha = 0.5,
  ...
)
```

Arguments

x	The object generated by the bmeta function.
n.samples	The number of posterior samples to plot.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot	Text for setting a title in the plot.
show.legend	A logical value indicating whether to show the legend.
legend.labels	A character vector of length 2 to customize the legend labels.
legend.title	A character value to customize the legend title.
show.histogram	A logical value indicating whether to show the histogram.
show.rug	A logical value indicating whether to show the rug plot.
show.vlines	A logical value indicating whether to show the vertical lines for the means.
binwidth	A numeric value specifying the bin width for the histogram.
adjust	A numeric value to adjust the bandwidth of the density curves. Defaults to 1.
density.colors	A character vector of length 2 for the density curve colors.
density.lwd	A numeric vector of length 2 for the density curve line widths.
density.lty	A numeric vector of length 2 for the density curve line types.
density.alpha	A numeric vector of length 2 for the density curve transparencies.
hist.color	A character value for the histogram border color.
hist.fill	A character value for the histogram fill color.

rug.color	A character value for the rug plot color.
rug.alpha	A numeric value between 0 and 1 for the rug plot transparency.
...	...

---

plot.dpmeta *Generic plot function for dpmeta object.*

Description

This function is built with 'ggplot2'. Parameters such as 'binwidth', 'adjust', 'density.color', 'density.lwd', 'density.lty', and 'density.alpha' correspond directly to arguments in the 'ggplot2' geoms.

Usage

```
## S3 method for class 'dpmeta'
plot(
  x,
  plot.type = "predictive_vs_mean",
  center = "median",
  n.samples = NULL,
  x.lim = NULL,
  y.lim = NULL,
  x.lab = expression(theta^{
     new
 }),
  y.lab = "Posterior Predictive Distribution",
  title.plot = "Dirichlet Process ",
  show.histogram = TRUE,
  show.rug = TRUE,
  show.legend = FALSE,
  binwidth = 0.08,
  adjust = 1,
  predictive.color = "blue",
  mean.color = "red",
  median.color = "black",
  density.lty = "solid",
  density.lwd = 1,
  density.alpha = 0.2,
  hist.color = "black",
  hist.fill = "grey95",
  rug.color = "green",
  rug.alpha = 0.5,
  ...
)
```

Arguments

x	The object generated by the dpmeta function.
plot.type	A character string specifying the type of plot: "predictive_vs_mean" (default), "predictive", "tau_posterior".
center	A character string specifying which central tendency of the DP to plot: "median" (default), "mean", "both".
n.samples	The number of posterior samples to plot.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis. Defaults to θ^{new}.
y.lab	Text with the label of the y-axis. Defaults to "Posterior Predictive Distribution".
title.plot	Text for setting a title in the plot. Defaults to "Dirichlet Process ".
show.histogram	A logical value indicating whether to show the histogram.
show.rug	A logical value indicating whether to show the rug plot.
show.legend	A logical value indicating whether to show the legend when multiple density curves are displayed.
binwidth	A numeric value specifying the bin width for the histogram. Defaults to 0.08.
adjust	A numeric value to adjust the bandwidth of the density curves. Defaults to 1.
predictive.color	A character value specifying the color of the posterior predictive density curve.
mean.color	A character value specifying the color of the posterior mean density curve.
median.color	A character value specifying the color of the posterior median density curve.
density.lty	A character value for the density curve line type. Defaults to "solid".
density.lwd	A numeric value for the density curve line width. Defaults to 1.
density.alpha	A numeric value between 0 and 1 for the density curve transparency. Defaults to 0.2.
hist.color	A character value for the histogram border color. Defaults to "black".
hist.fill	A character value for the histogram fill color. Defaults to "grey95".
rug.color	A character value for the rug plot color. Defaults to "green".
rug.alpha	A numeric value between 0 and 1 for the rug plot transparency. Defaults to 0.5.
...	...

plot.dpmmeta *Generic plot function for bmeta object in jarbes.*

Description

Generic plot function for bmeta object in jarbes.

Usage

```
## S3 method for class 'dpmmeta'
plot(
  x,
  x.lim = c(-3, 3),
  y.lim = c(0, 2),
  x.lab = "Treatment Effect: log(OR)",
  y.lab = "Posterior",
  title.plot = "Simple Bayesian Meta-Analysis",
  ...
)
```

Arguments

x	The object generated by the bmeta function.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot	Text for setting a title in the plot.
...	...

plot.hmr *Generic plot function for hmr object in jarbes.*

Description

Generic plot function for hmr object in jarbes.

Usage

