Inverse Probability Weighting

From backdoor criterion part, we learned that PA(X) always satisfies backdoor criterion. Hence, we can represent postintervention causal effect as such:

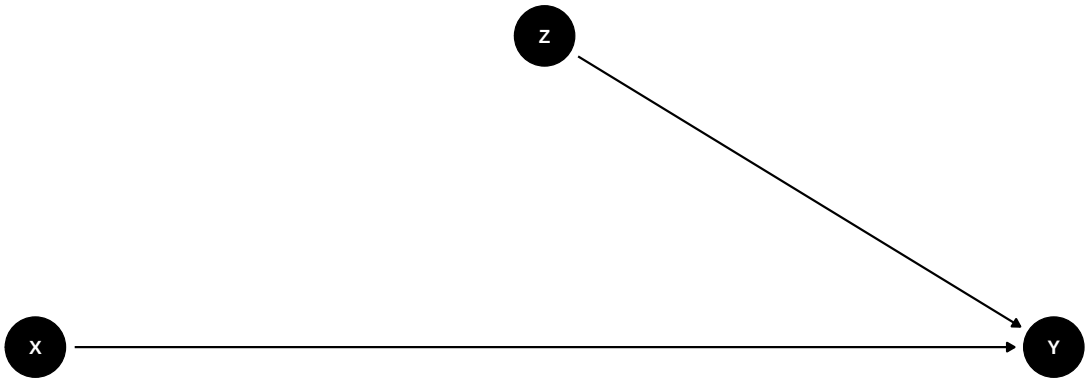
$P(Y = y \mid do(X = x)) = \sum_z P(Y = y \mid X = x, PA = z)P(PA = z)$

Modifying this equation, we can obtain the following:

$P(Y = y \mid do(X = x)) = \sum_z \frac{P(Y=y,X=x,PA=z)}{P(X=x|PA=z)}$

The factor $P(X = x \mid PA = z)$ in the denominator is known as the "propensity score."

Now, assume we have a graphical model with an intervention, do(X=x), on the model.



$P(Y = y \mid do(X = x))$

$= P_m(Y = y \mid X = x)$ (by definition)

$= \sum_z P_m(Y = y \mid X = x, Z = z)P(Z = z \mid X = x)$ (Bayes' rule)

$= \sum_z P_m(Y = y \mid X = x, Z = z)P(Z = z)$ $(X \perp\!\!\!\perp Z)$

$= \sum_z P(Y = y \mid X = x, Z = z)P(Z = z)$ (invariance relations)

$= \sum_z \frac{P(Y=y|X=x,Z=z)P(X=x|Z=z)P(Z=z)}{P(X=x|Z=z)}$

$= \sum_z \frac{P(Y=y,X=x,Z=z)}{P(X=x|Z=z)}$

From this result, we can see that postintervention causal effect can be computed by multiplying the pre-treatment distribution of (X,Y,Z) by a factor $1/P(X = x \mid Z = z)$, propensity score. Namely, each case $(Y = y, X = x, Z = z)$ in the population receives a weight of the inverse of the conditional probability of receiving the treatment level given a set of observed covariates. This is the reason why this method is called "inverse probability weighting."

Marginal structural model

A marginal structural model (MSM) is a model that relates potential outcomes $(Y \mid do(A = a))$ or Y^a to the treatment variable. The potential outcome is the outcome that would be observed if we intervened to set the treatment $A = a$.

Generally in causal inference, the models that describe potential outcomes are referred to as structural to infer relationships beyond associations. Plus, since a goal is to estimate a marginal mean as opposed to a conditional mean through a structural model, we call it a marginal structural model.

A linear regression MSM for continuous outcome: $E[Y^a] = \beta_0 + \beta_1 a$

The interpretation of β_1 when the treatment is binary: the average treatment effect or more specifically the change in Y on average when treated $(A = 1)$.

The reason is straightforward:

$E[Y^1] = \beta_0 + \beta_1$

$E[Y^0] = \beta_0$.

Subtracting two equations gives $E[Y^1] - E[Y^0] = \beta_1$

A logistic regression MSM for binary outcome: $log\left(\frac{P(Y^a=1)}{1-P(Y^a=1)}\right) = \beta_0 + \beta_1 a$

The interpretation of β_1 when the treatment is binary: the log odds ratio of $Y = 1$.

