Package 'mrbayes'

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Type Package

Title Bayesian Summary Data Models for Mendelian Randomization Studies

Version 0.5.3

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URL https://github.com/okezie94/mrbayes, https://okezie94.github.io/mrbayes/, https://mrcieu.r-universe.dev/mrbayes

BugReports https://github.com/okezie94/mrbayes/issues

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Contents

mrbayes-package 2
bmi_insulin 3
dodata 4
mrinput_mr_format 5
mr_egger_rjags 6
mr_egger_stan 7
mr_format 9
mr_ivw_rjags 10
mr_ivw_stan 11
mr_radialegger_rjags 12
mr_radialegger_stan 14
mvmr_egger_rjags 16
mvmr_egger_stan 18
mvmr_format 19
mvmr_ivw_rjags 20
mvmr_ivw_stan 22

Index **24**

`mrbayes-package` *mrbayes: Bayesian implementation of the IVW and MR-Egger models for two-sample Mendelian randomization analyses*

Description

Bayesian implementation of the IVW and MR-Egger models and their radial and multivariate versions for two-sample Mendelian randomization analyses.

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References

Stan Development Team (2019). RStan: the R interface to Stan. R package version 2.19.2. https://mc-stan.org

See Also

Useful links:

- https://github.com/okezie94/mrbayes
- https://okezie94.github.io/mrbayes/
- https://mrcieu.r-universe.dev/mrbayes
- Report bugs at https://github.com/okezie94/mrbayes/issues

`bmi_insulin` *Dataset from Richmond et al. 2017 investigating the association of BMI on insulin resistance*

Description

A two-sample summary level dataset, Richmond et al. (2017) doi:10.1101/155739, containing 14 single nucleotide polymorphisms (SNPs) which have genotype-phenotype associations (BMI) and genotype-outcome associations (insulin) with their respective standard errors.

Usage

```
bmi_insulin
```

Format

A data frame with 14 rows and 5 columns:

rsid SNP RSID number

beta.exposure The genotype-BMI associations

beta.outcome The genotype-outcome associations

se.exposure The standard errors of the genotype-phenotype associations

se.outcome The standard errors of the genotype-outcome associations

Details

bmi_insulin.

References

Richmond, R. et al., Investigating the role of insulin in increased adiposity: Bi-directional Mendelian randomization study. bioRxiv, 2017, doi:10.1101/155739.

`dodata` *Dataset from Do et al., Nat Gen, 2013 containing summary level data on associations of genotypes with lipid traits and the risk of coronary heart diseases*

Description

A summary-level dataset, from Do et al. (2013) doi:10.1038/ng.2795, containing 185 single nucleotide polymorphisms (SNPs) which have genotype-phenotype associations and standard errors for LDL-C, HDL-C, Triglycerides, and genotype-outcome associations for coronary heart disease with their respective standard errors.

Usage

```
dodata
```

Format

A data frame with 185 rows and 21 columns with the following variables:

rsid RSID number

a1 Allele 1

a2 Allele 2

chr Chromosome

pos Genomic position

ldlcbeta The genotype-low-density lipoprotein cholesterol associations

hdlcbeta The genotype-high-density lipoprotein cholesterol associations

tgbeta The genotype-triglyceride associations

chdbeta The genotype-coronary heart disease associations, on the log odds ratio scale

ldlcp2 P-value for genotype-LDL-C associations

hdlcp2 P-value for genotype-HDL-C associations

tgp2 P-value for genotype-triglyceride associations

chdp2 P-value for genotype-coronary heart disease associations

ldlcz Z-score for genotype-LDL-C associations

ldlcse The standard errors of the genotype-low-density lipoprotein cholesterol associations

hdlcz Z-score for genotype-HDL-C associations

hdlcse The standard errors of the genotype-high-density lipoprotein cholesterol associations

tgz Z-score for genotype-triglyceride associations

tgse The standard errors of the genotype-triglyceride associations

chdz Z-score for genotype-coronary heart disease associations

chdse The standard errors of the genotype-coronary heart disease associations

Details

dodata.

