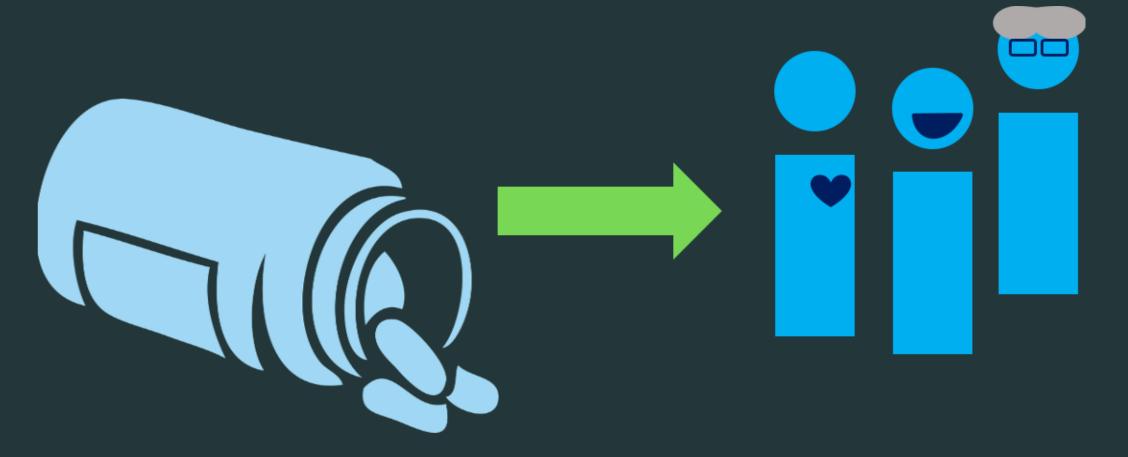
Causal Inference with group_by and summarise Lucy D'Agostino McGowan Wake Forest University

