Instrumental Variable (IV) Simulation Project

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```
library(dplyr)
library(tidyverse)
library(ggplot2)
library(gt)
library(AER)
set.seed(123)
```

1) Scenario

Imagine that we are doing a study in which 1000 adults from a neighborhood community were randomly assigned to one of the two conditions. One group was encouraged via a personalized email from their healthcare providers encouraging them to participate in a nutritional counseling program designed to help with weight management. People in the other were also allowed to participate but received no special encouragement. To be more specific, people who did not received the encouragement email would have to discover the existence of the nutritional counseling program by themselves. Whether or not a student was sent an encouragement email was determined randomly. Each adult has a 0.5 probability of being encouraged.

The outcome variable y denoted the change in BMI. y below 0 represents a decrease in BMI indicates successful weight management, whereas y equal to or greater than 0 indicates less successful or unsuccessful weight management.

2) IV Assumptions

- Ignorability of the instrument: The assignment to the treatment (i.e., receiving the encouraging email) is random.
- Non-zero correlation between instrument and treatment.
- Monotonicity: no defiers. D(1) >= D(0)
- Exclusion Restriction: any effect of Z on Y must be via an effect of Z on D. For always takers and never takers, the values need to be the same or the distribution of them should be the same.
- SUTVA: potential outcomes for each person i are unrelated to the treatment status of other individuals

3) Data Generating Process (DGP)

- We generate data from a sample of 1000 individuals (sample size N = 1000).
- Probability of encouragement (z) is .5 for all individuals (z is instrument)
- Assume that, on average, 30% of individuals in our sample are compliers.
- Assume that, on average, 60% are never takers.

- Assume that, on average, 10% are always takers.
- Status is a variable representing compliance status. status has 3 possible values: complier, always taker, or never taker.
- The exclusion restriction is satisfied.
- The average effect of z on y for the compliers is -1.5 (a decrese in BMI)
- The average y(z=0)=y(0) for never takers is 0 (no change in BMI)
- The average y(z=0)=y(0) for compliers is -1 (a decrease in BMI without encouragement)
- The average y(z=0)=y(0) for always takers is -2.2 (a decrease in BMI without the need for encouragement)
- The residual standard deviation is 0.5 for everyone in the sample (generated independently for each potential outcome).

```
# Thoughts on setting the BMI change
height_in_meters = 1.7
bmi_change = 0.5
kg_to_pounds = 2.20462

weight_change_kg = bmi_change * (height_in_meters ** 2)

# Converting weight to pounds to see whether the number is plausible
# for the situation of reducing weight over 6 months.
weight_change_pounds = weight_change_kg * kg_to_pounds
weight_change_pounds
```

```
## [1] 3.185676
```

We simulate data for three worlds:

(1). World A - all assumptions are satisfied

Formal model for WorldA:

$$
\begin{aligned}
D_i &= \gamma_0 + \gamma_1 Z_i + v_i \\
Y_i &= \beta_0 + \beta_1 D_i + \epsilon_i, \quad \text{where } v_i \text{ and } \epsilon_i \text{ are error terms.}
\end{aligned}
$$

Generating data for WorldA

```
#Effect of complier: E[Y(1) - Y(0)] = -1.5
#The average Y(Z=0)=Y(0) for compliers is -1
#Therefore, E[y(1)] = E(y(0)) + (-1) = -2.5
#The average Y(Z=0)=Y(0) for never takers is 0
#Therefore, E(y(1)) = E(y(0)) = 0
#The average Y(Z=0)=Y(0) for always takers is -2.2
#Therefore, E(y(1)) = E(y(0)) = -2.2
#The residual standard deviation is 0.5 for everyone in the sample (generated #independently
dgpA <- function(seed = 2){
      set.seed(seed)
      n <- 1000
      # create a vector of compliance status (30% complier , 10% always taker, 60% never taker)
```

