

Package: MRCorge (via r-universe)

October 8, 2026

Title Mendelian Randomization based on the core gene hypothesis for polygenic exposures

Version 0.1.0

Description This package performs Mendelian Randomization (MR) analyses based on the core gene hypothesis for polygenic exposures. MR CORGE identifies a small number of putative core instruments that are more likely to affect genes with a direct biological role in an exposure and obtains causal effect estimates based on these instruments, thereby reducing the risk of horizontal pleiotropy.

Depends R (>= 3.5.0)

Imports ggplot2, TwoSampleMR

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URL <https://github.com/zhwm/MRCORGE>, <https://zhwm.github.io/MRCorge/>

Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

Remotes MRCIEU/TwoSampleMR

Config/pak/sysreqs cmake make libicu-dev libuv1-dev libssl-dev

Repository <https://mrcieu.r-universe.dev>

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mrcorge	<i>Perform Mendelian Randomization based on the core gene hypothesis for polygenic exposures</i>
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Description

This function performs Mendelian Randomization (MR) analyses based on the core gene hypothesis for polygenic exposures. MR Corge identifies a small number of putative core instruments that are more likely to affect genes with a direct biological role in an exposure and obtains causal effect estimates based on these instruments, thereby reducing the risk of horizontal pleiotropy.

Usage

```
mrcorge(  
  harmonized_data,  
  rank = "beta",  
  K = 5,  
  method_list = c("mr_ivw", "mr_weighted_mode", "mr_weighted_median"),  
  seed = 1  
)
```

Arguments

harmonized_data	Data frame containing the harmonized data from the TwoSampleMR package.
rank	Character, method to rank instruments, one of 'beta' (absolute per-allele effect size), 'h2' (per-variant heritability), 'pval' (significance), or 'zscore' (sample size-normalized z-score). Default is 'beta'.
K	Integer, number of instrument groups. Default is 5.
method_list	Character vector, list of MR methods to apply. Default is c("mr_ivw", "mr_weighted_mode", "mr_weighted_median").
seed	Integer, seed for random number generation. Default is 1.

Value

A list containing:

- mrcorge** The main MR results.
- result** All MR results including group-specific and cumulative estimates.

instrument Data frame of instruments with their respective groups.

Q Q statistics for heterogeneity.

I2 I2 statistics for heterogeneity.

het_P P-values for heterogeneity tests.

Examples

```
# Example usage:
library(MRCorge)
data("HDL_CAD")
res <- mrcorge(HDL_CAD, rank='beta', K=20, method_list = c("mr_ivw"))
```

plot_mrcorge	<i>Plot MR CORGE Results</i>
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Description

This function plots the results of MR CORGE.

Usage

```
plot_mrcorge(mrcorge_result, scale = "linear")
```

Arguments

mrcorge_result List, result from the mrcorge function.

scale Character, scale for the plot, either "linear" or "exp". Default is "linear".

Value

ggplot object, the plot of MR sensitivity analysis results.

Examples

```
# Example usage:
library(MRCorge)
data("HDL_CAD")
res <- mrcorge(HDL_CAD, rank='beta', K=20, method_list = c("mr_ivw"))
plot_mrcorge(res, scale='exp')
```

`Qstatistic`*Calculate Q Statistic for Heterogeneity*

Description

This function calculates the Q statistic for heterogeneity in Mendelian Randomization analysis.

Usage

```
Qstatistic(b_group, se_group, b_overall)
```

Arguments

<code>b_group</code>	Numeric vector, effect sizes for each group.
<code>se_group</code>	Numeric vector, standard errors for each group.
<code>b_overall</code>	Numeric, overall effect size.

Value

Numeric, Q statistic for heterogeneity.

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