Goal: To answer a research question



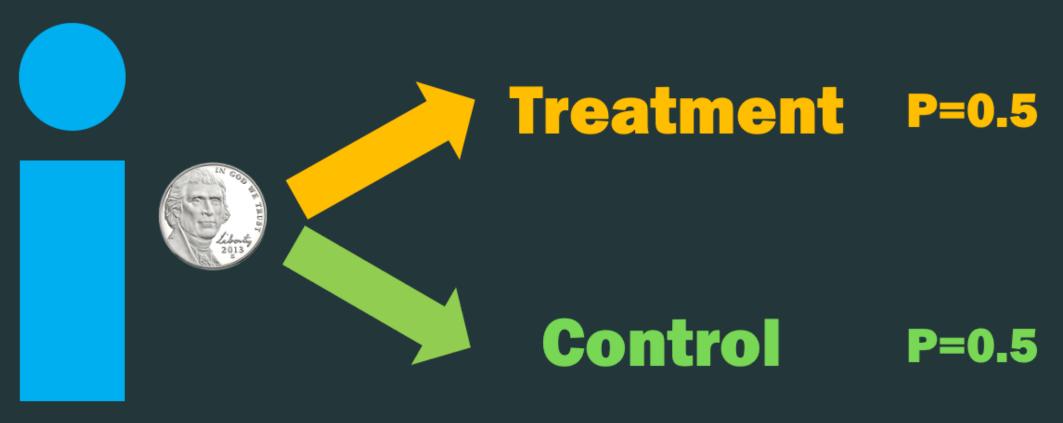
Goal: To answer a research question

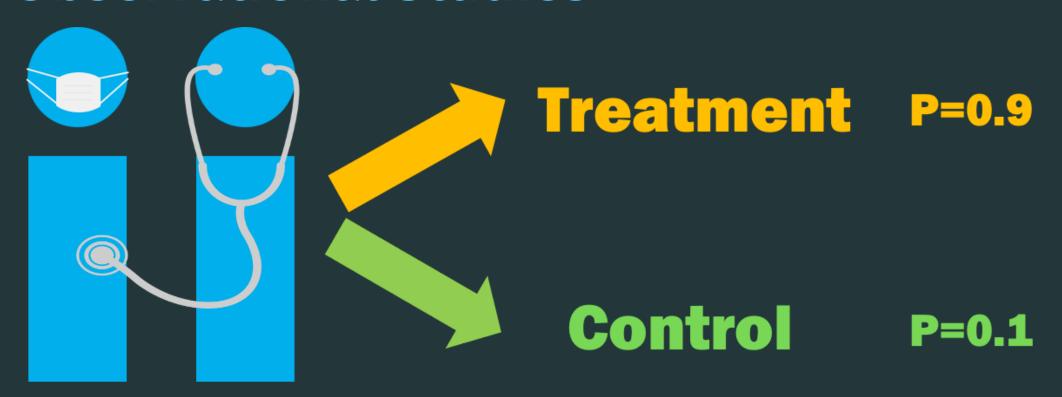


Randomized Controlled Trial



Randomized Controlled Trial

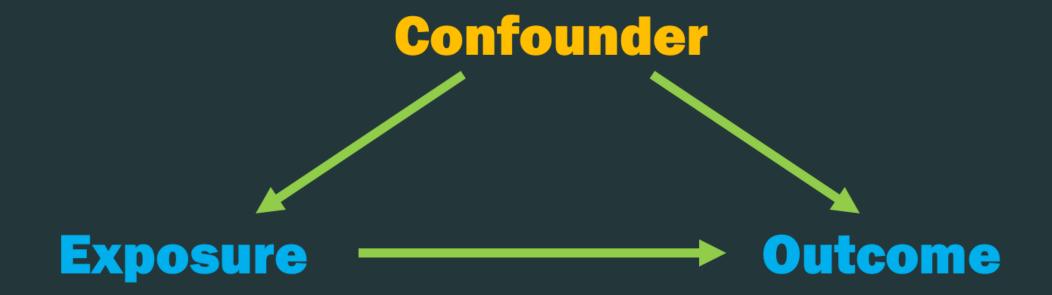




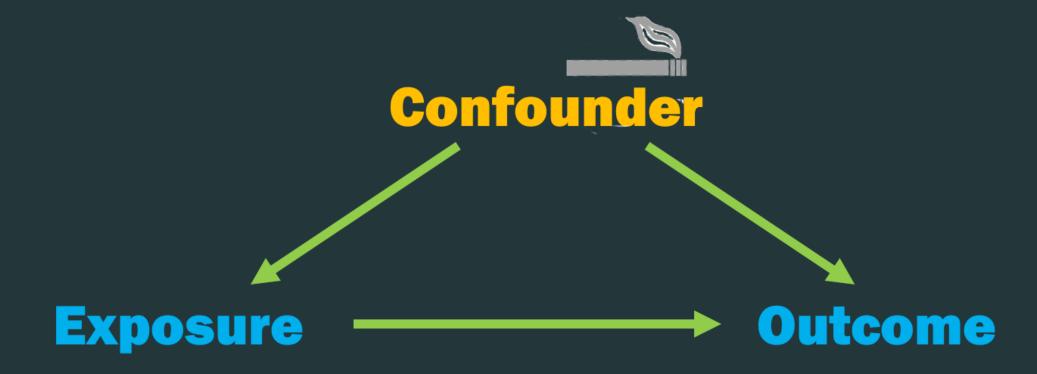




Confounding



Confounding



One binary confounder

```
1  n <- 1000
2  sim <- tibble(
3   confounder = rbinom(n, 1, 0.5),
4   p_exposure = case_when(
5   confounder == 1 ~ 0.75,
6   confounder == 0 ~ 0.25
7   ),
8   exposure = rbinom(n, 1, p_exposure),
9   outcome = confounder + rnorm(n)
10  ) |> select(-p_exposure)
11
12  sim
```

```
# A tibble: 1,000 × 3
   confounder exposure outcome
       <int> <int> <dbl>
                    0 1.13
                    0 1.11
                    1 0.129
                    0 1.21
                    0 0.0694
                    1 -0.663
                    1 1.81
                    1 -0.912
                    0 -0.247
10
                    0 0.998
```

```
1 sim |>
  group_by(exposure) |>
    summarise(avg_y = mean(outcome)) |>
     pivot_wider(
   names_from = exposure,
 6 values_from = avg_y,
  names_prefix = "x_"
  ) |>
     summarise(estimate = x_1 - x_0)
# A tibble: 1 × 1
  estimate
```

Your Turn 1 (03-ci-with-group-by-and-summarise-exercises.qmd)

Group the dataset by confounder and exposure

Group the dataset by confounder and exposure Calculate the mean of the outcome for the groups



Your Turn 1

Your Turn 1

```
1 sim |>
2   group_by(confounder, exposure) |>
3   summarise(avg_y = mean(outcome)) |>
4   pivot_wider(
5     names_from = exposure,
6     values_from = avg_y,
7     names_prefix = "x_"
8   ) |>
9   summarise(estimate = x_1 - x_0) |>
10   # note: we would need to weight this
11   # if the confounder groups were not equal sized
12   summarise(estimate = mean(estimate))
```

```
# A tibble: 1 × 1
   estimate
      <dbl>
1 -0.0794
```