Here is why:

$log\left(\frac{P(Y^1=1)}{1-P(Y^1=1)}\right) = \beta_0 + \beta_1$

$log\left(\frac{P(Y^0=1)}{1-P(Y^0=1)}\right) = \beta_0$

Subtracting two equations gives $log\left(\frac{\frac{P(Y^1=1)}{1-P(Y^1=1)}}{\frac{P(Y^0=1)}{1-P(Y^0=1)}}\right) = \beta_1$

Creating data (1000 individuals) and computing the true log odds ratio (B_1)

```
pre_data <- defData(varname = "L", formula = 0.37,
                dist = "binary")
pre_data <- defData(pre_data, varname = "Y0", formula = "-1.7 + 1.77*L",
                dist = "binary", link = "logit")
pre_data <- defData(pre_data, varname = "Y1", formula = "-0.7 + 1.77*L",
                dist = "binary", link = "logit")
pre_data <- defData(pre_data, varname = "A", formula = "0.27 + 0.37 * L",
                dist = "binary")
pre_data <- defData(pre_data, varname = "Y", formula = "Y0 + A * (Y1 - Y0)",
                dist = "nonrandom")

set.seed(77777)
df <- genData(1000, pre_data)

odds <- function(p) {
    return((p/(1 - p)))
}

log(odds(mean(df$Y1)) / odds(mean(df$Y0)))
```

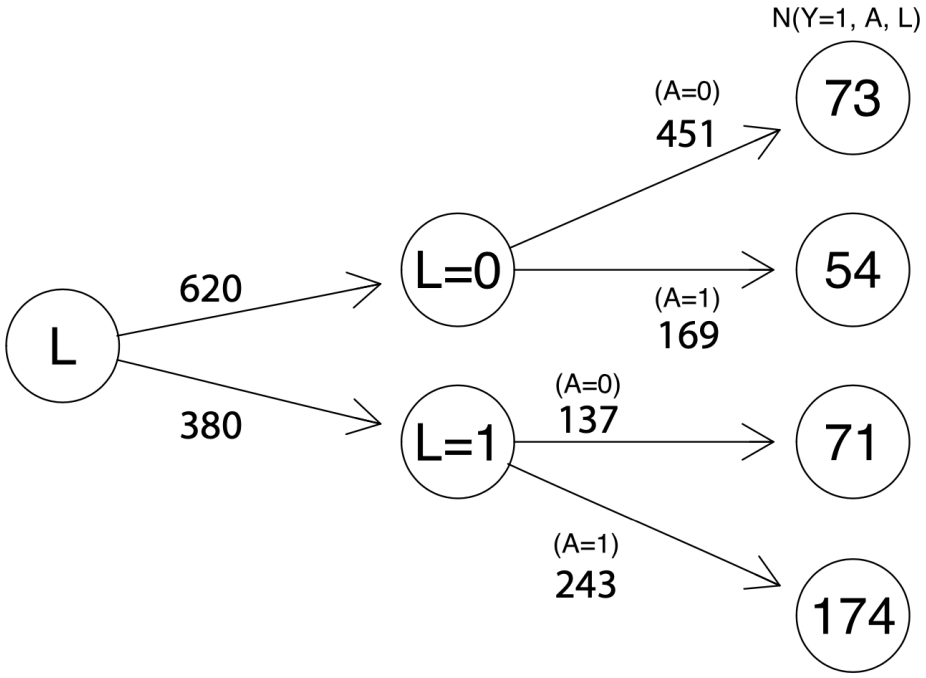
```
## [1] 0.7417183
```

Generating Joint Probability Distribution P(Y, A, L)

```
table <-
  df %>%
  group_by(L,A,Y) %>%
  summarise(percent_population = n()/1000)  %>%
  kbl(
      caption     = "Joint Probability Distribution P(Y,A,L)"
    , col.names   = c("L", "A", "Y", "% of Population")
    , format.args = list(big.mark = ',')
  ) %>%
  # further map to a more professional-looking table
  kable_paper("striped", full_width = F)
```

Table 1: Joint Probability Distribution P(Y,A,L)

L	A	Y	% of Population
0	0	0	0.378
0	0	1	0.073
0	1	0	0.115
0	1	1	0.054
1	0	0	0.066
1	0	1	0.071
1	1	0	0.069
1	1	1	0.174