References

Do, R. et al., Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352, doi:10.1038/ng.2795.

`mrinput_mr_format` *Convert an object of class MRInput from the MendelianRandomization package to the mrbayes mr_format class*

Description

Creates a data.frame with class `mr_format` from an object of class `MRInput` generated by `MendelianRandomization::mr_in`

Usage

```
mrinput_mr_format(dat)
```

Arguments

`dat`	Object from `MendelianRandomization::mr_input`.

Value

Object of class `mr_format`, the mrbayes format

Examples

```
if (requireNamespace("MendelianRandomization", quietly = TRUE)) {
dat <- MendelianRandomization::mr_input(
  bx = bmi_insulin$beta.exposure,
  bxse = bmi_insulin$se.exposure,
  by = bmi_insulin$beta.outcome,
  byse = bmi_insulin$se.outcome,
  snps = bmi_insulin$rsid
)
dat <- mrinput_mr_format(dat)
head(dat)
class(dat)
}
```

mr_egger_rjags *Bayesian implementation of the MR-Egger multivariate model with choice of prior distributions fitted using JAGS.*

Description

Bayesian implementation of the MR-Egger multivariate model with choice of prior distributions fitted using JAGS.

Usage

```
mr_egger_rjags(
  object,
  prior = "default",
  betaprior = "",
  sigmaprior = "",
  n.chains = 3,
  n.burn = 1000,
  n.iter = 5000,
  seed = NULL,
  rho = 0.5,
  ...
)
```

Arguments

object	A data object of class mr_format.
prior	A character string for selecting the prior distributions; • "default" selects a non-informative set of priors; • "weak" selects weakly informative priors; • "pseudo" selects a pseudo-horseshoe prior on the causal effect; • "joint" selects a joint prior on the intercept and slope.
betaprior	A character string in JAGS syntax to allow a user defined prior for the causal effect.
sigmaprior	A character string in JAGS syntax to allow a user defined prior for the residual standard deviation.
n.chains	Numeric indicating the number of chains used in the MCMC estimation, the default is 3 chains.
n.burn	Numeric indicating the burn-in period of the Bayesian MCMC estimation. The default is 1000 samples.
n.iter	Numeric indicating the number of iterations in the Bayesian MCMC estimation. The default is 5000 iterations.
seed	Numeric indicating the random number seed. The default is the rjags default.
rho	Numeric indicating the correlation coefficient input into the joint prior distribution. The default value is 0.5.
...	Additional arguments passed through to rjags::jags.model().

Value

An object of class `eggerjags` containing the following components:

AvgPleio The mean of the simulated pleiotropic effect

CausalEffect The mean of the simulated causal effect

StandardError Standard deviation of the simulated causal effect

sigma The value of the residual standard deviation

CredibleInterval The credible interval for the causal effect, which includes the lower (2.5%), median (50%) and upper intervals (97.5%)

samples Output of the Bayesian MCMC samples

Priors The specified priors

References

Bowden et al., Mendelian randomization with invalid instruments: effect estimation and bias detection through Egger regression. International Journal of Epidemiology 2015. 44(2): p. 512-525. doi:10.1093/ije/dyv080

Examples

```
if (requireNamespace("rjags", quietly = TRUE)) {
fit <- mr_egger_rjags(bmi_insulin)
summary(fit)
plot(fit$samples)
# 90% credible interval
fitdf <- do.call(rbind.data.frame, fit$samples)
cri90 <- sapply(fitdf, quantile, probs = c(0.05, 0.95))
print(cri90)
}
```

`mr_egger_stan` *Bayesian inverse variance weighted model with a choice of prior distributions fitted using Stan*

Description

Bayesian inverse variance weighted model with a choice of prior distributions fitted using Stan.

