Estimating average treatment effect for mixed variable domain graphical models

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Contents

Intro

Most real world cases involve working with mixed domain datasets (i.e continuous, count and categorical) rather than just gaussian continuous. In this script I show how the ATE can be estimated.

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:

```
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.

```
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)
```

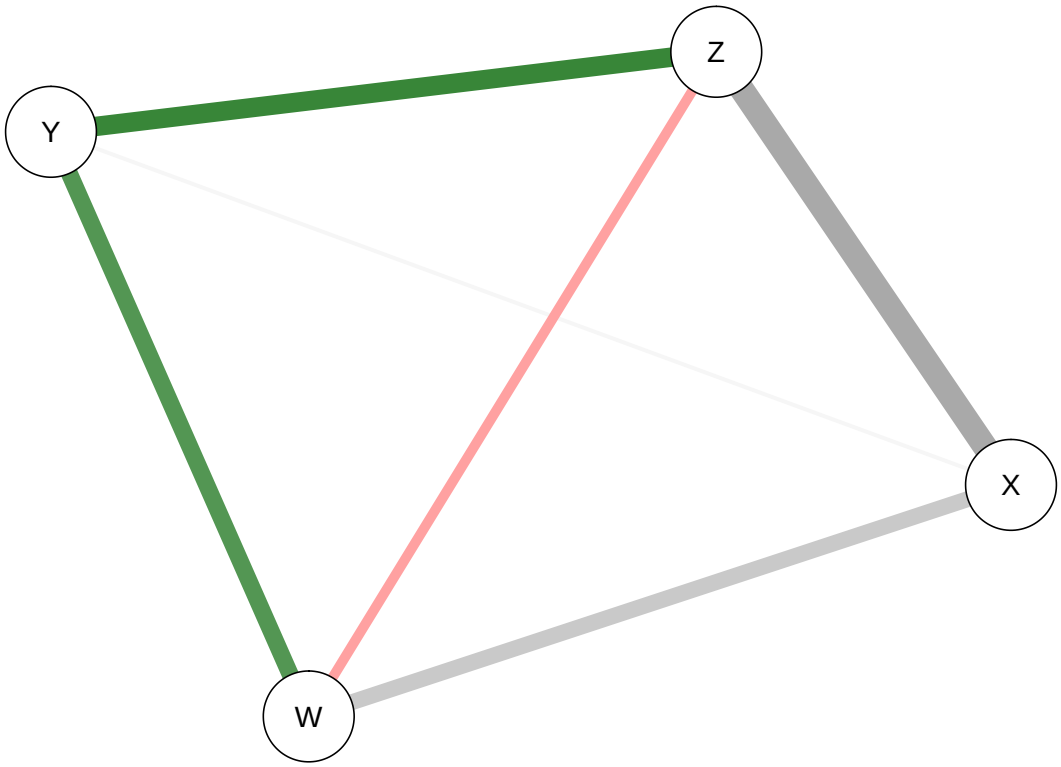
Estimate model DAG

In case domain knowledge is not enough to construct a reliable graph, the "mgm" package enables crude estimation of the model graph

```
sim_data_for_mgm <- sim_data %>%
  mutate(X = as.integer(X))
estimated_dag <- mgm(data = sim_data_for_mgm, type = c("c", "g", "g", "p"), level = c(3, rep(1, 3)), ve
```

```
## Note that the sign of parameter estimates is stored separately; see ?mgm
```

```
FactorGraph(estimated_dag, labels = names(sim_data_for_mgm), PairwiseAsEdge = T)
```



We can see that the result is close, but there is a redundant edge between Z and W. Also, it's un-oriented. More work is done at: https://github.com/benoslab/causalMGM

Estimate average treatment effect (ATE)

Below I assume the correct oriented DAG is used.

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").

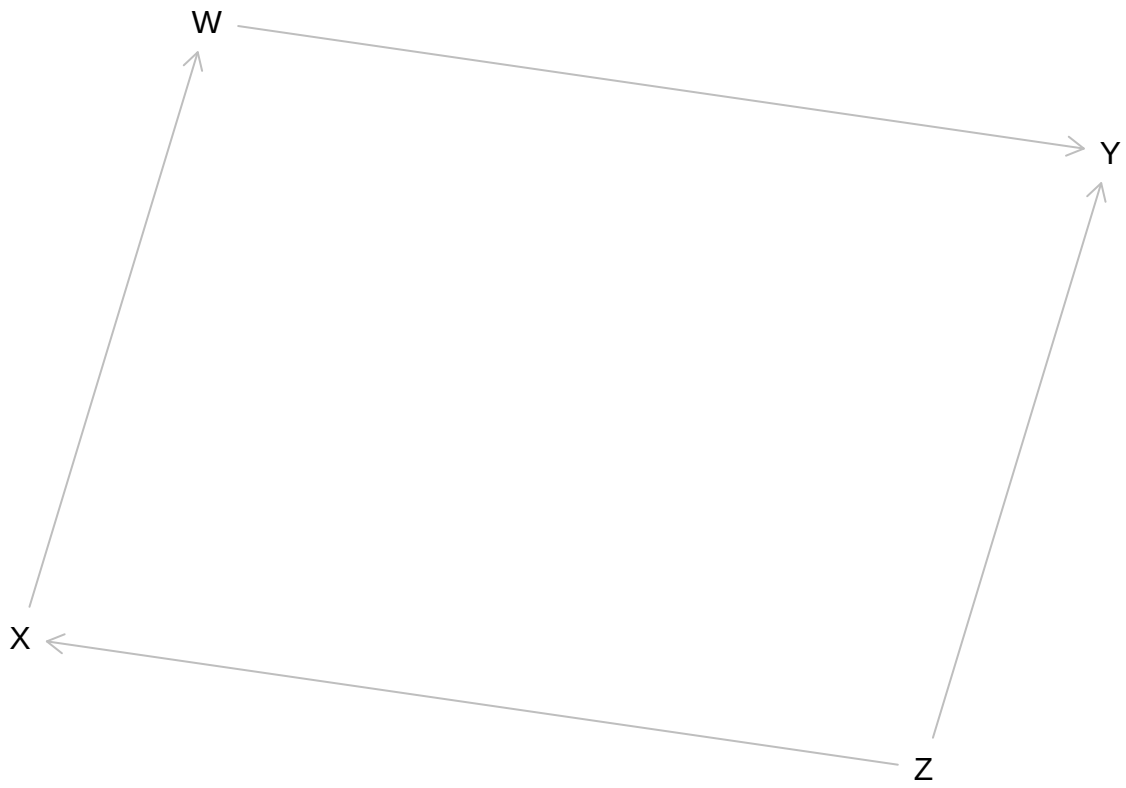
The ATE is given by:

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

We usually use regular machine learning framworks to estimate $\mathbb{E}(Y|x, z)$. When we predict for the original dataset we have the joint 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:

```
print(adjustmentSets(g))
```

```
## { 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

intervention	ATE
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!