

Example R and Stata code for a Mendelian randomization analysis

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Example R and Stata code to perform a multivariable Mendelian randomization (MVMR) analysis

R code

- Read in the data

```
suppressPackageStartupMessages({  
  library(tidyverse)  
  library(haven)  
  library(remotes)  
})  
dat <- read_dta("https://raw.githubusercontent.com/remlapmot/mrrobust/master/dodata.dta")  
dat <- dat %>% filter(ldlcp2 < 1e-8)
```

Example code using the MendelianRandomization package

- Install the package and load it into memory

```
library(MendelianRandomization)
```

- Convert our data frame to the required class

```
datfmt <- mr_mvinput(  
  bx = as.matrix(cbind(dat$ldlcbeta, dat$hdlcbeta, dat$tgbeta)),  
  bxse = as.matrix(cbind(dat$ldlcse, dat$hdlcse, dat$tgse)),  
  by = dat$chdbeta,  
  byse = dat$chdse,  
  exposure = "exposure",  
  outcome = "outcome",  
  snps = "snps",  
  effect_allele = dat$a1,  
  other_allele = dat$a2,  
  eaf = NA  
)
```

- Fit an MVMR/MVIVW model

```
mvivwfit <- mr_mvivw(datfmt)  
mvivwfit
```

```
##  
## Multivariable inverse-variance weighted method  
## (variants uncorrelated, random-effect model)  
##
```

```
## Number of Variants : 73
##
## -----
##      Exposure Estimate Std Error  95% CI      p-value
## exposure_1      0.429      0.061  0.309, 0.548    0.000
## exposure_2     -0.194      0.131 -0.451, 0.062    0.138
## exposure_3      0.226      0.123 -0.016, 0.468    0.067
## -----
## Residual standard error = 1.490
## Heterogeneity test statistic = 155.3766 on 70 degrees of freedom, (p-value = 0.0000)
```

- Fit an MVMR-Egger model

```
mvmreggerfit <- mr_mvegger(datfmt)
mvmreggerfit
```

```
##
## Multivariable MR-Egger method
## (variants uncorrelated, random-effect model)
##
## Orientated to exposure : 1
## Number of Variants : 73
## -----
##      Exposure Estimate Std Error  95% CI      p-value
## exposure_1      0.567      0.100  0.371, 0.764    0.000
## exposure_2     -0.136      0.133 -0.398, 0.125    0.306
## exposure_3      0.274      0.125  0.030, 0.518    0.028
## (intercept)    -0.009      0.005 -0.020, 0.001    0.084
## -----
## Residual standard error = 1.469
## Heterogeneity test statistic = 148.9290 on 69 degrees of freedom, (p-value = 0.0000)
```

Example code using the MVMR and RMVMR packages

- Install the package and load it into memory

```
if (!requireNamespace("MVMR", quietly = TRUE)) {
  remotes::install_github("WSpiller/MVMR")
}
library(MVMR)
```

- Create a data object of the required structure

```
r_input <- format_mvmmr(
  BXGs = dat[,c("ldlcbeta", "hdlcbeta", "tgbeta")],
  BYG = dat$chdbeta,
  seBXGs = dat[,c("ldlcse", "hdlcse", "tgse")],
  seBYG = dat$chdse,
  RSID = dat$rsid
)
```

- Fit an MVMR model

```
mvmrfit <- ivw_mvmmr(r_input)
```

```
##
## Multivariable MR
##
```

```
##           Estimate Std. Error   t value    Pr(>|t|)
## exposure1  0.4286200  0.0609661   7.030464 1.099077e-09
## exposure2 -0.1941989  0.1308289  -1.484372 1.421994e-01
## exposure3  0.2260456  0.1232828   1.833554 7.097168e-02
##
## Residual standard error: 1.49 on 70 degrees of freedom
```

- Conditional F-statistics for instrument strength (Sanderson, Spiller, and Bowden 2021)

```
strength_mvmm(r_input)
```

```
## Warning in strength_mvmm(r_input): Covariance between effect of genetic variants on each exposure
## not specified. Fixing covariance at 0.
```

```
##
## Conditional F-statistics for instrument strength
##
##           exposure1 exposure2 exposure3
## F-statistic  126.7447  35.29937  39.32731
##
##           exposure1 exposure2 exposure3
## F-statistic  126.7447  35.29937  39.32731
```