```
## S3 method for class 'hmr'
plot(
  x,
  x.lim = c(-5, 2.8),
  y.lim = c(-2, 1),
  x.lab = "Event rate of The Control Group (logit scale)",
  y.lab = "No improvement <- Effectiveness -> Improvement",
  title.plot = "HMR: Effectiveness Against Baseline Risk",
  AD.colour = "red",
  IPD.colour = "blue",
  Study.Types = c("AD-RCTs", "IPD-RWD"),
  ...
)
```

Arguments

x	The object generated by the hmr function.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot	Text for setting a title in the plot.
AD.colour	Colour of the location of the baseline risk of the aggregated data AD
IPD.colour	Colour of the location of the baseline risk of the individual participant data (IPD) data
Study.Types	Vector of text for the label of the study types
...	...

---

plot.metarisk *Generic plot function for metarisk object in jarbes.*

Description

Generic plot function for metarisk object in jarbes.

Usage

```
## S3 method for class 'metarisk'
plot(
  x,
  x.lim = c(-5, 2.8),
  y.lim = c(-2, 1),
  x.lab = "Rate of The Control Group (logit scale)",
```

```
  y.lab = "No improvement <- Treatment effect -> Improvement",
  title.plot = "Treatment Effect Against Baseline Risk",
  ...
)
```

Arguments

x	The object generated by the metarisk function.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
y.lim	Numeric vector of length 2 specifying the y-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot	Text for setting a title in the plot.
...	...

`plot.simData` *Forest Plot for simData Objects*

Description

Generates a forest plot of the simulated meta-analysis dataset, showing the observed effect sizes (TE) with 95

Arguments

x	A ‘simData‘ object created by ‘simData()‘.
x.lim	Numeric vector of length 2 specifying the x-axis limits.
x.lab	Text with the label of the x-axis.
y.lab	Text with the label of the y-axis.
title.plot	Text for the title of the plot.
bias_colors	Named character vector specifying colors for bias categories.
bias_legend_title	Text label for the bias legend.
ref_line_color	Color for the vertical reference line corresponding to the mean.
...	Additional arguments (currently not used).

plot_data *Plot Data Function*

Description

This function plots the treatment effect (TE) against specified covariates or creates a forest plot of treatment effects, arranging up to four plots in a grid.

Usage

```
plot_data(
  data,
  formula = ~1,
  group = NULL,
  group.colors = NULL,
  study.label = NULL,
  x.lab = NULL,
  y.lab = "TE",
  title.plot = NULL,
  errbar.width = 0.25,
  label.size = 6,
  forest.color = "blue",
  forest.shape = 19,
  forest.size = 3,
  forest.group = NULL,
  forest.group.colors = NULL,
  xlim = NULL,
  ylim = NULL
)
```

Arguments

data	A data frame with columns 'TE', 'seTE', and the covariates.
formula	A one-sided formula (e.g., '~ x1 + x2') for the x-axis variables. If not provided or set to '~1', a forest plot is generated.
group	A character string specifying the name of the column in 'data' to use for grouping the points (e.g., by color/fill) in covariate plots. Defaults to 'NULL'. This parameter is ignored for forest plots.
group.colors	A character vector specifying colors for the groups when 'group' is used in covariate plots. Can be a named vector where names match the levels of the grouping variable. Defaults to 'NULL', which uses ggplot2's default discrete colors.
study.label	A character string specifying the name of the column in 'data' that contains the study labels for the forest plot. If 'NULL', default labels ("Study 1", "Study 2", etc.) are created.

x.lab	A character vector for x-axis labels. Defaults to variable names.
y.lab	Text for the y-axis label. Defaults to "TE" or "Study" for forest plots.
title.plot	Text for the plot title. Defaults to 'NULL'.
errbar.width	The width of the error bars for covariate plots. Defaults to '0.25'.
label.size	A numeric value for the font size of the study labels in the forest plot. Defaults to '6'.
forest.color	The color of the points and error bars in a classic (ungrouped) forest plot. Defaults to '"blue"'.
forest.shape	The shape of the points in the forest plot. Defaults to '19' (filled circle).
forest.size	The size of the points in the forest plot. Defaults to '3'.
forest.group	A character string specifying the name of a column in 'data' used to group and color studies in the forest plot ('formula = ~1'). If 'NULL', a single-color forest plot is produced.
forest.group.colors	A character vector specifying colors for forest plot groups when 'forest.group' is used. Can be a named vector matching group levels. If 'NULL', colors are assigned automatically: two groups use blue and red; three or more groups use a Brewer palette.
xlim	A numeric vector of length 2 specifying x-axis limits.
ylim	A numeric vector of length 2 specifying y-axis limits.

Details

In forest plot mode ('formula = ~1'), studies can optionally be colored by a grouping variable using 'forest.group'.

Value

A 'ggplot' object for a single plot or a 'gridExtra' grob when multiple covariate plots are arranged in a grid.

---

plotdata_reg.bcbnp *Plot Meta-Regression Results from a BCBNP Model*

Description

This function visualizes the results of a bias-corrected Bayesian nonparametric meta-regression. It plots the raw data with error bars, colors points based on the posterior probability of bias (I > 0.5), and adds the posterior mean regression line, the credible interval for the true effects, and the prediction interval for new observations, including its median line.

Usage