```
      C <- sample(x = c('complier', 'always taker', 'never taker'),
                  size = n, replace = TRUE, p = c(.3, .1, .6))
      z <- rbinom(n, 1, 0.5)

      # simulate D0 (treatment|instrument = 0) and D1(treatment|instrument = 1)
      # start with empty vectors
      d0 <- vector()
      d1 <- vector()

      # fill in compliers
      d0[C== 'complier'] <- 0
      d1[C== 'complier'] <- 1

      # fill in always takers
      d0[C== 'always taker'] <- 1
      d1[C== 'always taker'] <- 1

      # fill in never takers
      d0[C== 'never taker'] <- 0
      d1[C== 'never taker'] <- 0

      # now that we have D0 and D1 for everyone realize D
      d <- ifelse(z == 1, d1, d0)

      # simulate y0 (outcome|treatment= 0) and Y1(outcome|treatment= 1)
      # start with empty vectors
      y0 <- vector()
      y1 <- vector()

      # fill in compliers
      y0[C== 'complier'] <- -1 + rnorm(n, 0, 0.5)
      y1[C== 'complier'] <- -2.5 + rnorm(n, 0, 0.5)

      # fill in always takers
      y0[C== 'always taker'] <- -2.2 + rnorm(n, 0, 0.5)
      y1[C== 'always taker'] <- -2.2 + rnorm(n, 0, 0.5)

      # fill in never takers
      y0[C== 'never taker'] <- 0 + rnorm(n, 0, 0.5)
      y1[C== 'never taker'] <- 0 + rnorm(n, 0, 0.5)

      # add error terms
      residuals <- rnorm(n, mean = 0, sd = 0.5)
      y0 <- y0 + residuals
      y1 <- y1 + residuals

      # now that we have y0 and Y1 for everyone realize Y
      y <- ifelse(d == 1, y1, y0)
      return(tibble(z = z, d = d, y = y))
}

worldA <- dgpA() # observed data
```

(2). World B - exclusion assumption violated

Formal model for WorldB (Exclusion restriction violated)

$$D_i = \gamma_0 + \gamma_1 Z_i + v_i$$
$$Y_i = \beta_0 + \beta_1 D_i + \theta Z_i + \epsilon_i$$

The inclusion of θZ_i denotes a direct effect of the instrument variable Z on Y.

```
dgpB <- function(seed = 2){
      set.seed(seed)
      n <- 1000
      theta <- -0.5
      C <- sample(x = c('complier', 'always taker', 'never taker'),
                  size = n, replace = TRUE, prob = c(0.3, 0.1, 0.6))

      z <- rbinom(n, 1, 0.5)

      d0 <- vector()
      d1 <- vector()

      d0[C== 'complier'] <- 0
      d1[C== 'complier'] <- 1

      d0[C== 'always taker'] <- 1
      d1[C== 'always taker'] <- 1

      d0[C== 'never taker'] <- 0
      d1[C== 'never taker'] <- 0

      # Realized treatment based on z
      d <- ifelse(z == 1, d1, d0)

      y0 <- vector()
      y1 <- vector()

      y0[C== 'complier'] <- -1 + rnorm(n, 0, 0.5)
      y1[C== 'complier'] <- -2.5 + rnorm(n, 0, 0.5)

      y0[C== 'always taker'] <- -2.2 + rnorm(n, 0, 0.5)
      y1[C== 'always taker'] <- -2.2 + rnorm(n, 0, 0.5)

      y0[C== 'never taker'] <- 0 + rnorm(n, 0, 0.5)
      y1[C== 'never taker'] <- 0 + rnorm(n, 0, 0.5)

      # Add error terms
      residuals <- rnorm(n, mean = 0, sd = 0.5)
      y0 <- y0 + residuals
      y1 <- y1 + residuals
```

```
      # Add Direct Effect of Z to Y
      y0 <- y0 + theta * z
      y1 <- y1 + theta * z