- Fit a radial MVMM model

```
if (!requireNamespace("RMVMM", quietly = TRUE)) {
  remotes::install_github("WSpiller/RMVMM")
}
library(RMVMM)

rmvmm_input <- mrmvininput_to_rmvmm_format(datfmt)

rmvmm_fit <- ivw_rmvmm(rmvmm_input, summary = TRUE)
```

```
##
## Radial Multivariable MR
##
##           Estimate Std. Error   t value    Pr(>|t|)
## exposure1  0.4286200  0.0609661   7.030464 1.099077e-09
## exposure2 -0.1941989  0.1308289  -1.484372 1.421994e-01
## exposure3  0.2260456  0.1232828   1.833554 7.097168e-02
##
## Residual standard error: 1.49 on 70 degrees of freedom
```

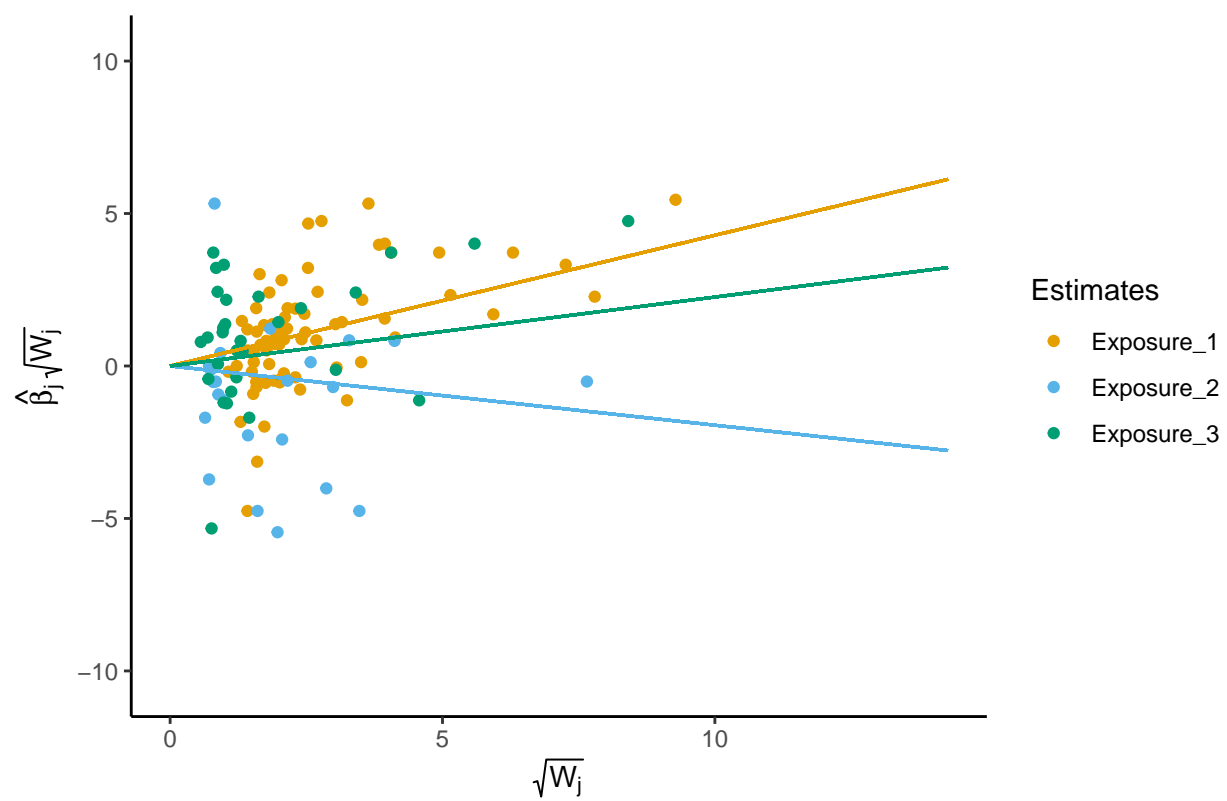
```
rmvmm_fit$coef
```

```
##           Estimate Std. Error   t value    Pr(>|t|)
## exposure1  0.4286200  0.0609661   7.030464 1.099077e-09
## exposure2 -0.1941989  0.1308289  -1.484372 1.421994e-01
## exposure3  0.2260456  0.1232828   1.833554 7.097168e-02
```

