

Mendelian randomization extension in the twin study design

Seminar - The University of Tennessee Health Science Center (UTHSC)

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Outline

- Introduction
- Mendelian randomization
- Equivalence in SEM
- Twin study design
- MRDoC2 paper
- Modeling with longitudinal data



Introduction

- Causal inference, gold standard: randomized controlled trial
- Not always feasible, ethics²
 - E.g. exposure to trauma → substance abuse
- Mendelian randomization,³ helps with these cases.

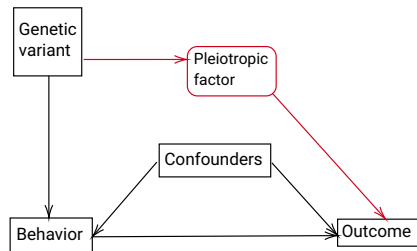


²Ohlsson, (2020), "Applying Causal Inference Methods in Psychiatric Epidemiology," *JAMA Psychiatry*.

³Katikireddi, (2018), "Assessing Causal Relationships Using Genetic Proxies for Exposures," *Addiction*.

Mendelian randomization⁴

- Uses genetic variants as instrumental variables
- Helps understand causation, but has strong assumptions
 1. G (instrument) is robustly associated with X (“relevance”);
 2. G does not share common causes (C and P) with Y (Outcome) (“independence” or “exchangeability”); and
 3. G affects Y exclusively through its effect on X (“exclusion restriction”).



⁴Richmond, (2022), “Mendelian Randomization,” *Cold Spring Harb Perspect Med*.

Mendelian Randomization⁵

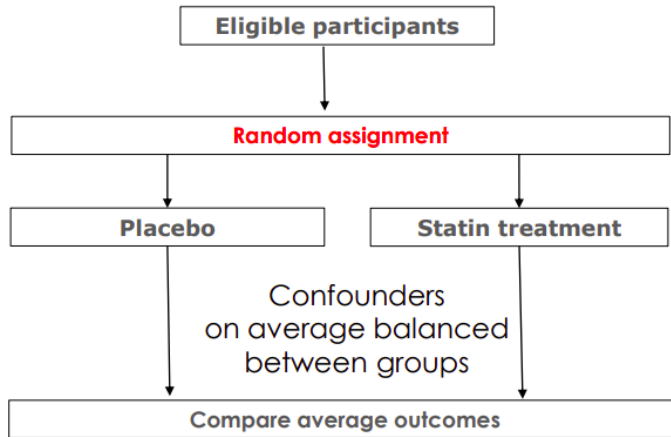
- Depends on instruments sufficiently predictive of exposure
- Psychiatric disorders polygenicity, weak instrument bias
- Cause is (typically) assessed in one direction

Table 4. Extensions to the basic Mendelian randomization (MR) approach

Method	Description	Directed acyclic graphs (DAGs)	Applications
Bidirectional or reciprocal MR (Timpson et al. 2011)	Used to evaluate the causal direction(s) of effect between two traits X and Y, with the use of valid instruments G_X and G_Y	$G_1 \longrightarrow X \longrightarrow Y$ $G_2 \longrightarrow Y \longrightarrow X$ - -	Body mass index (BMI) and vitamin D (Vimalleswaran et al. 2013)

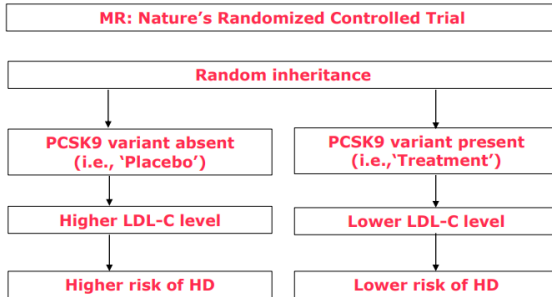
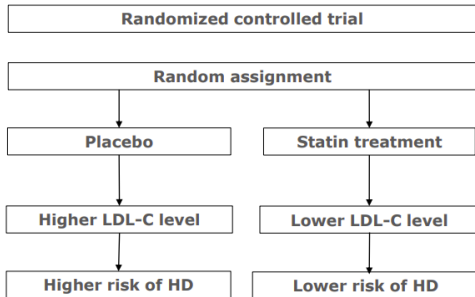


Randomized controlled trials⁶



⁶Camelia, 2017, "Mendelian Randomization," (VIPBG 2017).

