

## How to estimate in a conditionally randomized experiment

More formally: Nonparametric estimation by subgroup means under conditional exchangeability

Soc 114

## Nonparametric estimation

(a fancy words for model-free estimation, such as with `group_by` and `summarize()`)

## Simulated setting: In math

- ▶ Treatment  $a$  takes values 0 and 1
- ▶ Conditionally randomized within  $x$ , taking values 0, 1 and 2
  - ▶  $P(A = 1 | X = 0) = .3$
  - ▶  $P(A = 1 | X = 1) = .5$
  - ▶  $P(A = 1 | X = 2) = .8$
- ▶ Outcome  $Y$  is numeric

## Simulated setting: In data

```
# A tibble: 1,000 x 5
  id      x     a     y sampling_weight
  <int> <int> <int> <dbl>             <dbl>
1 1       1     1     1   2.84             1
2 2       2     2     1   1.96             1
3 3       0     0     1  -1.52             1
4 4       0     0     0  -2.24             1
5 5       0     0     0   0.523            1
# i 995 more rows
```

## 1) Estimate within subgroups

Estimate each mean potential outcome in each subgroup  $E(Y^a | X = x)$  by the subgroup sample weighted mean among those with  $X = x$  and  $A = a$ .

$$\begin{aligned}\hat{E}(Y^a | X = x) &= \hat{E}(Y | X = x, A = a) \\ &= \frac{\sum_{i:X_i=x, A_i=a} w_i Y_i}{\sum_{i:X_i=x, A_i=a} w_i}\end{aligned}$$

# 1) Estimate within subgroups

```
average_potential_outcomes <- simulated |>
  group_by(x,a) |>
  summarize(mean_y = weighted.mean(y, w = sampling_weight))
```

```
# A tibble: 6 x 3
# Groups:   x [3]
  x     a   mean_y
  <int> <int>   <dbl>
1 0     0 -0.105
2 0     1 -0.0336
3 1     0 -0.0168
4 1     1  1.05 
5 2     0 -0.100
6 2     1  2.03
```

## 2) Pivot across treatment $A$ to take differences

```
cate <- average_potential_outcomes |>
  # Pivot wider and difference over A to estimate CATE
  pivot_wider(
    names_from = a,
    names_prefix = "mean_y",
    values_from = "mean_y"
  ) |>
  mutate(cate = mean_y1 - mean_y0) |>
  print()
```

```
# A tibble: 3 x 4
# Groups:   x [3]
  x  mean_y0  mean_y1    cate
  <int>   <dbl>   <dbl>   <dbl>
1     0 -0.105 -0.0336 0.0712
2     1 -0.0168  1.05    1.06 
3     2 -0.100   2.03    2.13
```

### 3) Re-aggregate to the Average Treatment Effect

The average treatment effect (ATE) is the weighted average of the conditional average treatment effects (CATEs), weighted by size.

$$\underbrace{\hat{E}(Y^1 - Y^0)}_{\text{estimated overall average effect}} = \sum_x \underbrace{\hat{P}(X = x)}_{\substack{\text{size of subgroup} \\ \text{sum over subgroups}}} \underbrace{\hat{E}(Y^1 - Y^0 \mid X = x)}_{\text{average effect within subgroup}}$$

### 3) Re-aggregate to the Average Treatment Effect

First, determine the size of the subgroups:

```
stratum_sizes <- simulated |>
  # Count sum of sampling weight in each stratum
  count(x, wt = sampling_weight) |>
  # Convert count to a proportion of the population
  mutate(stratum_size = n / sum(n)) |>
  select(-n)
```

```
# A tibble: 3 x 2
  x stratum_size
  <int>      <dbl>
1     0        0.251
2     1        0.515
3     2        0.234
```

