# p8122\_HW1

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# Question 1a

```
individuals = data.frame(
    Individual = 1:8,
    Y0 = c(0, 1, 0, 1, 1, 0, 1, 0),
    Y1 = c(0, 0, 1, 0, 0, 1, 0, 0)
)

# calculate treatment effects
individuals = individuals |>
    mutate(TE = Y1 - Y0) # add a col TE

individuals |>
    kable()
```

Individual	Y0	Y1	TE
1	0	0	0
2	1	0	-1
3	0	1	1
4	1	0	-1
5	1	0	-1
6	0	1	1
7	1	0	-1
8	0	0	0

# Question 1b

```
ACE = individuals |>
   summarise(ACE = mean(TE)) |>
   pull(ACE)

cat("The average causal effect (ACE) is:", ACE, "\n")
```

## The average causal effect (ACE) is: -0.25

## Question 1c

Individual	Y0	Y1	Assigned_Treatment	Observed
1	0	0	1	0
2	1	0	0	1
3	0	1	1	1
4	1	0	1	0
5	1	0	0	1
6	0	1	0	0
7	1	0	0	1
8	0	0	1	0

```
mean_treatment = individuals |>
  filter(Assigned_Treatment == 1) |>
  summarise(mean_treatment = mean(Observed)) |>
  pull(mean_treatment)

mean_control = individuals |>
  filter(Assigned_Treatment == 0) |>
  summarise(mean_control = mean(Observed)) |>
  pull(mean_control)

association = mean_treatment - mean_control
association
```

# ## [1] -0.5

#### Interpretation:

The association between treatment and outcome under the specific treatment assignment is -0.5, which indicates individuals in the treatment group had worse health status (mean = 0.25) compared to the control group (mean = 0.75).

# Question 1d

```
set.seed(329)
random_assignment = sample(c(0, 1), size = 8, replace = TRUE)
individuals = individuals |>
```

Random_Assigned_Observed	$Random\_Assigned\_Treatment$	Y1	Y0	Individual
0	0	0	0	1
0	1	0	1	2
0	0	1	0	3
1	0	0	1	4
0	1	0	1	5
0	0	1	0	6
0	1	0	1	7
0	1	0	0	8

```
# Calculate the association for random assignment
mean_treatment_random = individuals |>
    filter(Random_Assigned_Treatment == 1) |>
    summarise(mean_treatment_random = mean(Random_Assigned_Observed)) |>
    pull(mean_treatment_random)

mean_control_random = individuals |>
    filter(Random_Assigned_Treatment == 0) |>
    summarise(mean_control_random = mean(Random_Assigned_Observed)) |>
    pull(mean_control_random)

association_random = mean_treatment_random - mean_control_random
association_random
```

## [1] -0.25

Interpretation:

• Compare with question 1b ACE -0.25, the ACE under random assignment is also -0.25.

#### Question 2a

The unit is the patient who is being treated for blood pressure management.

#### Question 2b

The treatment is the dosage of medication: 'High Dose' or 'Low Dose'

## Question 2c

In this case, we could define two potential outcomes:

- Y<sub>high</sub>: Blood pressure could be too high if the patient continues with the high dose of medication.
- Y<sub>low</sub>: Blood pressure could be perfect (or controlled) under the low dose of medication.

# Question 2d

```
outcomes_numeric = data.frame(
   Treatment = c("High Dose", "Low Dose"),
   Y_high = c(0, NA),
   Y_low = c(NA, 1)
)

# Calculate causal effect: Y_low - Y_high
causal_effect = outcomes_numeric$Y_low[2] - outcomes_numeric$Y_high[1]
causal_effect
```

#### ## [1] 1

Interpretation: Switching to the low dose results in better control of blood pressure.

## Question 2e

SUTVA is plausible in this scenario:

- No interference: The patient's outcome is not influenced by others' treatment.
- Consistency: The low dose consistently results in better blood pressure control.

# Question 2f

- SUTVA must be plausible to ensure that the potential outcome framework is valid.
- This ensures that the treatment's effect is not influenced by other external factors and the outcome is consistent across treatments.

### Question 2g

- Probabilistic: No, the assignment is deterministic based on blood pressure readings.
- Individualistic: Yes, the treatment is specifically tailored for this patient.
- Unconfounded: Yes, treatment is based directly on the observed blood pressure levels, minimizing confounding.
- Controlled: Yes, the physician adjusts the dosage in a controlled manner based on the outcome.

#### Question 2h

```
set.seed(123)
random_assignment = sample(c("High Dose", "Low Dose"), size = 1, replace = TRUE)
random_outcome = ifelse(random_assignment == "High Dose", "Too High", "Perfect")
n = 10  # Number of random assignments
results = data.frame(Trial = 1:n, Assigned_Treatment = NA, Outcome = NA)
```

```
for (i in 1:n) {
  assigned_treatment = sample(c("High Dose", "Low Dose"), size = 1, replace = TRUE)
  observed_outcome = ifelse(assigned_treatment == "High Dose", "Too High", "Perfect")
  results$Assigned_Treatment[i] = assigned_treatment
  results$Outcome[i] = observed_outcome
}
```

```
Trial Assigned_Treatment Outcome
## 1
         1
                    High Dose Too High
## 2
         2
                    High Dose Too High
## 3
                    Low Dose Perfect
## 4
         4
                    High Dose Too High
## 5
         5
                    Low Dose Perfect
## 6
         6
                    Low Dose Perfect
## 7
         7
                    Low Dose Perfect
## 8
                    High Dose Too High
         8
## 9
         9
                    High Dose Too High
## 10
        10
                    Low Dose Perfect
```