- Plot the radial MVMM models

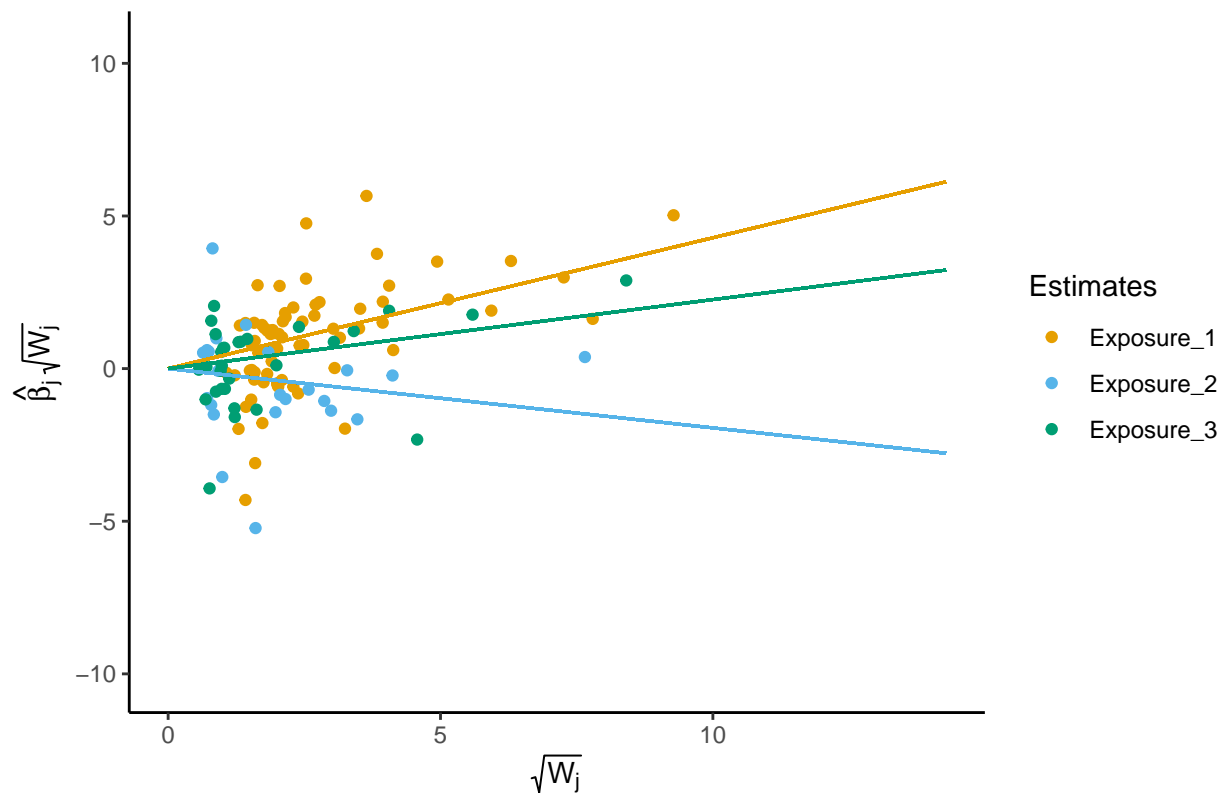
```
plt_rmvmm <- plot_rmvmm(rmvmm_input, rmvmm = rmvmm_fit)
plt_rmvmm$pl
```

Radial MVMR without correction



plt_rmvmr\$p2

Radial MVMR with correction



- Heterogeneity statistics

```
pleio_rmvmr <- pleiotropy_rmvmr(rmvmr_input, rmvmr = rmvmr_fit)
pleio_rmvmr$gq
```

```
##          q_statistic      p_value
## Exposure_1      76.37356 2.812609e-01
## Exposure_2      59.58894 8.243650e-06
## Exposure_3      45.88633 1.308596e-02
```

```
head(pleio_rmvmr$qdat)
```

```
##      snp      wj corrected_beta      qj      qj_p ref_exposure
## 1 snp_1 2.414215      0.3141338 0.031643343 0.85881269 Exposure_1
## 2 snp_2 3.938760      0.3821443 0.008507667 0.92650973 Exposure_1
## 3 snp_3 3.246657     -0.6057993 3.473998077 0.06234046 Exposure_1
## 4 snp_4 2.001191      0.3273484 0.020524059 0.88608310 Exposure_1
## 5 snp_5 9.278826      0.5414293 0.118081748 0.73112437 Exposure_1
## 6 snp_6 1.317671      1.0713541 0.544339092 0.46064001 Exposure_1
```