```
plotdata_reg.bcbnp(
  object,
  covariate,
  title.plot = NULL,
  ci.color = "green",
  pi.color = "purple",
  mean.line.color = "magenta",
  pi.mean.line.color = "gray",
  point.color.unbiased = "blue",
  point.color.biased = "red",
  show_ci = TRUE,
  show_pi = TRUE,
  errorbar_width = 0.25,
  x.lab = covariate,
  y.lab = "Treatment Effect (TE)",
  legend.name = "Posterior Bias",
  size.legend.name = "1/seTE",
  label.unbiased = "Unbiased",
  label.biased = "Biased"
)
```

Arguments

object	The output object from the bcbnp function.
covariate	A character string specifying the single covariate from the data to be plotted (e.g., '"baseline_va"').
title.plot	The title for the plot.
ci.color	The color of the credible interval lines. Defaults to "green".
pi.color	The color of the prediction interval lines. Defaults to "purple".
mean.line.color	The color of the mean regression line. Defaults to "magenta".
pi.mean.line.color	The color of the prediction interval median line. Defaults to "gray".
point.color.unbiased	The color of unbiased points. Defaults to "blue".
point.color.biased	The color of biased points. Defaults to "red".
show_ci	A logical value indicating whether to show the credible interval. Defaults to 'TRUE'.
show_pi	A logical value indicating whether to show the prediction interval. Defaults to 'TRUE'.
errorbar_width	The width of the error bars. Defaults to '0.25'.
x.lab	A character string for the x-axis label. Defaults to the covariate name.
y.lab	A character string for the y-axis label. Defaults to "Treatment Effect (TE)".

`legend.name` A character string for the color legend title. Defaults to "Posterior Bias".

`size.legend.name` A character string for the size legend title. Defaults to "1/seTE".

`label.unbiased` A character string for the label of the unbiased group. Defaults to "Unbiased".

`label.biased` A character string for the label of the biased group. Defaults to "Biased".

Value

A ggplot object.

`ppvcap` *Efficacy of Pneumococcal Polysaccharide Vaccine in Preventing Community Acquired Pneumonia*

Description

PPV23 (23-valent pneumococcal polysaccharide vaccine) with 16 Randomized Clinical Trials (RCTs); outcome variable CAP (community-acquired pneumonia).

This data frame corresponds to 16 randomized control trials (RCTs) reporting efficacy of the PPV (Pneumococcal Polysaccharide) vaccine in preventing CAP (community acquired pneumonia). The data frame contains the evaluation of Risk of Bias (RoB) of the trials and some study population characteristics.

Format

A matrix with 16 rows and 18 columns. Each row represents study results, the columns are:

Name_Year Name of the first author and year.

Year Year of publication.

yt Number of infections in the intervention group.

nt Number of patients in the intervention group.

yc Number of infections in the control group.

nc Number of patients in the control group.

TE Treatment Effect as Log Odds Ratio.

seTE Standard Error of the TE.

logitPc Observed baseline rate in logit scale.

N Total sample size.

Study_Design Description of the study design.

Intervention Type of vaccine used for itervention.

Valency 0 = PPV23; 1 = PPV-Other.

low_income Indicates low income patients population with 0 = no; 1 = yes.

R1 Random sequence generation (selection bias: low;high;unclear.

R2 Allocation concealment (selection bias): low;high;unclear.

R3 Confounding: low;high;unclear.

R4 Blinding of participants and personnel (performace bias): low;high;unclear.

R5 Blinding of outcome assessment (detection bias): low;high;unclear.

R6 Incomplete outcome data (attrition bias): low;high;unclear.

R7 Selective reporting (reporting bias): low;high;unclear.

Participants Comments on patients characteristics.

Source

The data were obtainded from: Moberley et al. (2013).

References

Moberley, S., Holden, J., Tatham, D., and Andrews, R. (2013), Vaccines for preventing pneumococcal infection in adults., Cochrane Database of Systematic Reviews, Issue 1. Art. No.: CD000422. DOI:10.1002/14651858.CD000422.pub3.

Verde, P.E. and Curcio, D. (2017) Hierarchical Meta-Regression Modelling: The Case of The Pneumococcal Polysaccharide Vaccine. Technical Report.

---

ppvipd — *Efficacy of Pneumococcal Polysaccharide Vaccine in Preventing Invasive Pneumococcal Disease*

Description

PPV23 (23-valent pneumococcal polysaccharide vaccine) with 3 Randomized Clinical Trials; 5 Cohort Studies and 3 Case-Control Studies.

The outcome variable IPD (Invasive Pneumococcal Disease).

Format

A matrix with 11 rows and 6 columns. Each row represents study results, the columns are:

name Name of the first author and year.

TE Treatment Effect as Log Odds Ratio.

seTE Standard Error of the TE.

