Package 'MRlap'

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Title What the Package Does (One Line, Title Case)

Version 0.0.0.9000

Description What the package does (one paragraph).

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Encoding UTF-8

LazyData true

Imports magrittr,
  tibble,
  dplyr,
  data.table,
  rlang,
  stringr,
  TwoSampleMR,
  GenomicSEM

Remotes MRCIEU/TwoSampleMR,
  MichelNivard/GenomicSEM

RoxygenNote 6.1.1

R topics documented:

MRlap   *MRlap - main function*

Description

Performs cross-trait LD score regression, IVW-MR analysis and provide a correction that simultaneously accounts for biases due to the overlap between the exposure and outcome samples, the use of weak instruments and Winner's curse.

Usage

```
MRlap(exposure, exposure_name = NULL, outcome, outcome_name = NULL, ld,
   hm3, MR_threshold = 5e-08, MR_pruning_dist = 500,
   MR_pruning_LD = 0, MR_reverse = 0.001, s = 10000,
   save_logfiles = FALSE, verbose = TRUE)
```

Arguments

exposure	The path to the file containing the GWAS summary statistics for the exposure, or a `data.frame` (character, or `data.frame`)
exposure_name	The name of the exposure trait, `default="exposure"` (character)
outcome	The path to the file containing the GWAS summary statistics for the exposure, or a `data.frame` (character, or `data.frame`)
outcome_name	The name of the outcome trait, `default="outcome"` (character)
ld	The path to the folder in which the LD scores used in the analysis are located. Expects LD scores formated as required by the original LD score regression software. (character)
hm3	The path to a file of SNPs with alt, ref alleles and rsid used to allign alleles across traits (character)
MR_threshold	The threshold used to select strong instruments for MR, should be lower than 1e-5, `default=5e-8` (numeric)
MR_pruning_dist	
	The distance used for pruning MR instruments (in Kb), should be between 10 and 1000, `default=500` (numeric)
MR_pruning_LD	The LD threshold (r2) used for pruning MR instruments, should be between 0 and 1 (if 0, distance-based pruning is used), `default=0` (numeric)
MR_reverse	The p-value used to exclude MR instruments that are more strongly associated with the outcome than with the exposure, `default=1e-3` (numeric)
s	The number of simulations in the sampling strategy to estimate the variance of the corrected causal effect and the covariance between observed and corrected effects `default=10,000` (numeric)
save_logfiles	A logical indicating if log files from LDSC should be saved, `default=FALSE`
verbose	A logical indicating if information on progress should be reported, `default=TRUE`

Details

`exposure` and `outcome` are required arguments. The input file / data.frame should contain the following columns (lower or upper case) :
SNPID (rs numbers) should be : `rs, rsid, snp, snpid, rnpid`
CHR (chromosome) should be : `chr`
POS (position) should be : `pos`
ALT (effect allele) should be : `a1, alt, alts`
REF (reference allele) should be : `a2, a0, ref`
Z (z-score) should be : `Z, zscore`
N (sample size) should be : `N`
If Z is not present, it can be calculated from BETA and SE.
BETA should be : `b, beta, beta1`
SE should be : `se, std`

Setting s to a smaller value is strongly discouraged, it can lead to an innacurate estimates of the corrected effect SE, therefore affecting the results of the difference testing between observed and corrected effects.

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