Analyses for FEV_1 in the UK Biobank (ukb-b-19657) with different exposures: ever/never smoking status (ukb-b-20261) in the UK biobank, ever stopped smoking for 6+ months (ukb-b-11355) in the UK biobank, and cigarettes per day (ieu-b-25) from Lui et al. 2019 (PMID 30643251). Based on the tutorial from https://explodecomputer.github.io/steiger_collider/lutz_reanalysis.nb.html

```
suppressMessages(suppressPackageStartupMessages(suppressWarnings({
    library(TwoSampleMR)
    library(ieugwasr)
    library(tidyverse)
    library(knitr)
})))
knitr::opts_chunk$set(warning = FALSE)
```

Analysis for FEV_1 (ukb-b-19657) and ever/never smoking status (ukb-b-20261) in the UK biobank

```
# UK biobank FEV1 (ukb-b-19657) using public GWAS summary data

gwasinfo("ukb-b-19657") %>% str()
```

```
## Classes 'GwasInfo' and 'data.frame': 1 obs. of  18 variables:
##  $ id         : chr "ukb-b-19657"
##  $ trait      : chr "Forced expiratory volume in 1-second (FEV1)"
##  $ sex        : chr "Males and Females"
##  $ mr         : int 1
##  $ ontology   : logi NA
##  $ build      : chr "HG19/GRCh37"
##  $ category   : chr "Continuous"
##  $ note       : chr "3063: Output from GWAS pipeline using Phesant derived variables from UKBioba
nk"
##  $ group_name : chr "public"
##  $ population : chr "European"
##  $ unit       : chr "SD"
##  $ nsnp       : int 9851867
##  $ subcategory: logi NA
##  $ consortium : chr "MRC-IEU"
##  $ author     : chr "Ben Elsworth"
##  $ priority   : int 1
##  $ year       : int 2018
##  $ sample_size: int 421986
```

```
# Never / ever smoking status (ukb-b-20261) in the UK biobank

gwasinfo("ukb-b-20261") %>% str()
```

```
## Classes 'GwasInfo' and 'data.frame': 1 obs. of  20 variables:
##  $ id         : chr "ukb-b-20261"
##  $ trait      : chr "Ever smoked"
##  $ sex        : chr "Males and Females"
##  $ mr         : int 1
##  $ ontology   : logi NA
##  $ build      : chr "HG19/GRCh37"
##  $ category   : chr "Binary"
##  $ note       : chr "20160: Output from GWAS pipeline using Phesant derived variables from UKBiob
ank"
##  $ group_name : chr "public"
##  $ population : chr "European"
##  $ unit       : chr "SD"
##  $ nsnp       : int 9851867
##  $ ncontrol   : int 180558
##  $ subcategory: logi NA
##  $ consortium : chr "MRC-IEU"
##  $ author     : chr "Ben Elsworth"
##  $ priority   : int 1
##  $ ncase      : int 280508
##  $ year       : int 2018
##  $ sample_size: int 461066
```

```
lutz_rs <- c("rs56113850", "rs12461383", "rs7260329", "rs11858836", "rs72738786", "rs11633958", "rs8
192482", "rs2869548")

e0a <- extract_outcome_data(lutz_rs, "ukb-b-20261")
```

```
## Extracting data for 8 SNP(s) from 1 GWAS(s)
```

```
e0 <- convert_outcome_to_exposure(e0a)
o0 <- extract_outcome_data(lutz_rs, "ukb-b-19657")
```

```
## Extracting data for 8 SNP(s) from 1 GWAS(s)
```

```
d0 <- harmonise_data(e0, o0)
```

```
## Harmonising Ever smoked || id:ukb-b-20261 (ukb-b-20261) and Forced expiratory volume in 1-second
(FEV1) || id:ukb-b-19657 (ukb-b-19657)
```

```
## Removing the following SNPs for being palindromic with intermediate allele frequencies:
## rs12461383
```

```
d0 <- add_metadata(d0)
d0 <- add_rsq(d0)
res0 <- mr(d0)
```

```
## Analysing 'ukb-b-20261' on 'ukb-b-19657'
```

```
kable(res0)
```