Usage

```
mr_egger_stan(
  data,
  prior = 1,
  n.chains = 3,
  n.burn = 1000,
```

```
  n.iter = 5000,
  seed = 12345,
  rho = 0.5,
  ...
)
```

Arguments

data	A data of class mr_format.
prior	An integer for selecting the prior distributions; • 1 selects a non-informative set of priors; • 2 selects weakly informative priors; • 3 selects a pseudo-horseshoe prior on the causal effect; • 4 selects joint prior of the intercept and causal effect estimate.
n.chains	Numeric indicating the number of chains used in the HMC estimation in rstan, the default is 3 chains.
n.burn	Numeric indicating the burn-in period of the Bayesian HMC estimation. The default is 1000 samples.
n.iter	Numeric indicating the number of iterations in the Bayesian HMC estimation. The default is 5000 iterations.
seed	Numeric indicating the random number seed. The default is 12345.
rho	Numeric indicating the correlation coefficient input into the joint prior distribution. The default is 0.5.
...	Additional arguments passed through to rstan::sampling().

Value

An object of class rstan::stanfit.

References

Bowden J, Davey Smith G, Burgess S. Mendelian randomization with invalid instruments: effect estimation and bias detection through Egger regression. International Journal of Epidemiology, 2015, 44, 2, 512-525. doi:10.1093/ije/dyv080.

Stan Development Team (2020). "RStan: the R interface to Stan." R package version 2.19.3, https://mc-stan.org/.

Examples

```
if (requireNamespace("rstan", quietly = TRUE)) {
# Note we recommend setting n.burn and n.iter to larger values
suppressWarnings(egger_fit <- mr_egger_stan(bmi_insulin, n.burn = 500, n.iter = 1000, refresh = 0L))
print(egger_fit)
}
```

`mr_format` *Organises the summary level data for use in the Bayesian MR functions*

Description

Organises the summary level data for use in the Bayesian MR functions

Usage

```
mr_format(rsid, xbeta, ybeta, xse, yse)
```

Arguments

`rsid`	A vector of genetic variants used for analysis, if unspecified a vector is automatically generated.
`xbeta`	A numeric vector of the instrument-phenotype associations.
`ybeta`	A numeric vector of the instrument-outcome associations.
`xse`	The standard errors of the instrument-phenotype associations `xbeta`.
`yse`	The standard errors of the instrument-outcome associations `ybeta`.

Value

A formatted data frame for analysis of class `mr_format`.

Examples

```
data(bmi_insulin)
dat <- mr_format(
  rsid = bmi_insulin[,"rsid"],
  xbeta = bmi_insulin[,"beta.exposure"],
  ybeta = bmi_insulin[,"beta.outcome"],
  xse = bmi_insulin[,"se.exposure"],
  yse = bmi_insulin[,"se.outcome"]
)
class(dat)
```

`mr_ivw_rjags` *Bayesian inverse variance weighted model with a choice of prior distributions fitted using JAGS.*

Description

Bayesian inverse variance weighted model with a choice of prior distributions fitted using JAGS.

Usage

```
mr_ivw_rjags(
  object,
  prior = "default",
  betaprior = "",
  n.chains = 3,
  n.burn = 1000,
  n.iter = 5000,
  seed = NULL,
  ...
)
```

Arguments

`object`	A data object of class `mr_format`.
`prior`	A character string for selecting the prior distributions; • `"default"` selects a non-informative set of priors; • `"weak"` selects weakly informative priors; • `"pseudo"` selects a pseudo-horseshoe prior on the causal effect.
`betaprior`	A character string in JAGS syntax to allow a user defined prior for the causal effect.
`n.chains`	Numeric indicating the number of chains used in the MCMC estimation, the default is `3` chains.
`n.burn`	Numeric indicating the burn-in period of the Bayesian MCMC estimation. The default is `1000` samples.
`n.iter`	Numeric indicating the number of iterations in the Bayesian MCMC estimation. The default is `5000` iterations.
`seed`	Numeric indicating the random number seed. The default is the rjags default.
`...`	Additional arguments passed through to `rjags::jags.model()`.

