

# Package ‘mrbayes’

September 21, 2021

**Type** Package

**Title** Bayesian Summary Data Models for Mendelian Randomization Studies

**Version** 0.5.0

**Description** Bayesian estimation of inverse variance weighted (IVW), Burgess et al. (2013) <[doi:10.1002/gepi.21758](https://doi.org/10.1002/gepi.21758)>, and MR-Egger, Bowden et al. (2015) <[doi:10.1093/ije/dyv080](https://doi.org/10.1093/ije/dyv080)>, summary data models for Mendelian randomization analyses.

**Depends** R (>= 3.5.0)

**Imports** methods, Rcpp (>= 0.12.0), rstan (>= 2.18.1), rstantools (>= 2.0.0), plyr

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Suggests** testthat, rjags (>= 4-9), tidyverse, knitr, ggplot2, ggmcmc, foreign, DescTools, bayesmeta, utils, kableExtra, roxygen2, bookdown, MendelianRandomization

**URL** <https://github.com/okezie94/mrbayes>

**BugReports** <https://github.com/okezie94/mrbayes/issues>

**RoxygenNote** 7.1.2

**SystemRequirements** GNU make

**Biarch** true

**LinkingTo** BH (>= 1.66.0), Rcpp (>= 0.12.0), RcppEigen (>= 0.3.3.3.0), rstan (>= 2.18.1), StanHeaders (>= 2.18.0)

**NeedsCompilation** yes

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**Repository** CRAN

**Date/Publication** 2021-09-21 13:10:31 UTC

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mrbayes-package	<i>mrbayes: Bayesian implementation of the IVW and MR-Egger models for two-sample Mendelian randomization analyses</i>
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### Description

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

### References

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

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bmi_insulin	<i>Dataset from Richmond et. al 2017 investigating the association of BMI on insulin resistance</i>
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### Description

A two-sample summary level dataset, Richmond et al. (2017) doi: [10.1101/155739](https://doi.org/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 44 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](https://doi.org/10.1101/155739).

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dodata	<i>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</i>
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**Description**

A summary-level dataset, from Do et al. (2013) doi: [10.1038/ng.2795](https://doi.org/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

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

**hdlcz** Z-score for genotype-HDL-C associations

**hdlcese** 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 cholesterol 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](https://doi.org/10.1038/ng.2795).

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mrinput_mr_format	<i>Convert an object of class MRInput from the MendelianRandomization package to the mrbayes mr_format class</i>
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---

## 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 `mr_bayes` 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)
}
```

---

<code>mr_egger_rjags</code>	<i>Bayesian implementation of the MR-Egger multivariate model with choice of prior distributions fitted using JAGS.</i>
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**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**

<code>object</code>	A data object of class <code>mr_format</code> .
<code>prior</code>	A character string for selecting the prior distributions; <ul style="list-style-type: none"> <li>• "default" selects a non-informative set of priors;</li> <li>• "weak" selects weakly informative priors;</li> <li>• "pseudo" selects a pseudo-horseshoe prior on the causal effect;</li> </ul>

- "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 <code>rjags::jags.model()</code> .

### Value

An object of class `egger_jags` 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](https://doi.org/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	<i>Bayesian inverse variance weighted model with a choice of prior distributions fitted using Stan</i>
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---

## 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 <a href="#">mr_format</a> .
prior	An integer for selecting the prior distributions; <ul style="list-style-type: none"> <li>• 1 selects a non-informative set of priors;</li> <li>• 2 selects weakly informative priors;</li> <li>• 3 selects a pseudo-horseshoe prior on the causal effect;</li> <li>• 4 selects joint prior of the intercept and causal effect estimate.</li> </ul>
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 <a href="#">rstan::sampling()</a> .

## Value

An object of class [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](https://doi.org/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
  egger_fit <- mr_egger_stan(bmi_insulin, n.burn = 500, n.iter = 1000)
  print(egger_fit)
}
```

---

mr_format	<i>Organises the summary level data for use in the Bayesian MR functions</i>
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---

## 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	<i>Bayesian inverse variance weighted model with a choice of prior distributions fitted using JAGS.</i>
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---

**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 <code>mr_format</code> .
prior	A character string for selecting the prior distributions; <ul style="list-style-type: none"> <li>• "default" selects a non-informative set of priors;</li> <li>• "weak" selects weakly informative priors;</li> <li>• "pseudo" selects a pseudo-horseshoe prior on the causal effect.</li> </ul>
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](https://doi.org/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 <code>mr_format</code> .
prior	An integer for selecting the prior distributions; <ul style="list-style-type: none"> <li>• 1 selects a non-informative set of priors;</li> <li>• 2 selects weakly informative priors;</li> <li>• 3 selects a pseudo-horseshoe prior on the causal effect.</li> </ul>
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 <code>rstan::sampling()</code> .