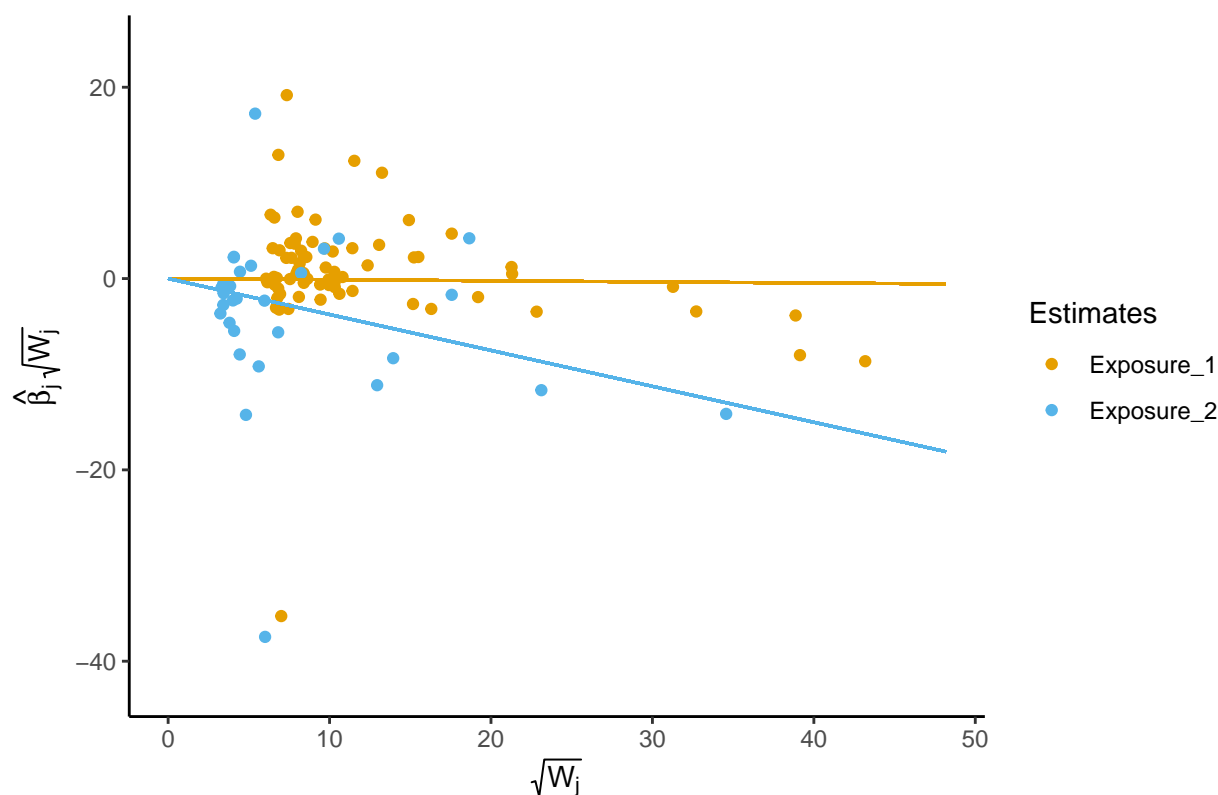
- Conditional F-statistics for instrument strength (Sanderson, Spiller, and Bowden 2021)

```
str_rmvmr <- strength_rmvmr(rmvmr_input)
```

```
## Warning in MVMR::strength_mvmm(r_input, gencov): Covariance between effect of genetic variants on
## each exposure not specified. Fixing covariance at 0.
```

```
str_rmvmr$plot[[2]]
```

Radial MVMR with correction



```
str_rmvnr$qstat[[2]]
```

```
##           q_statistic      p_value
## Exposure_1      335.0602 6.799449e-36
## Exposure_2      371.0830 1.403374e-61
```

Stata code

- Load the Statamarkdown package to enable Stata code chunks in an R Markdown file

```
if (!requireNamespace("Statamarkdown", quietly = TRUE)) {
  remotes::install_github("Hemken/Statamarkdown")
}
library(Statamarkdown)
```

