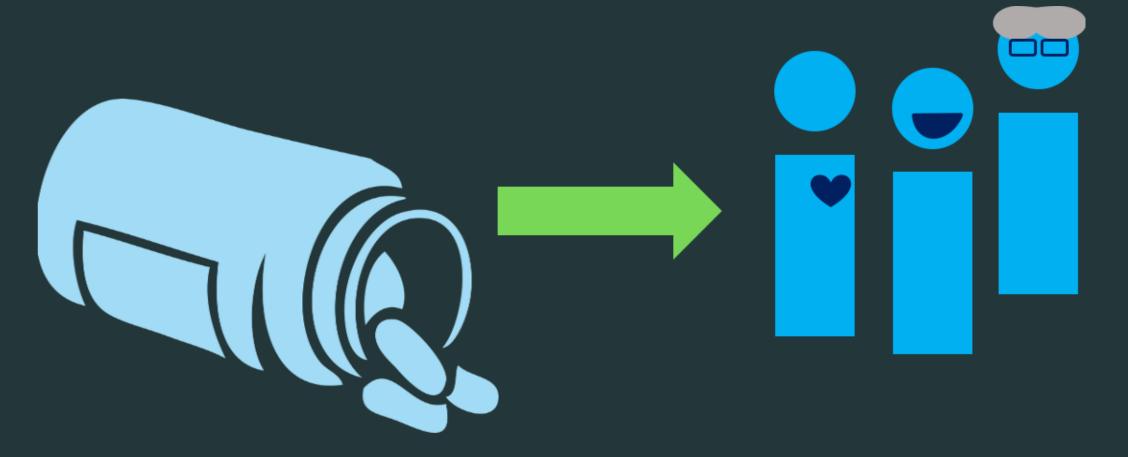
# Causal Inference with group\_by and summarise

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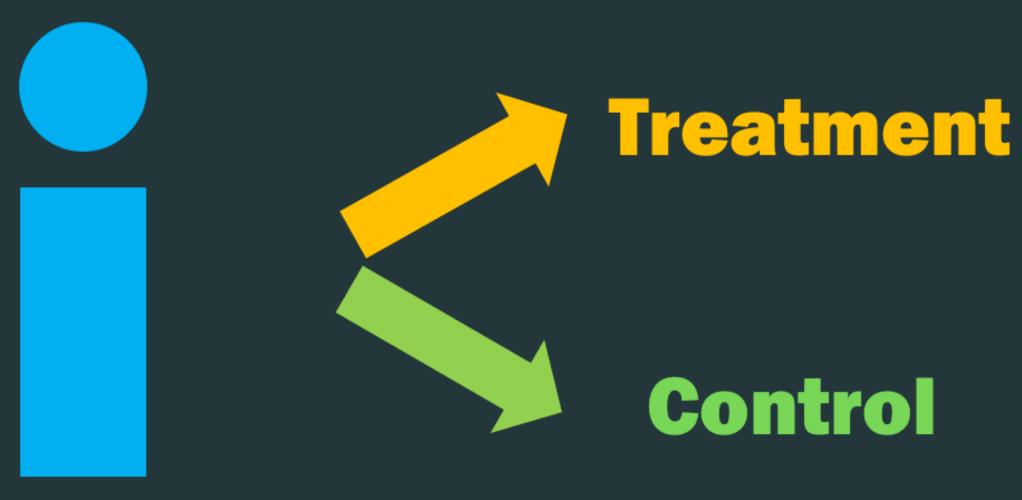
Goal: To answer a research question



