Estimating average treatment effect

Iyar Lin

04 December, 2018

Contents

Intro

Assuming we're able to find the DAG underlying the dataset, this script demonstrates average treatment effect (ATE) estimation using the backdoor criteria.

Define model and simulate dataset

Below I plot a graph model with the following variable set:

$$V = \{X, Y, Z, W\}$$

and function set (All disturbances U are distributed standard normal unless stated otherwise):

$$F = \{f_1, f_2, f_3, f_4\}$$

such that

$$X = f_1(Z, U_X) = \begin{cases} \text{a}, & \text{if } Z + U_X \geq 0.61 \\ \text{b}, & \text{if } Z + U_X \geq -0.61 \,\&\, Z + U_X < 0.61 \\ \text{c}, & \text{if } Z + U_X < -0.61 \end{cases}$$

$$Z = f_3(U_Z) = U_Z$$

$$W = f_4(X, U_W) \sim \begin{cases} poiss(1) & \text{if } X = a \\ poiss(2) & \text{if } X = b \\ poiss(3) & \text{if } X = c \end{cases}$$

and

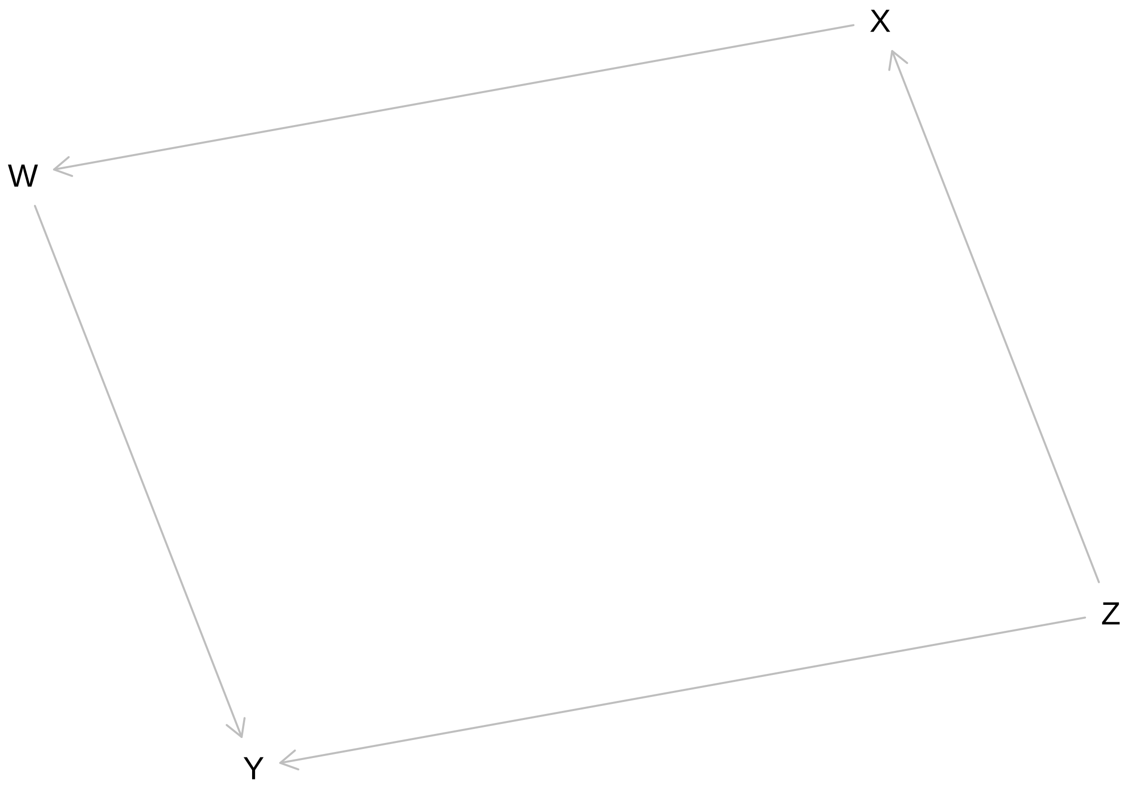
$$Y = f_2(W, Z, U_Y) \sim N(Z + W, 1)$$

So finally we have

$$E(Y|do(X = x)) = \begin{cases} 1, & \text{if } X = a \\ 2, & \text{if } X = b \\ 3, & \text{if } X = c \end{cases}$$

