

Package: mrsensemakr (via r-universe)

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Type Package

Title Sensitivity Analysis Tools for Mendelian Randomization

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Description The R package mrsensemakr implements sensitivity analysis tools for Mendelian Randomization.

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Encoding UTF-8

LazyData true

Imports sensemakr

Depends R (>= 2.10)

RoxygenNote 7.1.1

Suggests knitr, rmarkdown, testthat (>= 3.0.0), covr

VignetteBuilder knitr

Config/testthat/edition 3

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

RemoteUrl <https://github.com/carloscinelli/mrsensemakr>

RemoteRef HEAD

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 mr_sensemakr

MR-sensemakr

Description

MR-sensemakr

Usage

```
mr_sensemakr(
  outcome,
  exposure,
  instrument,
  covariates = NULL,
  data,
  benchmark_covariates = NULL,
  k = 1,
  alpha = 0.05
)
```

Arguments

outcome	A character vector with the name of the outcome trait.
exposure	A character vector with the name of the exposure trait.
instrument	A character vector with the name of the genetic instrument.
covariates	A character vector with the name of the control covariates, such as age, sex, genomic principal components, batch effect dummies and putative pleiotropic pathways.
data	An object of the class <code>data.frame</code> containing the variables used in the analysis.
benchmark_covariates	Covariates for benchmarking. Must be a subset of the <code>covariates</code> argument. The user has two options: (i) character vector of the names of covariates that will be used to bound the plausible strength of the unobserved confounders. Each variable will be considered separately; (ii) a named list with character vector names of covariates that will be used, as a group, to bound the plausible strength of the unobserved confounders. The names of the list will be used for the benchmark labels.
k	numeric vector. Parameterizes how many times stronger residual biases are related to the treatment and the outcome in comparison to the observed benchmark covariates.
alpha	significance level

Examples

```
## loads package
library(mrsensemakr)

## simulated data example
data("sim_data")

## create vectors indicating variable names in the data
outcome <- "out.trait" # name of outcome trait
exposure <- "exp.trait" # name of exposure trait
instrument <- "prs" # genetic instrument (e.g, polygenic risk score)
age.sex <- c("age", "sex") # age and sex variables (if applicable)
alc.smok <- c("alcohol", "smoking") # putative pleiotropic vars.
pcs <- paste0("pc", 1:20) # first 20 principal components pc1 ... pc20

## runs MR sensitivity analysis
mr.sense <- mr_sensemakr(outcome = outcome,
                          exposure = exposure,
                          instrument = instrument,
                          covariates = c(age.sex, alc.smok, pcs),
                          data = sim_data,
                          benchmark_covariates = list(alc.smok = alc.smok,
                                                       pcs = pcs))

## print results
mr.sense

## sensitivity contour plots
plot(mr.sense,
      benchmark_covariates = list(alc.smok = alc.smok,
                                   pcs = pcs),
      k = list(alc.smok = 25,
               pcs = 35))
```

sim_data

Simulated Data

Description

Simulated Data

Format

A data frame with 200,000 observations and 27 variables.

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* **dataset**

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