Computing the marginal causal effect ignoring L before applying IP weights

$P(Y = 1 \mid A = 0) = \frac{(451 \times \frac{73}{451} + 137 \times \frac{71}{137})}{(451+137)} = 0.245$

$P(Y = 1 \mid A = 1) = \frac{(169 \times \frac{54}{169} + 243 \times \frac{174}{243})}{(169+243)} = 0.186 = 0.553$

Computing crude log odds ratio

$LOR_{A=1 \ vs \ A=0} = log\left(\frac{(0.553/0.447)}{(0.245/0.755)}\right) = 1.34$

Comparing the result with coefficient of estimate (β_1) from a logistic model

```
glm(Y ~ A, data = df, family ="binomial") %>% broom::tidy()
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic  p.value
##   <chr>          <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)    -1.13    0.0959    -11.7  7.80e-32
## 2 A               1.34    0.138       9.72 2.48e-22
```

It is to be observed that the crude log odds ratio is the same as the coefficient of estimate. As expected, however, the crude log odds ratio is biased because we did not take into account the confounder L. The true odds ratio is 0.74 whereas the crude estimate is 1.34.

Computing Propensity Score

1. $P(A = 0 \mid L = 0) = \frac{451}{620}$
2. $P(A = 1 \mid L = 0) = \frac{169}{620}$
3. $P(A = 0 \mid L = 1) = \frac{137}{380}$
4. $P(A = 1 \mid L = 1) = \frac{243}{380}$

Let weight $W^A = \frac{1}{P(A|L)}$

$W_1^A = 1.37$

$W_2^A = 3.67$

$W_3^A = 2.77$

$W_4^A = 1.56$

Applying IP Weights to each individual

If we apply IP Weights to each individual, the hypothetical population becomes double the size of the original population and it's called the pseudo-population. This is because every individual gets to receive every level of treatment in the pseudo-population.

$N(Y = 1, A = 0, L = 0) \times W_1^A = 73 \times 1.37 = 100$

$N(Y = 1, A = 1, L = 0) \times W_1^A = 54 \times 3.67 = 198$

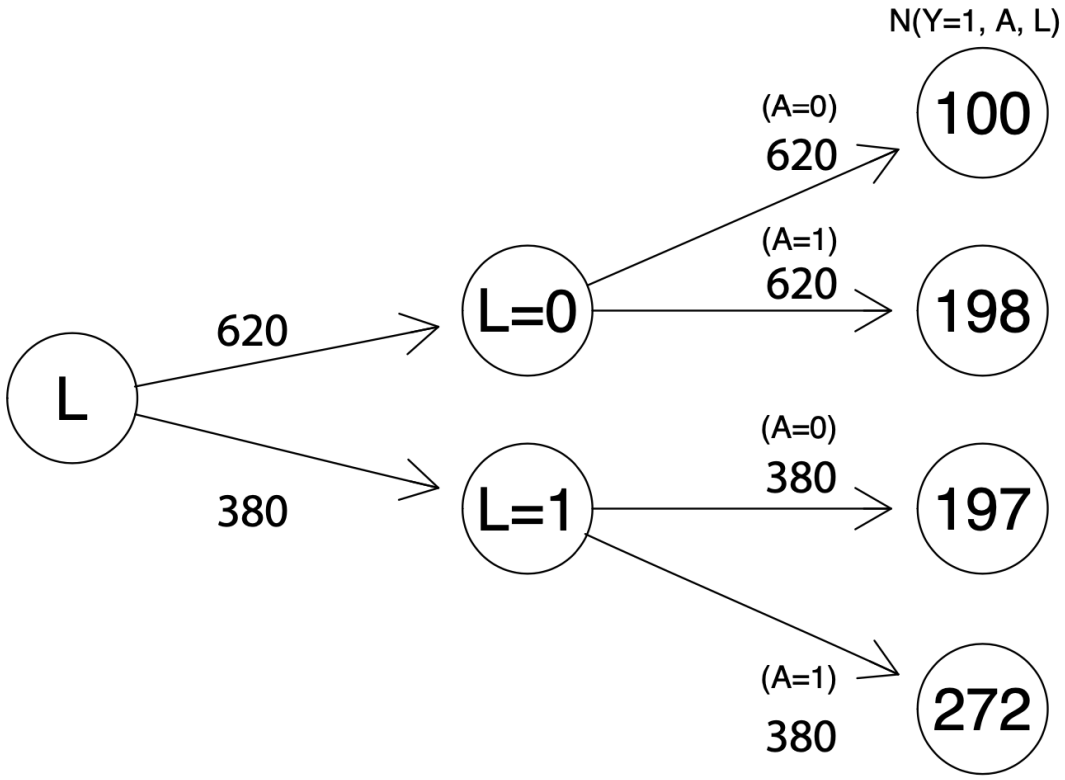
$N(Y = 1, A = 0, L = 1) \times W_1^A = 71 \times 2.77 = 197$

