Example R and Stata code for a Mendelian randomization analysis

Sanderson et al.

20 March 2023

R code

- Read in the data

```
library(tidyverse)
library(haven)
library(remotes)

dat <- read_dta("https://raw.github.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 = "snp",
  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_mvmr(
  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

```r
mvmrfit <- ivw_mvmr(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)

```r
strength_mvmr(r_input)
```

```
## Warning in strength_mvmr(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 MVMR model

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

rmvmr_input <- mrmvinput_to_rmvmr_format(datfmt)

rmvmr_fit <- ivw_rmvmr(rmvmr_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
```

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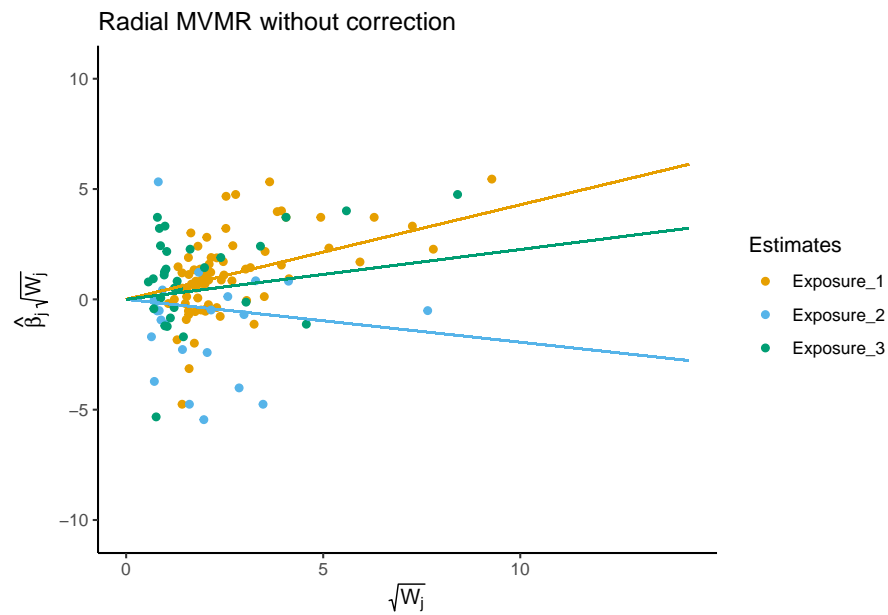
```
##             Estimate Std. Error    t value      Pr(>|t|)
## exposure1  0.4286200  0.0609661   7.030464 1.099077e-09
## exposure2 -0.1941989  0.1308289  -1.484372 1.421994e-01
## exposure3  0.2260456  0.1232828   1.833554 7.097168e-02
```