**Value**

An object of class `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](https://doi.org/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)) {
  ivw_fit <- mr_ivw_stan(bmi_insulin)
  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 <code>mr_format</code> .
prior	A character string for selecting the prior distributions; <ul style="list-style-type: none"> <li>• "default" selects a non-informative set of priors;</li> <li>• "weak" selects weakly informative priors;</li> <li>• "pseudo" selects a pseudo-horseshoe prior on the causal effect;</li> <li>• "joint" selects a joint prior on the intercept and slope.</li> </ul>
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 <code>rjags::jags.model()</code> .

**Value**

An object of class `radialegger_jags` 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](https://doi.org/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	<i>Bayesian inverse variance weighted model with a choice of prior distributions fitted using RStan.</i>
---------------------	--

---

**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 <code>mr_format</code> .
prior	An integer for selecting the prior distributions; <ul style="list-style-type: none"> <li>• 1 selects a non-informative set of priors;</li> <li>• 2 selects weakly informative priors;</li> <li>• 3 selects a pseudo-horseshoe prior on the causal effect;</li> <li>• 4 selects joint prior of the intercept and causal effect estimate.</li> </ul>
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 <code>rstan::sampling()</code> .

## Value

An object of class `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](https://doi.org/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
radegger_fit <- mr_radialegger_stan(bmi_insulin, n.burn = 500, n.iter = 1000)
print(radegger_fit)
}

```

---

mvmr_egger_rjags	<i>Bayesian implementation of the MVMR-Egger model with choice of prior distributions fitted using JAGS.</i>
------------------	--

---

### 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 <code>mvmr_format</code> .
prior	A character string for selecting the prior distributions; <ul style="list-style-type: none"> <li>• "default" selects a non-informative set of priors;</li> <li>• "weak" selects weakly informative priors;</li> <li>• "pseudo" selects a pseudo-horseshoe prior on the causal effect;</li> </ul>
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 `mvegger_jags` containing the following components: `if` (`requireNamespace("rjags", quietly = TRUE)`)

### 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](https://doi.org/10.1093/ije/dyv080)

### Examples

```
## 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 <code>mvmr_format</code> .
prior	An integer for selecting the prior distributions; <ul style="list-style-type: none"> <li>• 1 selects a non-informative set of priors;</li> <li>• 2 selects weakly informative priors;</li> <li>• 3 selects a pseudo-horseshoe prior on the causal effect;</li> </ul>
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 <code>rstan::sampling()</code> .

**Value**

An object of class `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](https://doi.org/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)
  mvegger_fit <- mvmr_egger_stan(dat, n.burn = 500, n.iter = 1000)
  print(mvegger_fit)
}

```

---

mvmr_format	<i>Organises the summary level data for use in the Bayesian MR functions</i>
-------------	--

---

**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	<i>Bayesian multivariate inverse variance weighted model with a choice of prior distributions fitted using JAGS.</i>
----------------	--

---

**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 <code>mvmr_format</code> .
prior	A character string for selecting the prior distributions; <ul style="list-style-type: none"> <li>• "default" selects a non-informative set of priors;</li> <li>• "weak" selects weakly informative priors;</li> <li>• "pseudo" selects a pseudo-horseshoe prior on the causal effect.</li> </ul>
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 <code>rjags::jags.model()</code> .

## Value

An object of class `mvi_vwjags` 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](https://doi.org/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	<i>Bayesian multivariate inverse variance weighted model with a choice of prior distributions fitted using RStan.</i>
---------------	---

---

## 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 <a href="#">mvmr_format</a> .
prior	An integer for selecting the prior distributions; <ul style="list-style-type: none"> <li>• 1 selects a non-informative set of priors;</li> <li>• 2 selects weakly informative priors;</li> <li>• 3 selects a pseudo-horseshoe prior on the causal effect.</li> </ul>
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 <a href="#">rstan::sampling()</a> .

## Value

An object of class [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](https://doi.org/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)  
  mvivw_fit <- mvmr_ivw_stan(dat)  
  print(mvivw_fit)  
  rstan::traceplot(mvivw_fit)  
}
```

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