**MR-PRESSO**

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

MR-PRESSO has three components, including:

1. detection of horizontal pleiotropy (*MR-PRESSO global test*)
2. correction of horizontal pleiotropy via outlier removal (*MR-PRESSO outlier test*)
3. testing of significant distortion in the causal estimates before and after outlier removal (*MR-PRESSO distortion test*).

**Reference**

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>

**1. Install and load MR-PRESSO**

To install the latest development builds directly from GitHub, run this instead:

if (!require("devtools")) { install.packages("devtools") } else {}

devtools::install\_github("rondolab/MR-PRESSO")

Load MR-PRESSO

library(MRPRESSO)

**2. Example**

# Load a simulated toy dataset

data(SummaryStats)

# Run MR-PRESSO global method

mr\_presso(BetaOutcome = "Y\_effect", BetaExposure = "E1\_effect", SdOutcome = "Y\_se", SdExposure = "E1\_se", OUTLIERtest = TRUE, DISTORTIONtest = TRUE, data = SummaryStats, NbDistribution = 1000, SignifThreshold = 0.05)

# Run MR-PRESSO on a multi-variable MR (MMR) model specifying several exposures

mr\_presso(BetaOutcome = "Y\_effect", BetaExposure = c("E1\_effect", "E2\_effect"), SdOutcome = "Y\_se", SdExposure = c("E1\_se", "E2\_se"), OUTLIERtest = TRUE, DISTORTIONtest = TRUE, data = SummaryStats, NbDistribution = 1000, SignifThreshold = 0.05)