Determining the direction of causality in the face of measurement error

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Abstract

With our ability to characterize the human phenome ever improving it is becoming increasingly common to use statistical tests to infer the causal relationships between correlated variables. A simple method for inferring if an exposure is on the causal pathway to an outcome is through mediation analysis, where the effect of an instrument on the outcome is tested before and after adjusting for the exposure. We show that in the face of measurement error this can lead to erroneous results, and that increasing sample size, rather than reducing bias, can often have the alarming effect of increasing certainty in the wrong answer. Commonly used tools that are predicated on this methodology such as the causal inference test (CIT) are shown to be susceptible. We demonstrate that Mendelian randomization (MR) is a method for causal inference that is robust to measurement error, and that a simple extension to MR can provide a method to estimate the direction of causality between correlated variables even when the biology of the instrument is unknown. We argue that because measurement error is ubiquitous in phenotypic data, mediation-based causal inference should be treated with caution.

Introduction

With the explosion in data that measures the human phenome, of great interest is understanding the causal nature of the emerging putitive correlations between measures of interest. Mediation is a commonly used statistical method for making causal inference in observational data[1–4], and it exists in many forms, from simple regression based systems to structural equation modeling. The principle behind mediation analysis can be explained as follows. Supposing an exposure has a causal effect on an outcome, then an 'instrument' that causes the exposure (a single nucleotide polymorophism (SNP), for example) should also influence the outcome. Therefore the influence of the instrument on the outcome conditional on the exposure should be zero. This forms the basis of a number of methods, such as the causal inference test (CIT)[1], which have been employed by a number of recent publications make causal inferences, often in large scale 'omics datasets[5–7].

While mediation based approaches are simple and convenient to implement, it is important to note where they may lead to unreliable results. One such mechanism is measurement error[8–11]. Measurement (or observational) error is the difference between a measured value of a quantity and its true value. Such variability can arise through a whole plethora of mechanisms, which are often unique to the study design and difficult to avoid[12,13]. Array technology is now commonly used to obtain high throughput phenotyping at low cost, but they come with the problem of having imperfect sensitivity, so for example methylation levels as measured by the Illumina450k chip are prone to have some amount of noise around the true value[14,15]. Sensitivity is also an issue, for example if the unit of measurement of biological interest is the methylation level in a T cell, then measurement error of this value can be introduced by using methylation levels from whole blood samples because the measured value will be an assay of many cell types[16].

Measurement error can indeed arise in more low-tech data too, for example when measuring body mass index (BMI) one is typically interested in using this as a proxy for obesity, but it is clear that the correlation

between BMI and obesity is not perfect[17]. A similar problem of biological misspecification is unavoidable in disease diagnosis. Measurement error can also be introduced after the data has been collected, for example the transformation of non-normal data for the purpose of statistical analysis will lead to a new variable that will typically have both bias and imprecision compared to the original variable. The sources of measurement error are not limited to this list[13], and its impact has been explored in the context of mediation analysis in the epidemiological literature extensively[8,11].

An alternative statistical method that gained prominence at least in part as a solution to the problem of measurement error[18] is Mendelian randomisation (MR)[19,20]. Here an instrumental variable (typically a SNP) that has a robost, causal association with the exposure is used to proxy the exposure in an association test with the outcome. If there is no measurement error in the SNP then the causal association between the exposure and the outcome can be estimated by scaling the association between the SNP and the outcome by the association between the SNP and the exposure. This approach also has the useful property that it guards against unmeasured confounders driving the association between exposure and outcome; and if the biological effect of the SNP is understood then it can also aid against reverse causality driving the association.

Here, however, arises a potential issue. Often the biological effect of a SNP is not known, and therefore it can be difficult to determine for which of the two variables in a putative exposure-outcome association is the SNP a valid instrument. By definition, we expect that if the association is causal then a SNP for the exposure will be associated with the outcome, so if the researcher erroneously uses the SNP as an instrument for the outcome then they are likely to see an apparently robust causal association of outcome on exposure. Such a situation can arise in many scenarios. For example genome wide association studies (GWASs) that identify genetic associations for complex traits are by design hypothesis free and agnostic of genomic function, and it often takes years of follow up studies to understand the biological nature of a putative GWAS hit[21]. Another situation is where the causal direction between 'omic measures need to be determined, for example if a DNA methylation probe is associated with expression of an adjacent gene, then is a cis-acting SNP an instrument for the DNA methylation level, or the gene expression level[7]?