- Plot the radial MVMR models

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


Radial MVMR without correction

```
plt_rmvmr$p2
```


Radial MVMR with correction
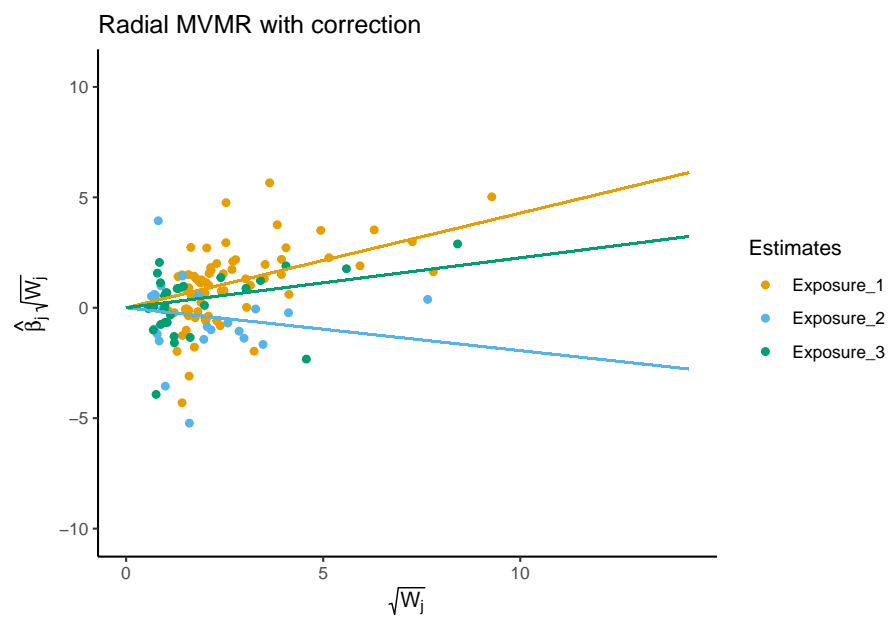
- Heterogeneity statistics

```
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
```

```r
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)

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

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

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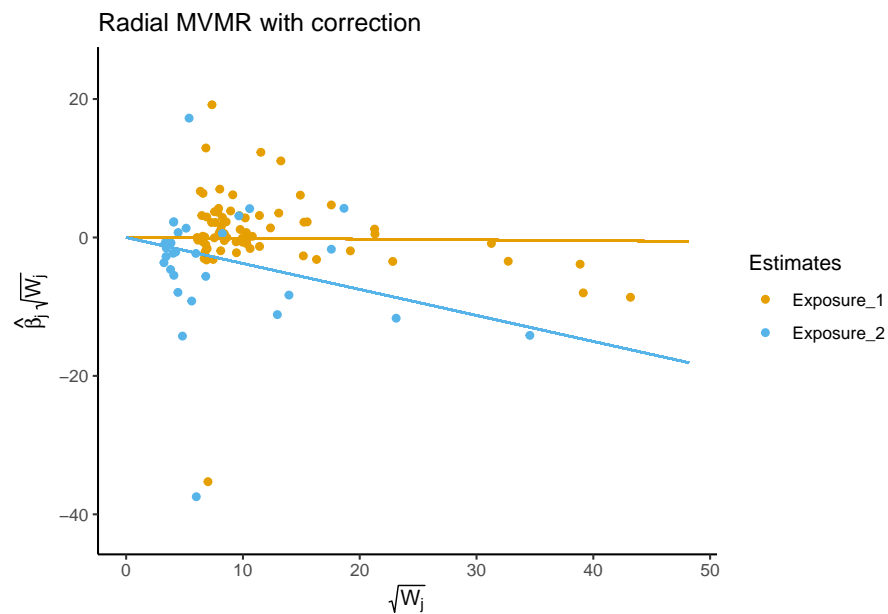


```r
str_rmvmr$qstat[[2]]
```

```
##            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

```r
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.github.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.github.com/remlapmot/mrrobust/master/")
mrdeps
```

- Fit IVW (with fixed effect standard errors)

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

```
                                    Number of genotypes = 73
                            Residual standard error constrained at 1
--------------------------------------------------------------------------
             | Coefficient  Std. err.      z    P>|z|     [95% conf. interval]
-------------+------------------------------------------------------------
chdbeta      |
    ldlcbeta |   .4815055    .038221    12.60   0.000     .4065938    .5564173
--------------------------------------------------------------------------
```