$N(Y = 1, A = 1, L = 1) \times W_1^A = 174 \times 1.56 = 272$

If we divide each $N(Y, A, L)$ by 1000, multiply it by each corresponding W^A, and sum them up, then we obtain the following form of the formula we saw previously:

$\sum_l \frac{P(Y=y,A=a,L=l)}{P(A=a|L=l)} = P(Y = y \mid do(A = a))$

Applying IP weights to each individual, resulting in the pseudo-population



Computing the marginal causal effect ignoring L after applying IP weights

$P(Y = 1 \mid do(A = 0)) = \frac{(620 \times \frac{100}{620} + 357 \times \frac{197}{380})}{(620+380)} = 0.297$

$P(Y = 1 \mid do(A = 1)) = \frac{(620 \times \frac{198}{620} + 380 \times \frac{272}{380})}{(620+380)} = 0.47$

$LOR_{A=1 \ vs \ A=0} = log\left(\frac{(0.47/0.53)}{(0.297/0.703)}\right) = 0.7414$

Comparing the result with coefficient of estimate (β_1) from a logistic model

```
msm.w <- glm(Y ~ A , data = df_with_weight, family = "binomial", weights = w)
Beta <- coef(msm.w)
cbind(Beta)
```

```
##                    Beta
## (Intercept) -0.8602406
## A            0.7409204
```

Through both manual calculation and logistic regression using inverse probability weights, we have been able to compute the log odds ratio(Y=1) very close to the true odds ratio (0.7417) without taking into account L. Important thing to note here is that the IP weighting is only valid when the set L satisfies the backdoor criterion.

Importing NHEFS data

```
nhefs <- read_csv("nhefs.csv")

nhefs_uncensored <-
  nhefs %>%
  mutate(cens = ifelse(is.na(wt82), 1, 0)) %>%
  relocate(cens, wt82) %>%
  filter(!is.na(wt82))
```

Estimating propensitiy score $P(A \mid L's)$ via a logistic model (multiple covariates)

