**MendelianRandomization**

MendelianRandomization is a package developed to carry out various Mendelian randomization analyses on summarized genetic data in R. The package uses various methods to assess whether a risk factor (also called an exposure) has a causal effect on an outcome.

MendelianRandomization has three main components, including:

1. the inverse-variance weighted (IVW) method
2. the median-based method
3. the MR-Egger method.

**Reference**

MendelianRandomization: an R package for performing Mendelian randomization analyses using summarized data. Olena O Yavorska, Stephen Burgess. International journal of epidemiology 2017. DOI: 10.1093/ije/dyx034

**1. Install and load** **MendelianRandomization**

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

install.packages("MendelianRandomization ")

library(MendelianRandomization)

**2. Example**

# Load a simulated toy dataset

Data (SummaryStats)

# Run the IVW method

##IVW random##

mr\_ivw(mr\_input(bx = dat$betaXG, bxse = dat$sebetaXG, by = dat$betaYG, byse = dat$sebetaYG),model = "random")

##IVW fixed##

mr\_ivw(mr\_input(bx = dat$betaXG, bxse = dat$sebetaXG, by = dat$betaYG, byse = dat$sebetaYG),model = "fixed")

# Run the median-based method

##weighted median##

mr\_median(mr\_input(bx = dat$betaXG, bxse = dat$sebetaXG, by = dat$betaYG, byse = dat$sebetaYG), weighting = "weighted", iterations = 1000)

##unweighted median##

mr\_median(mr\_input(bx = dat$betaXG, bxse = dat$sebetaXG, by = dat$betaYG, byse = dat$sebetaYG), weighting = "simple", iterations = 1000)

# Run the MR-Egger method.

mr\_egger(mr\_input(bx=dat$betaXG, bxse=dat$sebetaXG, by = dat$betaYG, byse = dat$sebetaYG))