

# G-Computation

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Normal regression estimates associations. But we want **causal** estimates: what would happen if **everyone** in the study were exposed to  $x$  vs if **no one** was exposed.

# G-Computation/G-Formula

- 1 Fit a model for  $y \sim x + z$  where  $z$  is all covariates**
- 2 Create a duplicate of your data set for each level of  $x$**
- 3 Set the value of  $x$  to a single value for each cloned data set (e.g  $x = 1$  for one,  $x = 0$  for the other)**

# G-Computation/G-Formula

- 1 Make predictions using the model on the cloned data sets
- 2 Calculate the estimate you want, e.g.  $\text{mean}(x_1) - \text{mean}(x_0)$

# Advantages of the parametric G-formula

**Often more statistically precise than propensity-based methods**

**Incredibly flexible**

**Basis of other important causal models, e.g. causal survival analysis and TMLE**

# Greek Pantheon data (greek\_data)

name	l	a	y
Rheia	0	0	0
Kronos	0	0	1
Demeter	0	0	0
Hades	0	0	0
Hestia	0	1	0
Poseidon	0	1	0
Hera	0	1	0
Zeus	0	1	1
Artemis	1	0	1
Apollo	1	0	1

+ 10 more rows

# 1. Fit a model for $y \sim a + l$

```
greek_model <- lm(y ~ a + l, data = greek_data)
```

## 2. Create a duplicate of your data set for each level of a

name	l	a	y
Rheia	0	0	0
Kronos	0	0	1
Demeter	0	0	0
Hades	0	0	0
Hestia	0	1	0
Poseidon	0	1	0
Hera	0	1	0
Zeus	0	1	1
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Apollo	1	0	1

### 3. Set the value of a to a single value for each cloned data set

name	l	a	y
Rheia	0	<b>0</b>	0
Kronos	0	<b>0</b>	1
Demeter	0	<b>0</b>	0
Hades	0	<b>0</b>	0
Hestia	0	<b>0</b>	0
Poseidon	0	<b>0</b>	0
Hera	0	<b>0</b>	0
Zeus	0	<b>0</b>	1
Artemis	1	<b>0</b>	1
Apollo	1	<b>0</b>	1

name	l	a	y
Rheia	0	<b>1</b>	0
Kronos	0	<b>1</b>	1
Demeter	0	<b>1</b>	0
Hades	0	<b>1</b>	0
Hestia	0	<b>1</b>	0
Poseidon	0	<b>1</b>	0
Hera	0	<b>1</b>	0
Zeus	0	<b>1</b>	1
Artemis	1	<b>1</b>	1
Apollo	1	<b>1</b>	1

### 3. Set the value of a to a single value for each cloned data set

```
# set all participants to have a = 0  
untreated_data <- greek_data %>%  
  mutate(a = 0)
```

```
# set all participants to have a = 1  
treated_data <- greek_data %>%  
  mutate(a = 1)
```

## 4. Make predictions using the model on the cloned data sets

```
# predict under the data where everyone is untreated
```

```
predicted_untreated <- greek_model %>%  
  augment(newdata = untreated_data) %>%  
  select(untreated = .fitted)
```

```
# predict under the data where everyone is treated
```

```
predicted_treated <- greek_model %>%  
  augment(newdata = treated_data) %>%  
  select(treated = .fitted)
```

```
predictions <- bind_cols(  
  predicted_untreated,  
  predicted_treated  
)
```

## 5. Calculate the estimate you want

```
predictions %>%  
  summarise(  
    mean_treated = mean(treated),  
    mean_untreated = mean(untreated),  
    difference = mean_treated - mean_untreated  
  )
```

```
## # A tibble: 1 × 3  
##   mean_treated mean_untreated difference  
##   <dbl>         <dbl>         <dbl>  
## 1         0.5         0.5         0
```

