

Package: mrcovreg (via r-universe)

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Type Package

Title Package for an efficient and robust approach to Mendelian randomization with measured pleiotropic effects

Version 1.0.0

Description Implement a method for an efficient and robust approach to Mendelian randomization with measured pleiotropic effects in a high-dimensional setting.

License GPL-3

Encoding UTF-8

LazyData true

Imports glmnet

RoxygenNote 6.1.1

Repository <https://mrcieu.r-universe.dev>

RemoteUrl <https://github.com/remlapmot/mrcovreg>

RemoteRef suggestions

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 cv.mr_covreg

Cross-validation for mr_covreg

Description

Implements K-fold cross-validation for mr_covreg where the target function is the mean squared error.

Usage

```
cv.mr_covreg(bx, bw, by, S, lambda = numeric(0), nlam = 100,
             nfolds = 10)
```

Arguments

bx	Vector of estimates of the genetic variant-risk factor associations.
bw	Matrix of estimates of the genetic variant-covariate associations estimates. The jth column of the matrix is a vector of the estimates of the genetic variant associations with the jth covariate.
by	Vector of estimates of the genetic variant-outcome associations.
S	Diagonal matrix where the jth diagonal entry is the inverse of the variance of the jth genetic variant-outcome association estimate.
lambda	Sequence of lambda values to be used in cross-validation. If not specified (which is the default setting), the sequence of lambda values is chosen by the glmnet package.
nlam	Number of lambda values to use in cross-validation. Default is 100. Note, if a lambda sequence is given, this parameter is redundant.
nfolds	Number of folds for cross-validation. Default is 10.

Value

glmnet.fit	List containing a matrix of coefficients and a vector of the number of non-zero coefficients.
lamseq	Sequence of lambda values used in cross-validation.
lambda.min	The value of lambda that minimised the test mean squared error.
lambda.1se	The value of lambda that minimised the test mean squared error with the 1 standard deviation rule applied.

Description

Estimates a causal effect by implementing regularization on potential pleiotropic covariates. The tuning parameter is chosen by cross-validation.

Usage

```
mr_covreg(bx, bw, by, S, klessp = TRUE, lambda = numeric(0),
          nlam = 100, K = 10, cv_mt = 2)
```

Arguments

bx	Vector of estimates of the genetic variant-risk factor associations.
bw	Matrix of estimates of the genetic variant-covariate associations estimates. The <i>j</i> th column of the matrix is a vector of the estimates of the genetic variant associations with the <i>j</i> th covariate.
by	Vector of estimates of the genetic variant-outcome associations.
S	Diagonal matrix where the <i>j</i> th diagonal entry is the inverse of the variance of the <i>j</i> th genetic variant-outcome association estimate.
klessp	Indicates whether the tuning parameter should be always sufficiently large such that there are always less than $p - 1$ covariates with a non-zero coefficient.
lambda	Sequence of lambda values to be used in cross-validation. If not specified (which is the default setting), the sequence of lambda values is chosen by the glmnet package.
nlam	Number of lambda values to use in cross-validation. Default is 100. Note, if a lambda sequence is given, this parameter is redundant.
K	Number of folds for cross-validation. Default is 10.
cv_mt	Controls which target function to use in cross-validation. If set at 1, the tuning parameter is selected independent of the genetic variant-risk factor associations. Otherwise, the target function is the mean squared error (which is the default).

Value

thest	Causal effect estimate.
thest_1se	Causal effect estimate with the 1 standard error rule applied.
a	Regularized covariate coefficients.
a_1se	Regularized covariate coefficients with the 1 standard error rule applied.
lambda	Value of lambda chosen by cross-validation.
lambda_1se	Value of lambda chosen by cross-validation with the 1 standard error rule applied.
lamseq	Sequence of lambda values used in cross-validation.

mr_covreg_lam	<i>Causal effect estimation via covariate regularization for a specified tuning parameter value</i>
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Description

Estimates a causal effect by implementing regularization on potential pleiotropic covariates for a given value of the tuning parameter.

Usage

```
mr_covreg_lam(bx, bw, by, S, lambda)
```

Arguments

bx	Vector of estimates of the genetic variant-risk factor associations.
bw	Matrix of estimates of the genetic variant-covariate associations estimates. The jth column of the matrix is a vector of the estimates of the genetic variant associations with the jth covariate.
by	Vector of estimates of the genetic variant-outcome associations.
S	Diagonal matrix where the jth diagonal entry is the inverse of the variance of the jth genetic variant-outcome association estimate.

Value

thest	Causal effect estimate.
a	Regularized covariate coefficients.

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