Mediation based methods, for example CIT and other related approaches typically attempt to use the data to resolve this issue using the following logic: if the SNP-exposure association is stronger than the SNP-outcome association then the causal effect must be in the direction of exposure to outcome. The same logic can indeed be applied to MR, but often when applied the sensitivity of these approaches to measurement error is not considered.

When being objective one must assume that measurement error is ubiquitous, and any measured variable is only an imperfect proxy of the biological quantity that the researcher intended to obtain. Here we show using theory and simulations how measurement error can lead to unreliable causal inference in the mediation-based CIT method, and we propose an extension to MR that, although does not eliminate the problem of measurement error, provides a framework in which to ascertain the causal direction when the biology of the instrument is not fully understood.

Methods

CIT test

The CIT method[1] is implemented in the R package *R/cit*[22]. The *cit.cp* function was used to obtain an omnibus p-value of causality between an exposure x and an outcome y using a mediator g. To infer the direction of causality using the CIT method, the omnibus p-value was estimated for x causing y, and for y causing x, and the model that returned the lowest p-value was taken as the one denoting the correct causal direction.

MR causal test

Supposing there are two correlated variables, x and y, with a variant g associated with both. Assuming no horizontal pleiotropy (i.e. g only has an effect on one of the variables through the other variable) it is desirable

to know which of the variables it has a direct influence on. This can be achieved by testing for a difference in the correlations $\rho_{g,x}$ and $\rho_{g,y}$ using Steiger's Z-test for correlated correlations within a population[???]. It is calculated as

$$Z = (Z_{gx} - Z_{gy})\frac{\sqrt{N-3}}{\sqrt{2(1-\rho_{xy})h}}$$

where Fisher's z-transformation is used to obtain $Z_{g*} = \frac{1}{2}\ln\left(\frac{1+\rho_{g*}}{1-\rho_{g*}}\right)$,

$$h = \frac{1-(frm^2)}{1-rm^2}$$

where

$$f = \frac{1-\rho_{xy}}{2(1-rm^2)}$$

and

$$rm^2 = \frac{1}{2}(\rho_{gx}^2 + \rho_{gy}^2).$$

The Z value is interpreted such that

$$Z\begin{cases} > 0, & x \to y \\ < 0, & y \to x \\ = 0, & x \perp\!\!\!\perp y \end{cases}$$

and a p-value is generated from the Z value to indicate confidence of difference in correlations ρ_{gx} and ρ_{gy}. The test for a causal association is then obtained by performing two sample MR in the direction that is predicted to be the correct model based on the Z score test. For simplicity, the test is deemed to have obtained a robust association if the Z score test has a p-value < 0.05 and the two sample MR analysis has a p-value < 0.05. Note that the same approach can be applied to a two-sample MR setting, where

Simulations

Simulations were conducting by creating variables of sample size n for the exposure x, the measured values of the exposure x_O, the outcome y, the measured values of the outcome y_O and the instrument g. In all models x causes y and g is an instrument for x. Each variable was simulated such that:

$$\begin{aligned} g &\sim Binom(2, 0.5) \\ x &= \beta_g g + \epsilon_g \\ x_O &= \beta_{mx} x + \epsilon_{mx} \\ y &= \beta_x x + \epsilon_x \\ y_O &= \beta_{my} y + \epsilon_{my} \end{aligned}$$

All β values were set to 1. Values of ϵ_* were generated such that

$$
\begin{aligned}
cor(g, x) &= \{0.01, 0.05, 0.1\} \\
cor(x, y) &= \{0.2, 0.4, 0.6, 0.8\} \\
var(\epsilon_{mx}) &= \{0, 0.2, 0.4, 0.6, 0.8, 1\} \\
var(\epsilon_{my}) &= \{0, 0.2, 0.4, 0.6, 0.8, 1\} \\
n &= \{100, 1000, 10000\}
\end{aligned}
$$

giving a total of 432 combinations of parameters. Each of these sets of variables was performed 100 times, and the CIT and MR methods were applied to each in order to evaluate the causal association of the simualted variables.

