Package: MRPRESSO (via r-universe)

May 28, 2026

Type Package

Title Performs the Mendelian Randomization Pleiotropy RESidual Sum and Outlier (MR-PRESSO) test.

Version 1.0

Date 2017-06-29

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Description MR-PRESSO (Mendelian Randomization Pleiotropy RESidual Sum and Outlier) is a framework that allows for the evaluation of pleiotropy in multi-instrument Mendelian Randomization utilizing genome-wide summary association statistics.

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NeedsCompilation no

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

Date/Publication 2023-07-25 16:33:23 UTC

RemoteUrl https://github.com/rondolab/MR-PRESSO

RemoteRef HEAD

RemoteSha 3e3c92d7eda6dce0d1d66077373ec0f7ff4f7e87

Contents

`MRPRESSO-package` *Performs the Mendelian Randomization Pleiotropy RESidual Sum and Outlier (MR-PRESSO) test.*

Description

MR-PRESSO (Mendelian Randomization Pleiotropy RESidual Sum and Outlier) is a unified framework that allows for the evaluation of pleiotropy in a standard MR model. The method extends on previous approaches that utilize the general model of multi-instrument MR on summary statistics. MR-PRESSO has three components, including: 1) detection of pleiotropy (MR-PRESSO global test); 2) correction of pleiotropy via outlier removal (MR-PRESSO outlier test); and 3) testing of significant distortion differences in the causal estimates before and after MR-PRESSO correction (MR-PRESSO bias assessment test).

Details

The DESCRIPTION file:

Author(s)

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References

Widespread pleiotropy confounds causal relationships between complex traits and diseases inferred from Mendelian randomization. Marie Verbanck*, Chia-Yen Chen*, Benjamin Neale, Ron Do.

Examples

```
data(SummaryStats)
mr_presso(BetaOutcome = ”Y_effect”, BetaExposure = ”E1_effect”, SdOutcome = ”Y_se”, SdExposure = ”E1_se”, OUTLIERt
```

`mr_presso` *a function to perform the Mendelian Randomization Pleiotropy RESidual Sum and Outlier (MR-PRESSO) test*

Description

MR-PRESSO (Mendelian Randomization Pleiotropy RESidual Sum and Outlier) is a unified framework that allows for the evaluation of pleiotropy in a standard MR model. The method extends on previous approaches that utilize the general model of multi-instrument MR on summary statistics. MR-PRESSO has three components, including: 1) detection of pleiotropy (MR-PRESSO global test); 2) correction of pleiotropy via outlier removal (MR-PRESSO outlier test); and 3) testing of significant distortion in the causal estimate before and after MR-PRESSO correction (MR-PRESSO distortion test).

Usage

```
mr_presso(BetaOutcome, BetaExposure, SdOutcome, SdExposure, data, OUTLIERtest = FALSE, DISTORTIONte
```

Arguments

`BetaOutcome`	character, name of the outcome variable
`BetaExposure`	vector of characters, name(s) of the exposure(s)
`SdOutcome`	character, name of the standard deviation of the outcome variable
`SdExposure`	vector of characters, name(s) of the standard deviation of the exposure(s)
`data`	dataframe of summary statistics containing the outcome and exposure variables
`OUTLIERtest`	boolean, if TRUE the MR-PRESSO outlier test will be performed, default is FALSE
`DISTORTIONtest`	boolean, if TRUE the MR-PRESSO distortion test on the causal estimate will be performed, default is FALSE
`SignifThreshold`	float, significance threshold to use between 0 and 1, default is 0.05
`NbDistribution`	integer, number of elements to simulate to form the null distribution to compute empirical P-values. This is directly impacting the precision of the empirical P-values, it is 1/NbDistribution for the global test and nrow(data)/NbDistribution
`seed`	a single value, interpreted as an integer to use in set.seed()

Value

`Main MR results`	Results of the MR analysis providing the causal estimate, sd and P-value of the raw and outlier-corrected MR analysis
`Global Test`	Results of the MR-PRESSO global test. List of the observed residual sum of squares 'RSSobs' and empirical P-value 'Pvalue'
`Outlier Test`	Results of the MR-PRESSO outlier test. Table of observed residual sum of squares 'RSSobs' and 'Pvalue' per SNV
`Distortion Test`	Results of the MR-PRESSO distortion test. List of the 'Outliers Indices' identified as outliers and excluded to calculate the 'Distortion Coefficient' (in percent) and its 'Pvalue'.

Author(s)

Marie Verbanck

References

Detection of widespread horizontal pleiotropy in causal relationships inferred from Mendelian randomization between complex traits and diseases. Marie Verbanck, Chia-Yen Chen, Benjamin Neale, Ron Do. Nature Genetics 2018. DOI: 10.1038/s41588-018-0099-7. https://www.nature.com/articles/s41588-018-0099-7

Examples

```
data(SummaryStats)
mr_presso(BetaOutcome = ”Y_effect”, BetaExposure = ”E1_effect”, SdOutcome = ”Y_se”, SdExposure = ”E1_se”, OUTLIERt
```

SummaryStats *Simulated toy dataset*

Description

’SummaryStats’ is a simulated toy dataset of summary statistics for Y the outcome and E1 and E2 two exposures. It is composed of 45 single ncleotide variants (SNVs) associated with E1 and 5 additional variants associated with E1 and E2 which are therefore submitted to pleiotropy. Test the function mr_presso() on this toy dataset.

Usage

```
data(”SummaryStats”)
```

Format

A data frame with 50 observations on the following 9 variables.

`E1_effect`	a numeric vector
`E1_se`	a numeric vector
`E1_pval`	a numeric vector
`E2_effect`	a numeric vector
`E2_se`	a numeric vector
`E2_pval`	a numeric vector
`Y_effect`	a numeric vector
`Y_se`	a numeric vector
`Y_pval`	a numeric vector

References

Detection of widespread horizontal pleiotropy in causal relationships inferred from Mendelian randomization between complex traits and diseases. Marie Verbanck, Chia-Yen Chen, Benjamin Neale, Ron Do. Nature Genetics 2018. DOI: 10.1038/s41588-018-0099-7. https://www.nature.com/articles/s41588-018-0099-7

Examples

```
data(SummaryStats)
mr_presso(BetaOutcome = ”Y_effect”, BetaExposure = ”E1_effect”, SdOutcome = ”Y_se”, SdExposure = ”E1_se”, OUTLIERt
```

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