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

```
mregger chdbeta ldlcbeta [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%)
--------------------------------------------------------------------------
             | Coefficient  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 ldlcbeta ldlcse if sel1==1
qui gr export mreggerplot-1.png, replace
```
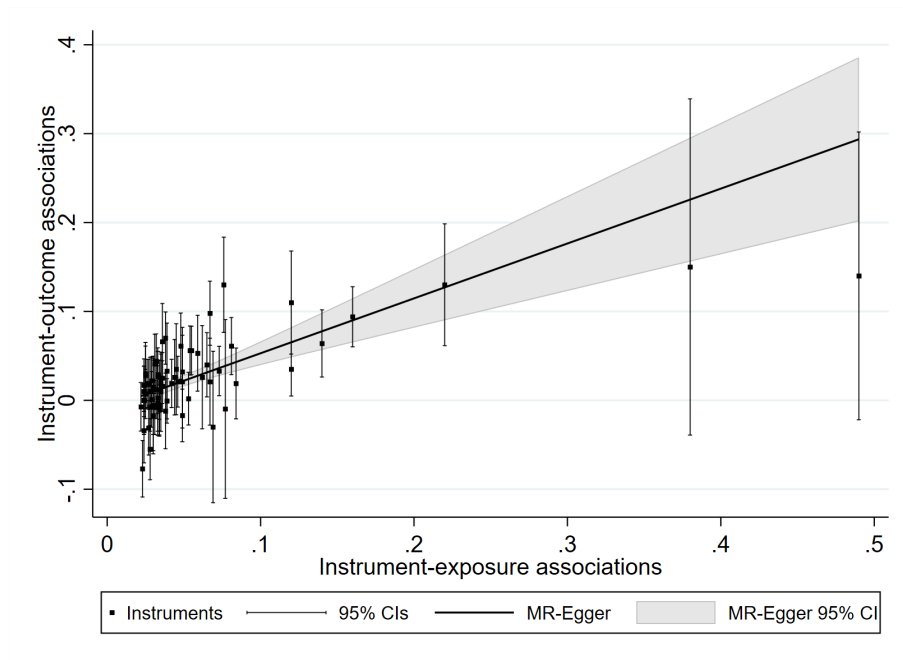
- Adding the modal and median estimates onto the plot

```
mreggerplot chdbeta chdse ldlcbeta ldlcse if sel1==1
mrmedian chdbeta chdse ldlcbeta 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 ldlcbeta 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
-------------------------------------------------------------------------
           | Coefficient  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
-------------------------------------------------------------------------
           | Coefficient  Std. err.      z    P>|z|   [95% conf. interval]
-----------+-------------------------------------------------------------
      beta |   .4198713   .2260632     1.86   0.063   -.0232045    .8629471
-------------------------------------------------------------------------
```
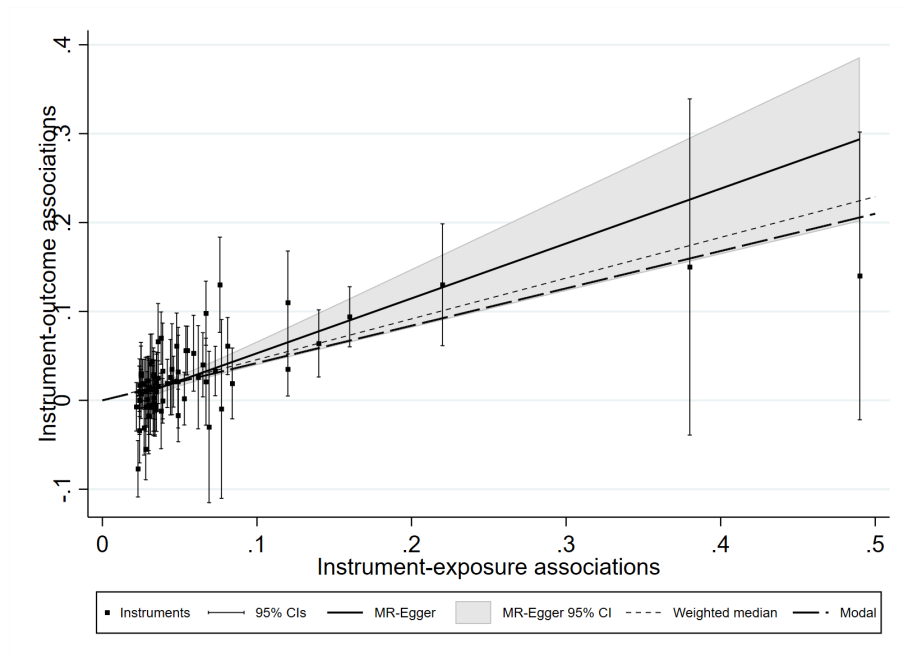
- Fit and MVMR model with phenotypes LDL-c and HDL-c (Burgess, Dudbridge, and Thompson 2015).

```
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
```

	Coefficient	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
```

	Coefficient	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).

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```
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
-----------------------------------------------------------------------------
             | Coefficient  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
-----------------------------------------------------------------------------
             | Coefficient  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)
```