Analogy RCT - Mendelian Randomization⁷



Two-stage least squares (2SLS)

- Stage 1: regress exposure on instrument and get predicted values
- Stage 2: use predicted exposure to predict the outcome



Two-stage least squares (2SLS)⁸

Stage 1

$$X_i = \beta_0 + \beta_1 * GV_i + \epsilon_i$$

- Regress exposure on GV & obtain **predicted** values

Stage 2

$$Y_i = g_0 + g_1 * \hat{X}_i + \epsilon_i$$

- Regress outcome on predicted exposure

g_1 difference in outcome per unit change in (genetically-predicted) exposure

Genetically determined exposure → “randomized” → can ascribe causality (if assumptions are met)



⁸Ibid.

Structural equation modeling - equivalence with 2SLS

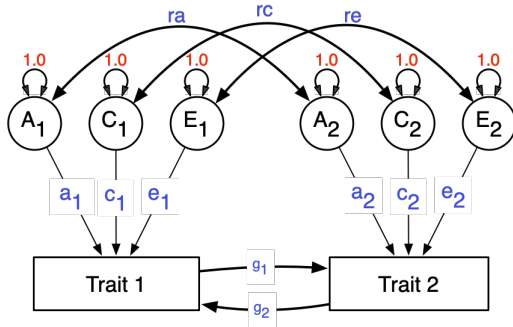
- Use of *structural equation modeling* to complement *mendelian randomization*, inspired by Direction of Causation (DoC) model⁹
- Reciprocal causation now possible to model



⁹Minică, (2018), "Extending Causality Tests with Genetic Instruments," *Behav Genet*.

Classic Direction of Causation model - reciprocal causation¹⁰

Model specification



Path diagram representing a Bidirectional DoC for one twin.

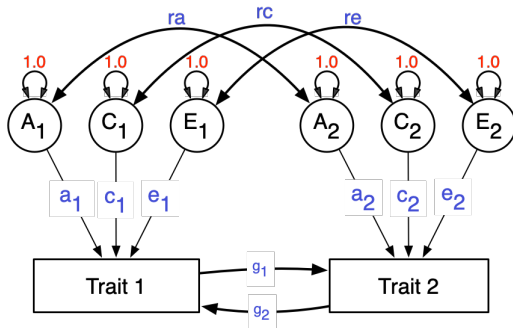
- causal paths are estimated affording information from the cross-twin cross-trait correlations.
- Cross-twin covariance between additive genetic effects is 0.5 (not shown) for DZ twins, as DZs are expected to share 50% of the genetic effects.
- Standard SEM symbology is used.



¹⁰Heath, (1993), "Testing Hypotheses About Direction of Causation Using Cross-Sectional Family Data," *Behav Genet*; Arumäe, (2021), "Two Genetic Analyses to Elucidate Causality Between Body Mass Index and Personality," *Int J Obes (Lond)*.

Classic Direction of Causation

Model specification



Problems

- Not identified as depicted
- Bias at the phenotypic level^a
- Bias due to E confounding^b
- Better detection of cause with different variance component proportions for each phenotype

^aGillespie, (2003), "Direction of Causation Modeling Between Cross-Sectional Measures of Parenting and Psychological Distress in Female Twins," *Behav Genet*.

^bRasmussen, (2019), "A Major Limitation of the Direction of Causation Model," *Twin Res Hum Genet*.