### 3) Re-aggregate to the Average Treatment Effect

Then, re-aggregate across subgroups:

```
cate_with_stratum_size <- cate |>
  left_join(stratum_sizes, by = join_by(x)) |>
  ungroup()
```

```
# A tibble: 3 x 5
  x mean_y0 mean_y1  cate stratum_size
  <int>   <dbl>   <dbl>  <dbl>      <dbl>
1 0 -0.105 -0.0336 0.0712     0.251
2 1 -0.0168  1.05    1.06      0.515
3 2 -0.100   2.03    2.13      0.234
```

```
ate <- cate_with_stratum_size |>
  summarize(ate = weighted.mean(cate, w = stratum_size))
```

```
# A tibble: 1 x 1
  ate
  <dbl>
1 1.06
```

## Takeaways

- ▶ In a **conditionally randomized experiment**, units are randomly assigned to treatment within subgroups of  $X$ .
- ▶ We get **conditional exchangeability**:

$$\underbrace{\{Y^1, Y^0\}}_{\text{Potential Outcomes}} \quad \underbrace{\parallel}_{\text{Are Independent of}} \quad \underbrace{A}_{\text{Treatment}} \quad \underbrace{|}_{\text{Within Subgroups}} \quad \underbrace{X}_{\text{of } X}$$

- ▶ Under conditional exchangeability, causal effects within subgroups can be estimated by a difference in means

## Bonus: Estimation by treatment weighting

Treatment weighting is an approach that begins from a different angle but ends up at a mathematically equivalent estimator.

For each unit, we observe  $Y^{A_i}$  with some probability

$$P(A = A_i | X = x_i)$$

We can estimate by the proportion within each subgroup to receive treatment  $A = A_i$ .

- ▶ For units with  $A_i = 1$ , this is the subgroup mean of  $A = 1$
- ▶ For units with  $A_i = 0$ , this is the subgroup mean of  $A = 0$

## Bonus: Estimation by treatment weighting

```
data_with_probabilities <- simulated |>
  group_by(x) |>
  mutate(probability_of_a = case_when(
    # For treated units, proportion treated
    a == 1 ~ mean(a),
    # For untreated units, proportion untreated
    a == 0 ~ mean(1 - a)
  )) |>
  ungroup() |>
  print()
```

# A tibble: 1,000 x 6						
	id	x	a	y	sampling_weight	probability_of_a
	<int>	<int>	<int>	<dbl>	<dbl>	<dbl>
1	1	1	1	2.84	1	0.480
2	2	2	1	1.96	1	0.808
3	3	0	1	-1.52	1	0.327
4	4	0	0	-2.24	1	0.673
5	5	0	0	0.523	1	0.673
6	6	1	0	-0.301	1	0.520
7	7	2	1	1.47	1	0.808
8	8	2	1	1.87	1	0.808

## Bonus: Estimation by treatment weighting

Sampling weights are 1 divided by the probability of inclusion in the sample. Likewise, treatment weights are 1 divided by the probability of receiving a particular treatment.

```
data_with_weights <- data_with_probabilities |>
  mutate(
    total_weight = sampling_weight * (1 / probability_of_a)
  ) |>
  print(n = 3)
```

```
# A tibble: 1,000 x 7
  id      x      a      y sampling_weight probability_of_a total_weight
  <int> <int> <int> <dbl>                <dbl>              <dbl>            <dbl>
1     1      1      1     1  2.84                  1        0.480       2.09
2     2      2      1     1  1.96                  1        0.808       1.24
3     3      0      1     1 -1.52                  1        0.327       3.06
# i 997 more rows
```

## Bonus: Estimation by treatment weighting

Once we have inverse probability of treatment weights, we can estimate by the sample weighted mean in each treatment group.

```
ate <- data_with_weights |>
  group_by(a) |>
  summarize(estimate = weighted.mean(y, w = total_weight)) |>
  pivot_wider(
    names_from = a,
    names_prefix = "mean_y",
    values_from = estimate
  ) |>
  mutate(ate = mean_y1 - mean_y0) |>
  print()
```

```
# A tibble: 1 x 3
  mean_y0  mean_y1    ate
  <dbl>    <dbl> <dbl>
1 -0.0585     1.01  1.06
```