id.exposure	id.outcome	outcome	exposure	method	nsnp	b	se	pval
ukb-b-20261	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Ever smoked || id:ukb-b-20261	MR Egger	7	5.299823	1.4688006	0.0154085
ukb-b-20261	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Ever smoked || id:ukb-b-20261	Weighted median	7	2.724055	0.4784397	0.0000000
ukb-b-20261	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Ever smoked || id:ukb-b-20261	Inverse variance weighted	7	2.454684	0.6600971	0.0002003
ukb-b-20261	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Ever smoked || id:ukb-b-20261	Simple mode	7	2.798306	0.4781745	0.0010991
ukb-b-20261	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Ever smoked || id:ukb-b-20261	Weighted mode	7	2.777025	0.4648569	0.0009868

```
s0 <- directionality_test(d0)
```

```
## r.exposure and/or r.outcome not present.
```

```
## Calculating approximate SNP-exposure and/or SNP-outcome correlations, assuming all are quantitati
ve traits. Please pre-calculate r.exposure and/or r.outcome using get_r_from_lor() for any binary tr
aits
```

```
str(s0)
```

```
## 'data.frame':    1 obs. of  8 variables:
##  $ id.exposure            : chr "ukb-b-20261"
##  $ id.outcome             : chr "ukb-b-19657"
##  $ exposure               : chr "Ever smoked || id:ukb-b-20261"
##  $ outcome                : chr "Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657"
##  $ snp_r2.exposure        : num 0.000166
##  $ snp_r2.outcome         : num 0.000515
##  $ correct_causal_direction: logi FALSE
##  $ steiger_pval           : num 4.23e-06
```

```
# Steiger filtering
d0 <- steiger_filtering(d0)

a0 <- d0 %>%
  select(SNP, chr, pos, pval.exposure, rsq.exposure, rsq.outcome, steiger_dir, steiger_pval) %>%
  arrange(chr, pos)
b0 <- mr_singlesnp(d0) %>% select(SNP, b, se)
a0 <- inner_join(b0, a0, by="SNP")
kable(a0)
```

SNP	b	se	chr	pos	pval.exposure	rsq.exposure	rsq.outcome	steiger_dir	steiger_pval
rs11633958	2.775228	0.4367444	15	78862064	0.0000750	7.9e-06	6.11e-05	FALSE	0.0189743

SNP	b	se	chr	pos	pval.exposure	rsq.exposure	rsq.outcome	steiger_dir	steiger_pval
rs11858836	3.555632	0.6117479	15	78783277	0.0047000	4.0e-06	5.04e-05	FALSE	0.0166257
rs2869548	2.654238	0.4644784	15	78922638	0.0002000	7.0e-06	4.96e-05	FALSE	0.0394252
rs56113850	-3.280212	0.8038733	19	41353107	0.0309999	2.3e-06	2.51e-05	FALSE	0.1019237
rs7260329	-5.173358	2.8715050	19	41521638	0.5500000	2.0e-07	4.90e-06	FALSE	0.4017562
rs72738786	3.074158	0.4505859	15	78828086	0.0001200	7.4e-06	7.03e-05	FALSE	0.0079469
rs8192482	2.678632	0.4317747	15	78886198	0.0000620	8.1e-06	5.81e-05	FALSE	0.0249880