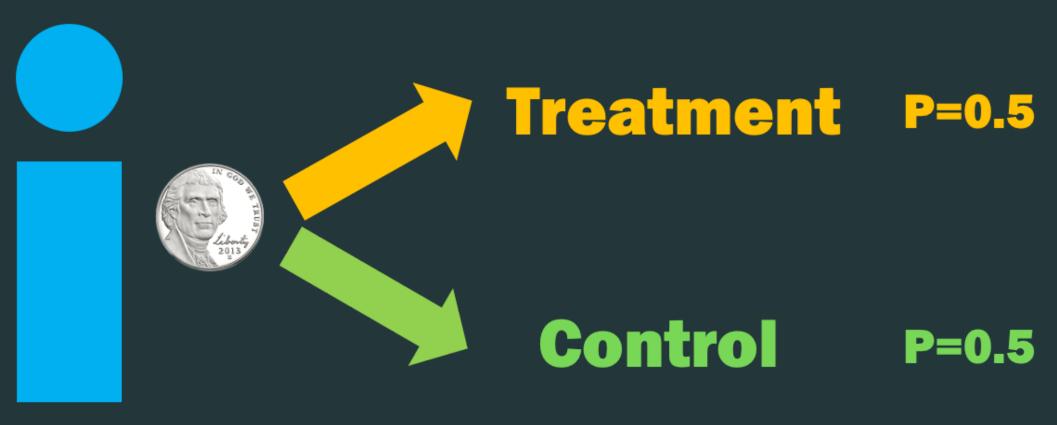
Goal: To answer a research question



**Randomized Controlled Trial** 



#### **Randomized Controlled Trial**

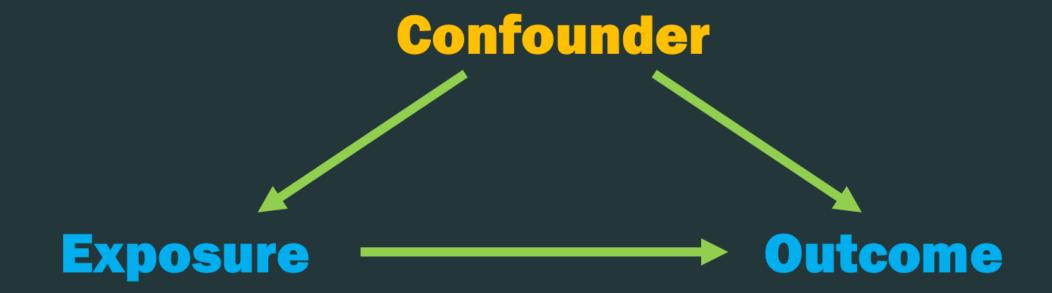




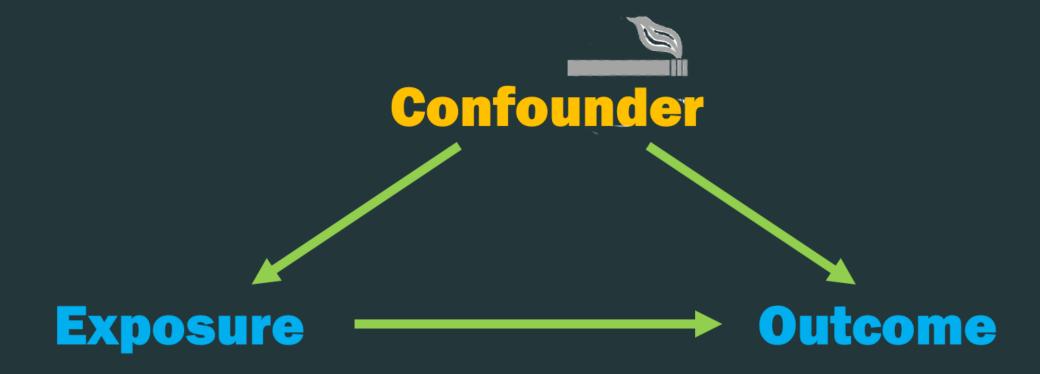




## Confounding



## 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 )</pre>
```

```
# A tibble: 1,000 \times 3
   confounder exposure outcome
        <int>
                 <int> <dbl>
                     0 1.13
                     0 1.11
            0
                     1 0.129
            1
                     0 1.21
                     0 0.0694
                     1 - 0.663
 6
                     1 1.81
            1
 8
            1
                     1 - 0.912
 9
            1
                     0 - 0.247
10
            0
                     0 0.998
# i 990 more rows
```

```
1 lm(outcome ~ exposure, data = sim)

Call:
lm(formula = outcome ~ exposure, data = sim)

Coefficients:
(Intercept) exposure
     0.2688      0.4070
```

```
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
```

```
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)
```



# Two binary confounders

```
1 n < -1000
 2 sim2 <- tibble(</pre>
     confounder 1 = rbinom(n, 1, 0.5),
     confounder 2 = rbinom(n, 1, 0.5),
 4
 5
     p exposure = case when(
        confounder 1 == 1 \& confounder 2 == 1 \sim 0.75,
 7
        confounder 1 == 0 \& confounder 2 == 1 \sim 0.9,
 8
 9
        confounder 1 == 1 \& confounder 2 == 0 \sim 0.2
        confounder 1 == 0 \& confounder 2 == 0 \sim 0.1,
10
11
12
     exposure = rbinom(n, 1, p exposure),
     outcome = confounder 1 + confounder 2 + rnorm(n)
13
14 )
```

```
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)
```

```
1 n < 100000
 2 sim2 <- tibble(</pre>
     confounder 1 = rbinom(n, 1, 0.5),
     confounder 2 = rbinom(n, 1, 0.5),
 4
 5
     p exposure = case when(
        confounder 1 == 1 \& confounder 2 == 1 \sim 0.75,
 7
        confounder 1 == 0 \& confounder 2 == 1 \sim 0.9,
 8
 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
14 )
```

```
# A tibble: 100,000 \times 4
  confounder 1 confounder 2 exposure outcome
         <int>
                     <int>
                             <int>
                                     <dbl>
                                1 2.35
                         1
                                 0 3.71
                                 0 2.08
                                 1 0.516
                                 0 -0.166
                                 1 1.58
                                 0 0.472
 8
                                 0 3.22
9
                         1
                                 1 0.929
10
                                 1 1.41
# i 99,990 more rows
```

#### **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 )</pre>
```

```
# A tibble: 10,000 × 3
  confounder exposure outcome
                <int>
       <dbl>
                       <dbl>
      -0.167
                    0 -0.560
       0.252
                    1 0.628
      -0.321
                    1 -0.608
 3
       0.621
                    0 1.58
 5
      -0.619
                    1 0.358
      -0.897
                    0 - 1.95
      -2.01
                    0 -2.50
      0.296
                    0 -1.10
      -0.504
                    1 - 0.316
      -0.536
1.0
                    1 1.12
# i 9,990 more rows
```

```
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)
```

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