Results

The influence of measurement error on CIT

Measurement error of an exposure can be modeled as some transformation of the true value that leads to the observed value, $x_O = f(x)$. For example, we can define $f(x) = \alpha_m + \beta_m x + \epsilon_m$, where α_m and β_m influence the bias in the measurement of x, and ϵ_m represents the imprecision in the measurement of x. Here the true value of the exposure is partially explained by the genetic instrument, g, such that

$$x = \alpha_g + \beta_g g + \epsilon_g$$

where β_g is the effect of the SNP on the exposure, and ϵ_g is the residual value of x; and the outcome is partially explained by the exposure

$$y = \alpha_x + \beta_x x + \epsilon_x$$

where β_x is the true effect of the exposure on the outcome. In the causal inference test (CIT), an omnibus p-value is generated from four hypothesis tests: 1) g is associated with x; 2) g is associated with y; 3) g is associated with $x|y$; and 4) g is independent of $y|x$. The 4th condition is necessary for causal inference, and can be expressed as $cov(g, y - \hat{y}) = 0$, where $\hat{y} = \hat{\alpha}_x + \hat{\beta}_x x_O$. When measurement error is introduced we can show using basic covariance properties (Appendix 1) that

$$
\begin{aligned}
cov(g, y - \hat{y}) &= cov(g, y) - cov(g, \hat{y}) \\
&= \beta_g \beta_x var(g) - D\beta_g \beta_x var(g)
\end{aligned}
$$

where

$$D = \frac{\beta_m^2 var(x)}{\beta_m^2 var(x) + var(\epsilon_m)}$$

Thus an observational study will find $cov(g, y - \hat{y}) = 0$ when the true model is causal only when $D = 1$. Therefore, if there is any measurement error that incurs imprecision (i.e. $var(\epsilon_m) \neq 0$) then there will remain an association between g and $y|x$, which is in violation of the the 4th condition of the CIT. Note that measurement bias alone is insufficient to lead to a violation of the test statistic assumptions.

We performed simulations to verify that this problem does arise using the CIT method. Figure 1 shows that when there is no measurement error in the exposure or outcome variables ($\rho_{x,x_O} = 1$) the CIT is reliable in identifying the correct causal direction. However, as measurement error increases in the exposure variable, eventually the CIT is more likely to infer a robust causal association in the wrong direction. Also of concern here is that increasing sample size does not solve the issue, indeed it only strengthens the evidence of the incorrect inference.

Inferring direction of causality using MR

When selecting an instrument g that has a direct influence on x and x is causally related to y, one can reason that the influence of g on y is the proportion of the effect of x on y that is explained by the effect of g on x. Hence the effect estimate β_{MR} of x on y is estimated as

$$\beta_{MR} = \frac{\beta_y}{\beta_g} = \frac{cov(y, g)}{cov(x_O, g)} = \frac{cov(\beta_x x + \epsilon_x, g)}{cov(x + \epsilon_x, g)}$$

which reduces to

$$\lim_{n\to\infty} \hat{\beta}_{MR} = \frac{\beta_x cov(x + \epsilon_x)}{cov(x + \epsilon_x)} = \beta_x$$

thus we obtain an estimate of the effect of x_O on y that is unbiased by measurement error in x.

However, if we do not know whether the SNP g has a direct influence on x or y then further efforts are required. If x causes y and g is a valid instrument for x then we expect that the Steiger test will obtain the correct result because the value $d = \rho_{g,x_O} - \rho_{g,y_O}$ is greater than 0 when the causal association between x and y is $\rho_{x,y} < 1$. But it can be shown that in the presence of measurement error, $d = \rho_{x,x_O} - \rho_{x,y}\rho_{y,y_O}$ (Appendix 2), thus it is important to note that under certain conditions when measurement error is present the Steiger test could make erroneous inference about causal direction because the value of d is not restricted to being greater than 0. However, using the MR approach there are two potential advantages over the CIT. First, we can conduct a formal test for the direction of causality. Second the correct direction of causality can be inferred when measurement error in the exposure variable is present, as long as it is lower than the product of the measurement error in the outcome and the causal correlation between the exposure and the outcome. Figure 2 shows that in most cases, especially when the causal effect between x and y is not very large, the condition of $d > 0$ is satisfied.