Analysis for FEV$_1$ (ukb-b-19657) and ever stopped smoking for 6+ months (ukb-b-11355) in the UK biobank

```
# Ever stopped smoking for 6+ months (ukb-b-11355)

gwasinfo("ukb-b-11355") %>% str()
```

```
## Classes 'GwasInfo' and 'data.frame': 1 obs. of  20 variables:
##  $ id         : chr "ukb-b-11355"
##  $ trait      : chr "Ever stopped smoking for 6+ months"
##  $ sex        : chr "Males and Females"
##  $ mr         : int 1
##  $ ontology   : logi NA
##  $ build      : chr "HG19/GRCh37"
##  $ category   : chr "Binary"
##  $ note       : chr "2907: Output from GWAS pipeline using Phesant derived variables from UKBioba
nk"
##  $ group_name : chr "public"
##  $ population : chr "European"
##  $ unit       : chr "SD"
##  $ nsnp       : int 9851867
##  $ ncontrol   : int 64249
##  $ subcategory: logi NA
##  $ consortium : chr "MRC-IEU"
##  $ author     : chr "Ben Elsworth"
##  $ priority   : int 1
##  $ ncase      : int 48981
##  $ year       : int 2018
##  $ sample_size: int 113230
```

```
e3a <- extract_outcome_data(lutz_rs, "ukb-b-11355")
```

```
## Extracting data for 8 SNP(s) from 1 GWAS(s)
```

```
e3 <- convert_outcome_to_exposure(e3a)
o3 <- extract_outcome_data(lutz_rs, "ukb-b-19657")
```

```
## Extracting data for 8 SNP(s) from 1 GWAS(s)
```

```
d3 <- harmonise_data(e3, o3)
```

```
## Harmonising Ever stopped smoking for 6+ months || id:ukb-b-11355 (ukb-b-11355) and Forced expirat
ory volume in 1-second (FEV1) || id:ukb-b-19657 (ukb-b-19657)
```

```
## Removing the following SNPs for being palindromic with intermediate allele frequencies:
## rs12461383
```

```
d3 <- add_metadata(d3)
d3 <- add_rsq(d3)
res3 <- mr(d3)
```

```
## Analysing 'ukb-b-11355' on 'ukb-b-19657'
```

```
kable(res3)
```

id.exposure	id.outcome	outcome	exposure	method	nsnp	b	se	pval
ukb-b-11355	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Ever stopped smoking for 6+ months || id:ukb-b-11355	MR Egger	7	1.9204109	0.3314394	0.0021571
ukb-b-11355	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Ever stopped smoking for 6+ months || id:ukb-b-11355	Weighted median	7	0.9535886	0.1274894	0.0000000
ukb-b-11355	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Ever stopped smoking for 6+ months || id:ukb-b-11355	Inverse variance weighted	7	0.8380467	0.2039978	0.0000399
ukb-b-11355	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Ever stopped smoking for 6+ months || id:ukb-b-11355	Simple mode	7	0.9620765	0.1222313	0.0002227
ukb-b-11355	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Ever stopped smoking for 6+ months || id:ukb-b-11355	Weighted mode	7	0.9566156	0.1217473	0.0002248

```
s3 <- directionality_test(d3)
```

```
## r.exposure and/or r.outcome not present.
```

```
## Calculating approximate SNP-exposure and/or SNP-outcome correlations, assuming all are quantitati
ve traits. Please pre-calculate r.exposure and/or r.outcome using get_r_from_lor() for any binary tr
aits
```

```
str(s3)
```

```
## 'data.frame':    1 obs. of  8 variables:
##  $ id.exposure            : chr "ukb-b-11355"
##  $ id.outcome             : chr "ukb-b-19657"
##  $ exposure               : chr "Ever stopped smoking for 6+ months || id:ukb-b-11355"
##  $ outcome                : chr "Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657"
##  $ snp_r2.exposure        : num 0.00144
##  $ snp_r2.outcome         : num 0.000515
##  $ correct_causal_direction: logi TRUE
##  $ steiger_pval           : num 5.15e-06
```

```
# Steiger filtering
d3 <- steiger_filtering(d3)

a3 <- d3 %>%
  select(SNP, chr, pos, pval.exposure, rsq.exposure, rsq.outcome, steiger_dir, steiger_pval) %>%
  arrange(chr, pos)
b3 <- mr_singlesnp(d3) %>% select(SNP, b, se)
a3 <- inner_join(b3, a3, by="SNP")
kable(a3)
```

SNP	b	se	chr	pos	pval.exposure	rsq.exposure	rsq.outcome	steiger_dir	steiger_pval
rs11633958	0.9594136	0.1509853	15	78862064	0.0000000	6.69e-05	6.11e-05	TRUE	0.9131243
rs11858836	0.9728156	0.1673733	15	78783277	0.0000005	5.38e-05	5.04e-05	TRUE	0.9444722
rs2869548	0.8823986	0.1544153	15	78922638	0.0000001	6.41e-05	4.96e-05	TRUE	0.7729347
rs56113850	-1.3182090	0.3230502	19	41353107	0.0098001	1.44e-05	2.51e-05	FALSE	0.7165944
rs7260329	-1.5037222	0.8346505	19	41521638	0.3200000	2.20e-06	4.90e-06	FALSE	0.8239965
rs72738786	1.0086821	0.1478447	15	78828086	0.0000000	6.96e-05	7.03e-05	FALSE	0.9913019
rs8192482	0.9336674	0.1504999	15	78886198	0.0000000	6.72e-05	5.81e-05	TRUE	0.8634373