Fig. 4 Path diagrammatic representation of the MR-DoC model in DZ twins. The parameter x equals the standard deviation of the observed instrument, i.e., PGS in the circle is standardized. The model as depicted is not identified (see Table 1)

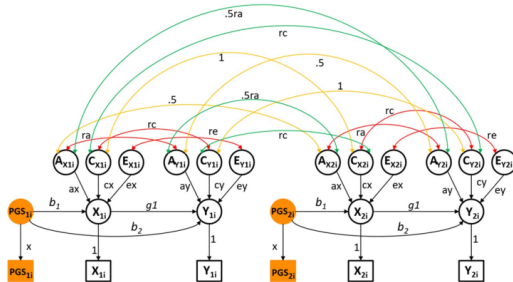
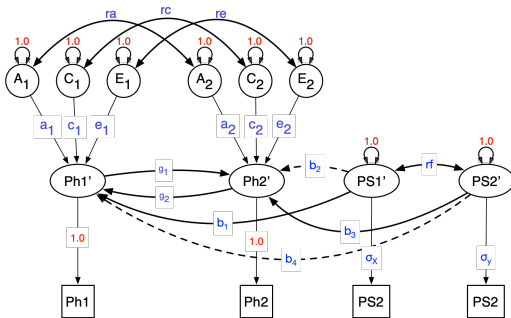


Figure 1: MR-DoC extension. Some confounding, not bidirectional. Not identified as depicted.

Model specification



Modified MR-DOC

- Path diagram of the MR-DoC2 model for an individual.
- The model includes the effects of additive genetic (A), common environment (C) and specific environment (E) factors for both X and Y, and their effects may correlate (parameters ra , rc and re).
- All latent variables have fixed unit variance (not shown).

- Which parameters drive power?

Revisiting limitations

- Do we need phenotypes with distinct inheritance patterns
- What about measurement error at the phenotypic level?
- How robust it is regarding pleiotropy

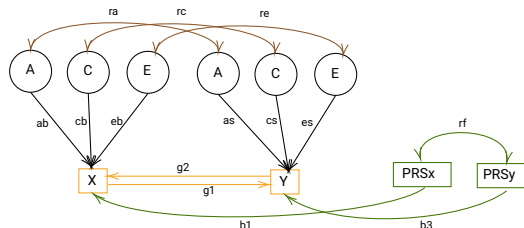


Which parameters drive power?

Table 1: Variance explained in statistical power (non-centrality parameter; NCP) by model parameters.

	$g1 = 0$	$g2 = 0$	$g1 = g2 = 0$
$g1$	0.517	0.000	0.289
$g2$	0.000	0.517	0.289
$b1$	0.365	0.000	0.181
$b3$	0.000	0.365	0.181
ra	0.000	0.000	0.000
rc	0.000	0.000	0.000
re	0.002	0.002	0.000
rf	0.041	0.041	0.000
ay	0.002	0.000	0.001
ax	0.000	0.002	0.001
cy	0.002	0.000	0.001
cx	0.000	0.002	0.001
Total R2	0.929	0.929	0.945

- Distinct inheritance patterns from phenotypes - not needed
- $b1$, $b2$, $g1$, and $g2$ are what drives power
- slightly better power without C variance