n.v Number of patients in the vaccination group.

n.c Number of patients in the control group.

design Description of the study design.

Source

The data were obtainded from: Falkenhorst et al. (2017).

References

Falkenhorst, G., Remschmidt, C., Harder, T., Hummers-Pradier, E., Wichmann, O., and Bogdan, C. (2017) Effectiveness of the 23-Valent Pneumococcal Polysaccharide Vaccine(PPV23) against Pneumococcal Disease in the Elderly: Systematic Review and Meta-Analysis. PLoS ONE 12(1): e0169368. doi:10.1371/journal.pone.0169368.

Verde, P.E. and Curcio, D. (2017) Hierarchical Meta-Regression Modelling: The Case of The Pneumococcal Polysaccharide Vaccine. Technical Report.

---

preterm *Meta-analysis of Cognitive Outcomes in Very Preterm Children*

Description

This dataset contains study-level data extracted from the systematic review and meta-analysis Trends Over Time in Cognitive Outcomes of Children Born Very Preterm by Behboodi et al. (JAMA Pediatrics, 2025). The review synthesizes evidence from observational cohort and matched studies comparing cognitive outcomes of children born very preterm (VPT) or extremely preterm (EPT) with children born at full term (FT).

Format

A data frame with 61 rows and 18 columns. Each row represents a single study included in the meta-analysis. The columns include:

study First author and publication year.

n_EPT.VPT Number of children born extremely or very preterm.

mean_EPT.VPT Mean cognitive score in the EPT/VPT group.

sd_EPT.VPT Standard deviation of cognitive scores in the EPT/VPT group.

n_FT Number of children born full term.

mean_FT Mean cognitive score in the full-term group.

sd_FT Standard deviation of cognitive scores in the full-term group.

SMD Standardized mean difference (Hedges' g) comparing EPT/VPT with FT.

seSMD Standard error of the standardized mean difference.

mean_age Mean age at cognitive assessment.

mean_ga Mean gestational age of the study population.

mean_bw Mean birth weight of the study population.

median_birth_year Median year of birth of the cohort included in the study.

quality Methodological quality score based on a modified Newcastle–Ottawa Scale, ranging from 0 to 7, with higher values indicating better study quality.

matched Indicator of whether the study used a matched design to compare preterm and full-term participants ("yes" or "no").

birth_level Classification of the preterm subgroup included in the comparison: `VPT` for very preterm only, `EPT` for extremely preterm only, and `VPT_and_EPT` for combined very and extremely preterm groups.

country Country where the study was conducted.

analysis Indicator of whether the study contributed data to the primary analysis, secondary analysis, or both, as defined in Behboodi et al.

Details

The standardized mean difference (SMD) is a measure of the difference between two group means, expressed in units of their pooled standard deviation. In this dataset it quantifies the difference in mean cognitive test scores between children born preterm (EPT/VPT) and those born full term (FT), with negative values indicating lower scores in the preterm group.

The SMD is calculated as Hedges' g. First, Cohen's d is computed as

$$d = \frac{\bar{X}_{EPT.VPT} - \bar{X}_{FT}}{s_p},$$

where $\bar{X}_{EPT.VPT}$ and $\bar{X}_{FT}$ are the mean cognitive scores in the EPT/VPT and FT groups, respectively, and s_p is the pooled standard deviation.

The pooled standard deviation is given by

$$s_p = \sqrt{\frac{(n_{EPT.VPT} - 1)\, s^2_{EPT.VPT} + (n_{FT} - 1)\, s^2_{FT}}{n_{EPT.VPT} + n_{FT} - 2}}.$$

Here, $n_{EPT.VPT}$ and n_{FT} are the group sample sizes, and $s_{EPT.VPT}$ and s_{FT} are the corresponding standard deviations.

Cohen's d is multiplied by the small-sample correction factor

$$J = 1 - \frac{3}{4\,(n_{EPT.VPT} + n_{FT} - 2) - 1}$$

to obtain Hedges' g:

$$SMD = g = J \times d.$$

The standard error of the standardized mean difference (seSMD) measures the uncertainty of the estimated SMD. Smaller values indicate more precise estimates of the difference between the preterm (EPT/VPT) and full-term (FT) groups.

The seSMD is calculated as

$$seSMD = \sqrt{J^2 \left(\frac{n_{EPT.VPT} + n_{FT}}{n_{EPT.VPT}\, n_{FT}} + \frac{d^2}{2\,(n_{EPT.VPT} + n_{FT} - 2)} \right)}.$$

Source

Behboodi S, Chaimani A, Benhammou V, Twilhaar ES, Johnson S, Zeitlin J, Sentenac M. Trends Over Time in Cognitive Outcomes of Children Born Very Preterm: A Systematic Review and Meta-Analysis. JAMA Pediatrics. 2025;179(10):1074–1081. doi:10.1001/jamapediatrics.2025.2221.

---

print.b3lmeta *Generic print function for b3lmeta object in jarbes.*

Description

Generic print function for b3lmeta object in jarbes.

Usage