Analysis for FEV$_1$ (ukb-b-19657) in the UK biobank and cigarettes per day (ieu-b-25) from Lui et al. 2019 (PMID 30643251)

```
# cigarettes per day (ieu-b-25) from Lui et al. 2019 (PMID 30643251)
gwasinfo("ieu-b-25") %>% str()
```

```
## Classes 'GwasInfo' and 'data.frame': 1 obs. of  19 variables:
##  $ id         : chr "ieu-b-25"
##  $ trait      : chr "Cigarettes per Day"
##  $ sex        : chr "Males and Females"
##  $ mr         : int 1
##  $ ontology   : logi NA
##  $ build      : chr "HG19/GRCh37"
##  $ category   : chr "Continuous"
##  $ note       : logi NA
##  $ group_name : chr "public"
##  $ population : chr "European"
##  $ unit       : logi NA
##  $ nsnp       : int 11913712
##  $ subcategory: chr "Behavioural"
##  $ consortium : chr "GWAS and Sequencing Consortium of Alcohol and Nicotine use"
##  $ author     : chr "Liu, M"
##  $ priority   : int 1
##  $ year       : int 2019
##  $ sample_size: int 337334
##  $ pmid       : int 30643251
```

```
e1a <- extract_outcome_data(lutz_rs, "ieu-b-25")
```

```
## Extracting data for 8 SNP(s) from 1 GWAS(s)
```

```
e1 <- convert_outcome_to_exposure(e1a)
o1 <- extract_outcome_data(lutz_rs, "ukb-b-19657")
```

```
## Extracting data for 8 SNP(s) from 1 GWAS(s)
```

```
d1 <- harmonise_data(e1, o1)
```

```
## Harmonising Cigarettes per Day || id:ieu-b-25 (ieu-b-25) and Forced expiratory volume in 1-second
(FEV1) || id:ukb-b-19657 (ukb-b-19657)
```

```
## Removing the following SNPs for being palindromic with intermediate allele frequencies:
## rs12461383
```

```
d1 <- add_metadata(d1)
d1 <- add_rsq(d1)
res1 <- mr(d1)
```

```
## Analysing 'ieu-b-25' on 'ukb-b-19657'
```

```
kable(res1)
```

id.exposure	id.outcome	outcome	exposure	method	nsnp	b	se	pval

id.exposure	id.outcome	outcome	exposure	method	nsnp	b	se	pval
ieu-b-25	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Cigarettes per Day || id:ieu-b-25	MR Egger	7	-0.0627877	0.0148340	0.0082270
ieu-b-25	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Cigarettes per Day || id:ieu-b-25	Weighted median	7	-0.0659147	0.0055386	0.0000000
ieu-b-25	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Cigarettes per Day || id:ieu-b-25	Inverse variance weighted	7	-0.0660318	0.0045409	0.0000000
ieu-b-25	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Cigarettes per Day || id:ieu-b-25	Simple mode	7	-0.0658609	0.0069561	0.0000790
ieu-b-25	ukb-b-19657	Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657	Cigarettes per Day || id:ieu-b-25	Weighted mode	7	-0.0653982	0.0067429	0.0000689

```
s1 <- directionality_test(d1)
```

```
## r.exposure and/or r.outcome not present.
```

```
## Calculating approximate SNP-exposure and/or SNP-outcome correlations, assuming all are quantitati
ve traits. Please pre-calculate r.exposure and/or r.outcome using get_r_from_lor() for any binary tr
aits
```

```
str(s1)
```

```
## 'data.frame':    1 obs. of  8 variables:
##  $ id.exposure            : chr "ieu-b-25"
##  $ id.outcome             : chr "ukb-b-19657"
##  $ exposure               : chr "Cigarettes per Day || id:ieu-b-25"
##  $ outcome                : chr "Forced expiratory volume in 1-second (FEV1) || id:ukb-b-19657"
##  $ snp_r2.exposure        : num 0.0146
##  $ snp_r2.outcome         : num 0.000515
##  $ correct_causal_direction: logi TRUE
##  $ steiger_pval           : num 0
```

```
# Steiger filtering
d1 <- steiger_filtering(d1)

a1 <- d1 %>%
  select(SNP, chr, pos, pval.exposure, rsq.exposure, rsq.outcome, steiger_dir, steiger_pval) %>%
  arrange(chr, pos)
b1 <- mr_singlesnp(d1) %>% select(SNP, b, se)
a1 <- inner_join(b1, a1, by="SNP")
kable(a1)
```