Below is a plot of the resulting DAG:

```r
g <- dagitty("dag {
Y [outcome]
X [exposure]
X -> W
W -> Y
Z -> X
Z -> Y
}")

plot(graphLayout(g))
```



Below I simulate a dataset according to the above toy model.

```r
N <- 1000
Z <- rnorm(N)
X_tag <- Z + rnorm(N)
X <- ifelse(X_tag > qnorm(2/3, 0, sqrt(2)), "a",
            ifelse(X_tag > qnorm(1/3, 0, sqrt(2)), "b", "c"))
```

```
W <- sapply(X, function(x){
  if(x == "a") rpois(1, 1)
  else if(x == "b") rpois(1, 2)
  else rpois(1, 3)
})

Y <- mapply(function(z,w){
  rnorm(1, z + w, 1)
  }, Z, W)

sim_data <- data.frame(X,Y,Z,W)
```

Estimate average treatment effect (ATE)

In Pearl eq 3.5 (p. 57) the post intervention of Y given $do(X = x)$ is given by

$$P(Y = y|do(X = x)) = \sum_z P(Y = y|X = x, Z = z)P(Z = z)$$

Where Z is a variable set satisfying the backdoor criteria (A.K.A "adjustment set").

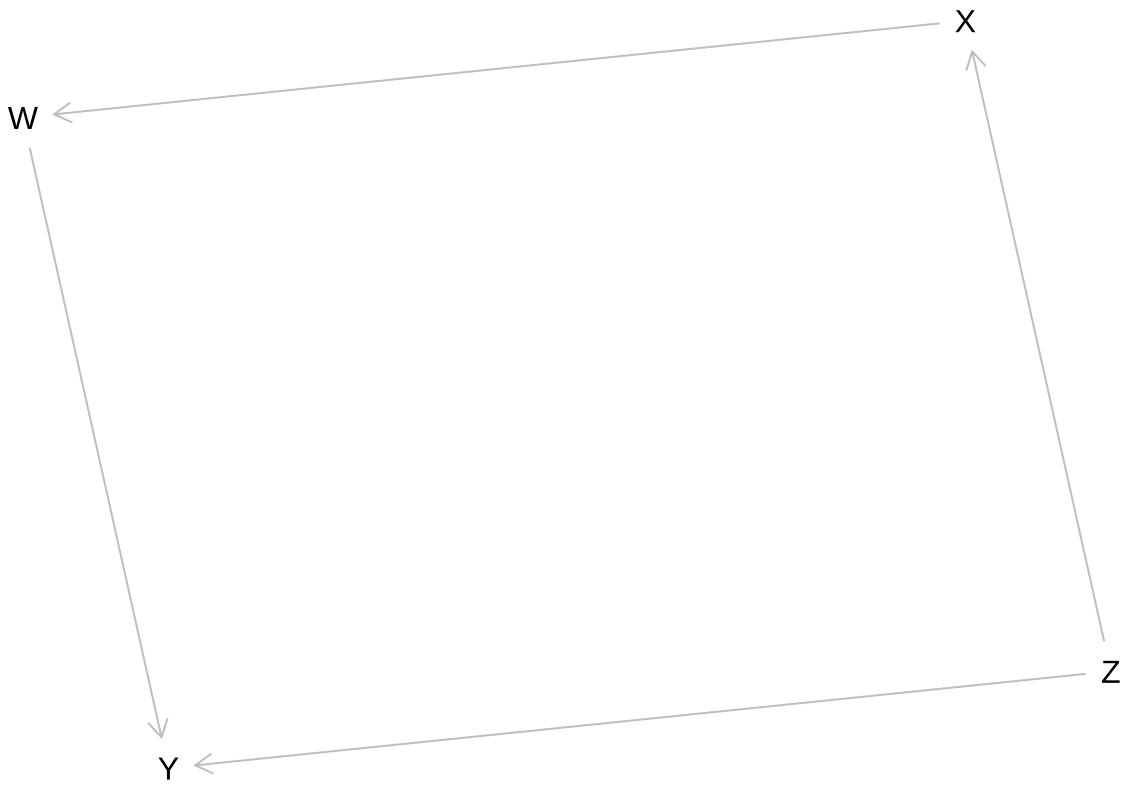
The ATE is given by:

$$\begin{gathered}\mathbb{E}(Y|do(X = x)) = \sum_y \sum_z yP(Y = y|X = x, Z = z)P(Z = z) = \\ \sum_z P(Z = z) \sum_y yP(Y = y|X = x, Z = z) = \sum_z P(Z = z)\mathbb{E}(Y|x, z)\end{gathered} \tag{1}$$

We usually use regular machine learning framworks to estimate $\mathbb{E}(Y|x, z)$. When we predict for the original dataset we have the join probability of Z: $P(Z = z)$ preserved so no need to estimate it. I'll validate that in the results below.

Looking at the graph below:

```
plot(graphLayout(g))
```



we can see that the adjustment set is $Z = \{Z\}$.

We'll use a linear regression to estimate $\mathbb{E}(Y|x, z)$.

Below are the estimated ATE using the correct procedure:

```
model <- lm(Y ~ Z + X, data = sim_data)
Z_prob <- density(x = sim_data$Z)

interventions <- levels(sim_data$X)
ATE <- vector(length = length(interventions))
for(i in 1:length(interventions)){
  intervention_data <- data.frame(X = interventions[i], Z = Z_prob$x)
  ATE[i] <- sum(Z_prob$y*predict(model, intervention_data)/sum(Z_prob$y))
}

pandoc.table(data.frame(intervention = interventions, ATE = ATE))
```

intervention	ATE
a	0.985
b	2.157
c	3.145

Below are the ATE estimates when regressing Y on X:

```
model <- lm(Y ~ X, data = sim_data)
ATE <- vector(length = length(interventions))
for(i in 1:length(interventions)){
  intervention_data <- data.frame(X = interventions[i])
  ATE[i] <- predict(model, intervention_data)
}
pandoc.table(data.frame(intervention = interventions, ATE = ATE))
```

intervention	ATE
a	1.811
b	2.204
c	2.28

We can see that the ordering is preserved but the estimates are all bundeled together.

Below are the ATE estimates when regressing Y on all variables:

```
model <- lm(Y ~ ., data = sim_data)
ATE <- vector(length = length(interventions))
for(i in 1:length(interventions)){
  intervention_data <- sim_data %>%
    mutate(X = interventions[i])
  ATE[i] <- mean(predict(model, intervention_data))
}
pandoc.table(data.frame(intervention = interventions, ATE = ATE))
```

intervention	ATE
a	2.178
b	2.152
c	1.966

We can see here X is estimated to have virtually no effect.

Below are the ATE estimates when using the correct adjustment set but without re-weighting:

```
model <- lm(Y ~ X + Z, data = sim_data)
ATE <- vector(length = length(interventions))
for(i in 1:length(interventions)){
  intervention_data <- sim_data %>%
    mutate(X = interventions[i])
  ATE[i] <- mean(predict(model, intervention_data))
}
pandoc.table(data.frame(intervention = interventions, ATE = ATE))
```