```
## S3 method for class 'b3lmeta'
print(x, digits, ...)
```

Arguments

x	The object generated by the function b3lmeta.
digits	The number of significant digits printed. The default value is 3.
...	...

---

print.bcbnp_0 *Generic print function for bcbnp object in jarbes.*

Description

Generic print function for bcbnp object in jarbes.

Usage

```
## S3 method for class 'bcbnp_0'
print(x, digits, ...)
```

Arguments

x	The object generated by the function bcbnp.
digits	The number of significant digits printed. The default value is 3.
...	...

`print.bcdpmeta` *Generic print function for bcdpmeta object in jarbes.*

Description

Generic print function for bcdpmeta object in jarbes.

Usage

```
## S3 method for class 'bcdpmeta'
print(x, digits, ...)
```

Arguments

`x`	The object generated by the function bcdpmeta.
`digits`	The number of significant digits printed. The default value is 3.
`...`	...

`print.bchmr` *Generic print function for hmr object in jarbes.*

Description

Generic print function for hmr object in jarbes.

Usage

```
## S3 method for class 'bchmr'
print(x, digits = 3, intervals = c(0.025, 0.25, 0.5, 0.75, 0.975), ...)
```

Arguments

`x`	The object generated by the function bchmr.
`digits`	The number of significant digits printed. The default value is 3.
`intervals`	A numeric vector of probabilities with values in [0,1]. The default value is intervals = c(0.025, 0.5, 0.975).
`...`	...

print.bcmeta *Generic print function for bcmeta object in jarbes.*

Description

Generic print function for bcmeta object in jarbes.

Usage

```
## S3 method for class 'bcmeta'
print(x, digits, ...)
```

Arguments

x	The object generated by the function bcmeta.
digits	The number of significant digits printed. The default value is 3.
...	...

print.bcmixmeta *Generic print function for bcmixmeta object in jarbes.*

Description

Generic print function for bcmixmeta object in jarbes.

Usage

```
## S3 method for class 'bcmixmeta'
print(x, digits, ...)
```

Arguments

x	The object generated by the function bcmixmeta.
digits	The number of significant digits printed. The default value is 3.
...	...

print.dpmeta *Generic print function for dpmeta object in jarbes.*

Description

Generic print function for dpmeta object in jarbes.

Usage

```
## S3 method for class 'dpmeta'
print(x, digits, ...)
```

Arguments

x	The object generated by the function dpmeta.
digits	The number of significant digits printed. The default value is 3.
...	...

print.dpmetareg *Generic print function for dpmeta object in jarbes.*

Description

Generic print function for dpmeta object in jarbes.

Usage