We performed simulations to explore the performance of this approach in comparison to CIT. Figure 3 shows that, as predicted, when $d < 0$ the MR analysis is liable to infer the wrong direction of causality, and that this erroneous result is more likely to occur with increasing sample size. However, in all cases the MR analysis infers the wrong direction of causality at the same or a lower rate than the CIT. When $d > 0$ is satisfied we observe that in many cases the MR method has greater power to obtain evidence for causality than CIT, and always obtains the correct direction of causality.

Discussion

Researchers are often confronted with the problem of making causal inferences using a statistical framework on observational data, and unfortunately there are no solutions that work perfectly in all scenarios. In the face of measurement error it is evident that causal inference drawn through mediation analysis will be difficult to interpret, and this is a serious problem considering that it is often impossible to estimate the extent of measurement error for most experimental designs.

In the epidemiological literature this is relatively well understood and our initial analysis simply confirms that for widely used methods such as CIT that it is indeed liable to the same issues as standard mediation based analysis. Under many circumstances a practical solution to this problem is to use Mendelian randomisation instead of mediation based methods. Mendelian randomisation is robust in the face of measurement error and, given that the researcher has knowledge about the biology of the instrument being used in the analysis, can offer a direct solution to the issues that CIT faces. This assumption is often reasonable, for example exposures such as CRP

Pleiotropy

Appendix 1

Given the following model

$$x = \alpha_g + \beta_g g + \epsilon_g x_O = \alpha_m + \beta_m x + \epsilon_m y = \alpha_x + \beta_x x + \epsilon_x$$

where x is the exposure on the outcome y, g is an instrument that has a direct effect on x, and x_O is the measured quantity of x, where measurement error is incurred from bias in α_m and β_m and imprecision from ϵ_m, our objective is to estimate the expected magnitude of association between g and y after conditioning on x. Under the CIT, this is expected to be $cov(g, y - \hat{y}) = 0$ when x causes y, where $\hat{y} = \hat{a}_{x_O} + \hat{b}_{x_O} x_O + \epsilon_{x_O}$ is the predicted value of y using the measured value of x_O.

We can split $cov(g, y - \hat{y})$ into two parts, $cov(g, y)$ and $cov(g, \hat{y})$.

Part 1

$$\begin{aligned} cov(g, y) &= cov(g, \beta_x x) \\ &= cov(g, \beta_x \beta_g g) \\ &= \beta_x \beta_g var(g) \end{aligned}$$

Part 2

$$\begin{aligned} cov(g, \hat{y}) &= cov(g, \hat{\beta}_{x_O} x_O) \\ &= cov(g, \hat{\beta}_{x_O} \beta_m x) \\ &= cov(g, \hat{\beta}_{x_O} \beta_m \beta_g g) \\ &= \hat{\beta}_{x_O} \beta_m \beta_g var(g) \end{aligned}$$

Simpifying further

$$\begin{aligned} \hat{\beta}_{x_O} &= \frac{cov(y, x_O)}{var(x_O)} \\ &= \frac{\beta_m cov(y, x)}{var(x_O)} \\ &= \frac{\beta_m \beta_x var(x)}{var(x_O)} \\ &= \frac{\beta_m \beta_x var(x)}{\beta_m^2 var(x) + var(\epsilon_m)} \end{aligned}$$

which can be substituted back to give

$$\begin{aligned} cov(g, \hat{y}) &= \frac{\beta_x \beta_g var(g) \beta_m^2 var(x)}{\beta_m^2 var(x) + var(\epsilon_m)} \\ &= D \beta_x \beta_g var(g) \end{aligned}$$

where

$$D = \frac{\beta_m^2 var(x)}{\beta_m^2 var(x) + var(\epsilon_m)}$$

Appendix 2

Steiger test is used to infer if the variant g has a direct influence on x or y when it is known that it associates with both, but the direction of causality between x and y is unknown. Assuming the causal direction is $x \rightarrow y$, two stage MR is formulated using the following regression models:

$$x = \alpha_1 + \beta_1 g + e_1$$

for the first stage and

$$y = \alpha_2 + \beta_2 \hat{x} + e_2$$

where $\hat{x} = \hat{alpha}_1 + \hat{\beta}_1 g$. Writing in scale free terms, $\rho_{g,x}$ denotes the correlation between g and the exposure variable x, and it is expected that $\rho_{g,x} > \rho_{g,y}$ because $\rho_{g,y} = \rho_{g,x}\rho_{x,y}$, where $\rho_{x,y}$ is the causal association between x and y (which is likely to be less than 1). In the presence of measurement error in x and y, however, Steiger test will instead be assessing the inequality $\rho_{g,x_O} > \rho_{g,y_O}$, which can be simplified:

$$\begin{aligned}
\rho_{g,x_O} &> \rho_{g,y_O} \\
\rho_{g,x}\rho_{x,x_O} &> \rho_{g,y}\rho_{y,y_O} \\
\rho_{g,x}\rho_{x,x_O} &> \rho_{g,x}\rho_{x,y}\rho_{y,y_O} \\
\rho_{x,x_O} &> \rho_{x,y}\rho_{y,y_O}
\end{aligned}$$

Tables

Figures

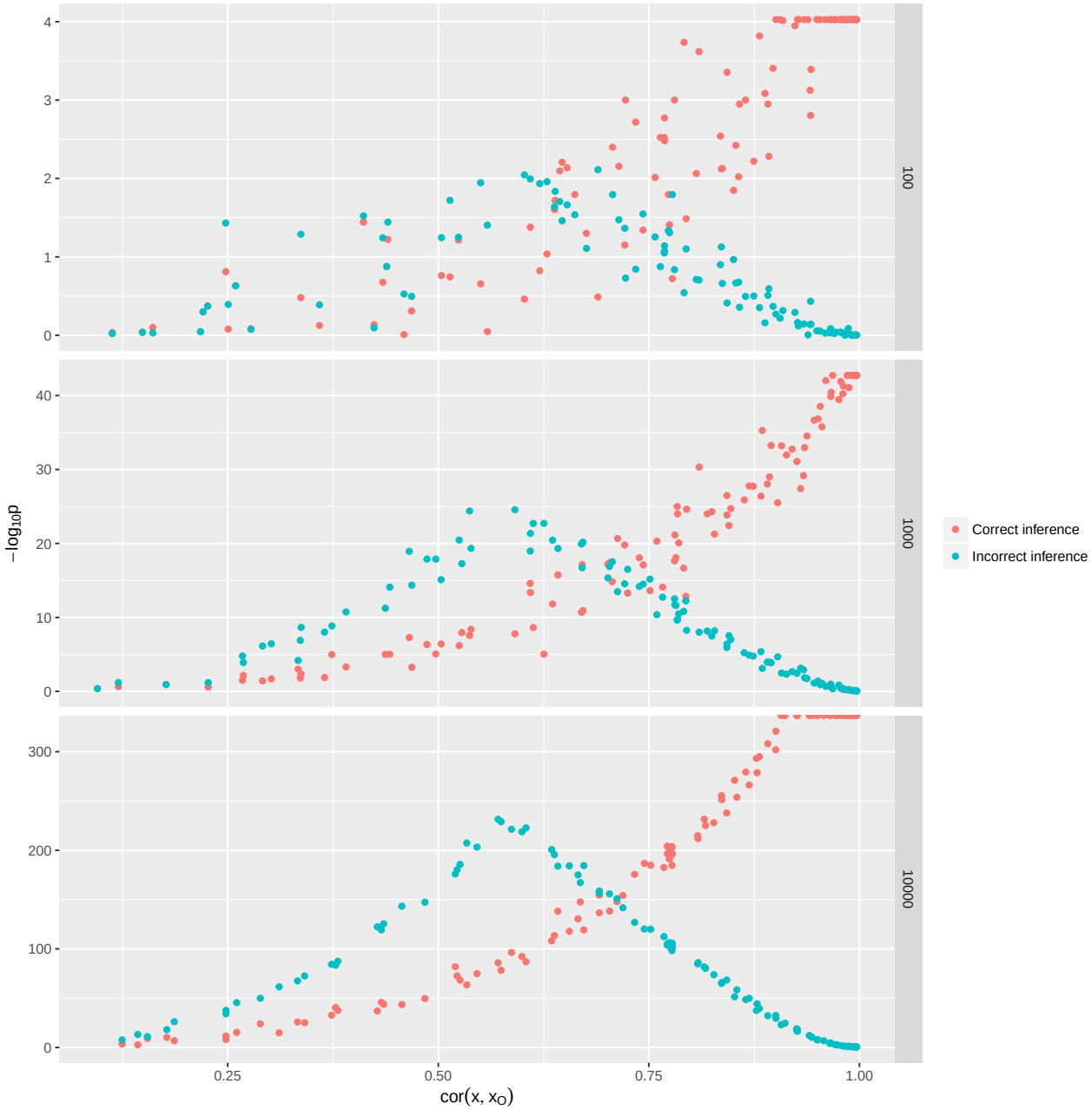

Figure 1: The CIT was performed on simulated variables where the exposure influenced the outcome and the exposure was instrumented by a SNP. The test statistic from CIT when testing if the exposure caused