Value

An object of class `ivwjags` containing the following components:

CausalEffect The mean of the simulated causal effects

StandardError Standard deviation of the simulated causal effects

CredibleInterval The credible interval for the causal effect, which indicates the lower (2.5%), median (50%) and upper intervals (97.5%)

samples Output of the Bayesian MCMC samples with the different chains

Priors The specified priors

References

Burgess, S., Butterworth, A., Thompson S.G. Mendelian randomization analysis with multiple genetic variants using summarized data. Genetic Epidemiology, 2013, 37, 7, 658-665 doi:10.1002/gepi.21758.

Examples

```
if (requireNamespace("rjags", quietly = TRUE)) {
fit <- mr_ivw_rjags(bmi_insulin)
print(fit)
summary(fit)
plot(fit$samples)
# 90% credible interval
fitdf <- do.call(rbind.data.frame, fit$samples)
cri90 <- quantile(fitdf$Estimate, probs = c(0.05, 0.95))
print(cri90)
}
```

`mr_ivw_stan` *Bayesian inverse variance weighted model with a choice of prior distributions fitted using RStan.*

Description

Bayesian inverse variance weighted model with a choice of prior distributions fitted using RStan.

Usage

```
mr_ivw_stan(
  data,
  prior = 1,
  n.chains = 3,
  n.burn = 1000,
  n.iter = 5000,
  seed = 12345,
  ...
)
```

Arguments

data	A data of class mr_format.
prior	An integer for selecting the prior distributions; • 1 selects a non-informative set of priors; • 2 selects weakly informative priors; • 3 selects a pseudo-horseshoe prior on the causal effect.
n.chains	Numeric indicating the number of chains used in the HMC estimation in rstan, the default is 3 chains.
n.burn	Numeric indicating the burn-in period of the Bayesian HMC estimation. The default is 1000 samples.
n.iter	Numeric indicating the number of iterations in the Bayesian MCMC estimation. The default is 5000 iterations.
seed	Numeric indicating the random number seed. The default is 12345.
...	Additional arguments passed through to rstan::sampling().

Value

An object of class rstan::stanfit.

References

Burgess, S., Butterworth, A., Thompson S.G. Mendelian randomization analysis with multiple genetic variants using summarized data. Genetic Epidemiology, 2013, 37, 7, 658-665 doi:10.1002/gepi.21758.

Stan Development Team (2020). "RStan: the R interface to Stan." R package version 2.19.3, https://mc-stan.org/.

Examples

```
if (requireNamespace("rstan", quietly = TRUE)) {
suppressWarnings(ivw_fit <- mr_ivw_stan(bmi_insulin, refresh = 0L))
print(ivw_fit)
rstan::traceplot(ivw_fit)
}
```

---

mr_radialegger_rjags *Bayesian radial MR-Egger model with a choice of prior distributions fitted using JAGS.*

Description

Bayesian radial MR-Egger model with a choice of prior distributions fitted using JAGS.

Usage

```
mr_radialegger_rjags(
  object,
  prior = "default",
  betaprior = "",
  sigmaprior = "",
  n.chains = 3,
  n.burn = 1000,
  n.iter = 5000,
  seed = NULL,
  rho = 0.5,
  ...
)
```

Arguments

object	A data object of class mr_format.
prior	A character string for selecting the prior distributions; • "default" selects a non-informative set of priors; • "weak" selects weakly informative priors; • "pseudo" selects a pseudo-horseshoe prior on the causal effect; • "joint" selects a joint prior on the intercept and slope.
betaprior	A character string in JAGS syntax to allow a user defined prior for the causal effect.
sigmaprior	A character string in JAGS syntax to allow a user defined prior for the residual standard deviation.
n.chains	Numeric indicating the number of chains used in the MCMC estimation, the default is 3 chains.
n.burn	Numeric indicating the burn-in period of the Bayesian MCMC estimation. The default is 1000 samples.
n.iter	Numeric indicating the number of iterations in the Bayesian MCMC estimation. The default is 5000 iterations.
seed	Numeric indicating the random number seed. The default is the rjags default.
rho	Numeric indicating the correlation coefficient input into the joint prior distribution. The default is 0.5.
...	Additional arguments passed through to rjags::jags.model().