SNP	b	se	chr	pos	pval.exposure	rsq.exposure	rsq.outcome	steiger_dir	steiger_pval
rs11633958	-0.0655063	0.0103089	15	78862064	0	0.0026992	6.11e-05	TRUE	0.0e+00
rs11858836	-0.0669645	0.0115213	15	78783277	0	0.0021387	5.04e-05	TRUE	0.0e+00
rs2869548	-0.0631335	0.0110480	15	78922638	0	0.0023807	4.96e-05	TRUE	0.0e+00
rs56113850	-0.0669264	0.0164015	19	41353107	0	0.0010838	2.51e-05	TRUE	0.0e+00
rs7260329	-0.0764538	0.0424362	19	41521638	0	0.0001630	4.90e-06	TRUE	4.9e-06
rs72738786	-0.0693134	0.0101594	15	78828086	0	0.0027788	7.03e-05	TRUE	0.0e+00
rs8192482	-0.0639848	0.0103139	15	78886198	0	0.0027051	5.81e-05	TRUE	0.0e+00

Analysis for FEV_1 (data code = 20150) and current/former smoking status (based on data code = 20116) in the UK biobank

In the UK biobank, we used the smoking status phenotype to identify current/former smoking status (data code=20116) and FEV_1 (best measure) (data code=20150) in participants with European ancestry, resulting in 160,183 participants. We considered the unadjusted FEV_1 as well as FEV_1 adjusted for age, sex and genetic ancestry via 10 PCs. Below is the correlation matrix: corGX is the correlation between the SNP and current/former smoking status, corGY is the correlation between the SNP and FEV_1, and corXY is the correlation between current/former smoking status and FEV_1. As recommended by the TwoSampleMR package, for the binary current/former smoking status phenotype, we calculated the corGX using the get_r_from_lor function from the TwoSampleMR package. (Lee et al. A Better Coefficient of Determination for Genetic Profile Analysis. Genetic Epidemiology 36: 214–224 (2012))

```
library(psych)
```

```
##
## Attaching package: 'psych'
```

```
## The following objects are masked from 'package:ggplot2':
##
##     %+%, alpha
```

```
# Correlations
dataSmk<-matrix(c(160183,160183,160183,160183,160183,160183,160183,0.004,-0.024,0.005,0.004,0.009,0.
004,0.005,-0.02,-0.01,-0.02,-0.02,0.01,-0.02,-0.02,-0.03,-0.03,-0.03,-0.03,-0.03,-0.03,-0.03),nrow=7
,ncol=4)
rownames(dataSmk)<-c("rs11858836_A","rs56113850_C","rs11633958_T","rs2869548_A","rs7260329_A","rs727
38786_T","rs8192482_T")
colnames(dataSmk)<-c("n","corGX","corGY","corXY")
dataSmk
```

```
##                    n  corGX corGY corXY
## rs11858836_A 160183  0.004 -0.02 -0.03
## rs56113850_C 160183 -0.024 -0.01 -0.03
## rs11633958_T 160183  0.005 -0.02 -0.03
## rs2869548_A  160183  0.004 -0.02 -0.03
## rs7260329_A  160183  0.009  0.01 -0.03
## rs72738786_T 160183  0.004 -0.02 -0.03
## rs8192482_T  160183  0.005 -0.02 -0.03
```

```
# Matrix to store results
nSNP<-nrow(dataSmk)
matS<-matrix(0,nrow=(nSNP),ncol=2)
colnames(matS)<-c("Direction","SteigerP")
rownames(matS)<-rownames(dataSmk)

#cycle through SNPs
for(ss in 1:nSNP){

# William test of correlation from the Steiger paper (1980) for dependent samples.
matS[ss,"SteigerP"]<-signif(r.test(dataSmk[ss,"n"], r12 = dataSmk[ss,"corGX"], r13=dataSmk[ss,"corGY"], r23=dataSmk[ss,"corXY"], twotailed = TRUE)$p,1)

matS[ss,"Direction"]<-paste(((dataSmk[ss,"corGX"])^2>(r13=dataSmk[ss,"corGY"])^2))
}

matS
```

```
##              Direction SteigerP
## rs11858836_A "FALSE"   "2e-11"
## rs56113850_C "TRUE"    "9e-05"
## rs11633958_T "FALSE"   "3e-12"
## rs2869548_A  "FALSE"   "2e-11"
## rs7260329_A  "FALSE"   "0.8"
## rs72738786_T "FALSE"   "2e-11"
## rs8192482_T  "FALSE"   "3e-12"
```