the outcome (the true model) is in red, and the test for the outcome causing the exposure (false model) is in green. Rows of plots represent the sample sizes used for the simulations. As measurement error increases (decreasing values on x-axis) the test statistic for the incorrect model gets stronger and the test statistic for the correct model gets weaker.

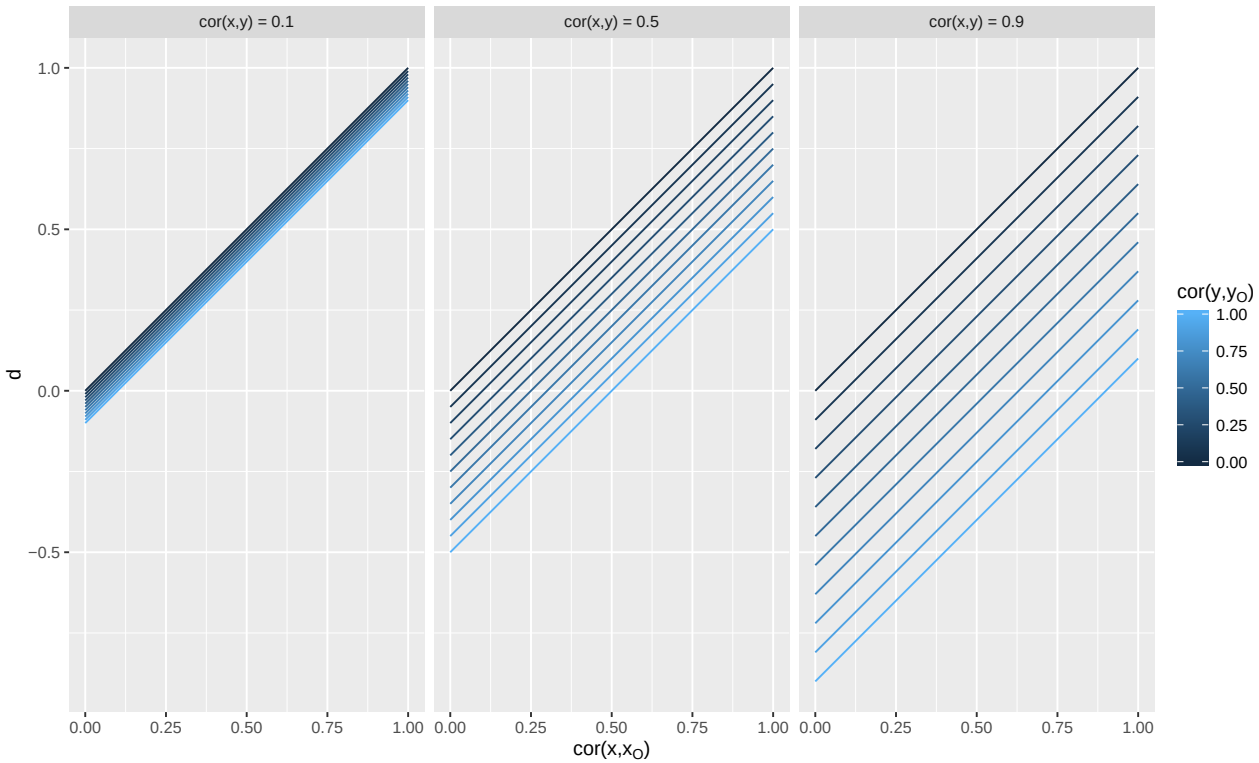

Figure 2: Plots depicting the function $d = cor(x, x_O) - cor(x, y)cor(y, y_O)$.