- Read in the data and create an indicator variable to select observations with p -value between the genotype and LDL-C $< 10^{-8}$

```
use https://raw.githubusercontent.com/remlapmot/mrrobust/master/dodata, clear
gen byte sel1 = (ldlcp2 < 1e-8)
```

Example code using the mrrobust package

- Install the mrrobust package using the github package

```
// Note: output suppressed
net install mrrobust, from("https://raw.githubusercontent.com/remlapmot/mrrobust/master/")
mrdeps
```

- Fit IVW (with fixed effect standard errors)

```
mregger chdbeta ldldbata [aw=1/(chdse^2)] if sel1==1, ivw fe
```

Number of genotypes = 73						
Residual standard error constrained at 1						
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
chdbeta						
ldldbata	.4815055	.038221	12.60	0.000	.4065938	.5564173

- Fit MR-Egger reporting I2GX statistic and heterogeneity Q-test

```
mregger chdbeta ldldbata [aw=1/(chdse^2)] if sel1==1, gxse(ldlcse) heterogi
```

Q_GX statistic (weighted) = 3454.26						
I ² _GX statistic (weighted) = 97.92%						
Number of genotypes = 73						
Residual standard error = 1.548						
Ruecker's Q for heterogeneity; chi2(71) = 170.11 (p = 0.0000)						
I-squared statistic = 58.3% (95% CI 45.8%, 67.8%)						
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
chdbeta						
slope	.6173131	.1034573	5.97	0.000	.4145405	.8200858
_cons	-.0087706	.0054812	-1.60	0.110	-.0195136	.0019723

- Simple plot of IVW and MR-Egger univariate estimates

```
mreggerplot chdbeta chdse ldldbata ldlcse if sel1==1
```

- Adding the modal and median estimates onto the plot

```
mreggerplot chdbeta chdse ldldbata ldlcse if sel1==1
mrmedian chdbeta chdse ldldbata ldlcse if sel1==1, weighted
addplot : function _b[beta]*x if sel1==1, ///
    range(0 0.5) lc(gs0) lp(shortdash) lw(vthin)
mrmodal chdbeta chdse ldldbata ldlcse if sel1==1, phi(.25)
addplot : function _b[beta]*x if sel1==1, ///
    range(0 0.5) lc(gs0) lp(longdash) ///
    legend(order(5 "Instruments" ///
        4 "95% CIs" 3 "MR-Egger" 2 "MR-Egger 95% CI" ///
        6 "Weighted median" 7 "Modal") ///
    rows(1) si(vsmall) symx(*.5))
```

Number of genotypes = 73						
Replications = 1000						
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
beta	.4582573	.0633137	7.24	0.000	.3341648	.5823499

Number of genotypes = 73
Replications = 1000
Phi = .25

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
beta	.4198713	.2260632	1.86	0.063	-.0232045 .8629471

- Fit and MVMR model with phenotypes LDL-c and HDL-c (Burgess, Dudbridge, and Thompson 2015).

```
mvmr chdbeta ldlcbeta hdlcbeta [aw=1/(chdse^2)] if sel1==1
```

Number of genotypes = 73
Number of phenotypes = 2
Standard errors: Random effect
Residual standard error = 1.514

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
chdbeta					
ldlcbeta	.4670719	.0581901	8.03	0.000	.3530214 .5811224
hdlcbeta	-.2930048	.1211822	-2.42	0.016	-.5305175 -.0554921

- Additionally include a third phenotype – triglycerides.

```
mvmr chdbeta ldlcbeta hdlcbeta tgbeta [aw=1/(chdse^2)] if sel1==1
```

Number of genotypes = 73
Number of phenotypes = 3
Standard errors: Random effect
Residual standard error = 1.490

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
chdbeta					
ldlcbeta	.42862	.0609661	7.03	0.000	.3091286 .5481113
hdlcbeta	-.1941989	.1308289	-1.48	0.138	-.4506189 .0622211
tgbeta	.2260456	.1232828	1.83	0.067	-.0155842 .4676755

- Report the QA statistic for instrument validity and the conditional F-statistics for instrument strength for each phenotype (Sanderson et al. 2019; Sanderson, Spiller, and Bowden 2021).

```
mvmr chdbeta ldlcbeta hdlcbeta tgbeta [aw=1/(chdse^2)] if sel1==1, gxse(ldlcse hdlcse tgse)
> e hdlcse tgse)
```

Number of genotypes = 73
Number of phenotypes = 3
Standard errors: Random effect
Residual standard error = 1.490

