

Package: MRTool (via r-universe)

November 25, 2024

Title Simulating Data for Mendelian Randomization Scenarios Based on Genotype Data

Version 0.0.0.9000

Description This package can be used to simulate data in R for Mendelian Randomization scenarios including confounder, exposure and outcome. Recommended MR package is MendelianRandomization.

License What license it uses

Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

Date Sys.Date()

VignetteBuilder knitr

Imports data.table, foreach, broom, knitr, rmarkdown, MendelianRandomization, ggplot2, parallel

Depends stats, utils, datasets, methods, base

Config/pak/sysreqs libgmp3-dev make libicu-dev libssl-dev

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

RemoteUrl <https://github.com/askieslinger/MRTool>

RemoteRef HEAD

RemoteSha eea664f1c3cf32314a4a5853afe61bd844bbbed60

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cal_betas	<i>calculates betacoefficients from explained variances</i>
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Description

For examples see vignette `browseVignettes('MRTool')`

Usage

```
cal_betas(pves, maf, gy_direct = T)
```

Arguments

pves	a named list of parameters and percentages of variance explained for each one. If multiple snps, each param is a list of snp-vectors, each vector the scenarios for this snp
maf	a named list of maf for every snp
gy_direct	should there be a direct effect of G on Y. default true. does not need to be changed.

Value

a list of two data.tables. a data.table containing all valid combinations of coefficients, one row is one snp in one scenario. A data.table with the adjusted combinations of percentages of variance explained

CreateMRInputObject	<i>Create MRInput Object</i>
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Description

For examples see vignette `browseVignettes('MRTool')`

Usage

```
CreateMRInputObject(MR_data = my_MR_data, MR_Scenario = "V1", correlation = T)
```

Arguments

correlation

get_corrs	<i>calculate correlation for a datatable of snps</i>
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Description

returns 2 snps each that have lowest, positive high, positive low, negative high, negative low correlation. uses pearson correlation For examples see vignette `browseVignettes('MRTool')`

Usage

```
get_corrs(genedose_test, method = "pearson")
```

Arguments

genedose_test	snp datatable. first two columns identifiers
method	used to compute correlation coefficient. 'pearson' (default), 'kendall' or 'spearman'

MRTool	<i>MRTool: A package to simulate data for mendelian randomization</i>
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Description

For examples see vignette `browseVignettes('MRTool')`

SetMRParams	<i>Set MR Parameters (betacoefficients)</i>
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Description

Create a testplan for different parameter combinations or create a custom plan for different IV parameters. If `Vary_between_SNP`, The Parameters set for `G_U`, `G_X` and `G_Y` will not create individual scenarios but one, where the different parameters are distributed to the individual SNP, cycled through all give SNP, based on the number of parameters provided by the user, accepting only one parameter (the first) for `U_Y`, `U_X` and `X_Y` For examples see vignette `browseVignettes('MRTool')`

Usage

```
SetMRParams(
  Vary_between_SNP = F,
  G_X_randomization = F,
  SNP = NULL,
  G_U = c(0, 0.1),
  G_Y = c(0, 0.1),
  X_Y = c(0, 0.1),
  G_X = c(0.03, 0.1),
  U_X = c(0, 0.1),
  U_Y = c(0, 0.1),
  sim_sd = 1,
  maf
)
```

Arguments

maf

SimulateMRData	<i>Simulate MR Data</i>
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Description

For examples see vignette `browseVignettes('MRTool')`

Usage

```
SimulateMRData(SNP_data = SNP_data, SNP = NULL, Parameters = NULL)
```

Arguments

Parameters

sim_and_mr	<i>Simulate U,X and Y and run MR on them</i>
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Description

Simulates confounder U, exposure X and outcome Y based on genotype data and betacoefficients. For examples see vignette `browseVignettes('MRTool')`

Usage

```
sim_and_mr(SNP_data, SNP, my_Parameters, reverse = FALSE)
```

Arguments

reverse=FALSE TRUE if MR should be conducted with X as putative outcome and Y as putative exposure

Value

list(reg_res,sim_data,mr_res)

transform_results *Transform result of iterations of simulation and MR*

Description

Transforms results of x iterations with each n scenario simulations into median per scenario for relevant variables. For examples see vignette `browseVignettes('MRTool')`

Usage

```
transform_results(results, SNP, iterations, pve_grid, rev = FALSE)
```

Arguments

results list of results of single iteration. result of single iteration is list(reg_res,sim_data,mr_res)
 SNP names of snps used
 iterations integer how many times the simulation was repeated
 pve_grid grid of percentages of variance explained as output of cal_betas
 rev true if mr was executed in the anticausal direction. false for causal direction

Value

list(res_list,sim_data). res_list is list of regression results and mr results. sim_data is result of simulation

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