Two binary confounders

```
1 n <- 1000
 2 sim2 <- tibble(</pre>
     confounder_1 = rbinom(n, 1, 0.5),
     confounder_2 = rbinom(n, 1, 0.5),
     p_exposure = case_when(
       confounder_1 == 1 \& confounder_2 == 1 \sim 0.75,
       confounder 1 == 0 \& confounder 2 == 1 \sim 0.9,
       confounder_1 == 1 \& confounder_2 == 0 \sim 0.2,
        confounder_1 == 0 & confounder_2 == 0 \sim 0.1,
10
11
     exposure = rbinom(n, 1, p_exposure),
     outcome = confounder_1 + confounder_2 + rnorm(n)
12
13
   ) |> select(-p_exposure)
14
15 sim2
```

```
# A tibble: 1,000 × 4
  confounder_1 confounder_2 exposure outcome
                    <int> <int> <dbl>
         <int>
                                0 0.521
                                0 1.38
                                   -0.624
                                1 0.427
                                1 1.31
                                   -0.707
                                1 2.52
                                0 1.45
                                0 -0.505
10
                                    0.793
```

Your Turn 2

Group the dataset by the confounders and exposure

Calculate the mean of the outcome for the groups

Your Turn 2

```
1 sim2 |>
2   group_by(confounder_1, confounder_2, exposure) |>
3   summarise(avg_y = mean(outcome)) |>
4   pivot_wider(
5    names_from = exposure,
6    values_from = avg_y,
7    names_prefix = "x_"
8   ) |>
9   summarise(estimate = x_1 - x_0, .groups = "drop") |>
10   summarise(estimate = mean(estimate))
```

```
# A tibble: 1 × 1
estimate
<dbl>
<dbl>
1 -0.0731
```

```
1 n <- 100000
 2 big sim2 <- tibble(</pre>
     confounder_1 = rbinom(n, 1, 0.5),
     confounder_2 = rbinom(n, 1, 0.5),
     p_exposure = case_when(
       confounder_1 == 1 \& confounder_2 == 1 \sim 0.75,
       confounder 1 == 0 \& confounder 2 == 1 \sim 0.9,
       confounder_1 == 1 \& confounder_2 == 0 \sim 0.2,
        confounder_1 == 0 & confounder_2 == 0 \sim 0.1,
10
11
     exposure = rbinom(n, 1, p_exposure),
     outcome = confounder_1 + confounder_2 + rnorm(n)
12
13
   ) |> select(-p_exposure)
14
15 big_sim2
```

```
# A tibble: 100,000 × 4
  confounder_1 confounder_2 exposure outcome
                     <int>
         <int>
                             <int> <dbl>
                                 1 2.35
                                 0 3.71
                                 0 2.08
                                 1 0.516
                                    -0.166
                                    1.58
                                 0 0.472
                                    3.22
                                 1 0.929
10
                                    1.41
```

```
big_sim2 |>
group_by(confounder_1, confounder_2, exposure) |>
summarise(avg_y = mean(outcome)) |>
pivot_wider(
names_from = exposure,
values_from = avg_y,
names_prefix = "x_"
) |>
summarise(estimate = x_1 - x_0, .groups = "drop") |>
summarise(estimate = mean(estimate))
# A tibble: 1 x 1
```

Continuous confounder?

```
1 n <- 10000
2 sim3 <- tibble(
3    confounder = rnorm(n),
4    p_exposure = exp(confounder) / (1 + exp(confounder)),
5    exposure = rbinom(n, 1, p_exposure),
6    outcome = confounder + rnorm(n)
7 ) |> select(-p_exposure)
8
9 sim3
```

```
# A tibble: 10,000 × 3
  confounder exposure outcome
       <dbl> <int> <dbl>
      -0.167
                     -0.560
                  1 0.628
      0.252
      -0.321
                     -0.608
     0.621
                   0 1.58
5
                  1 0.358
     -0.619
     -0.897
                     -1.95
     -2.01
                     -2.50
     0.296
                     -1.10
9
                     -0.316
     -0.504
10
      -0.536
                    1.12
```

Your Turn 3

Use ntile() from dplyr to calculate a binned version of confounder called confounder_q. We'll create a variable with 5 bins.

Group the dataset by the binned variable you just created and exposure

Calculate the mean of the outcome for the groups

03:00

Your Turn 3

```
1 sim3 |>
2  mutate(confounder_q = ntile(confounder, 5)) |>
3  group_by(confounder_q, exposure) |>
4  summarise(avg_y = mean(outcome)) |>
5  pivot_wider(
6   names_from = exposure,
7  values_from = avg_y,
8   names_prefix = "x_"
9  ) |>
10  summarise(estimate = x_1 - x_0) |>
11  summarise(estimate = mean(estimate))
```

```
# A tibble: 1 × 1
estimate
<dbl>
<dbl>
1 0.0728
```

What if we could come up with a summary score of all confounders?