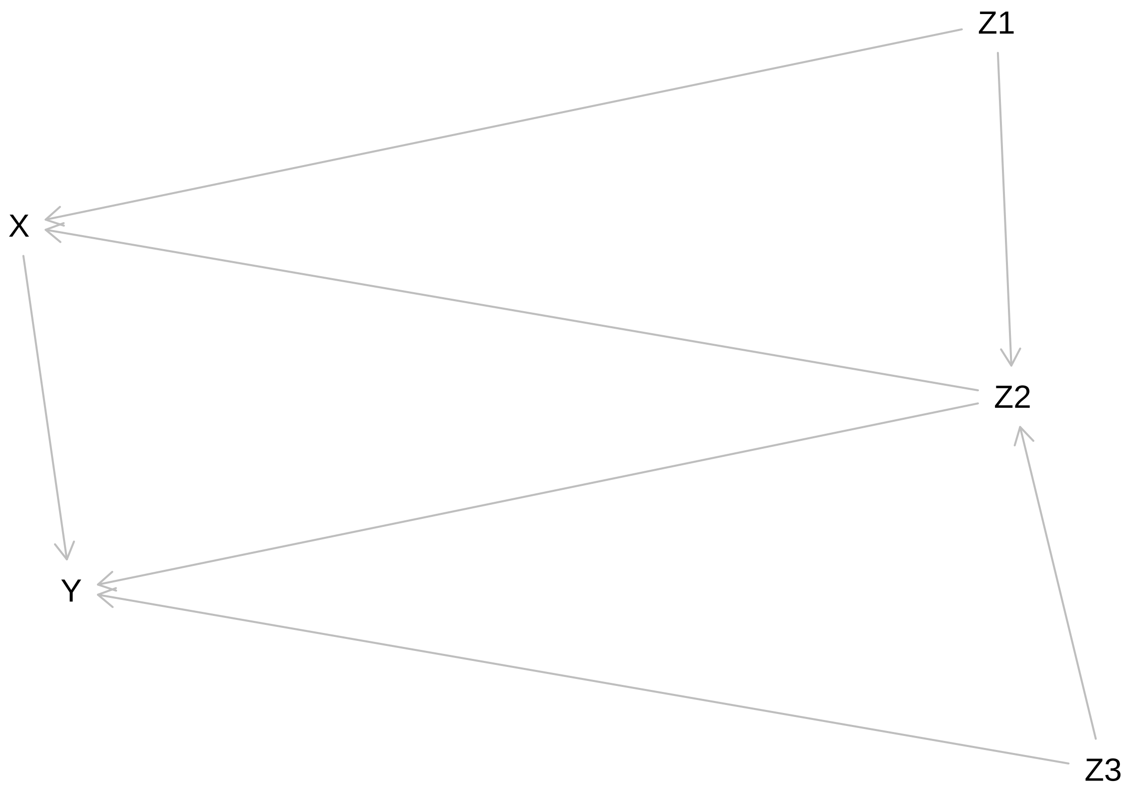
intervention	ATE
a	0.985
b	2.157
c	3.145

Looks like we're getting similar results! So no need to estimate density!

Does the size of the adjustment set follows the same variance-bias trade off as in classic ML?

Let's look at the DAG below:

```r
g <- dagitty("dag {
Y [outcome]
X [exposure]
X -> Y [beta = 0.2]
Z1 -> X [beta = 0.1]
Z1 -> Z2 [beta = -0.1]
Z2 -> X [beta = 0.3]
Z2 -> Y [beta = 0.05]
Z3 -> Z2 [beta = -0.05]
Z3 -> Y [beta = -0.1]
}")

plot(graphLayout(g))
```



If we're interesting in estimating $\mathbb{E}(Y|do(X=x)$ there's several confounding paths that we need to block.

The exact possible adjustment sets are:

```r
M = 1000
print(adjustmentSets(g, type = "all"))
```

```
## { Z1, Z2 }
## { Z2, Z3 }
## { Z1, Z2, Z3 }
```

