Package ‘mrbayes’

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Description

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

References


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

A two-sample summary level dataset, Richmond et al. (2017) https://dx.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
**do_data**

**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**


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**do_data**

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) https://dx.doi.org/10.1038/ng.2795, containing 185 single nucleotide polymorphisms (SNPs) which have genotype-phenotype associations and standard errors for low-density lipoprotein cholestrol, and genotype-outcome associations for coronary heart disease with their respective standard errors.

**Usage**

do_data

**Format**

A data frame with 185 rows and 9 columns:

- **rsid**: SNPs RSID number
- **beta.exposure**: The genotype-phenotype associations for low-density lipoprotein cholestrol
- **beta.outcome**: The genotype-outcome associations in this case the outcome is coronary heart disease
- **se.exposure**: The standard errors of the genotype-low-density lipoprotein cholestrol associations
- **se.outcome**: The standard errors of the genotype-outcome coronary heart disease associations
Details

do_data.

References


---

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

Description

Bayesian implementation of the MR-Egger 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.
mr_egger_rjags

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 <- quantile(fitdf$Estimate, 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 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 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 \texttt{rjags::jags.model()}.

\section*{Value}

An object of class \texttt{ivwjags} containing the following components:

\begin{itemize}
  \item **CausalEffect**  The mean of the simulated causal effects
  \item **StandardError**  Standard deviation of the simulated causal effects
  \item **CredibleInterval**  The credible interval for the causal effect, which indicates the lower(2.5%), median (50%) and upper intervals (97.5%)
  \item **samples**  Output of the Bayesian MCMC samples with the different chains
  \item **Priors**  The specified priors
\end{itemize}

\section*{References}


\section*{Examples}

\begin{verbatim}
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)
\end{verbatim}

---

\texttt{mr_ivw_stan} \hspace{1cm} \textit{Bayesian inverse variance weighted model with a choice of prior distributions fitted using RStan.}

\section*{Description}

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

\section*{Usage}

\begin{verbatim}
mr_ivw_stan(
  data,
  prior = 1,
  n.chains = 3,
  n.burn = 1000,
\end{verbatim}
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)
```
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

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

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)
```

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

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

`mr_radialegger_stan`

```r
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**

```r
# 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)
```
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