# Package: MRPRESSO (via r-universe)

September 17, 2024

**Type** Package

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

**Version** 1.0

**Date** 2017-06-29

**Author** Marie Verbanck

**Maintainer** Marie Verbanck <marie.verbanck@mssm.edu>

**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.

**License** GPL-3

**NeedsCompilation** no

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

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

**RemoteRef** HEAD

**RemoteSha** 3e3c92d7eda6dce0d1d66077373ec0f7ff4f7e87

# Contents

1

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

Marie Verbanck

Maintainer: Marie Verbanck <marie.verbanck@mssm.edu>

### 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
```

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

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SummaryStats                    *Simulated toy dataset*

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### 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

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data(SummaryStats)
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# Index