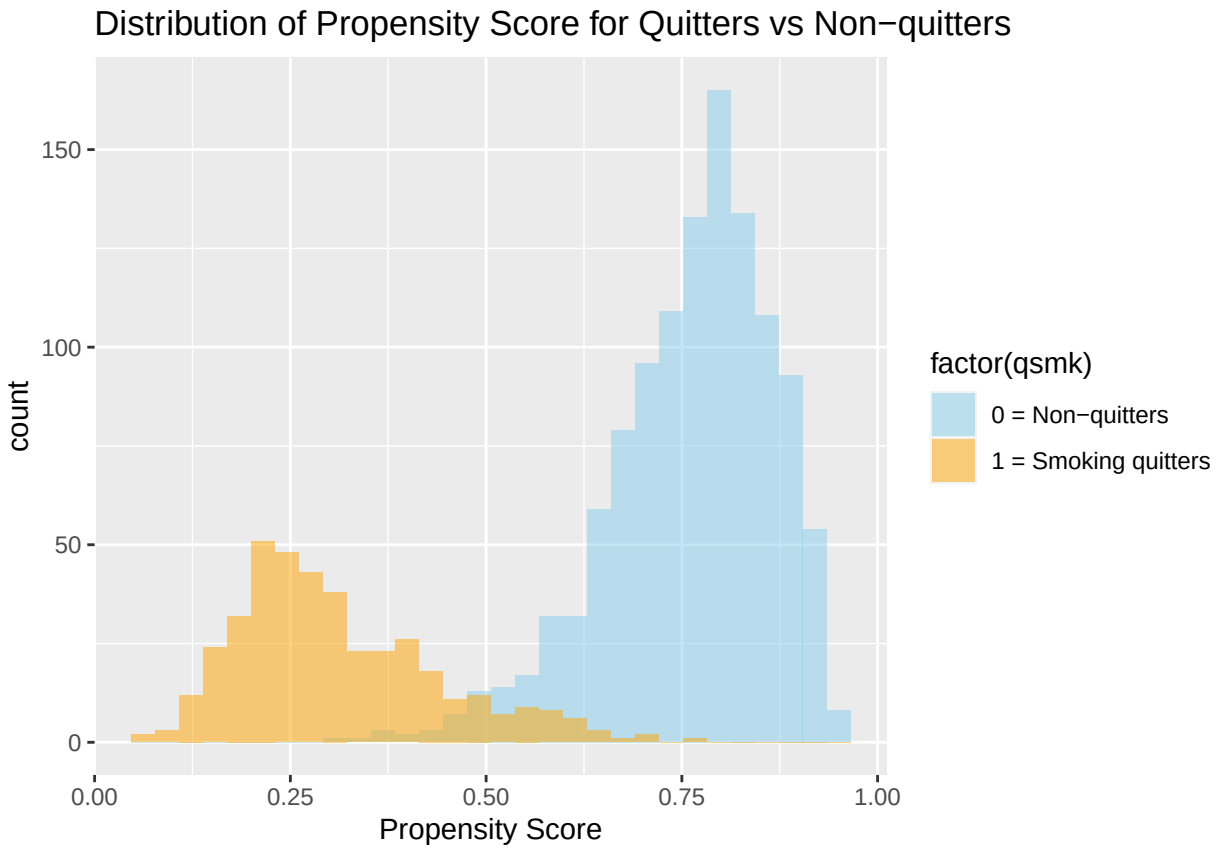
```
propensity_model <- glm(
  qsmk ~ sex + race + age + I(age ^ 2) +
    as.factor(education) + smokeintensity +
    I(smokeintensity ^ 2) + smokeyrs + I(smokeyrs ^ 2) +
    as.factor(exercise) + as.factor(active) + wt71 + I(wt71 ^ 2),
  family = binomial(),
  data = nhefs_uncensored
)
```

Computing propensity score. Note that Pr[A=0|L] = 1-Pr[A=1|L]

```
p.qsmk.obs <-
  ifelse(nhefs_uncensored$qsmk == 0,
         1 - predict(propensity_model, type = "response"),
         predict(propensity_model, type = "response"))

nhefs_uncensored <-
  nhefs_uncensored %>%
  mutate(w = 1/p.qsmk.obs, #inverse propensity score (weight)
         ps = p.qsmk.obs) #propensity score
```

In this data from NHEFS, the continuous outcome Y is weight. The binary treatment A is smoking cessation. Additionally, there are 9 confounders included as covariates. It should be noted that positivity should hold. Namely, we must ensure every combination of $P(A \mid L)$ is greater than zero.



Computing the coefficient of β_1 of the marginal structural model

```
msm.w <- geeglm(
  wt82_71 ~ qsmk,
  data = nhefs_uncensored,
  weights = w,
  id = seqn,
  corstr = "independence"
)

beta <- coef(msm.w)
SE <- coef(summary(msm.w))[, 2]
Lower_CI <- beta - qnorm(0.975) * SE
Upper_CI <- beta + qnorm(0.975) * SE
cbind(beta, Lower_CI, Upper_CI)
```

```
##                beta Lower_CI Upper_CI
## (Intercept) 1.779978 1.339514 2.220442
## qsmk        3.440535 2.410587 4.470484
```

Here, the parameter estimate, β_1, is 3.4. This estimated value indicates that quitting smoking ($A = 1$) increases weight (Y) by 3.4kg on average.

Reference

Pearl, J., Glymour, M., & Jewell, N. P. (2016). Causal inference in statistics a primer. Wiley.

Hernán MA, Robins JM (2020). Causal Inference: What If. Boca Raton: Chapman & Hall/CRC.

Stat 394: Causal inference. Leslie Myint. (n.d.). https://lmyint.github.io/causal_spring_2020/