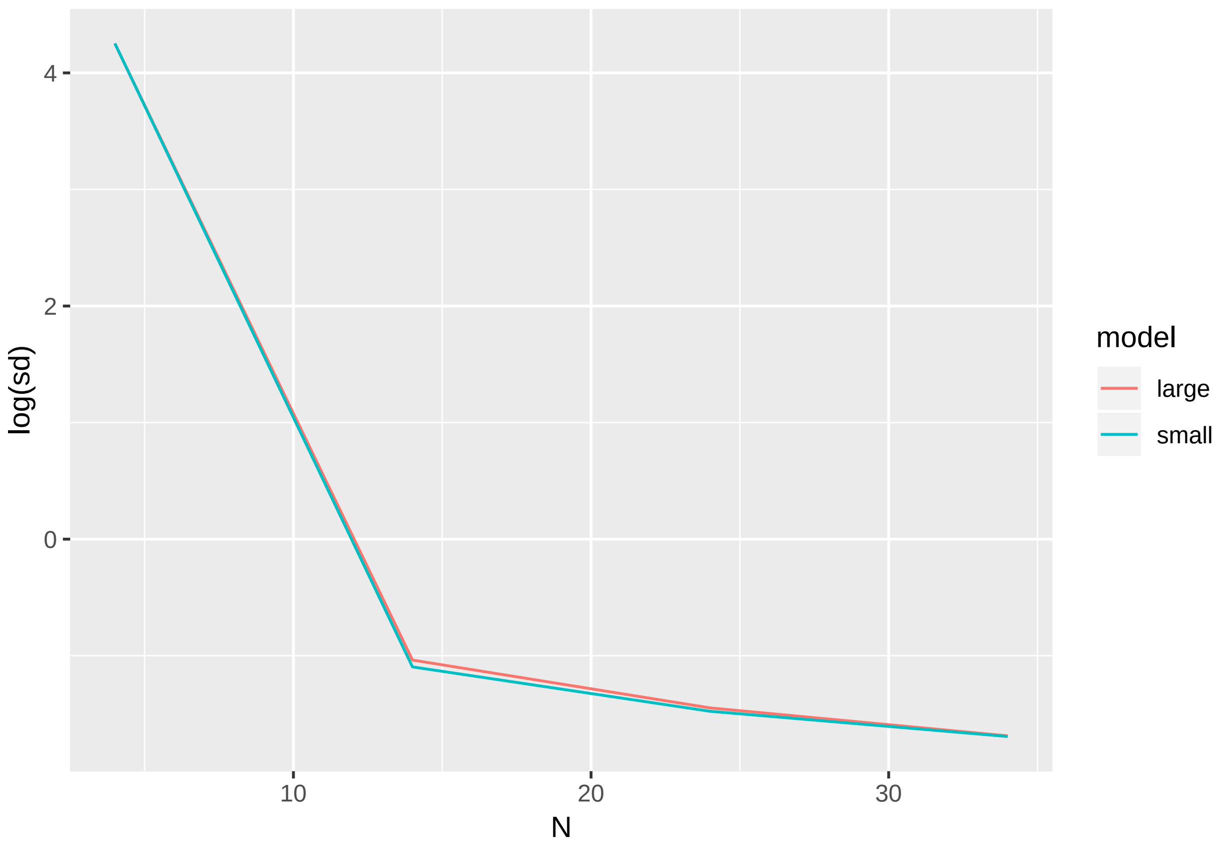
We can see that we can either control for 2 or 3 out of the confounding variables. Assuming we can measure them all, and we know from the graph they are all "relevant" (e.g. not white noise) does it make sense to use all 3 instead of just a subset?

Below I simulate 1000 dataset for a grid of sample size N and compare the standard deviation of the coefficient estimate as well as the R-squered on a hold out test set:

```
N_grid <- seq(4, 40, 10)
model_performance <- data.frame(model = rep(c("small", "large"), length(N_grid)),
                      N = rep(N_grid, each = 2),
                      sd = NA,
                      R_2 = NA)

for(n in N_grid){
  sim_data <- replicate(M, simulateSEM(g, N = n), simplify = F)
  sim_test_data <- replicate(M, simulateSEM(g, N = n), simplify = F)
  sim_small_model <- lapply(sim_data, function(data) lm(Y ~ X + Z1 + Z2, data = data))
  sim_large_model <- lapply(sim_data, function(data) lm(Y ~ X + Z1 + Z2 + Z3, data = data))

  model_performance$sd[model_performance$N == n & model_performance$model == "small"] <- sd(sapply(sim_s
  model_performance$sd[model_performance$N == n & model_performance$model == "large"] <- sd(sapply(sim_l

  model_performance$R_2[model_performance$N == n & model_performance$model == "small"] <- mean(mapply(fu
    sqrt(mean((predict(model, data) - data$Y)^2))
  },
  data = sim_test_data, model = sim_small_model))

  model_performance$R_2[model_performance$N == n & model_performance$model == "large"] <- mean(mapply(fu
    sqrt(mean((predict(model, data) - data$Y)^2))
  },
  data = sim_test_data, model = sim_large_model))

}
```