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
chdbeta					

ldlcbeta		.42862	.0609661	7.03	0.000	.3091286	.5481113
hdlcbeta		-.1941989	.1308289	-1.48	0.138	-.4506189	.0622211
tgbeta		.2260456	.1232828	1.83	0.067	-.0155842	.4676755

Q_A statistic for instrument validity; $\chi^2(70) = 152.88$ ($p = 0.0000$)

Conditional F-statistics for instrument strength:

F_x1 = 130.31 (ldlcbeta)

F_x2 = 36.29 (hdlcbeta)

F_x3 = 40.44 (tgbeta)

- Fit an MVMR-Egger regression (Rees, Wood, and Burgess 2017), orienting the model with respect to the first phenotype in the main *varlist*.

```
mrmmvegger chdbeta ldlcbeta hdlcbeta tgbeta [aw=1/(chdse^2)] if sel1==1
```

MVMR-Egger model oriented wrt: ldlcbeta

Number of genotypes = 73

Number of phenotypes = 3

Residual standard error = 1.469

		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
chdbeta						
ldlcbeta		.5672993	.1002611	5.66	0.000	.370791 .7638075
hdlcbeta		-.1364113	.1332727	-1.02	0.306	-.3976209 .1247983
tgbeta		.2739803	.1246927	2.20	0.028	.0295871 .5183735
_cons		-.0093655	.0054187	-1.73	0.084	-.019986 .001255

We can also orient the model with respect to HDL-C.

```
mrmmvegger chdbeta ldlcbeta hdlcbeta tgbeta [aw=1/(chdse^2)] if sel1==1, orient(2)
```

```
> t(2)
```

MVMR-Egger model oriented wrt: hdlcbeta

Number of genotypes = 73

Number of phenotypes = 3

Residual standard error = 1.501

		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
chdbeta						
ldlcbeta		.4286398	.0614056	6.98	0.000	.308287 .5489926
hdlcbeta		-.1989637	.1541909	-1.29	0.197	-.5011723 .1032449
tgbeta		.2256794	.1243221	1.82	0.069	-.0179875 .4693463
_cons		.0002155	.0036218	0.06	0.953	-.006883 .0073141

Or we can orient the model with respect to triglycerides.

```
mrmmvegger chdbeta ldlcbeta hdlcbeta tgbeta [aw=1/(chdse^2)] if sel1==1, orient(3)
```

```
> t(3)
```

MVMR-Egger model oriented wrt: tgbeta

Number of genotypes = 73

Number of phenotypes = 3

Residual standard error = 1.499

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
chdbeta						
ldlcbeta	.4203073	.0660026	6.37	0.000	.2909447	.54967
hdlcbeta	-.1903089	.1321536	-1.44	0.150	-.4493252	.0687075
tgbeta	.2065651	.1365427	1.51	0.130	-.0610537	.474184
_cons	.0013499	.003951	0.34	0.733	-.0063939	.0090936

R session information for reproducibility

```
library(sessioninfo)
session_info()
```

```
- Session info -----
setting value
version R version 4.1.1 (2021-08-10)
os Windows 10 x64
system x86_64, mingw32
ui RTerm
language (EN)
collate English_United Kingdom.1252
ctype English_United Kingdom.1252
tz Europe/London
date 2021-09-24
```

```
- Packages -----
package      * version date      lib source
arrangements 1.1.9   2020-09-13 [1] CRAN (R 4.1.0)
assertthat    0.2.1   2019-03-21 [1] CRAN (R 4.1.0)
backports     1.2.1   2020-12-09 [1] CRAN (R 4.1.0)
broom         0.7.9   2021-07-27 [1] CRAN (R 4.1.0)
cellranger    1.1.0   2016-07-27 [1] CRAN (R 4.1.0)
cli           3.0.1   2021-07-17 [1] CRAN (R 4.1.0)
codetools     0.2-18  2020-11-04 [2] CRAN (R 4.1.1)
colorspace    2.0-2   2021-06-24 [1] CRAN (R 4.1.0)
conquer       1.0.2   2020-08-27 [1] CRAN (R 4.1.0)
crayon        1.4.1   2021-02-08 [1] CRAN (R 4.1.0)
curl          4.3.2   2021-06-23 [1] CRAN (R 4.1.0)
data.table    1.14.0  2021-02-21 [1] CRAN (R 4.1.0)
DBI           1.1.1   2021-01-15 [1] CRAN (R 4.1.0)
dbplyr        2.1.1   2021-04-06 [1] CRAN (R 4.1.0)
DEoptimR      1.0-9   2021-05-24 [1] CRAN (R 4.1.0)
digest        0.6.27  2020-10-24 [1] CRAN (R 4.1.0)
dplyr         * 1.0.7   2021-06-18 [1] CRAN (R 4.1.0)
ellipsis      0.3.2   2021-04-29 [1] CRAN (R 4.1.0)
evaluate      0.14    2019-05-28 [1] CRAN (R 4.1.0)
fans          0.5.0   2021-05-25 [1] CRAN (R 4.1.0)
farver        2.1.0   2021-02-28 [1] CRAN (R 4.1.0)
fastmap       1.1.0   2021-01-25 [1] CRAN (R 4.1.0)
forcats       * 0.5.1   2021-01-27 [1] CRAN (R 4.1.0)
foreach       1.5.1   2020-10-15 [1] CRAN (R 4.1.0)
```

