Package: MVMRcML (via r-universe)

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Type Package

Title Multivariable Mendelian randomization based on constrained
maximum likelihood

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Description Robust multivariable Mendelian randomization based on
constrained maximum likelihood.

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Encoding UTF-8

LazyData true

Imports numDeriv, Rcpp, RcppArmadillo

LinkingTo Rcpp, RcppArmadillo

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

RemoteUrl https://github.com/ZhaotongL/MVMR-cML

RemoteRef HEAD

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Contents

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invcov_mvmr	*Generate the list of inverse of covariance matrices used in* MVMR-cML-DP

Description

Generate the list of inverse of covariance matrices used in MVMR-cML-DP

Usage

```
invcov_mvmr(se_bx, se_by, rho_mat)
```

Arguments

se_bx	A m*L matrix of standard errors of SNP-exposure association
se_by	A vector of standard errors of SNP-outcome association
rho_mat	A $(L+1) \times (L+1)$ correlation matrix among the L exposures and the outcome, note that the upper-left $L \times L$ submatrix corresponding to the L exposures.

Value

A list of inverse of covariance matrices with respect to each genetic variant, retaining the ordering in se_bx

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MVcML_SdTheta	*Standard error estimate for MVMR-cML-BIC*

Description

This is based on the profile likelihood of the set of valid IVs, which is not robust to uncertainty in model selection.

Usage

```
MVcML_SdTheta(b_exp, b_out, Sig_inv_l, theta, zero_ind, r_vec = NULL)
```

Arguments

b_exp	A matrix of SNP effects on the exposure variable.
b_out	A vector of SNP effects on the outcome variable.
Sig_inv_l	A list of inverse of covariance matrix.
theta	A vector of final estimates of causal effect of each exposure by MVMR-cML-BIC obtained from MVmr_cML_DP.
zero_ind	A vector of the index of valid IVs.
r_vec	A vector of estimated horizontal pleiotropic effects.

Value

A vector

| MVmr_cML | *MVMRcML method with BIC selection* |

Description

This is the main function of MVMR-cML.

Usage

```
MVmr_cML(
  b_exp,
  b_out,
  se_bx,
  Sig_inv_l,
  n,
  K_vec = as.numeric(c()),
  random_start = 1L,
  maxit = 100L,
  thres = 1e-04
)
```

Arguments

b_exp	A m*L matrix of SNP effects on the exposure variable.
b_out	A m*1 matrix of SNP effects on the outcome variable.
se_bx	A m*L matrix of standard errors of b_exp.
Sig_inv_l	A list of the inverse of m covariance matrices, generated by invcov_mvmr().
n	The smallest sample size of the L+1 GWAS dataset.
K_vec	Sets of candidate K's, the constraint parameter representing number of invalid IVs.
random_start	Number of random start points, default is 1.
maxit	Maximum number of iterations for each optimization, default is 100.
thres	Threshold for convergence criterion.

Value

A list

BIC_theta Estimated causal effect from MVMR-cML-BIC

BIC_invalid Invalid IVs selected by MVMR-cML-BIC

K_vec K_vec to be searched from

Converge 0 if converge; 1 otherwise

BIC_vec BIC vector corresponding to K_vec

MVmr_cML_DP   *MVMRcML method with Data Perturbation*

Description

This is the main function of MVMR-cML.

Usage

```
MVmr_cML_DP(
  b_exp,
  b_out,
  se_bx,
  Sig_inv_l,
  n,
  K_vec = as.numeric(c()),
  random_start = 1L,
  num_pert = 100L,
  maxit = 100L,
  thres = 1e-04
)
```

Arguments

b_exp	A m*L matrix of SNP effects on the exposure variable.
b_out	A m*1 matrix of SNP effects on the outcome variable.
se_bx	A m*L matrix of standard errors of b_exp.
Sig_inv_l	A list of the inverse of m covariance matrices, generated by invcov_mvmr().
n	The smallest sample size of the L+1 GWAS dataset.
K_vec	Sets of candidate K's, the constraint parameter representing number of invalid IVs.
random_start	Number of random start points, default is 1.
num_pert	Number of perturbation, default is 100.
maxit	Maximum number of iterations for each optimization, default is 100.
thres	Threshold for convergence criterion.

Value

A list

BIC_theta Estimated causal effect from MVMR-cML-BIC

BIC_invalid Invalid IVs selected by MVMR-cML-BIC

BIC_DP_theta Estimated causal effect from MVMR-cML-DP

BIC_DP_se Estimate standard error for BIC_DP_theta

eff_DP_B Data perturbation with successful convergence

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