      # Direct effect of z on y
      y <- ifelse(d == 1, y1, y0)
      return(tibble(z = z, d = d, y = y))
  }

worldB <- dgpB()
```

(3). World C - Non-zero correlation between instrument and treatment assumption violated

Formal model for WorldC

$$D_i = \gamma_0 + v_i$$
$$Y_i = \beta_0 + \beta_1 D_i + \epsilon_i$$

```
dgpC <- function(seed = 2){
      set.seed(seed)
      n <- 1000

      C <- sample(x = c('complier', 'always taker', 'never taker'),
                  size = n, replace = TRUE, prob = c(0.3, 0.1, 0.6))

      z <- rbinom(n, 1, 0.5)
      d <- rbinom(n, 1, 0.5)

      y0 <- vector()
      y1 <- vector()

      y0[C== 'complier'] <- -1 + rnorm(n, 0, 0.5)
      y1[C== 'complier'] <- -2.5 + rnorm(n, 0, 0.5)

      y0[C== 'always taker'] <- -2.2 + rnorm(n, 0, 0.5)
      y1[C== 'always taker'] <- -2.2 + rnorm(n, 0, 0.5)

      y0[C== 'never taker'] <- 0 + rnorm(n, 0, 0.5)
      y1[C== 'never taker'] <- 0 + rnorm(n, 0, 0.5)

      y <- ifelse(d == 1, y1, y0)

      return(tibble(z = z, d = d, y = y))
}

worldC <- dgpC()
```

4) Causal estimate and interpretation

** CACE for worldA **

```
# CACE estimated using as-treated approach for world A
as_treated_A <- lm(y ~ d, data = worldA)
summary(as_treated_A)
```

```
##
## Call:
## lm(formula = y ~ d, data = worldA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.55893 -0.48962  0.02318  0.51726  2.28343
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.17641    0.02728  -6.467 1.57e-10 ***
## d           -2.11185    0.05489 -38.474  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7486 on 998 degrees of freedom
## Multiple R-squared:  0.5973, Adjusted R-squared:  0.5969
## F-statistic:  1480 on 1 and 998 DF,  p-value: < 2.2e-16
```

```
as_treated_effectA <- summary(as_treated_A)$coef[2, 1:2]
as_treated_effectA <- c(Estimate = round(summary(as_treated_A)$coef[2, 1], 2),
            Std_Error = round(summary(as_treated_A)$coef[2, 2], 2),
            t_value = round(summary(as_treated_A)$coef[2, 3], 2),
            Pr_t = round(summary(as_treated_A)$coef[2, 4], 2))
as_treated_effectA
```

```
##  Estimate Std_Error   t_value      Pr_t
##     -2.11      0.05    -38.47      0.00
```

```
# CACE estimated using tsls approach for world A
fitA <- ivreg(y ~ d|z, data = worldA)
summaryA <- summary(fitA)
summaryA
```

```
##
## Call:
## ivreg(formula = y ~ d | z, data = worldA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.36797 -0.55494  0.05221  0.56157  2.47439
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)  -0.3674     0.0503  -7.304 5.72e-13 ***
## d            -1.3387     0.1745  -7.671 4.06e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8196 on 998 degrees of freedom
## Multiple R-Squared: 0.5172,  Adjusted R-squared: 0.5168
## Wald test: 58.84 on 1 and 998 DF,  p-value: 4.059e-14
```

```
CACE_A <- c(Estimate = round(summaryA$coef[2, 1], 2),
            Std_Error = round(summaryA$coef[2, 2], 2),
            t_value = round(summaryA$coef[2, 3], 2),
            Pr_t = round(summaryA$coef[2, 4], 2))
CACE_A
```

