

Example R and Stata code for a Mendelian randomization analysis

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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 MVMMR model

```

mvmmrfit <- 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_mvmmr(r_input)

```

```

## Warning in strength_mvmmr(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 MVMMR model

```

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

rmvmmr_input <- mrmvininput_to_rmvmmr_format(datfmt)

rmvmmr_fit <- ivw_rmvmmr(rmvmmr_input, summary = TRUE)

```

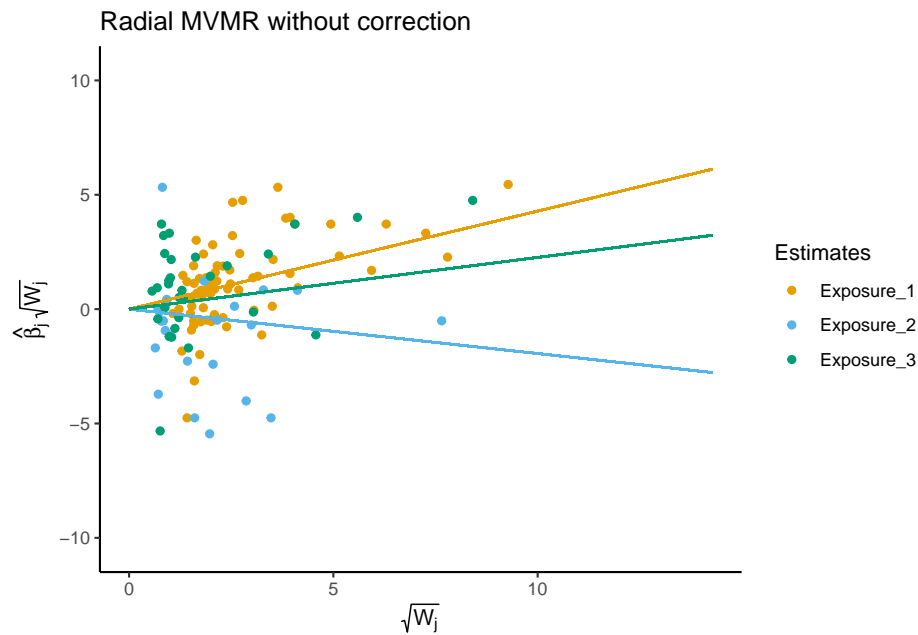
```
##
## Radial Multivariable MR
##
##           Estimate Std. Error   t value    Pr(>|t|)
## exposure1  0.4286200  0.0609661   7.030464 1.099077e-09
## exposure2 -0.1941989  0.1308289  -1.484372 1.421994e-01
## exposure3  0.2260456  0.1232828   1.833554 7.097168e-02
##
## Residual standard error: 1.49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

```
rmvmr_fit$coef
```

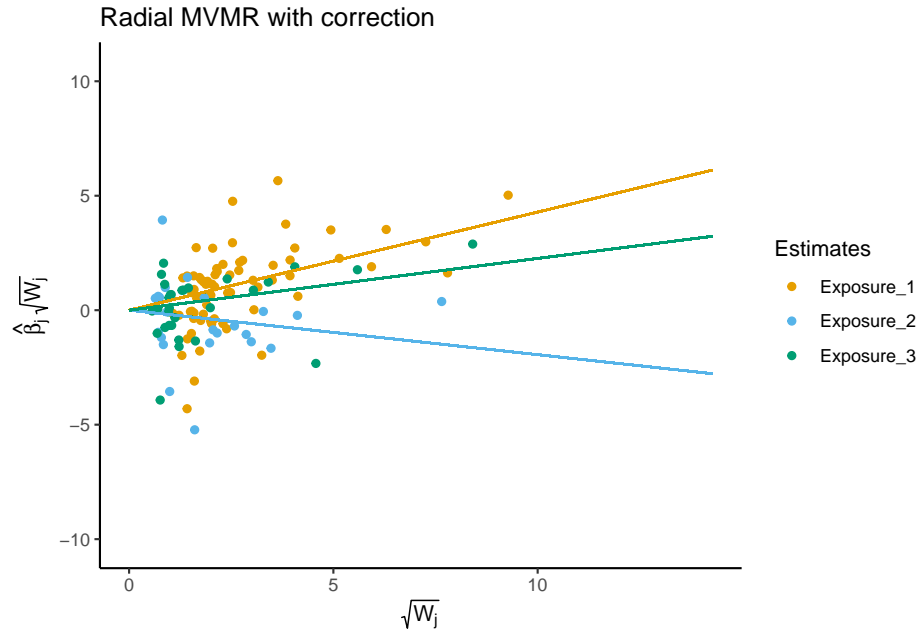
```
##           Estimate Std. Error   t value    Pr(>|t|)
## exposure1  0.4286200  0.0609661   7.030464 1.099077e-09
## exposure2 -0.1941989  0.1308289  -1.484372 1.421994e-01
## exposure3  0.2260456  0.1232828   1.833554 7.097168e-02
```