fs	1.5.0	2020-07-31	[1]	CRAN	(R 4.1.0)
generics	0.1.0	2020-10-31	[1]	CRAN	(R 4.1.0)
ggplot2	* 3.3.5	2021-06-25	[1]	CRAN	(R 4.1.0)
glmnet	4.1-2	2021-06-24	[1]	CRAN	(R 4.1.0)
glue	1.4.2	2020-08-27	[1]	CRAN	(R 4.1.0)
gmp	0.6-2	2021-01-07	[1]	CRAN	(R 4.1.0)
gtable	0.3.0	2019-03-25	[1]	CRAN	(R 4.1.0)
haven	* 2.4.3	2021-08-04	[1]	CRAN	(R 4.1.0)
highr	0.9	2021-04-16	[1]	CRAN	(R 4.1.0)
hms	1.1.0	2021-05-17	[1]	CRAN	(R 4.1.0)
htmltools	0.5.2	2021-08-25	[1]	CRAN	(R 4.1.1)
htmlwidgets	1.5.4	2021-09-08	[1]	CRAN	(R 4.1.1)
httr	1.4.2	2020-07-20	[1]	CRAN	(R 4.1.0)
iterators	1.0.13	2020-10-15	[1]	CRAN	(R 4.1.0)
iterpc	0.4.2	2020-01-10	[1]	CRAN	(R 4.1.0)
jsonlite	1.7.2	2020-12-09	[1]	CRAN	(R 4.1.0)
knitr	1.34	2021-09-09	[1]	CRAN	(R 4.1.1)
labeling	0.4.2	2020-10-20	[1]	CRAN	(R 4.1.0)
lattice	0.20-44	2021-05-02	[2]	CRAN	(R 4.1.1)
lazyeval	0.2.2	2019-03-15	[1]	CRAN	(R 4.1.0)
lifecycle	1.0.0	2021-02-15	[1]	CRAN	(R 4.1.0)
lubridate	1.7.10	2021-02-26	[1]	CRAN	(R 4.1.0)
magrittr	2.0.1	2020-11-17	[1]	CRAN	(R 4.1.0)
Matrix	1.3-4	2021-06-01	[2]	CRAN	(R 4.1.1)
MatrixModels	0.5-0	2021-03-02	[1]	CRAN	(R 4.1.0)
matrixStats	0.61.0	2021-09-17	[1]	CRAN	(R 4.1.1)
MendelianRandomization	* 0.5.1	2021-04-16	[1]	CRAN	(R 4.1.0)
modelr	0.1.8	2020-05-19	[1]	CRAN	(R 4.1.0)
munsell	0.5.0	2018-06-12	[1]	CRAN	(R 4.1.0)
MVMR	* 0.3	2021-08-03	[1]	Github	(wspiller/mvmr@a6388a8)
pillar	1.6.2	2021-07-29	[1]	CRAN	(R 4.1.0)
pkgconfig	2.0.3	2019-09-22	[1]	CRAN	(R 4.1.0)
plotly	4.9.4.1	2021-06-18	[1]	CRAN	(R 4.1.0)
purrr	* 0.3.4	2020-04-17	[1]	CRAN	(R 4.1.0)
quantreg	5.86	2021-06-06	[1]	CRAN	(R 4.1.0)
R6	2.5.1	2021-08-19	[1]	CRAN	(R 4.1.1)
RadialMR	1.0	2021-07-09	[1]	Github	(wspiller/radialmr@d63d3fc)
Rcpp	1.0.7	2021-07-07	[1]	CRAN	(R 4.1.0)
readr	* 2.0.1	2021-08-10	[1]	CRAN	(R 4.1.1)
readxl	1.3.1	2019-03-13	[1]	CRAN	(R 4.1.0)
remotes	* 2.4.0	2021-06-02	[1]	CRAN	(R 4.1.0)
reprex	2.0.1	2021-08-05	[1]	CRAN	(R 4.1.0)
rjson	0.2.20	2018-06-08	[1]	CRAN	(R 4.1.0)
rlang	0.4.11	2021-04-30	[1]	CRAN	(R 4.1.0)
rmarkdown	2.11	2021-09-14	[1]	CRAN	(R 4.1.1)
RMVMR	* 0.2	2021-05-18	[1]	Github	(wspiller/rmvmr@5b1198b)
robustbase	0.93-8	2021-06-02	[1]	CRAN	(R 4.1.0)
rstudioapi	0.13	2020-11-12	[1]	CRAN	(R 4.1.0)
rvest	1.0.1	2021-07-26	[1]	CRAN	(R 4.1.0)
scales	1.1.1	2020-05-11	[1]	CRAN	(R 4.1.0)
sessioninfo	* 1.1.1	2018-11-05	[1]	CRAN	(R 4.1.0)
shape	1.4.6	2021-05-19	[1]	CRAN	(R 4.1.0)
SparseM	1.81	2021-02-18	[1]	CRAN	(R 4.1.0)
Statamarkdown	* 0.7.0	2021-08-02	[1]	Github	(Hemken/Statamarkdown@a68a8b9)