Factorial design simulation - factors

θ	Design 1 (ACE)	Design 2 (AE)	Design 3 (AE)
b1	$\sqrt{0.025}, \sqrt{0.05}$	$\sqrt{0.025}, \sqrt{0.05}, \sqrt{0.075}$	$-\sqrt{0.075}, -\sqrt{0.03}, \sqrt{0.03}, \sqrt{0.075}$
b3	$\sqrt{0.025}, \sqrt{0.05}$	$\sqrt{0.025}, \sqrt{0.05}, \sqrt{0.075}$	$-\sqrt{0.075}, -\sqrt{0.03}, \sqrt{0.03}, \sqrt{0.075}$
g1	$\sqrt{0.020}, \sqrt{0.05}$	$\sqrt{0.020}, \sqrt{0.04}, \sqrt{0.06}$	$-\sqrt{0.050}, -\sqrt{0.020}, \sqrt{0.050}, \sqrt{0.020}$
g2	$\sqrt{0.020}, \sqrt{0.05}$	$\sqrt{0.020}, \sqrt{0.04}, \sqrt{0.06}$	$-\sqrt{0.050}, -\sqrt{0.020}, \sqrt{0.050}, \sqrt{0.020}$
ra	0.25, 0.50	0.0, 0.25, 0.50	0.3
rc	0.25, 0.50	0	0
re	0.25, 0.50	0.0, 0.25, 0.50	0.3
rf	0.25, 0.50	0.0, 0.25, 0.50	0.3
ax	$\sqrt{0.10}, \sqrt{0.25}$	$\sqrt{0.10}, \sqrt{0.25}$	$\sqrt{0.5}$
ay	$\sqrt{0.10}, \sqrt{0.25}$	$\sqrt{0.10}, \sqrt{0.25}$	$\sqrt{0.3}$
cx	$\sqrt{0.10}, \sqrt{0.25}$	0	0
cy	$\sqrt{0.10}, \sqrt{0.25}$	0	0
Total cells	$2^{12}=4096$	$3^7 \cdot 2^2 = 8748$	$4^4=256$

Parameter levels on the three factorial designs, with respective total number of cells for each design simulation. Also, ex was specified as $\sqrt{1 - ax^2 - cx^2}$ and ey as $\sqrt{1 - ay^2 - cy^2}$.

Revisiting limitations: Error at the phenotypic level

Reliability

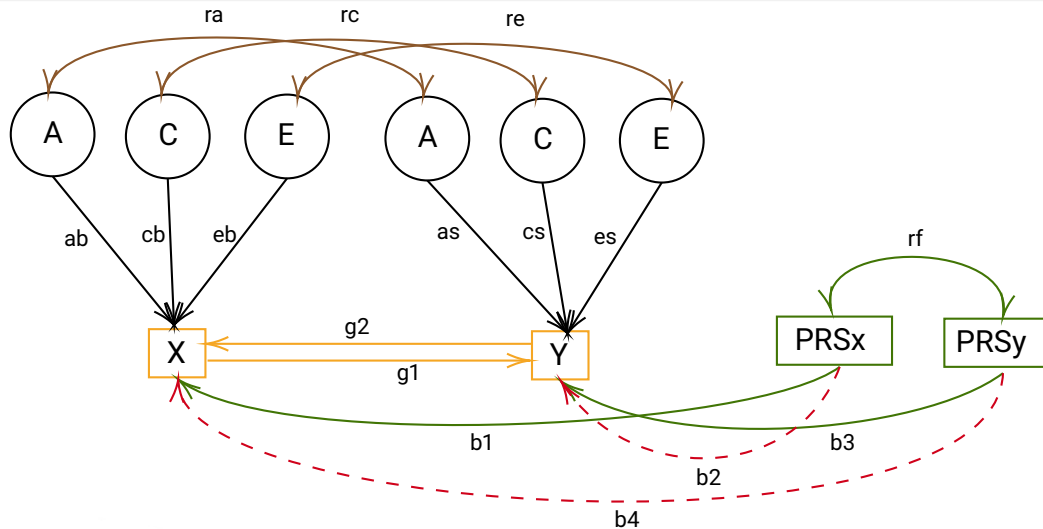
$$\text{relB} = \text{var}(B) / \{\text{var}(B) + \text{var}(\text{errorB})\}$$

$$\text{relS} = \text{var}(S) / \{\text{var}(S) + \text{var}(\text{errorS})\}$$

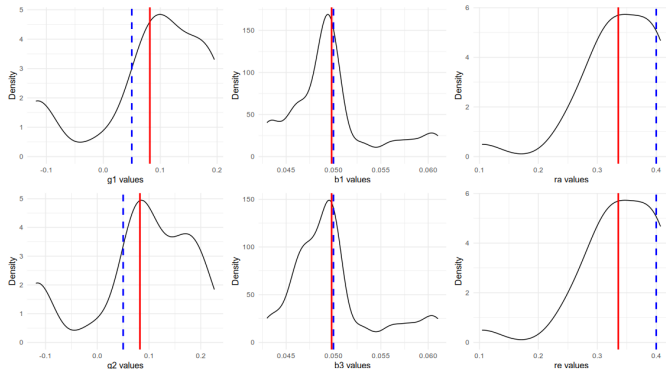
- power reduces
- but no bias in estimation of b_1 , b_2 , g_1 , g_2