- Plot the radial MVMR models

```
plt_rmvmr <- plot_rmvmr(rmvmr_input, rmvmr = rmvmr_fit)
plt_rmvmr$p1
```



```
plt_rmvmr$p2
```



- 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)
```

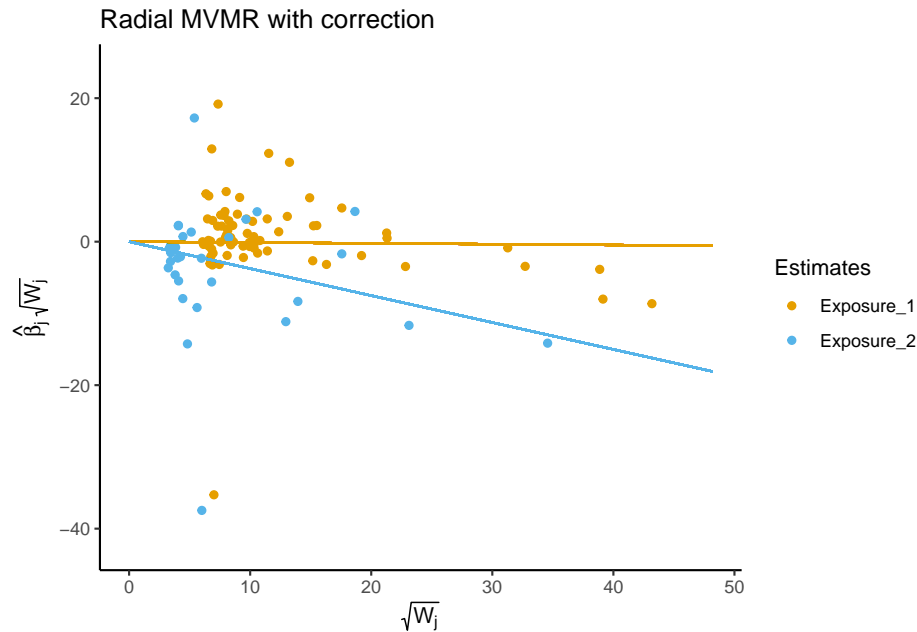
```
##      snp      wj corrected_beta      qj      qj_p ref_exposure
## 1 snp_1 2.414215      0.3141338 0.031643343 0.85881269 Exposure_1
## 2 snp_2 3.938760      0.3821443 0.008507667 0.92650973 Exposure_1
## 3 snp_3 3.246657     -0.6057993 3.473998077 0.06234046 Exposure_1
## 4 snp_4 2.001191      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]]
```



```
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
```

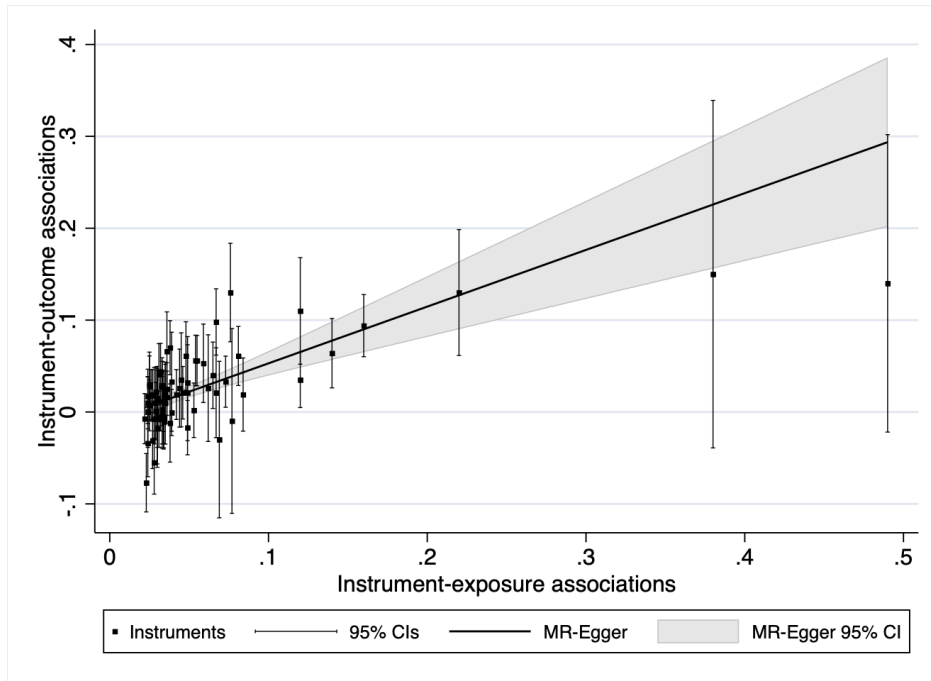
```