stringi	1.7.4	2021-08-25	[1]	CRAN	(R 4.1.1)
stringr	* 1.4.0	2019-02-10	[1]	CRAN	(R 4.1.0)
survival	3.2-13	2021-08-24	[2]	CRAN	(R 4.1.1)
tibble	* 3.1.4	2021-08-25	[1]	CRAN	(R 4.1.1)
tidyr	* 1.1.3	2021-03-03	[1]	CRAN	(R 4.1.0)
tidyselect	1.1.1	2021-04-30	[1]	CRAN	(R 4.1.0)
tidyverse	* 1.3.1	2021-04-15	[1]	CRAN	(R 4.1.0)
tzdb	0.1.2	2021-07-20	[1]	CRAN	(R 4.1.0)
utf8	1.2.2	2021-07-24	[1]	CRAN	(R 4.1.0)
vctrs	0.3.8	2021-04-29	[1]	CRAN	(R 4.1.0)
viridisLite	0.4.0	2021-04-13	[1]	CRAN	(R 4.1.0)
withr	2.4.2	2021-04-18	[1]	CRAN	(R 4.1.0)
xfun	0.26	2021-09-14	[1]	CRAN	(R 4.1.1)
xml2	1.3.2	2020-04-23	[1]	CRAN	(R 4.1.0)
yaml	2.2.1	2020-02-01	[1]	CRAN	(R 4.1.0)

[1] C:/Users/tom/Documents/R/win-library/4.1

[2] C:/Program Files/R/R-4.1.1/library

Stata session information for reproducibility

```
about
ado describe mrrobust
```

Stata/MP 16.1 for Windows (64-bit x86-64)

Revision 08 Jul 2021

Copyright 1985-2019 StataCorp LLC

Total physical memory: 32.00 GB

Available physical memory: 16.66 GB

Stata license: Unlimited-user 2-core network, expiring 21 Jan 2022

Serial number: 501609352178

Licensed to: Tom Palmer

University of Bristol

```
-----
[40] package mrrobust from https://raw.githubusercontent.com/remlapmot/mrrobust
> /master
-----
```

TITLE

'mrrobust': Stata package for two-sample Mendelian randomization analyses

DESCRIPTION/AUTHOR(S)

Author: Tom Palmer

Distribution-Date: 20210917

INSTALLATION FILES

m\mrmedian.ado

m\mrmedian.sthlp

m\mrmedianobs.ado

m\mrmedianobs_work.ado

```

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m\mrleaveoneout.sthlp
m\mrrobust-author.ihlp

```

INSTALLED ON
 24 Sep 2021

References

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