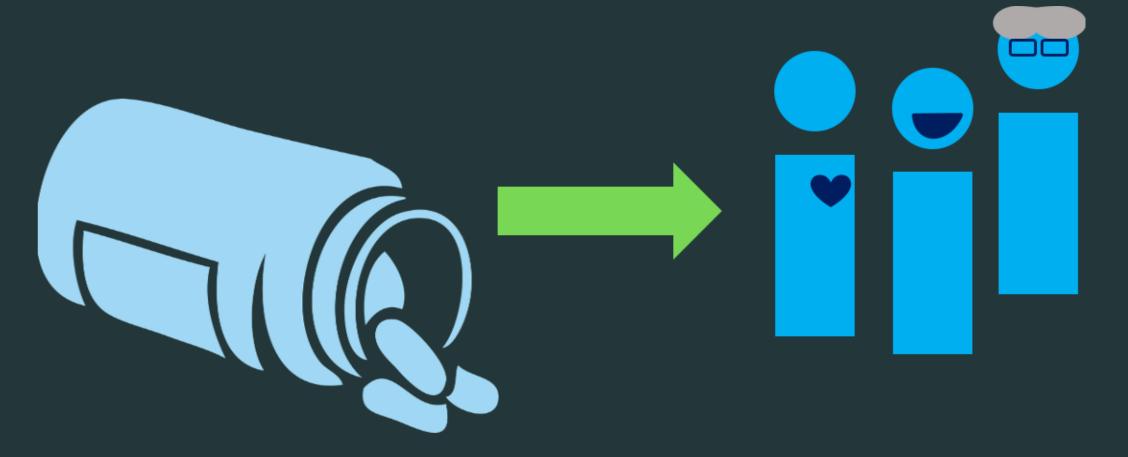
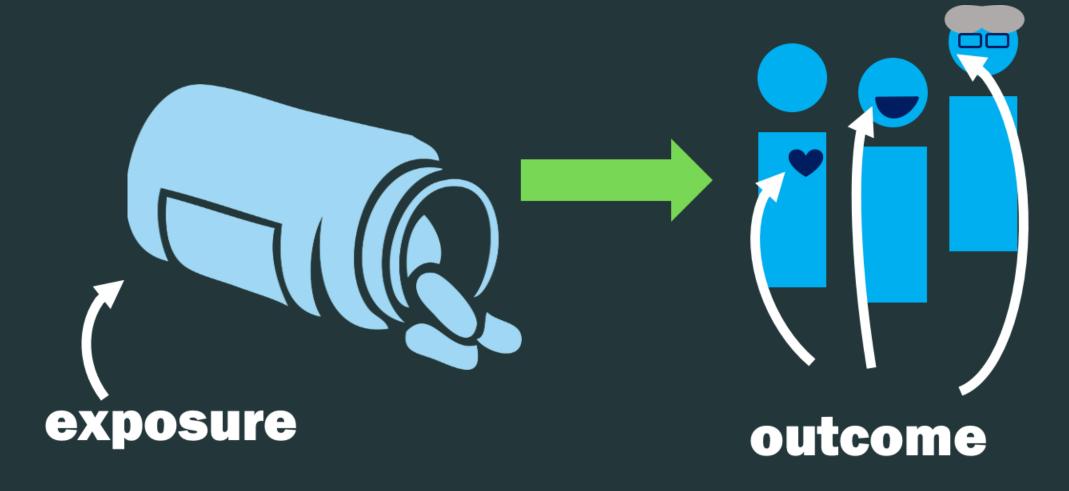
# Causal Inference with group\_by and summarise