                                     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
qui gr export mreggerplot-1.png, replace
```



- 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))
qui gr export mreggerplot-2.png, replace
```

Number of genotypes = 73

Replications = 1000

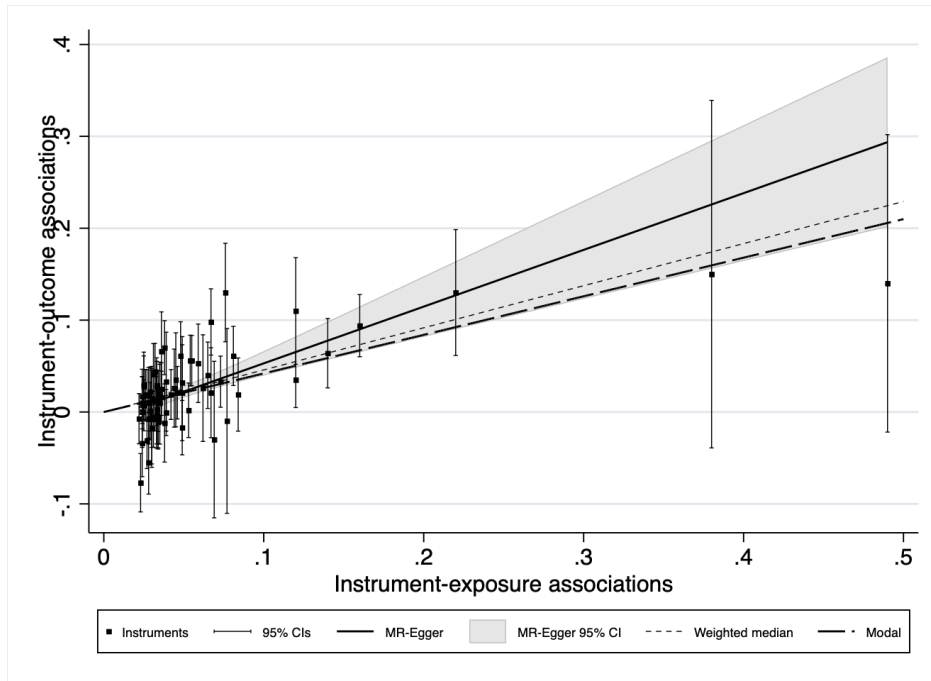
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
beta	.4582573	.0633137	7.24	0.000	.3341648	.5823499

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)
```

```
> 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; chi2(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*.

```
mrmvegger 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.

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

> (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.

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

> (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

Session information for reproducibility

R session information

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

```
- Session info -----
setting  value
version  R version 4.1.1 (2021-08-10)
os       macOS Big Sur 11.6
system   aarch64, darwin20
ui       X11
language (EN)
collate  en_GB.UTF-8
```

