Package: MRAID (via r-universe)

Type Package

Title MRAID(Mendelian Randomization with Automated Instrument Determination)

Version 1.0

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Description MRAID is an R package for efficient statistical inference of two-sample Mendelian Randomization. MRAID takes GWAS summary statistics as inputs to estimate causal effects of one trait on another. MRAID is able to model an initial set of candidate SNP instruments that are in high LD with each other and perform automated instrument selection to identify suitable SNPs to serve as instrumental variables. MRAID simultaneously accounts for both uncorrelated and correlated horizontal pleiotropy, relies on a scalable sampling-based inference algorithm to perform numerical integration, circumventing the difficulty in likelihood function, leading to calibrated p-values that enable reasonably large-scale exposure screening.

License GPL-3

Imports Rcpp (>= 1.0.6)

LinkingTo Rcpp, RcppArmadillo, RcppDist

RoxygenNote 7.1.1

NeedsCompilation yes

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

RemoteUrl https://github.com/yuanzhongshang/MRAID

RemoteRef HEAD

RemoteSha 87692470047baeb0061f48c7f316fe11c6fcdad7

Contents

MRAID   *The function of MRAID method two sample Mendelian Randomization*

Description

MRAID is able to model an initial set of candidate SNP instruments that are in high LD with each other and perform automated instrument selection to identify suitable SNPs to serve as instrumental variables. MRAID simultaneously accounts for both uncorrelated and correlated horizontal pleiotropy, relies on a scalable sampling-based inference algorithm to perform numerical integration, circumventing the difficulty in likelihood function

Usage

```
MRAID(
  Zscore_1,
  Zscore_2,
  Sigma1sin,
  Sigma2sin,
  samplen1,
  samplen2,
  Gibbsnumber = 1000,
  burninproportion = 0.2,
  pi_beta_shape = 0.5,
  pi_beta_scale = 4.5,
  pi_c_shape = 0.5,
  pi_c_scale = 9.5,
  pi_1_shape = 0.5,
  pi_1_scale = 1.5,
  pi_0_shape = 0.05,
  pi_0_scale = 9.95
)
```

Arguments

Zscore_1	the Zscore vector of the SNP effect size vector for the exposure
Zscore_2	the Zscore vector of the SNP effect size vector for the outcome
Sigma1sin	the LD matrix for the SNPs in the exposure GWAS data
Sigma2sin	the LD matrix for the SNPs in the outcome GWAS data,both Sigma2sin and sigma1sin are often from the same reference panel
samplen1	the sample size of exposure GWAS

samplen2	the sample size of outcome GWAS
Gibbsnumber	the number of Gibbs sampling iterations with the default to be 1000
burninproportion	
	the proportion to burn in from Gibbs sampling iterations, with default to be 0.2
pi_beta_shape	the prior shape paramter for pi_beta with the default to be 0.5
pi_beta_scale	the prior scale paramter for pi_beta with the default to be 4.5
pi_c_shape	the prior shape paramter for pi_c with the default to be 0.5
pi_c_scale	the prior shape paramter for pi_c with the default to be 9.5
pi_1_shape	the prior shape paramter for pi_1 with the default to be 0.5
pi_1_scale	the prior scale paramter for pi_1 with the default to be 1.5
pi_0_shape	the prior shape paramter for pi_0 with the default to be 0.05
pi_0_scale	the prior scale paramter for pi_0 with the default to be 9.95

Value

A list of estimated parameters including the p values for the causal effect test

causal_effect	The estimate of causal effect
causal_pvalue	The p value for the causal effect
correlated_pleiotropy_effect	
	The estimate of correlated pleiotropy effect
sigmaeta	The variance estimate for the uncorrelated pleiotropy effect
sigmabeta	The variance estimate for the SNP effect sizes on the exposure
sigma_error_1	The variance estimate of the error in exposure GWAS model
sigma_error_2	The variance estimate of the error in outcome GWAS model

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MRAID_CPP	*MRAID*

Description

MRAID

Usage

```
MRAID_CPP(
  betaxin,
  betayin,
  Sigma1sin,
  Sigma2sin,
  samplen1,
  samplen2,
  Gibbsnumberin,
```

```
        burninproportion,
        initial_betain,
        pi_beta_shape_in,
        pi_beta_scale_in,
        pi_c_shape_in,
        pi_c_scale_in,
        pi_1_shape_in,
        pi_1_scale_in,
        pi_0_shape_in,
        pi_0_scale_in,
        maxvarin,
        alphain
)
```

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