```
##  Estimate Std_Error   t_value      Pr_t
##     -1.34      0.17     -7.67      0.00
```

Interpretation:

In world A, where all assumptions are satisfied,the CACE estimate is a valid representation of the causal effect of participating in the nutritional counseling program on BMI change.

The CACE estimated for World A using the as-treated analysis is statistically significant, indicated by a value of -2.11 and a standard error of 0.05. It suggests that th effect of participating the nutritional counseling program (versus not participating it) for those who will actually take it when encouraged and won't if not encouraged (compliers) is a a reduction of 2.11 units in BMI.

The CACE estimated for World A using the tsls approach is also statistically significant, indicated by a value of -1.34 and a standard error of 0.17. It implies that th effect of participating the nutritional counseling program (versus not participating it) for those who will actually take it when encouraged and won't if not encouraged (compliers) is a a reduction of 1.34 units in BMI.

** CACE for worldB **

```
# CACE estimated using as-treated approach for world B
as_treated_B <- lm(y ~ d, data = worldB)
summary(as_treated_B)
```

```
##
## Call:
## lm(formula = y ~ d, data = worldB)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.47620 -0.49583 -0.01591  0.53228  2.48463
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.37761    0.02722  -13.87   <2e-16 ***
## d           -2.31147    0.05478  -42.20   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.747 on 998 degrees of freedom
```

```
## Multiple R-squared:  0.6408, Adjusted R-squared:  0.6405
## F-statistic:  1781 on 1 and 998 DF,  p-value: < 2.2e-16
```

```
as_treated_effectB <- summary(as_treated_B)$coef[2, 1:2]
as_treated_effectB <- c(Estimate = round(summary(as_treated_B)$coef[2, 1], 2),
            Std_Error = round(summary(as_treated_B)$coef[2, 2], 2),
            t_value = round(summary(as_treated_B)$coef[2, 3], 2),
            Pr_t = round(summary(as_treated_B)$coef[2, 4], 2))
as_treated_effectB
```

```
##  Estimate Std_Error   t_value      Pr_t
##     -2.31      0.05    -42.20      0.00
```

```
# CACE estimated using tsls approach for world B
fitB <- ivreg(y ~ d|z, data = worldB)
summaryB <- summary(fitB)
summaryB
```

```
##
## Call:
## ivreg(formula = y ~ d | z, data = worldB)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.65174 -0.53161 -0.01222  0.52726  2.68549
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.20207    0.04956  -4.077 4.92e-05 ***
## d           -3.02216    0.17197 -17.574  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8076 on 998 degrees of freedom
## Multiple R-Squared: 0.5803,  Adjusted R-squared: 0.5798
## Wald test: 308.9 on 1 and 998 DF,  p-value: < 2.2e-16
```

```
CACE_B <- c(Estimate = round(summaryB$coef[2, 1], 2),
            Std_Error = round(summaryB$coef[2, 2], 2),
            t_value = round(summaryB$coef[2, 3], 2),
            Pr_t = round(summaryB$coef[2, 4], 2))
CACE_B
```

```
##  Estimate Std_Error   t_value      Pr_t
##     -3.02      0.17    -17.57      0.00
```

Interpretation:

The CACE estimated using the as-treated analysis for World B is statistically significant, indicated by a value of -2.31 and a standard error of 0.05. The CACE estimate using the tsls approach for World B is also statistically significant, indicated by a value of -3.02 and a standard error of 0.17. In World B, the exclusion restriction is violated. Therefore, the CACE estimated through the as-treated approach does not

exclusively represent the causal effect of the treatment but may include the direct effect of the instrument on the outcome.

** CACE for worldC **

```
# CACE estimated using as-treated approach for world C
as_treated_C <- lm(y ~ d, data = worldC)
summary(as_treated_C)
```

```
##
## Call:
## lm(formula = y ~ d, data = worldC)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.8361 -0.9805  0.2837  0.8849  2.5038
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.54850    0.05084 -10.788  < 2e-16 ***
## d           -0.39211    0.07051  -5.561 3.44e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.114 on 998 degrees of freedom
## Multiple R-squared:  0.03006,    Adjusted R-squared:  0.02909
## F-statistic: 30.93 on 1 and 998 DF,  p-value: 3.439e-08
```