```

ctype    en_GB.UTF-8
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)
base64enc    0.1-3 2015-07-28 [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)
checkmate    2.0.0 2020-02-06 [1] CRAN (R 4.1.1)
cli          3.0.1 2021-07-17 [1] CRAN (R 4.1.0)
cluster      2.1.2 2021-04-17 [1] CRAN (R 4.1.1)
codetools    0.2-18 2020-11-04 [1] CRAN (R 4.1.1)
colorspace   2.0-2 2021-06-24 [1] CRAN (R 4.1.1)
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 4.1.1)
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       0.6.28 2021-09-23 [1] CRAN (R 4.1.1)
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 4.1.1)
foreach      1.5.1 2020-10-15 [1] CRAN (R 4.1.0)
foreign      0.8-81 2020-12-22 [1] CRAN (R 4.1.1)
Formula      * 1.2-4 2020-10-16 [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 4.1.1)
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)
gridExtra    2.3 2017-09-09 [1] CRAN (R 4.1.1)
gtable       0.3.0 2019-03-25 [1] CRAN (R 4.1.1)
haven        * 2.4.3 2021-08-04 [1] CRAN (R 4.1.1)
Hmisc        * 4.5-0 2021-02-28 [1] CRAN (R 4.1.0)
hms          1.1.0 2021-05-17 [1] CRAN (R 4.1.0)
htmlTable    2.2.1 2021-05-18 [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)
jpeg         0.1-9 2021-07-24 [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	* 0.20-45	2021-09-22	[1]	CRAN (R 4.1.1)
latticeExtra	0.6-29	2019-12-19	[1]	CRAN (R 4.1.0)
lazyeval	0.2.2	2019-03-15	[1]	CRAN (R 4.1.0)
lifecycle	1.0.1	2021-09-24	[1]	CRAN (R 4.1.1)
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	[1]	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 4.1.1)
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	2021-09-24	[1]	Github (wspiller/mvmr@3a0b54b)
nnet	7.3-16	2021-05-03	[1]	CRAN (R 4.1.1)
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)
png	0.1-7	2013-12-03	[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	2021-08-13	[1]	Github (WSpiller/RadialMR@d63d3fc)
RColorBrewer	1.1-2	2014-12-07	[1]	CRAN (R 4.1.0)
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 4.1.1)
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	2021-09-24	[1]	Github (WSpiller/RMVMR@a162f9e)
robustbase	0.93-8	2021-06-02	[1]	CRAN (R 4.1.0)
rpart	4.1-15	2019-04-12	[1]	CRAN (R 4.1.1)
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	2021-08-26	[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 4.1.1)
survival	* 3.2-13	2021-08-24	[1]	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] /Library/Frameworks/R.framework/Versions/4.1-arm64/Resources/library
```

Stata session information

```
about
ado describe mrrobust
```

```
Stata/MP 16.1 for Mac (Apple Silicon)
Revision 08 Jul 2021
Copyright 1985-2019 StataCorp LLC
```

```
Total physical memory: 8.01 GB
```

```
Stata license: Unlimited-user 2-core network, expiring 21 Jan 2022
Serial number: 501609352178
  Licensed to: Tom Palmer
              University of Bristol
```

```
-----
[15] 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
m/mrmedianobs.sthlp
m/mregger.ado
m/mregger.sthlp
m/mrrobust.sthlp
m/mreggerplot.ado
m/mreggerplot.sthlp
m/mrmodal.ado
m/mrmodal.sthlp
m/mrratio.ado
m/mrratio.sthlp
m/mrivests.ado
m/mrivests.sthlp
```

```

m/mrforest.ado
m/mrforest.sthlp
m/mreggersimex.ado
m/mreggersimex.sthlp
m/mreggersimexonce.ado
m/mrmodalplot.ado
m/mrmodalplot.sthlp
m/mrfunnel.ado
m/mrfunnel.sthlp
m/mrdeps.ado
m/mrdeps.sthlp
m/mr.ado
m/mr.sthlp
m/mrmvivw.ado
m/mrmvivw.sthlp
m/mvivw.ado
m/mvivw.sthlp
m/mvmr.ado
m/mvmr.sthlp
m/mrmvegger.ado
m/mrmvegger.sthlp
m/mrleaveoneout.ado
m/mrleaveoneout.sthlp
m/mrrobust-author.ihlp

```

INSTALLED ON
 24 Sep 2021

References

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- Sanderson, E, G Davey Smith, F Windmeijer, and J Bowden. 2019. "An examination of multivariable Mendelian randomization in the single-sample and two-sample summary data settings." *International Journal of Epidemiology* 48: 713--27. <https://doi.org/10.1093/ije/dyy262>.
- Sanderson, E, W Spiller, and J Bowden. 2021. "Testing and Correcting for Weak and Pleiotropic Instruments in Two-Sample Multivariable Mendelian Randomization." *Statistics in Medicine*. <https://doi.org/10.1002/sim.9133>.