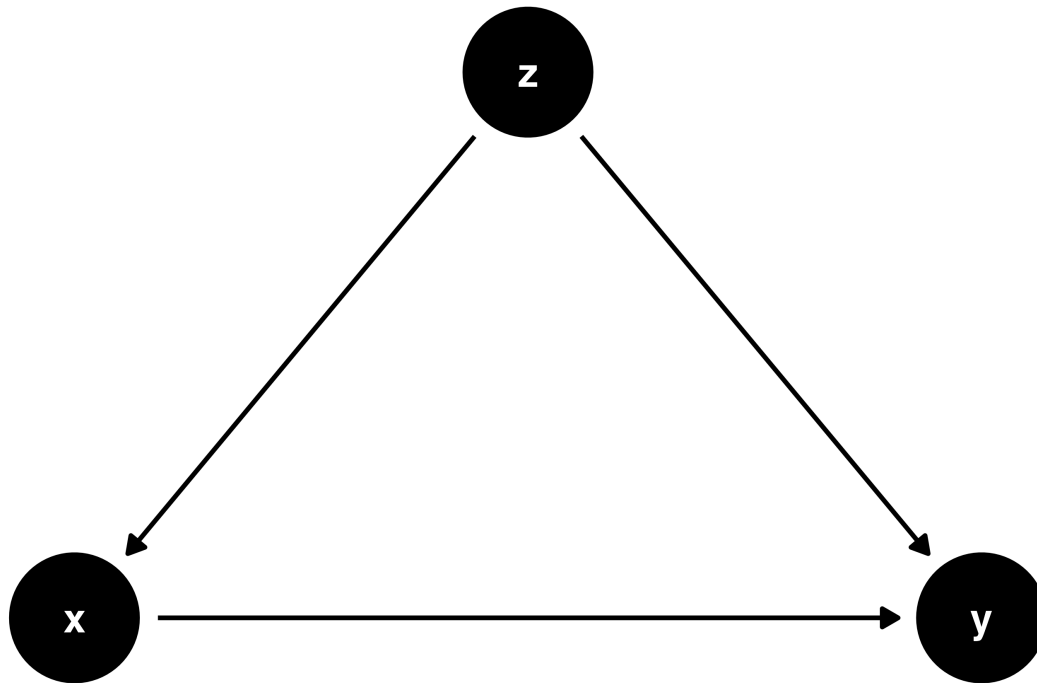
# Your Turn

**Work through Your Turns 1-3 in 07-g-computation-exercises.Rmd**

10:00

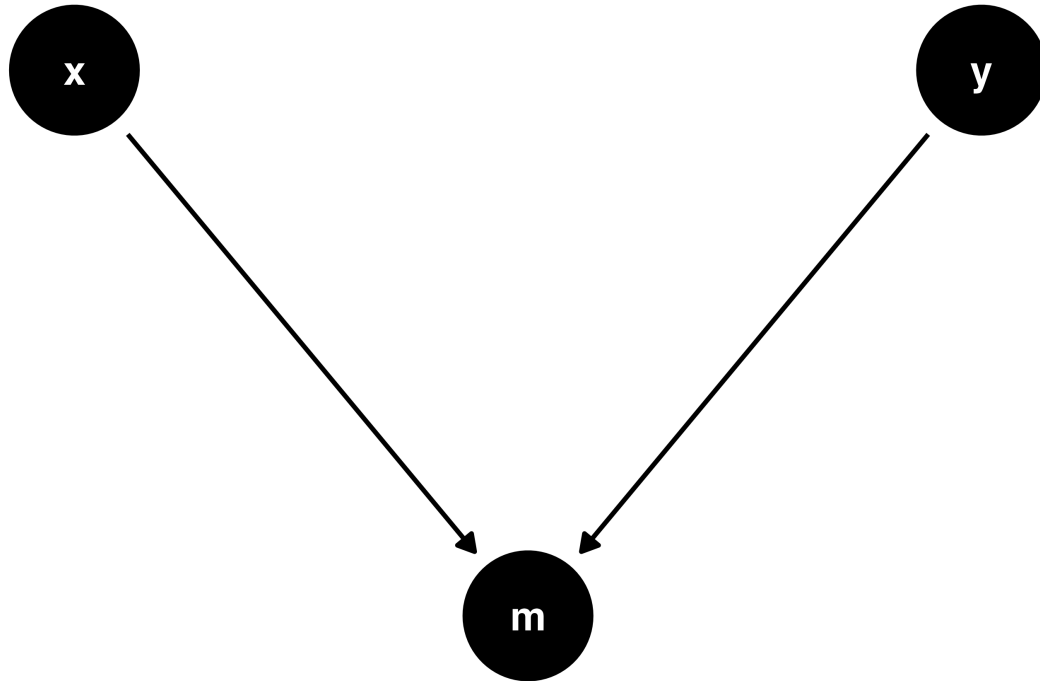
# **Detour:** Colliders, selection bias, and loss to follow-up