> t(2)

```
                                    MVMR-Egger model oriented wrt: hdlcbeta
                                          Number of genotypes = 73
                                          Number of phenotypes =  3
                                          Residual standard error =  1.501
-----------------------------------------------------------------------------
             | Coefficient  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)
```

```
> t(3)

                                    MVMR-Egger model oriented wrt: tgbeta
                                            Number of genotypes = 73
                                            Number of phenotypes = 3
                                     Residual standard error =  1.499
------------------------------------------------------------------------------
             | Coefficient  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 4.2.3 (2023-03-15 ucrt)
 os       Windows 10 x64 (build 22621)
 system   x86_64, mingw32
 ui       RTerm
 language (EN)
 collate  English_United Kingdom.utf8
 ctype    English_United Kingdom.utf8
 tz       Europe/London
 date     2023-03-20
 pandoc   2.19.2 @ C:/Program Files/RStudio/resources/app/bin/quarto/bin/tools/ (via rmarkdown)

- Packages -------------------------------------------------------------------
 package              * version  date (UTC) lib source
 arrangements           1.1.9    2020-09-13 [1] CRAN (R 4.2.2)
 backports              1.4.1    2021-12-13 [1] CRAN (R 4.2.0)
 base64enc              0.1-3    2015-07-28 [1] CRAN (R 4.2.0)
 checkmate              2.1.0    2022-04-21 [1] CRAN (R 4.2.1)
 cli                    3.6.0    2023-01-09 [1] CRAN (R 4.2.2)
 cluster                2.1.4    2022-08-22 [2] CRAN (R 4.2.3)
```

```
codetools                0.2-19    2023-02-01 [2] CRAN (R 4.2.3)
colorspace               2.1-0     2023-01-23 [1] CRAN (R 4.2.2)
curl                     5.0.0     2023-01-12 [1] CRAN (R 4.2.2)
data.table               1.14.8    2023-02-17 [1] CRAN (R 4.2.2)
DEoptimR                 1.0-11    2022-04-03 [1] CRAN (R 4.2.0)
digest                   0.6.31    2022-12-11 [1] CRAN (R 4.2.2)
dplyr                  * 1.1.0     2023-01-29 [1] CRAN (R 4.2.2)
ellipsis                 0.3.2     2021-04-29 [1] CRAN (R 4.2.0)
evaluate                 0.20      2023-01-17 [1] CRAN (R 4.2.2)
fansi                    1.0.4     2023-01-22 [1] CRAN (R 4.2.2)
farver                   2.1.1     2022-07-06 [1] CRAN (R 4.2.1)
fastmap                  1.1.1     2023-02-24 [1] CRAN (R 4.2.2)
forcats                * 1.0.0     2023-01-29 [1] CRAN (R 4.2.2)
foreach                  1.5.2     2022-02-02 [1] CRAN (R 4.2.2)
foreign                  0.8-84    2022-12-06 [2] CRAN (R 4.2.3)
Formula                  1.2-5     2023-02-24 [1] CRAN (R 4.2.2)
generics                 0.1.3     2022-07-05 [1] CRAN (R 4.2.1)
ggplot2                * 3.4.1     2023-02-10 [1] CRAN (R 4.2.2)
glmnet                   4.1-6     2022-11-27 [1] CRAN (R 4.2.2)
glue                     1.6.2     2022-02-24 [1] CRAN (R 4.2.0)
gmp                      0.7-1     2023-02-07 [1] CRAN (R 4.2.2)
gridExtra                2.3       2017-09-09 [1] CRAN (R 4.2.1)
gtable                   0.3.2     2023-03-17 [1] CRAN (R 4.2.3)
haven                  * 2.5.2     2023-02-28 [1] CRAN (R 4.2.2)
Hmisc                  * 5.0-1     2023-03-08 [1] CRAN (R 4.2.2)
hms                      1.1.2     2022-08-19 [1] CRAN (R 4.2.1)
htmlTable                2.4.1     2022-07-07 [1] CRAN (R 4.2.1)
htmltools                0.5.4     2022-12-07 [1] CRAN (R 4.2.2)
htmlwidgets              1.6.2     2023-03-17 [1] CRAN (R 4.2.3)
httr                     1.4.5     2023-02-24 [1] CRAN (R 4.2.2)
iterators                1.0.14    2022-02-05 [1] CRAN (R 4.2.2)
iterpc                   0.4.2     2020-01-10 [1] CRAN (R 4.2.2)
jsonlite                 1.8.4     2022-12-06 [1] CRAN (R 4.2.2)
knitr                    1.42.5    2023-03-14 [1] Github (yihui/knitr@c50d307)
labeling                 0.4.2     2020-10-20 [1] CRAN (R 4.2.0)
lattice                  0.20-45   2021-09-22 [2] CRAN (R 4.2.3)