```
## S3 method for class 'dpmetareg'
print(x, digits, ...)
```

Arguments

x	The object generated by the function dpmmeta.
digits	The number of significant digits printed. The default value is 3.
...	...

print.dpmmeta *Generic print function for dpmmeta object in jarbes.*

Description

Generic print function for dpmmeta object in jarbes.

Usage

```
## S3 method for class 'dpmmeta'
print(x, digits, ...)
```

Arguments

x	The object generated by the function dpmmeta.
digits	The number of significant digits printed. The default value is 3.
...	...

print.hmr *Generic print function for hmr object in jarbes.*

Description

Generic print function for hmr object in jarbes.

Usage

```
## S3 method for class 'hmr'
print(x, digits = 3, intervals = c(0.025, 0.25, 0.5, 0.75, 0.975), ...)
```

Arguments

x	The object generated by the function hmr.
digits	The number of significant digits printed. The default value is 3.
intervals	A numeric vector of probabilities with values in [0,1]. The default value is intervals = c(0.025, 0.5, 0.975).
...	...

print.metarisk *Generic print function for metarisk object in jarbes.*

Description

Generic print function for metarisk object in jarbes.

Usage

```
## S3 method for class 'metarisk'
print(x, digits, ...)
```

Arguments

x	The object generated by the function metarisk.
digits	The number of significant digits printed. The default value is 3.
...	...

print.simData *Generic print function for simData object.*

Description

Generic print function for simData object.

Usage

```
## S3 method for class 'simData'
print(x, ...)
```

Arguments

x	An object of class simData generated by the simData function.
...	Additional arguments passed to print.data.frame.

simData *Simulate Data for Meta-Analysis*

Description

This function simulates aggregated data for a meta-analysis, introducing biased studies at different levels.

Usage

```
simData(
  mu,
  sigma,
  n.total,
  tau,
  N,
  mu.beta.1,
  mu.beta.2,
  mu.beta.3,
  n.B.1,
  n.B.2,
  n.B.3
)
```

Arguments

mu	Scalar with the true pooled effect value.
sigma	Scalar with the true intra-study standard deviation.
n.total	A vector with the sample sizes of the studies.
tau	Scalar with the between-studies standard deviation.
N	Scalar with the total number of studies in the meta-analysis.
mu.beta.1	Scalar with the mean bias of studies in the mild bias class.
mu.beta.2	Scalar with the mean bias of studies in the large bias class.
mu.beta.3	Scalar with the mean bias of studies in the extreme bias class.
n.B.1	Scalar with the number of studies in the mild bias class.
n.B.2	Scalar with the number of studies in the large bias class.
n.B.3	Scalar with the number of studies in the extreme bias class.

Value

A dataframe with columns:

TE	Observed study's effect.
seTE	Standard error of the study's effect.

theta	True study's effect.
n.total	Sample size of the study.
B.flag	Bias category: "No B", "Mild B", "Large B", "Extreme B".

Examples

```
set.seed(123)
simData(mu = 0, sigma = 1, n.total = rep(100, 10), tau = 0.5, N = 10,
        mu.beta.1 = 0.2, mu.beta.2 = 0.5, mu.beta.3 = 1,
        n.B.1 = 2, n.B.2 = 2, n.B.3 = 2)
```

---

stemcells *Meta-analysis: 31 randomized controled trials (RCTs) with reported discrepancies*

Description

Meta-analysis of 31 randomized controled trials (RCTs) of two treatment groups of heart disease patients, where the treatment group received bone marrow stem cells and the control group a placebo treatment.

Format

A matrix with 31 rows and 11 columns. Each row represents study results, the columns are:

trial ID name of the trial.

TE effect.size= treatment effect is measured as the difference of the ejection fraction between groups, which measures the improvement of left ventricular function in the heart.

seTE Standard Error of the effect.size.

sample.size Total number of patients in the trial.

n.discrep Number of detected discrepancies in the published trial. Discrepancies are defined as two or more reported facts that cannot both be true because they are logically or mathematically incompatible.

Sequence Bias arising from the randomization process.

Allocation Bias due to deviations from intended interventions.

Blinding Bias introduced by lack of blinding.

Outcome Bias in measurement of the outcome.

Reporting Bias in selection of the reported result.

Other Selection bias, performance bias, detection bias, attrition bias, etc.

Source

Nowbar, A N, et al. (2014) Discrepancies in autologous bone marrow stem cell trials and enhancement of ejection fraction (DAMASCENE): weighted regression and meta-analysis. BMJ, 348,1-9.

References

Verde, P. E. (2017) Two Examples of Bayesian Evidence Synthesis with the Hierarchical Meta-Regression Approach. Chap.9, pag 189-206. Bayesian Inference, ed. Tejedor, Javier Prieto. InTech.

`summary.b3lmeta` *Generic summary function for bmeta object in jarbes*

Description

Generic summary function for bmeta object in jarbes

Usage