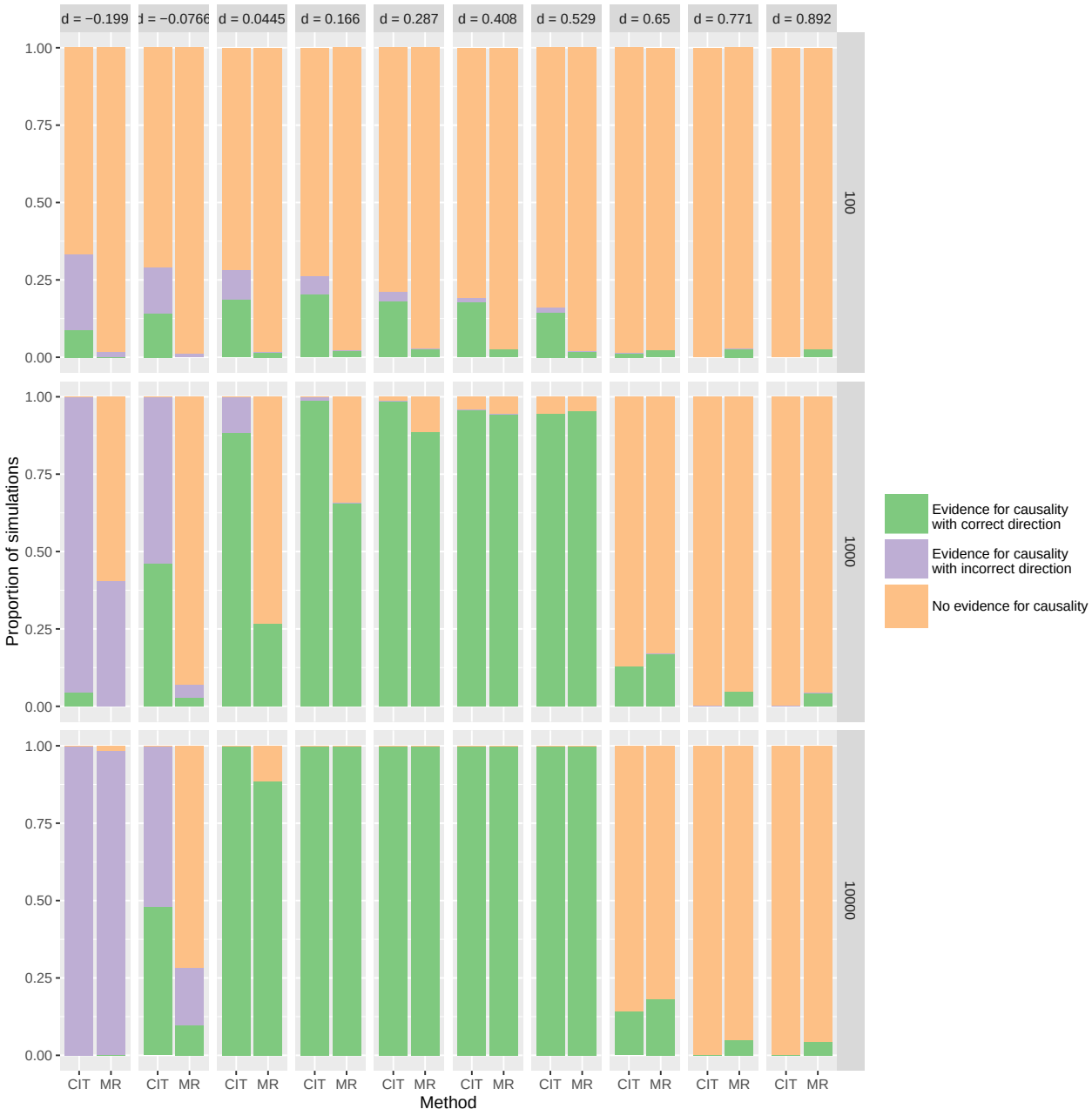

Figure 3: Outcomes were simulated to be causally influenced by exposures, with varying degrees of measurement error applied to both. CIT and MR were used to infer evidence for causality between the exposure and outcome, and to infer the direction of causality. The value of $d = \rho_{x,x_O} - \rho_{x,y}\rho_{y,y_O}$, such that when d is negative we expect the Steiger test to be more likely to be wrong about the direction of causality. Rows of graphs represent the sample size used in the simulations.

Supplementary tables

Supplementary figures

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