lazyeval                 0.2.2     2019-03-15 [1] CRAN (R 4.2.1)
lifecycle                1.0.3     2022-10-07 [1] CRAN (R 4.2.1)
lubridate              * 1.9.2     2023-02-10 [1] CRAN (R 4.2.2)
magrittr                 2.0.3     2022-03-30 [1] CRAN (R 4.2.0)
MASS                     7.3-58.3  2023-03-07 [1] CRAN (R 4.2.2)
Matrix                   1.5-3     2022-11-11 [1] CRAN (R 4.2.2)
MatrixModels             0.5-1     2022-09-11 [1] CRAN (R 4.2.1)
MendelianRandomization * 0.7.0     2023-01-09 [1] CRAN (R 4.2.2)
munsell                  0.5.0     2018-06-12 [1] CRAN (R 4.2.0)
MVMR                   * 0.3       2023-03-20 [1] Github (WSpiller/MVMR@3a0b54b)
nnet                     7.3-18    2022-09-28 [2] CRAN (R 4.2.3)
pillar                   1.8.1     2022-08-19 [1] CRAN (R 4.2.1)
pkgconfig                2.0.3     2019-09-22 [1] CRAN (R 4.2.0)
plotly                   4.10.1    2022-11-07 [1] CRAN (R 4.2.2)
purrr                  * 1.0.1     2023-01-10 [1] CRAN (R 4.2.2)
quantreg                 5.94      2022-07-20 [1] CRAN (R 4.2.1)
R6                       2.5.1     2021-08-19 [1] CRAN (R 4.2.0)
RadialMR                 1.0       2023-02-17 [1] Github (WSpiller/RadialMR@d63d3fc)
Rcpp                     1.0.10    2023-01-22 [1] CRAN (R 4.2.2)
readr                  * 2.1.4     2023-02-10 [1] CRAN (R 4.2.2)
remotes                * 2.4.2     2021-11-30 [1] CRAN (R 4.2.0)
rjson                    0.2.21    2022-01-09 [1] CRAN (R 4.2.0)
```

```
rlang                1.1.0    2023-03-14 [1] CRAN (R 4.2.2)
rmarkdown            2.20     2023-01-19 [1] CRAN (R 4.2.2)
RMVMR              * 0.2      2023-03-20 [1] Github (WSpiller/RMVMR@a162f9e)
robustbase           0.95-0   2022-04-02 [1] CRAN (R 4.2.2)
rpart                4.1.19   2022-10-21 [2] CRAN (R 4.2.3)
rstudioapi           0.14     2022-08-22 [1] CRAN (R 4.2.1)
scales               1.2.1    2022-08-20 [1] CRAN (R 4.2.1)
sessioninfo        * 1.2.2    2021-12-06 [1] CRAN (R 4.2.1)
shape                1.4.6    2021-05-19 [1] CRAN (R 4.2.0)
SparseM              1.81     2021-02-18 [1] CRAN (R 4.2.0)
Statamarkdown      * 0.7.2    2023-02-15 [1] CRAN (R 4.2.2)
stringi              1.7.12   2023-01-11 [1] CRAN (R 4.2.2)
stringr            * 1.5.0    2022-12-02 [1] CRAN (R 4.2.2)
survival             3.5-5    2023-03-12 [2] CRAN (R 4.2.2)
tibble             * 3.2.1    2023-03-20 [1] CRAN (R 4.2.3)
tidyr              * 1.3.0    2023-01-24 [1] CRAN (R 4.2.2)
tidyselect           1.2.0    2022-10-10 [1] CRAN (R 4.2.1)
tidyverse          * 2.0.0    2023-02-22 [1] CRAN (R 4.2.2)
timechange           0.2.0    2023-01-11 [1] CRAN (R 4.2.2)
tzdb                 0.3.0    2022-03-28 [1] CRAN (R 4.2.0)
utf8                 1.2.3    2023-01-31 [1] CRAN (R 4.2.2)
vctrs                0.6.0    2023-03-16 [1] CRAN (R 4.2.2)
viridisLite          0.4.1    2022-08-22 [1] CRAN (R 4.2.1)
withr                2.5.0    2022-03-03 [1] CRAN (R 4.2.0)
xfun                 0.37     2023-01-31 [1] CRAN (R 4.2.2)
yaml                 2.3.7    2023-01-23 [1] CRAN (R 4.2.2)

 [1] C:/Users/tom/AppData/Local/R/win-library/4.2
 [2] C:/Program Files/R/R-4.2.3/library

----------------------------------------------------------------------------
```

Stata session information

```
about
ado describe mrrobust
```

```
Stata/MP 17.0 for Windows (64-bit x86-64)
Revision 08 Mar 2023
Copyright 1985-2021 StataCorp LLC

Total physical memory:        32.00 GB
Available physical memory:    15.27 GB

Stata license: Unlimited-user 2-core network, expiring 21 Jan 2024
Serial number: 501709378202
  Licensed to: Tom Palmer
               University of Bristol


----------------------------------------------------------------------------
[47] 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
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      m\mrmedianobs.ado
      m\mrmedianobs_work.ado
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      m\mrrobust-author.ihlp

INSTALLED ON
      17 Feb 2023
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```

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.

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