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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.

References


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 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**


---

**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 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

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_input.

Usage

mrinput_mr_format(dat)

Arguments

dat  Object from MendelianRandomization::mr_input.
mr_egger_rjags

Value

Object of class mr_format, the mrbayes format

Examples

```r
dat <- MendelianRandomization::mr_input(bx = bmi_insulin$beta.exposure,
bxse = bmi_insulin$se.exposure,
by = bmi_insulin$beta.outcome,
byse = bmi_insulin$se.outcome,
spns = 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

```r
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


Examples

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)
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 `stanfit`. 

References


Examples

# 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

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
xbeta
ybeta
xse
yse

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


Examples

```r
fit <- mr_ivw_rjags(bmi_insulin)
print(fit)
summary(fit)
plot(fit$samples)
# 90% credible interval
fitdf <- do.call(rbind.data.frame, fit$samples)
crit90 <- quantile(fitdf$Estimate, probs = c(0.05,0.95))
print(crit90)
```

**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

```r
mr_ivw_stan(
  data,
  prior = 1,
  n.chains = 3,
  n.burn = 1000,
```
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 `stanfit`.

References


Examples

```r
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 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 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 distribu-
tion. 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


Examples

```r
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)
```

Description

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

Usage

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

```
  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 `stanfit`.

References


Examples

```
# 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**  
*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

```r
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;

- **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


Examples

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)
crid <- sapply(fitdf, quantile, probs = c(0.05, 0.95))
print(crid)
Bayesian implementation of the MVMR-Egger model with choice of prior distributions fitted using RStan.

Usage

```r
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 `stanfit`.
References


Examples

# 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

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


Examples

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)
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**

```r
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 `stanfit`.
References


Examples

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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