

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
 - ▶ $P(A = 1 \mid X = 0) = .3$
 - ▶ $P(A = 1 \mid X = 1) = .5$
 - ▶ $P(A = 1 \mid X = 2) = .8$
- ▶ 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	0.814	1
2	2	0	0	0.750	1
3	3	0	0	-0.699	1
4	4	1	0	0.507	1
5	5	1	0	1.65	1

```
# i 995 more rows
```

1) Estimate within subgroups

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

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

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 -0.0206  
2     0     1 -0.0369  
3     1     0 -0.0849  
4     1     1  0.907  
5     2     0 -0.241  
6     2     1  1.91
```

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	-0.0206	-0.0369	-0.0163
2	1	-0.0849	0.907	0.992
3	2	-0.241	1.91	2.15

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.

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

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	0.255
2	1	0.492
3	2	0.253

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	-0.0206	-0.0369	-0.0163	0.255
2	1	-0.0849	0.907	0.992	0.492
3	2	-0.241	1.91	2.15	0.253

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

```
# A tibble: 1 x 1
```

	ate
	<dbl>
1	1.03

Takeaways

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

$$\underbrace{\{Y^1, Y^0\}}_{\text{Potential Outcomes}} \perp\!\!\!\perp \underbrace{A}_{\text{Treatment}} \mid \underbrace{X}_{\text{Within Subgroups of } X}$$

- ▶ 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

$$P(A = A_i \mid X = x_i)$$

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	0.814	1	0.530
2	2	0	0	0.750	1	0.655
3	3	0	0	-0.699	1	0.655
4	4	1	0	0.507	1	0.470
5	5	1	0	1.65	1	0.470
6	6	1	1	0.641	1	0.530
7	7	1	0	-0.584	1	0.470
8	8	1	0	-0.519	1	0.470

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	0.814	1	0.530	1.8
2	2	0	0	0.750	1	0.655	1.5
3	3	0	0	-0.699	1	0.655	1.5

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 -0.108  0.920  1.03
```