Value

An object of class radialeggerjags containing the following components:

AvgPleio The mean of the simulated pleiotropic effect

CausalEffect The mean of the simulated causal effect

StandardError Standard deviation of the simulated causal effect

sigma The mean of the simulated residual standard deviation

CredibleInterval The credible interval for the causal effect, which includes the lower (2.5%), median (50%) and upper intervals (97.5%)

samples Output of the Bayesian MCMC samples

Prior The specified priors

References

Bowden, J., et al., Improving the visualization, interpretation and analysis of two-sample summary data Mendelian randomization via the Radial plot and Radial regression. International Journal of Epidemiology, 2018. 47(4): p. 1264-1278. doi:10.1093/ije/dyy101.

Examples

```
if (requireNamespace("rjags", quietly = TRUE)) {
fit <- mr_radialegger_rjags(bmi_insulin)
summary(fit)
plot(fit$samples)
# 90% credible interval
fitdf <- do.call(rbind.data.frame, fit$samples)
cri90 <- quantile(fitdf$Estimate, probs = c(0.05, 0.95))
print(cri90)
}
```

`mr_radialegger_stan` *Bayesian inverse variance weighted model with a choice of prior distributions fitted using RStan.*

Description

Bayesian inverse variance weighted model with a choice of prior distributions fitted using RStan

Usage

```
mr_radialegger_stan(
  data,
  prior = 1,
  n.chains = 3,
  n.burn = 1000,
  n.iter = 5000,
  rho = 0.5,
  seed = 12345,
  ...
)
```

Arguments

data	A data of class mr_format.
prior	An integer for selecting the prior distributions; • 1 selects a non-informative set of priors; • 2 selects weakly informative priors; • 3 selects a pseudo-horseshoe prior on the causal effect; • 4 selects joint prior of the intercept and causal effect estimate.
n.chains	Numeric indicating the number of chains used in the HMC estimation in rstan, the default is 3 chains.
n.burn	Numeric indicating the burn-in period of the Bayesian HMC estimation. The default is 1000 samples.
n.iter	Numeric indicating the number of iterations in the Bayesian HMC estimation. The default is 5000 iterations.
rho	Numeric indicating the correlation coefficient input into the joint prior distribution. The default is 0.5.
seed	Numeric indicating the random number seed. The default is 12345.
...	Additional arguments passed through to rstan::sampling().

Value

An object of class rstan::stanfit.

References

Bowden, J., et al., Improving the visualization, interpretation and analysis of two-sample summary data Mendelian randomization via the Radial plot and Radial regression. International Journal of Epidemiology, 2018. 47(4): p. 1264-1278. doi:10.1093/ije/dyy101.

Stan Development Team (2020). "RStan: the R interface to Stan." R package version 2.19.3, https://mc-stan.org/.

Examples

```
if (requireNamespace("rstan", quietly = TRUE)) {
# Note we recommend setting n.burn and n.iter to larger values
suppressWarnings({
 radegger_fit <- mr_radialegger_stan(bmi_insulin, n.burn = 500, n.iter = 1000, refresh = 0L)
})
print(radegger_fit)
}
```

`mvmr_egger_rjags` *Bayesian implementation of the MVMR-Egger model with choice of prior distributions fitted using JAGS.*

Description

Bayesian implementation of the MVMR-Egger model with choice of prior distributions fitted using JAGS.