```
## S3 method for class 'b3lmeta'
summary(object, digits = 3, ...)
```

Arguments

`object`	The object generated by the bmeta function.
`digits`	The number of significant digits printed. The default value is 3.
`...`	...

`summary.bcbnp` *Generic summary function for bcbnp object in jarbes.*

Description

Generic summary function for bcbnp object in jarbes.

Usage

```
## S3 method for class 'bcbnp'
summary(object, digits = 3, show.clustering = FALSE, show.neff = FALSE, ...)
```

Arguments

`object`	The object generated by the bcbnp function.
`digits`	The number of significant digits printed. The default value is 3.
`show.clustering`	A logical value indicating whether to show the clustering parameters table. Defaults to 'TRUE'.
`show.neff`	A logical value indicating whether to show the effective sample size column (n.eff) and Rhat. Defaults to 'TRUE'.
`...`	...

summary.bcbnp_0 *Generic summary function for bcbnp_0 object in jarbes.*

Description

Generic summary function for bcbnp_0 object in jarbes.

Usage

```
## S3 method for class 'bcbnp_0'
summary(object, digits = 3, show.clustering = FALSE, show.neff = FALSE, ...)
```

Arguments

object	The object generated by the bcbnp function.
digits	The number of significant digits printed. The default value is 3.
show.clustering	A logical value indicating whether to show the clustering parameters table. Defaults to 'TRUE'.
show.neff	A logical value indicating whether to show the effective sample size column (n.eff) and Rhat. Defaults to 'TRUE'.
...	...

summary.bcdpmeta *Generic summary function for bcdpmeta object in jarbes*

Description

Generic summary function for bcdpmeta object in jarbes

Usage

```
## S3 method for class 'bcdpmeta'
summary(object, digits = 3, ...)
```

Arguments

object	The object generated by the bcmeta function.
digits	The number of significant digits printed. The default value is 3.
...	...

summary.bcmeta *Generic summary function for bcmeta object.*

Description

Generic summary function for bcmeta object.

Usage

```
## S3 method for class 'bcmeta'
summary(object, digits = 3, show.neff = FALSE, ...)
```

Arguments

object	The object generated by the bcmeta function.
digits	The number of significant digits printed. The default value is 3.
show.neff	A logical value indicating whether to show the effective sample size column (n.eff) and Rhat. Defaults to 'FALSE'.
...	...

summary.bcmixmeta *Generic summary function for bcmixmeta object in jarbes.*

Description

Generic summary function for bcmixmeta object in jarbes.

Usage

```
## S3 method for class 'bcmixmeta'
summary(object, digits = 3, show.clustering = FALSE, show.neff = FALSE, ...)
```

Arguments

object	The object generated by the bcmixmeta function.
digits	The number of significant digits printed. The default value is 3.
show.clustering	A logical value indicating whether to show the clustering parameters table. Defaults to 'TRUE'.
show.neff	A logical value indicating whether to show the effective sample size column (n.eff) and Rhat. Defaults to 'TRUE'.
...	...

summary.bmeta *Generic summary function for bmeta object in jarbes*

Description

Generic summary function for bmeta object in jarbes

Usage

```
## S3 method for class 'bmeta'
summary(object, digits = 3, show.neff = FALSE, ...)
```

Arguments

object	The object generated by the bmeta function.
digits	The number of significant digits printed. The default value is 3.
show.neff	A logical value indicating whether to show the effective sample size column (n.eff) and Rhat. Defaults to 'FALSE'.
...	...

summary.dpmeta *Generic summary function for dpmeta object in jarbes.*

Description

Generic summary function for dpmeta object in jarbes.

Usage

```
## S3 method for class 'dpmeta'
summary(
  object,
  digits = 3,
  show.clustering = TRUE,
  show.neff = FALSE,
  max.clusters = 10,
  ...
)
```

Arguments

object	The object generated by the dpmeta function.
digits	The number of significant digits printed. The default value is 3.
show.clustering	A logical value indicating whether to show the clustering parameters table. Defaults to 'TRUE'.
show.neff	A logical value indicating whether to show the effective sample size column (n.eff) and Rhat. Defaults to 'TRUE'.
max.clusters	Maximum number of clusters printed in the clustering table. Default is 10.
...	...

---

summary.dpmmeta *Generic summary function for dpmmeta object in jarbes*

Description

Generic summary function for dpmmeta object in jarbes

Usage