```
as_treated_effectC <- summary(as_treated_C)$coef[2, 1:2]
as_treated_effectC <- c(Estimate = round(summary(as_treated_C)$coef[2, 1], 2),
            Std_Error = round(summary(as_treated_C)$coef[2, 2], 2),
            t_value = round(summary(as_treated_C)$coef[2, 3], 2),
            Pr_t = round(summary(as_treated_C)$coef[2, 4], 2))
as_treated_effectC
```

```
##  Estimate Std_Error   t_value      Pr_t
##     -0.39      0.07     -5.56      0.00
```

```
# CACE estimated using tsls approach for world C
fitC <- ivreg(y ~ d|z, data = worldC)
summaryC <- summary(fitC)
summaryC
```

```
##
## Call:
## ivreg(formula = y ~ d | z, data = worldC)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.9416 -0.9867  0.3300  0.8673  2.3479
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept) -0.71737    0.97696  -0.734    0.463
## d           -0.06736    1.87753  -0.036    0.971
##
## Residual standard error: 1.126 on 998 degrees of freedom
## Multiple R-Squared: 0.00944, Adjusted R-squared: 0.008447
## Wald test: 0.001287 on 1 and 998 DF,  p-value: 0.9714
```

```
CACE_C <- c(Estimate = round(summaryC$coef[2, 1], 2),
            Std_Error = round(summaryC$coef[2, 2], 2),
            t_value = round(summaryC$coef[2, 3], 2),
            Pr_t = round(summaryC$coef[2, 4], 2))
CACE_C
```

```
##  Estimate Std_Error   t_value      Pr_t
##     -0.07      1.88     -0.04      0.97
```

Interpretation:

The CACE estimated using the as-treated analysis for World C is statistically significant, as indicated by a value of -0.39 with a large standard error of 0.07. The CACE estimated using tsls for World C is not statistically significant, as indicated by a value of -0.07 with a large standard error of 1.88. In World C, the assumption of non-zero correlation between the instrument and the treatment was designed to be violated. This violation means that receiving the encouragement email did not effectively influence people's decision on whether to participate the nutritional counseling program or not. Therefore, even though we have a numerical estimate obtained, it does not carry any causal interpretation. The CACE estimate in World C does not provide any reliable insights into the causal impact of the nutritional counseling program on BMI change.

```
results <- data.frame(
  World = c("A", "B", "C", "A", "B", "C"),
  Method = c("TSLS", "TSLS", "TSLS", "As-Treated", "As-Treated", "As-Treated"),
  Estimate = c(CACE_A["Estimate"], CACE_B["Estimate"], CACE_C["Estimate"],
               as_treated_effectA["Estimate"], as_treated_effectB["Estimate"],
               as_treated_effectC["Estimate"]),
  Std_Error = c(CACE_A["Std_Error"], CACE_B["Std_Error"], CACE_C["Std_Error"],
                as_treated_effectA["Std_Error"], as_treated_effectB["Std_Error"],
                as_treated_effectC["Std_Error"]),
  t_value = c(CACE_A["t_value"], CACE_B["t_value"],
              CACE_C["t_value"],as_treated_effectA["Std_Error"],
              as_treated_effectB["Std_Error"], as_treated_effectC["Std_Error"]),
  Pr_t = c(CACE_A["Pr_t"], CACE_B["Pr_t"], CACE_C["Pr_t"],
           as_treated_effectA["Pr_t"], as_treated_effectB["Pr_t"],
           as_treated_effectC["Pr_t"])
)
knitr::kable(results, caption = "CACE Estimates and Statistics for Worlds A, B, and C")
```

Table 1: CACE Estimates and Statistics for Worlds A, B, and C

World	Method	Estimate	Std_Error	t_value	Pr_t
A	TSLS	-1.34	0.17	-7.67	0.00
B	TSLS	-3.02	0.17	-17.57	0.00
C	TSLS	-0.07	1.88	-0.04	0.97

World	Method	Estimate	Std_Error	t_value	Pr_t
A	As-Treated	-2.11	0.05	0.05	0.00
B	As-Treated	-2.31	0.05	0.05	0.00
C	As-Treated	-0.39	0.07	0.07	0.00

5) Evaluating Bias

In summary, biases are observed in both methods even using sampling distribution with 10,000 iterations. Notably, the tsls method's CACE estimate for World A is the most accurate, exhibiting minimal bias and closely aligning with the true average effect. This accuracy can be attributed to World A's adherence to the IV assumptions. The the biases in both Worlds B and C suggest that violating key IV assumptions can lead to substantial biases.

By comparing the result, we can clearly see that the tsls outperformed the as-treated approach. The tsls framework uses instruments that are correlated with the treatment and only correlated with the outcome through the treatment, not through random assignment. This helps to isolate the variation in treatment that is not confounded by unobserved factors, providing a more accurate estimate of the causal effect. These biases highlight the importance of choosing the appropriate method for causal inference and the critical role played by the underlying assumptions of each method.