Usage

```
mvmr_egger_rjags(
  object,
  prior = "default",
  betaprior = "",
  sigmaprior = "",
  orientate = 1,
  n.chains = 3,
  n.burn = 1000,
  n.iter = 5000,
  seed = NULL,
  rho = 0.5,
  ...
)
```

Arguments

`object`	A data object of class `mvmr_format`.
`prior`	A character string for selecting the prior distributions; • `"default"` selects a non-informative set of priors; • `"weak"` selects weakly informative priors; • `"pseudo"` selects a pseudo-horseshoe prior on the causal effect; • `"joint"` selects a joint prior on the intercept and slopes.
`betaprior`	A character string in JAGS syntax to allow a user defined prior for the causal effect.
`sigmaprior`	A character string in JAGS syntax to allow a user defined prior for the residual standard deviation.
`orientate`	Numeric value to indicate the oriented exposure
`n.chains`	Numeric indicating the number of chains used in the MCMC estimation, the default is `3` chains.
`n.burn`	Numeric indicating the burn-in period of the Bayesian MCMC estimation. The default is `1000` samples.
`n.iter`	Numeric indicating the number of iterations in the Bayesian MCMC estimation. The default is `5000` iterations.

seed	Numeric indicating the random number seed. The default is the rjags default.
rho	Numeric indicating the correlation coefficient input into the joint prior distribution. The default value is 0.5.
...	Additional arguments passed through to rjags::jags.model().

Value

An object of class mveggerjags containing the following components:

AvgPleio The mean of the simulated pleiotropic effect

CausalEffect The mean of the simulated causal effect

StandardError Standard deviation of the simulated causal effect

sigma The value of the residual standard deviation

CredibleInterval The credible interval for the causal effect, which includes the lower (2.5%), median (50%) and upper intervals (97.5%)

samples Output of the Bayesian MCMC samples

Priors The specified priors

References

Bowden et al., Mendelian randomization with invalid instruments: effect estimation and bias detection through Egger regression. International Journal of Epidemiology 2015. 44(2): p. 512-525. doi:10.1093/ije/dyv080

Examples

```
if (requireNamespace("rjags", quietly = TRUE)) {
## Not run:
dat <- mvmr_format(
  rsid = dodata$rsid,
  xbeta = cbind(dodata$ldlcbeta,dodata$hdlcbeta,dodata$tgbeta),
  ybeta = dodata$chdbeta,
  xse = cbind(dodata$ldlcse,dodata$hdlcse,dodata$tgse),
  yse = dodata$chdse
)

fit <- mvmr_egger_rjags(dat)
summary(fit)
plot(fit$samples)
# 90% credible interval
fitdf <- do.call(rbind.data.frame, fit$samples)
cri90 <- sapply(fitdf, quantile, probs = c(0.05, 0.95))
print(cri90)

## End(Not run)
}
```

`mvmr_egger_stan` *Bayesian implementation of the MVMR-Egger model with choice of prior distributions fitted using RStan.*

Description

Bayesian implementation of the MVMR-Egger model with choice of prior distributions fitted using RStan.

Usage

```
mvmr_egger_stan(
  data,
  prior = 1,
  n.chains = 3,
  n.burn = 1000,
  n.iter = 5000,
  seed = 12345,
  rho = 0.5,
  orientate = 1,
  ...
)
```

Arguments

`data`	A data of class `mvmr_format`.
`prior`	An integer for selecting the prior distributions; • `1` selects a non-informative set of priors; • `2` selects weakly informative priors; • `3` selects a pseudo-horseshoe prior on the causal effect;
`n.chains`	Numeric indicating the number of chains used in the HMC estimation in rstan, the default is `3` chains.
`n.burn`	Numeric indicating the burn-in period of the Bayesian HMC estimation. The default is `1000` samples.
`n.iter`	Numeric indicating the number of iterations in the Bayesian HMC estimation. The default is `5000` iterations.
`seed`	Numeric indicating the random number seed. The default is `12345`.
`rho`	Numeric indicating the correlation coefficient input into the joint prior distribution. The default is `0.5`.
`orientate`	Numeric value to indicate the oriented exposure.
`...`	Additional arguments passed through to `rstan::sampling()`.

Value

An object of class `rstan::stanfit`.