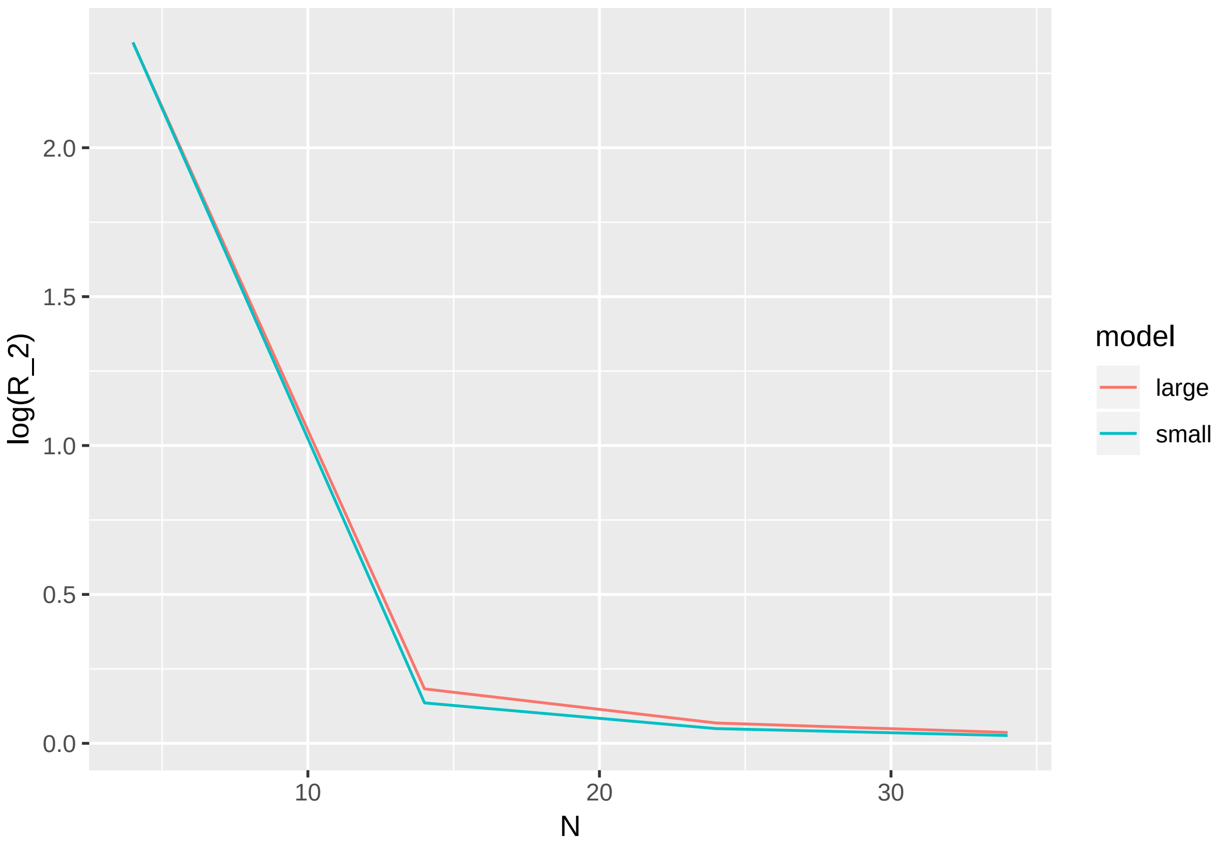
Below are the sd results:

```
model_performance %>% ggplot(aes(N, log(sd), color = model)) + geom_line()
```



Below are the R-squared results:

```
model_performance %>% ggplot(aes(N, log(R_2), color = model)) + geom_line()
```



Oddly enough it looks like if anything, using less variables is better!