# Confounders and chains

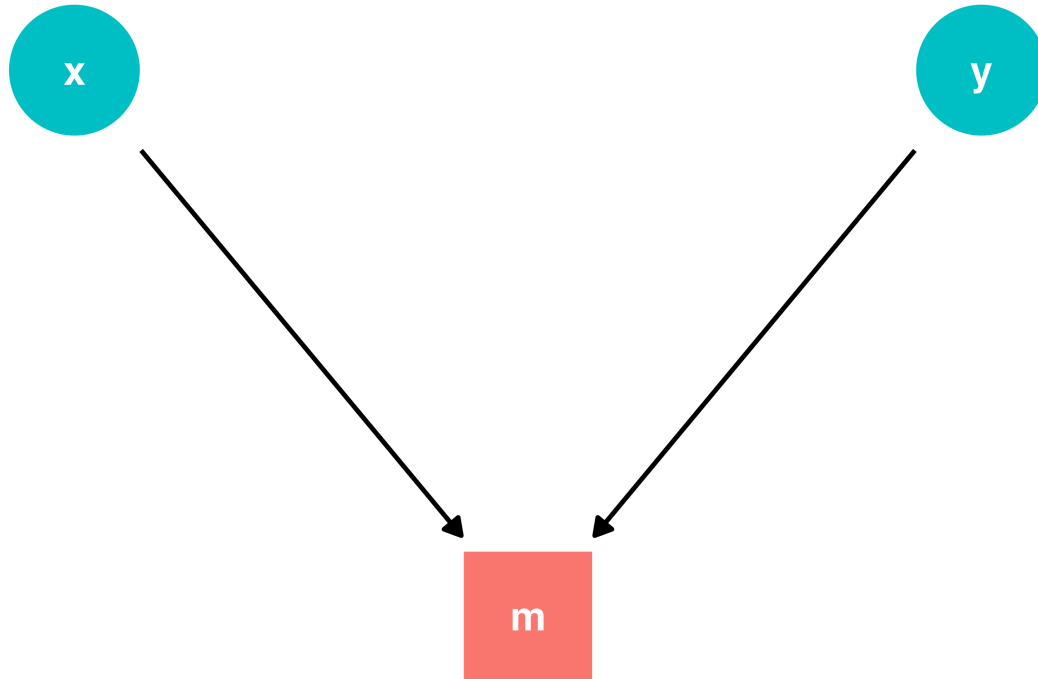




# Colliders



# Colliders



# Let's prove it!

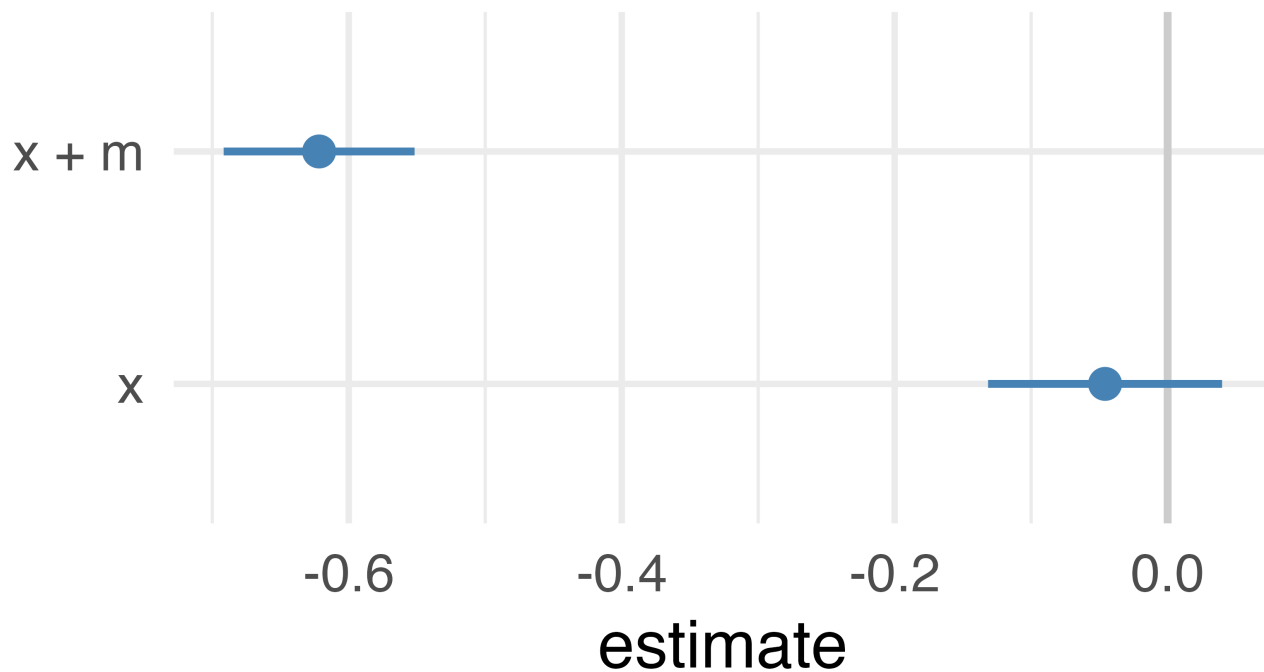
```
set.seed(1234)
collider_data <- collider_triangle() |>
  simulate_data(-.6)
```