Note that the Steiger_filtering function from TwoSampleMR package uses the William test of correlation from the Steiger paper (1980) for independent samples. Given that both phenotypes are from the same overlapping sample in the UK Biobank, the William test of correlation from the Steiger paper (1980) for dependent samples needs to be used here. For this specific example, the Steiger p-values were similar for the 2 formulas.

Below is the mr_steiger function from https://github.com/MRCIEU/TwoSampleMR/blob/master/R/steiger.R on Feb 1, 2022. Note that the correlation for the exposure and the outcome is the square root of the sum of the absolute values of all the correlations.

```
r_exp <- sqrt(sum(r_exp[!is.na(r_exp) | is.na(r_out)]^2))
r_out <- sqrt(sum(r_out[!is.na(r_exp) | is.na(r_out)]^2))
```

```
mr_steiger <- function(p_exp, p_out, n_exp, n_out, r_exp, r_out, r_xxo = 1, r_yyo=1, ...)
{
    requireNamespace("psych", quietly=TRUE)

    r_exp <- abs(r_exp)
    r_out <- abs(r_out)

    ir_exp <- is.na(r_exp)
    ir_out <- is.na(r_out)

    ip_exp <- is.na(p_exp) | is.na(n_exp)
    ip_out <- is.na(p_out) | is.na(n_out)

    if(any(ir_exp))
    {
        r_exp[ir_exp] <- get_r_from_pn(p_exp[ir_exp & !ip_exp], n_exp[ir_exp & !ip_exp])
    }

    if(any(ir_out))
    {
        r_out[ir_out] <- get_r_from_pn(p_out[ir_out & !ip_out], n_out[ir_out & !ip_out])
    }

    r_exp <- sqrt(sum(r_exp[!is.na(r_exp) | is.na(r_out)]^2))
    r_out <- sqrt(sum(r_out[!is.na(r_exp) | is.na(r_out)]^2))

    stopifnot(r_xxo <= 1 & r_xxo >= 0)
    stopifnot(r_yyo <= 1 & r_yyo >= 0)

    r_exp_adj <- sqrt(r_exp^2 / r_xxo^2)
    r_out_adj <- sqrt(r_out^2 / r_yyo^2)

    sensitivity <- steiger_sensitivity(r_exp, r_out, ...)

    rtest <- psych::r.test(n = mean(n_exp), n2 = mean(n_out), r12 = r_exp, r34 = r_out)

    rtest_adj <- psych::r.test(n = mean(n_exp), n2 = mean(n_out), r12 = r_exp_adj, r34 = r_out_adj)

    l <- list(
        r2_exp = r_exp^2,
        r2_out = r_out^2,
        r2_exp_adj = r_exp_adj^2,
        r2_out_adj = r_out_adj^2,
        correct_causal_direction = r_exp > r_out,
        steiger_test = pnorm(-abs(rtest[["z"]])) * 2,
        correct_causal_direction_adj = r_exp_adj > r_out_adj,
        steiger_test_adj = pnorm(-abs(rtest_adj[["z"]])) * 2,
        vz = sensitivity$vz,
        vz0 = sensitivity$vz0,
        vz1 = sensitivity$vz1,
        sensitivity_ratio = sensitivity$sensitivity_ratio,
        sensitivity_plot = sensitivity$pl
    )
    return(l)
}
```