Horizontal pleiotropy



Not robust to pleiotropy (b_2 and $b_4 \neq 0$)

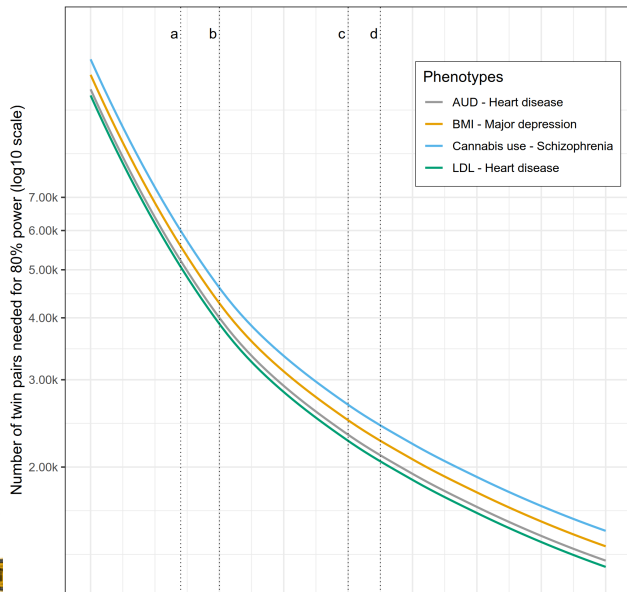


The solid red lines indicate the observed mean of the distribution while the dotted blue lines indicated the simulated value for the parameter. If the solid red line is on the right of the dotted blue line, then the parameter is overestimated and if the solid red line is on the left of the dotted blue line the parameter is underestimated.

Results from simulation with 1024 replications, with variation on the factor level of b_2 and b_4 ($0, \sqrt{.001}, \sqrt{.002}, \sqrt{.003}, \sqrt{.004}$).



Reasonable sample sizes in relevant scenarios



A and C variances for the groups:

1. alcohol use (a^2 49%, c^2 10%) (Verhulst et al., 2015) and heart disease (a^2 22%, c^2 0%) (Wu et al., 2014);
2. BMI (a^2 7.9%, c^2 3%) (Rokholm et al., 2011) and major depression (a^2 37%, c^2 1%) (Scherrer et al., 2003);
3. cannabis use (a^2 51%, c^2 20%) (Verweij et al., 2010) and schizophrenia (a^2 81%, c^2 11%) (Sullivan et al., 2003);
4. dyslipidemia (LDL) (a^2 60%, c^2 28%) (Zhang et al., 2010) and heart disease (a^2 22%, c^2 0%) (Wu et al., 2014).

MR-DoC2: bidirectional causal modeling with instrumental variables and data from relatives

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This article is a preprint and has not been certified by peer review [what does this mean?].



Abstract

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Abstract

Establishing causal associations is an essential step towards developing interventions for psychiatric, substance use and many other disorders. While randomized controlled trials (RCTs) are considered the gold standard for causal inference, they are unethical in many scenarios. Mendelian randomization (MR) can instead be used, but both methods focus on



¹³Castro-de-Araujo, March 2022, "MR-DoC2," (2022).

Conclusion

MR-DoC2

- Can complement MR within twin studies framework with a bidirectional causal model
- Improves on some limitations of classic DoC

Future directions

- Apply MR-DoC2 and the versions of CLPM to real data



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Contact