References

Bowden J, Davey Smith G, Burgess S. Mendelian randomization with invalid instruments: effect estimation and bias detection through Egger regression. International Journal of Epidemiology, 2015, 44, 2, 512-525. doi:10.1093/ije/dyv080.

Stan Development Team (2020). "RStan: the R interface to Stan." R package version 2.19.3, https://mc-stan.org/.

Examples

```
if (requireNamespace("rstan", quietly = TRUE)) {
# Note we recommend setting n.burn and n.iter to larger values
dat <- mvmr_format(
  rsid = dodata$rsid,
  xbeta = cbind(dodata$ldlcbeta,dodata$hdlcbeta,dodata$tgbeta),
  ybeta = dodata$chdbeta,
  xse = cbind(dodata$ldlcse,dodata$hdlcse,dodata$tgse),
  yse = dodata$chdse
)
suppressWarnings(mvegger_fit <- mvmr_egger_stan(dat, n.burn = 500, n.iter = 1000, refresh = 0L))
print(mvegger_fit)
}
```

`mvmr_format` *Organises the summary level data for use in the Bayesian MR functions*

Description

Organises the summary level data for use in the Bayesian MR functions

Usage

```
mvmr_format(rsid, xbeta, ybeta, xse, yse)
```

Arguments

`rsid`	A vector of genetic variants used for analysis, if unspecified a vector is automatically generated.
`xbeta`	A matrix of multiple instrument-phenotypes associations.
`ybeta`	A numeric vector of the instrument-outcome associations.
`xse`	The matrix for corresponding standard errors of the instrument-phenotypes associations `xbeta`.
`yse`	The standard errors of the instrument-outcome associations `ybeta`.

Value

A formatted data frame for analysis of class `mvmr_format`.

Examples

```
data(dodata)
dat <- mvmr_format(
  rsid = dodata$rsid,
  xbeta = cbind(dodata$ldlcbeta,dodata$hdlcbeta,dodata$tgbeta),
  ybeta = dodata$chdbeta,
  xse = cbind(dodata$ldlcse,dodata$hdlcse,dodata$tgse),
  yse = dodata$chdse
)
class(dat)
```

`mvmr_ivw_rjags` *Bayesian multivariate inverse variance weighted model with a choice of prior distributions fitted using JAGS.*

Description

Bayesian multivariate inverse variance weighted model with a choice of prior distributions fitted using JAGS.

Usage

```
mvmr_ivw_rjags(
  object,
  prior = "default",
  betaprior = "",
  n.chains = 3,
  n.burn = 1000,
  n.iter = 5000,
  seed = NULL,
  ...
)
```

Arguments

`object`	A data object of class `mvmr_format`.
`prior`	A character string for selecting the prior distributions; • `"default"` selects a non-informative set of priors; • `"weak"` selects weakly informative priors; • `"pseudo"` selects a pseudo-horseshoe prior on the causal effect.
`betaprior`	A character string in JAGS syntax to allow a user defined prior for the causal effect.
`n.chains`	Numeric indicating the number of chains used in the MCMC estimation, the default is `3` chains.
`n.burn`	Numeric indicating the burn-in period of the Bayesian MCMC estimation. The default is `1000` samples.

n.iter	Numeric indicating the number of iterations in the Bayesian MCMC estimation. The default is 5000 iterations.
seed	Numeric indicating the random number seed. The default is the rjags default.
...	Additional arguments passed through to rjags::jags.model().

Value

An object of class mvivwjags containing the following components:

CausalEffect The mean of the simulated causal effects

StandardError Standard deviation of the simulated causal effects

CredibleInterval The credible interval for the causal effect, which indicates the lower (2.5%), median (50%) and upper intervals (97.5%)

samples Output of the Bayesian MCMC samples with the different chains

Priors The specified priors

References

Burgess, S., Butterworth, A., Thompson S.G. Mendelian randomization analysis with multiple genetic variants using summarized data. Genetic Epidemiology, 2013, 37, 7, 658-665 doi:10.1002/gepi.21758.