```
## S3 method for class 'dpmmeta'
summary(object, digits = 3, ...)
```

Arguments

object	The object generated by the dmpmeta function.
digits	The number of significant digits printed. The default value is 3.
...	...

---

summary.hmr *Generic summary function for hmr object in jarbes*

Description

Generic summary function for hmr object in jarbes

Usage

```
## S3 method for class 'hmr'
summary(object, digits = 3, ...)
```

Arguments

object	The object generated by the hmr function.
digits	The number of significant digits printed. The default value is 3.
...	...

summary.metarisk *Generic summary function for metarisk object in jarbes*

Description

Generic summary function for metarisk object in jarbes

Usage

```
## S3 method for class 'metarisk'
summary(object, digits = 3, ...)
```

Arguments

object	The object generated by the metarisk function.
digits	The number of significant digits printed. The default value is 3.
...	...

summary.simData *Summary method for simData objects*

Description

Provides a summary of the simulated meta-analysis dataset using the known simulation parameters.

Usage

```
## S3 method for class 'simData'
summary(object, digits = 3, ...)
```

Arguments

object	A simData object created by simData().
digits	The number of significant digits printed. The default value is 3.
...	Additional arguments (currently not used).

Value

A formatted summary of the meta-analysis simulation.

trisomy21 — *Meta-analysis: Observational studies assessing the relationship of a positive ICPC (Isolated Choroid Plexus Cyst) on Trisomy 21*

Description

Meta-analysis of 22 Observational Studies from PubMed, Cochrane Library and SciELO databases that assessed the relationship of a positive ICPC (Isolated Choroid Plexus Cyst) on Trisomy 21

Format

A dataframe with 22 rows and 6 columns. Each row represents study results, the columns are:

year Year of publication.

author Principal author of the publication.

y Number of cases of ICPC with Trisomy 21.

n Total number o cases with ICPC.

mean.GA Mean gestational time in weeks.

study.design Study design: prospective or retrospective cohort.

Source

Kürten C, Knippel A, Verde P, Kozlowski P. A Bayesian risk analysis for Trisomy 21 in isolated choroid plexus cyst: combining a prenatal database with a meta-analysis. J Matern Fetal Neonatal Med. 2019 Jun 11:1-9. doi: 10.1080/14767058.2019.1622666. Epub ahead of print. PMID: 31113245.

tyge_2011 — *Mortality data from the tigecycline meta-analysis (Curcio & Verde, 2011)*

Description

Mortality data from the tigecycline meta-analysis (Curcio & Verde, 2011)

Format

A data frame with 15 randomized clinical trials and 5 variables:

author_year Character string identifying the study.

event_e Number of deaths in the tigecycline treatment group.

n_e Total number of patients in the tigecycline group.

event_c Number of deaths in the comparator treatment group.

n_c Total number of patients in the comparator group.

RR Relative risk calculated using the 0.5 correction when event is 0.

TE Treatment effect as log(RR).

seTE Standard error of the TE.

Details

The dataset is typically analyzed using the **log relative risk**

$$TE_i = \log(RR_i)$$

where

$$RR_i = \frac{event_e/n_e}{event_c/n_c}$$

and the approximate sampling variance

$$seTE_i^2 = \frac{1}{event_e} - \frac{1}{n_e} + \frac{1}{event_c} - \frac{1}{n_c}$$

The data were used to illustrate how **profile likelihood methods can evaluate the support for different values of the between-study heterogeneity parameter** in a random-effects meta-analysis.

Source

Yahav D., Lador A., Paul M., Leibovici L. (2011). Efficacy and safety of tigecycline: a systematic review and meta-analysis. Journal of Antimicrobial Chemotherapy, 66:1963–1971.

References

Curcio D., Verde P.E. (2011). Comment on: Efficacy and safety of tigecycline: a systematic review and meta-analysis. Journal of Antimicrobial Chemotherapy.

Examples

```
data(tyge_2011)

# compute log relative risks
TE <- log((tyge_2011$event_e / tyge_2011$n_e) /
          (tyge_2011$event_c / tyge_2011$n_c))

seTE <- sqrt(
  1 / tyge_2011$event_e - 1 / tyge_2011$n_e +
  1 / tyge_2011$event_c - 1 / tyge_2011$n_c
)

head(data.frame(TE, seTE))
```

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