

# Package: MRPRESSO (via r-universe)

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**Type** Package

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

**Version** 1.0

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**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

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MRPRESSO-package	<i>Performs the Mendelian Randomization Pleiotropy RESidual Sum and Outlier (MR-PRESSO) test.</i>
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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", OUTLIER
```

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mr_presso	<i>a function to perform the Mendelian Randomization Pleiotropy RESidual Sum and Outlier (MR-PRESSO) test</i>
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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, DISTORTIONtest = FALSE)
```

**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 for the outlier test
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 nucleotide 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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