Lucy D'Agostino McGowan
Wake Forest University

Goal: To answer a research question



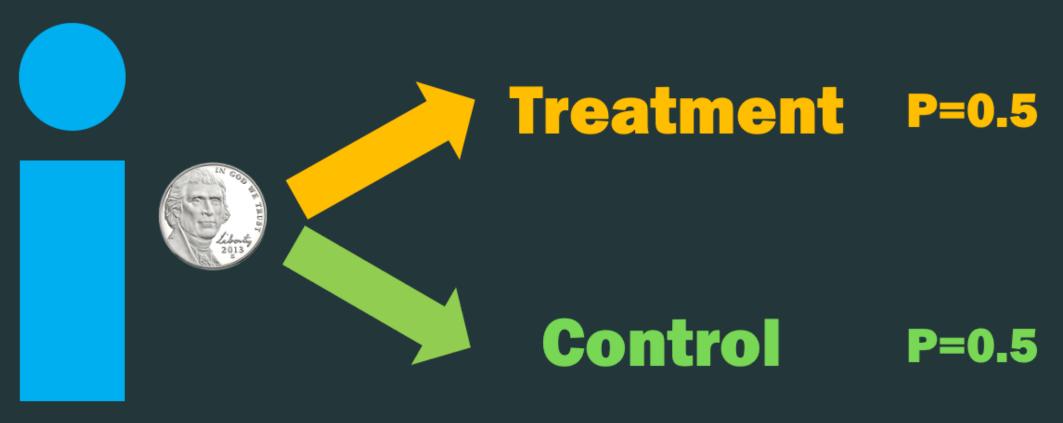
Goal: To answer a research question



**Randomized Controlled Trial** 



#### **Randomized Controlled Trial**

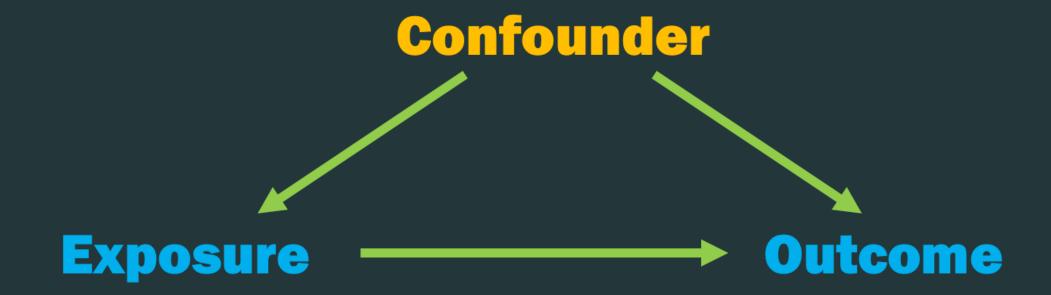




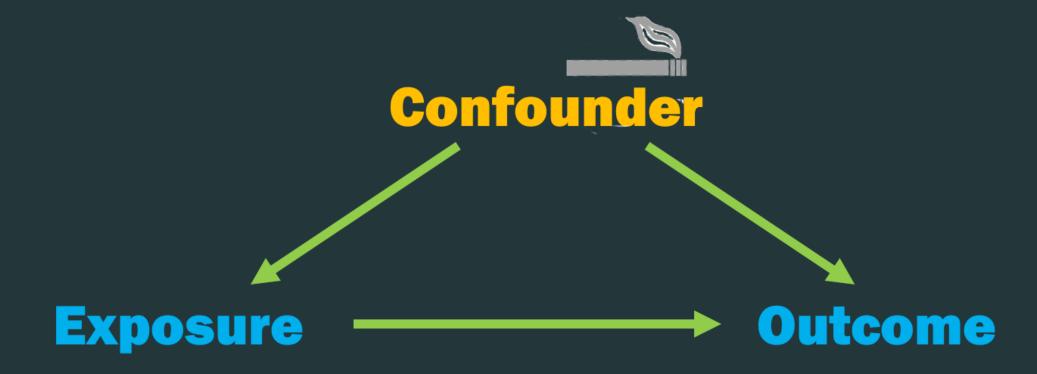




#### Confounding



#### Confounding



#### One binary confounder

```
1 n < -1000
2 sim <- tibble(</pre>
   confounder = rbinom(n, 1, 0.5),
   p_exposure = case_when(
  confounder == 1 \sim 0.75,
  confounder == 0 \sim 0.25
   ),
   exposure = rbinom(n, 1, p_exposure),
   outcome = confounder + rnorm(n)
10 ) |> select(-p_exposure)
11
12 sim
```

```
# A tibble: 1,000 \times 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,
       values_from = avg_y,
       names_prefix = "x_"
   ) |>
     summarise(estimate = x_1 - x_0)
# A tibble: 1 × 1
  estimate
    <dbl>
 0.407
```

## Your Turn 1 (03-ci-with-group-by-and-summarise-exercises.qmd) Group the dataset by confounder and exposure

Calculate the mean of the outcome for the groups

#### **Your Turn 1**

```
1 sim |>
2  group_by(confounder, exposure) |>
3  summarise(avg_y = mean(outcome))

# A tibble: 4 × 3
# Groups: confounder [2]
  confounder exposure avg_y
```

#### **Your Turn 1**

```
1 \sin >
     group by(confounder, exposure) >
     summarise(avg y = mean(outcome)) |>
    pivot wider(
       names from = exposure,
       values from = avg y,
       names prefix = "x "
    ) |>
     summarise(estimate = x 1 - x 0) |>
   # note: we would need to weight this
10
# if the confounder groups were not equal sized
     summarise(estimate = mean(estimate))
12
```



#### Two binary confounders

```
1 n < -1000
 2 sim2 <- tibble(</pre>
    confounder 1 = rbinom(n, 1, 0.5),
    confounder 2 = rbinom(n, 1, 0.5),
 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),
12  outcome = confounder 1 + confounder 2 + rnorm(n)
13 ) |> select(-p exposure)
14
15 sim2
```

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

#### **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))
```

```
1 n < -100000
 2 big sim2 <- tibble(</pre>
    confounder 1 = rbinom(n, 1, 0.5),
    confounder 2 = rbinom(n, 1, 0.5),
 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
    ),
  exposure = rbinom(n, 1, p_exposure),
11
12  outcome = confounder 1 + confounder 2 + rnorm(n)
13 ) |> select(-p exposure)
14
15 big sim2
```

```
# A tibble: 100,000 \times 4
  confounder_1 confounder_2 exposure outcome
         <int>
                     <int> <int> <dbl>
                                 1 2.35
                                 0 3.71
                                 0 2.08
                                 1 0.516
                                 0 - 0.166
                                 1 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))
```

#### 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 \times 3
  confounder exposure outcome
       <dbl> <int> <dbl>
                   0 - 0.560
      -0.167
      0.252
                   1 0.628
      -0.321
                   1 -0.608
      0.621
                   0 1.58
 5
                  1 0.358
     -0.619
     -0.897
                   0 - 1.95
                   0 -2.50
    -2.01
      0.296
                   0 -1.10
                   1 -0.316
9
    -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))
```

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