Examples

```
if (requireNamespace("rjags", quietly = TRUE)) {
dat <- mvmr_format(
  rsid = dodata$rsid,
  xbeta = cbind(dodata$ldlcbeta,dodata$hdlcbeta,dodata$tgbeta),
  ybeta = dodata$chdbeta,
  xse = cbind(dodata$ldlcse,dodata$hdlcse,dodata$tgse),
  yse = dodata$chdse
)

fit <- mvmr_ivw_rjags(dat)
print(fit)
summary(fit)
plot(fit$samples)
# 90% credible interval
fitdf <- do.call(rbind.data.frame, fit$samples)
cri90 <- sapply(fitdf, quantile, probs = c(0.05, 0.95))
print(cri90)
}
```

`mvmr_ivw_stan` *Bayesian multivariate inverse variance weighted model with a choice of prior distributions fitted using RStan.*

Description

Bayesian multivariate inverse variance weighted model with a choice of prior distributions fitted using RStan.

Usage

```
mvmr_ivw_stan(
  data,
  prior = 1,
  n.chains = 3,
  n.burn = 1000,
  n.iter = 5000,
  seed = 12345,
  ...
)
```

Arguments

`data`	A data of class `mvmr_format`.
`prior`	An integer for selecting the prior distributions; • `1` selects a non-informative set of priors; • `2` selects weakly informative priors; • `3` selects a pseudo-horseshoe prior on the causal effect.
`n.chains`	Numeric indicating the number of chains used in the HMC estimation in rstan, the default is `3` chains.
`n.burn`	Numeric indicating the burn-in period of the Bayesian HMC estimation. The default is `1000` samples.
`n.iter`	Numeric indicating the number of iterations in the Bayesian MCMC estimation. The default is `5000` iterations.
`seed`	Numeric indicating the random number seed. The default is `12345`.
`...`	Additional arguments passed through to `rstan::sampling()`.

Value

An object of class `rstan::stanfit`.

References

Burgess, S., Butterworth, A., Thompson S.G. Mendelian randomization analysis with multiple genetic variants using summarized data. Genetic Epidemiology, 2013, 37, 7, 658-665 doi:10.1002/gepi.21758.

Stan Development Team (2020). "RStan: the R interface to Stan." R package version 2.19.3, https://mc-stan.org/.

Examples

```
if (requireNamespace("rstan", quietly = TRUE)) {
dat <- mvmr_format(
  rsid = dodata$rsid,
  xbeta = cbind(dodata$ldlcbeta,dodata$hdlcbeta,dodata$tgbeta),
  ybeta = dodata$chdbeta,
  xse = cbind(dodata$ldlcse,dodata$hdlcse,dodata$tgse),
  yse = dodata$chdse
)
suppressWarnings(mvivw_fit <- mvmr_ivw_stan(dat, refresh = 0L))
print(mvivw_fit)
rstan::traceplot(mvivw_fit)
}
```

Index

∗ **datasets**
bmi_insulin, 3
dodata, 4

bmi_insulin, 3

dodata, 4

MendelianRandomization::mr_input, *5*
mr_egger_rjags, 6
mr_egger_stan, 7
mr_format, *6*, *8*, 9, *10*, *12*, *13*, *15*
mr_ivw_rjags, 10
mr_ivw_stan, 11
mr_radialegger_rjags, 12
mr_radialegger_stan, 14
mrbayes *(*mrbayes-package*)*, 2
mrbayes-package, 2
mrinput_mr_format, 5
mvmr_egger_rjags, 16
mvmr_egger_stan, 18
mvmr_format, *16*, *18*, 19, *20*, *22*
mvmr_ivw_rjags, 20
mvmr_ivw_stan, 22

rjags::jags.model(), *6*, *10*, *13*, *17*, *21*
rstan::sampling(), *8*, *12*, *15*, *18*, *22*
rstan::stanfit, *8*, *12*, *15*, *18*, *22*