```
suppressWarnings({
    true_average_effect <- -1.5
    nItr <- 10000
    as_treatedA <- function() {
      dataA <- dgpA()
      fit1 <- lm(y~d, data = dataA)
      return(summary(fit1)$coef[2, 1]) # Return the estimate
    }

    as_treatedB <- function() {
      dataB <- dgpB()
      fit2 <- lm(y~d, data = dataB)
      return(summary(fit2)$coef[2, 1]) # Return the estimate
    }

    as_treatedC <- function() {
      dataC <- dgpC()
      fit3 <- lm(y~d, data = dataC)
      return(summary(fit3)$coef[2, 1]) # Return the estimate
    }

    bias_worldA_1 <- mean(replicate(nItr, as_treatedA()) - true_average_effect)
    bias_worldB_1 <- mean(replicate(nItr, as_treatedB()) - true_average_effect)
    bias_worldC_1 <- mean(replicate(nItr, as_treatedC()) - true_average_effect)
})
```

```
suppressWarnings({
    true_average_effect <- -1.5
    nItr <- 10000
    calculate_CACE_A <- function() {
      simA <- dgpA()
      regA <- ivreg(y ~ d | z, data = simA)
```

```
    return(summary(regA)$coef[2, 1]) # Return the estimate
  }

  calculate_CACE_B <- function() {
    simB <- dgpB()
    regB <- ivreg(y ~ d | z, data = simB)
    return(summary(regB)$coef[2, 1]) # Return the estimate
  }

  calculate_CACE_C <- function() {
    simC <- dgpC()
    regC <- ivreg(y ~ d | z, data = simC)
    return(summary(regC)$coef[2, 1]) # Return the estimate
  }

  bias_worldA <- mean(replicate(nItr, calculate_CACE_A()) - true_average_effect)
  bias_worldB <- mean(replicate(nItr, calculate_CACE_B()) - true_average_effect)
  bias_worldC <- mean(replicate(nItr, calculate_CACE_C()) - true_average_effect)
})
```

```
# Creating a data frame to hold the results
results <- data.frame(
  Method = c("As-Treated", "As-Treated", "As-Treated", "TSLS", "TSLS", "TSLS"),
  World = c("A", "B", "C", "A", "B", "C"),
  Bias = c(bias_worldA_1, bias_worldB_1, bias_worldC_1, bias_worldA, bias_worldB, bias_worldC)
)
knitr::kable(results, caption = "Bias Calculations for As-Treated and IV Methods across Worlds")
```

Table 2: Bias Calculations for As-Treated and IV Methods across Worlds

Method	World	Bias
As-Treated	A	-0.6118516
As-Treated	B	-0.8114661
As-Treated	C	1.1078919
TSLS	A	0.1612692
TSLS	B	-1.5221577
TSLS	C	1.4326426