

# Package: MRTool (via r-universe)

September 26, 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

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

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

**RemoteRef** HEAD

**RemoteSha** eea664f1c3cf32314a4a5853afe61bd844bbbed60

## Contents

|                               |          |
|-------------------------------|----------|
| cal_betas . . . . .           | 2        |
| CreateMRInputObject . . . . . | 2        |
| get_corr . . . . .            | 3        |
| MRTool . . . . .              | 3        |
| SetMRParams . . . . .         | 3        |
| SimulateMRData . . . . .      | 4        |
| sim_and_mr . . . . .          | 4        |
| transform_results . . . . .   | 5        |
| <b>Index</b>                  | <b>6</b> |

---

|           |   |
|-----------|---|
| cal_betas | <i>calculates betacoefficients from explained variances</i> |
|-----------|---|

---

**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> |
|---------------------|------------------------------|

---

**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> |
|-----------|--|

---

### 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> |
|--------|---|

---

### Description

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

---

|             |   |
|-------------|---|
| SetMRParams | <i>Set MR Parameters (betacoefficients)</i> |
|-------------|---|

---

### 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

*Simulate MR Data*

---

**Description**

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

**Usage**

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

**Arguments**

Parameters

---

sim\_and\_mr

*Simulate U,X and Y and run MR on them*

---

**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

# Index

cal\_betas, [2](#)  
CreateMRInputObject, [2](#)  
  
get\_corrs, [3](#)  
  
MRTool, [3](#)  
  
SetMRParams, [3](#)  
sim\_and\_mr, [4](#)  
SimulateMRData, [4](#)  
  
transform\_results, [5](#)