Package ‘mrbayes’

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

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mrbayes-package

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

bmi_insulin

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

Description

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

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

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 cholesterol, high-density lipoprotein cholesterol and triglycerides, 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
- **ldlcbeta** The genotype-phenotype associations for low-density lipoprotein cholesterol
- **hdlcbeta** The genotype-phenotype associations for high-density lipoprotein cholesterol
- **tgbeta** The genotype-phenotype associations for triglycerides
- **chdbeta** The genotype-outcome associations in this case the outcome is coronary heart disease
- **ldlcse** The standard errors of the genotype-low-density lipoprotein cholesterol associations
- **hdlcse** The standard errors of the genotype-high-density lipoprotein cholesterol associations
- **tgse** The standard errors of the genotype-triglyceride associations
- **chdse** 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
mr_egger_rjags(object, prior = "default", betaprior = "", sigmaprior = "", n.chains = 1, 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 1 chain.
- **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
The result object of class eggerjags contains 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**

```r
data(bmi_insulin)
fit <- mr_egger_rjags(bmi_insulin, n.chains = 1)
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_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**

```r
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 = 1,
              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 1 chain.
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

data(bmi_insulin)
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)
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 1 chain.

**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

Examples

data(bmi_insulin)
fit <- mr_radialegger_rjags(bmi_insulin, n.chains = 1)
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)
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