# Let's prove it!

```
collider_data
```

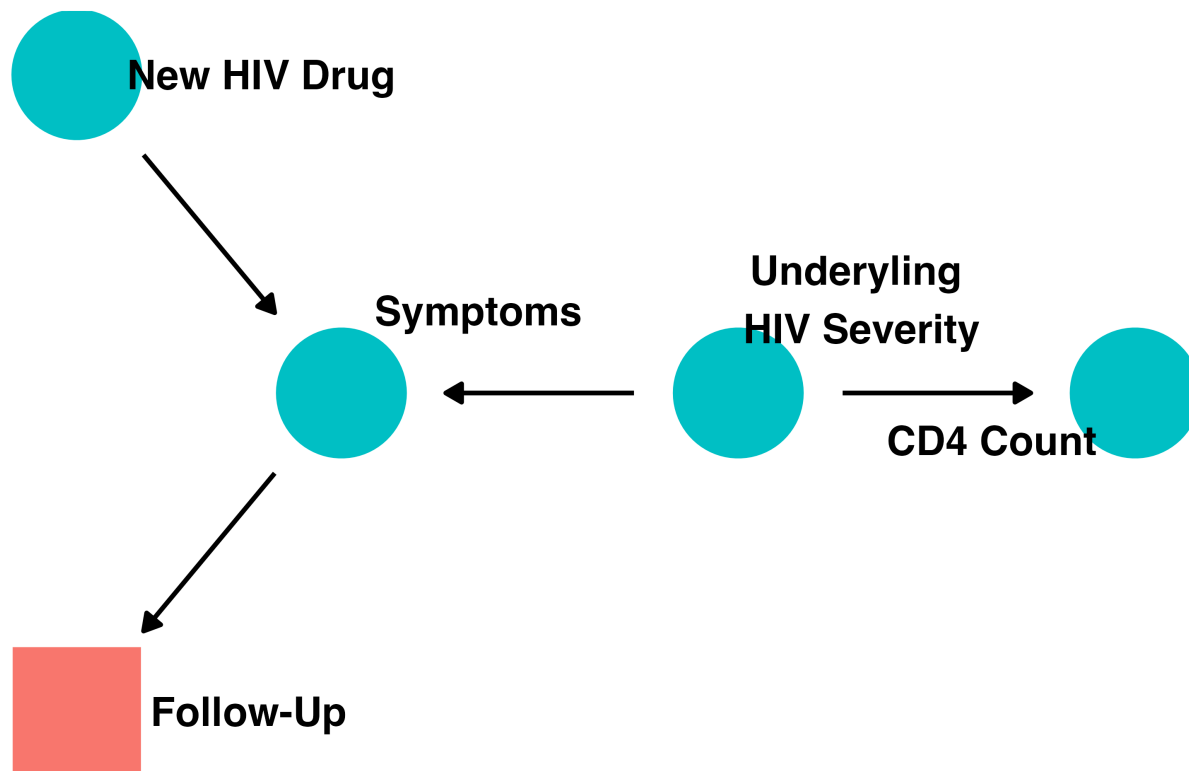
```
## # A tibble: 500 × 3
##       m       x       y
##   <dbl> <dbl> <dbl>
## 1 -0.457 -0.410  1.28
## 2  0.281  1.79  -0.550
## 3  0.0835 1.31  -0.169
## 4  0.640  1.06  -1.40
## 5 -1.30    0.435  1.16
## 6 -0.569  0.630 -0.000667
## 7 -0.793  1.50  -1.10
## 8 -0.482  0.748 -0.411
## 9 -0.706  1.03  -0.381
## 10  1.42  -0.841 -0.420
## # ... with 490 more rows
```

# Let's prove it!



correct effect size: 0

# Loss to follow-up



# Adjusting for selection bias

- 1 Fit a probability of censoring model, e.g. `glm(censoring ~ predictors, family = binomial())`
- 2 Create weights using inverse probability strategy
- 3 Use weights in your causal model

We won't do it here, but you can include many types of weights in a given model. Just take their product, e.g. **multiply inverse propensity of treatment weights by inverse propensity of censoring weights.**



# Your Turn

**Work through Your Turns 4-6 in 07-g-computation-exercises.Rmd**

10:00