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 ~ 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

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`)

The name of a Greek god	A prognostic factor	The treatment, a heart transplant	The outcome, death
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 ~ a + l`

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

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

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

The name of a Greek god	A prognostic factor	a	The outcome, death
Rheia	0	**0**	0
Kronos	0	**0**	1
Demeter	0	**0**	0
Hades	0	**0**	0
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The name of a Greek god	A prognostic factor	a	The outcome, death
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Hades	0	**1**	0
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Hera	0	**1**	0
Zeus	0	**1**	1
Artemis	1	**1**	1
Apollo	1	**1**	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

```r
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
```

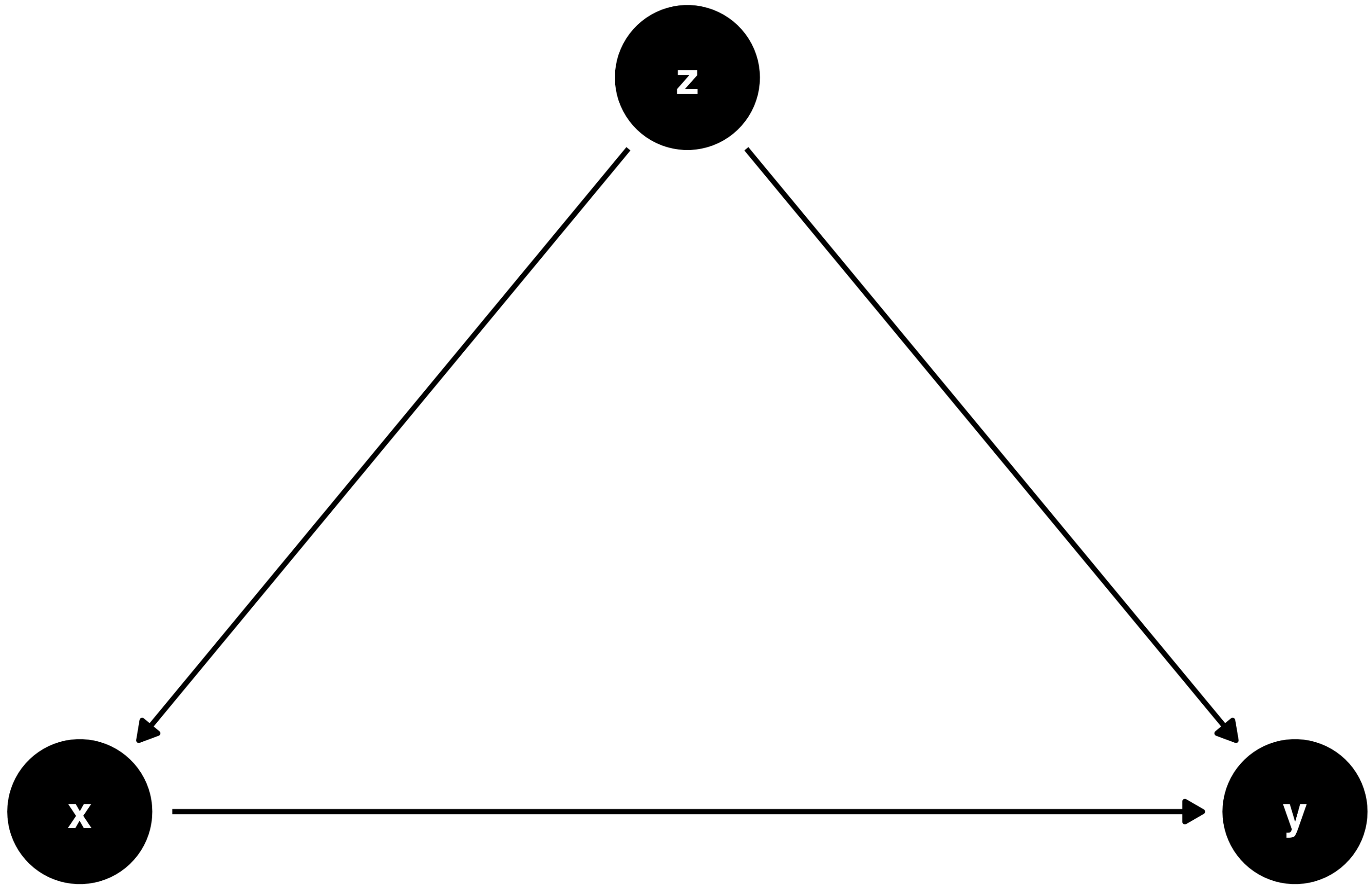
Your Turn

Work through Your Turns 1-3 in `07-g-computation-exercises.qmd`

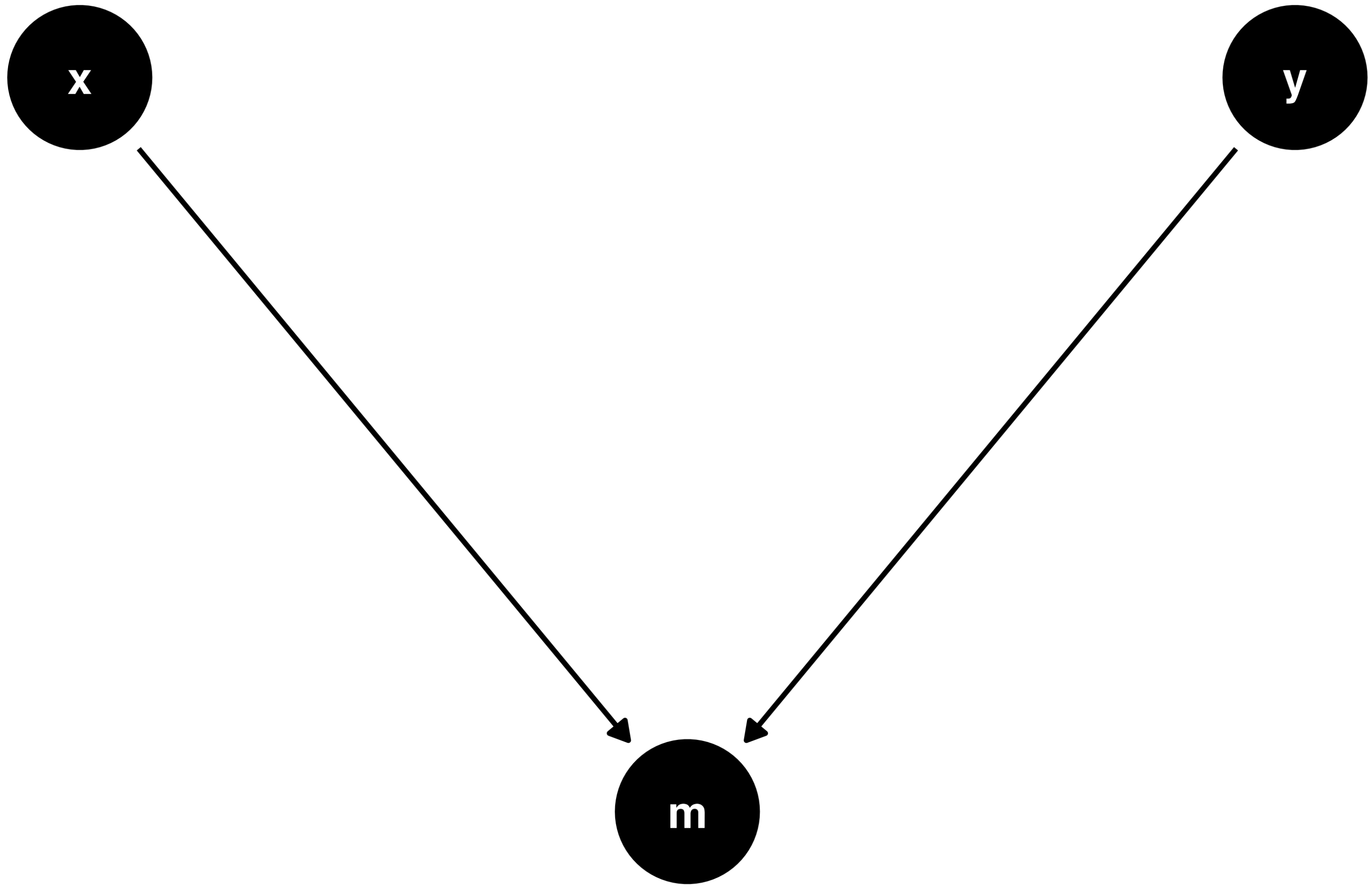
10:00

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

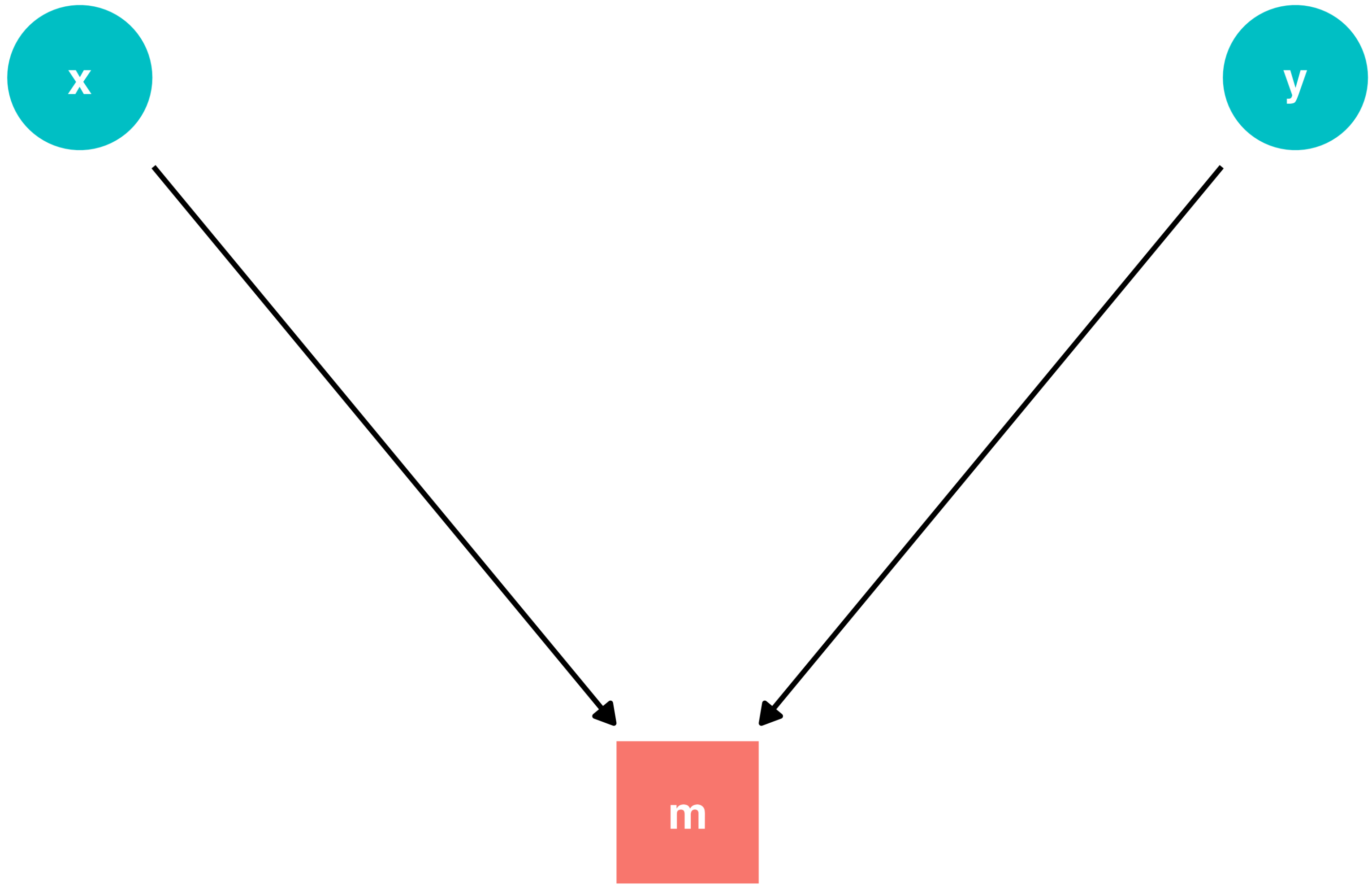
Confounders and chains



Colliders



Colliders



Let’s prove it!

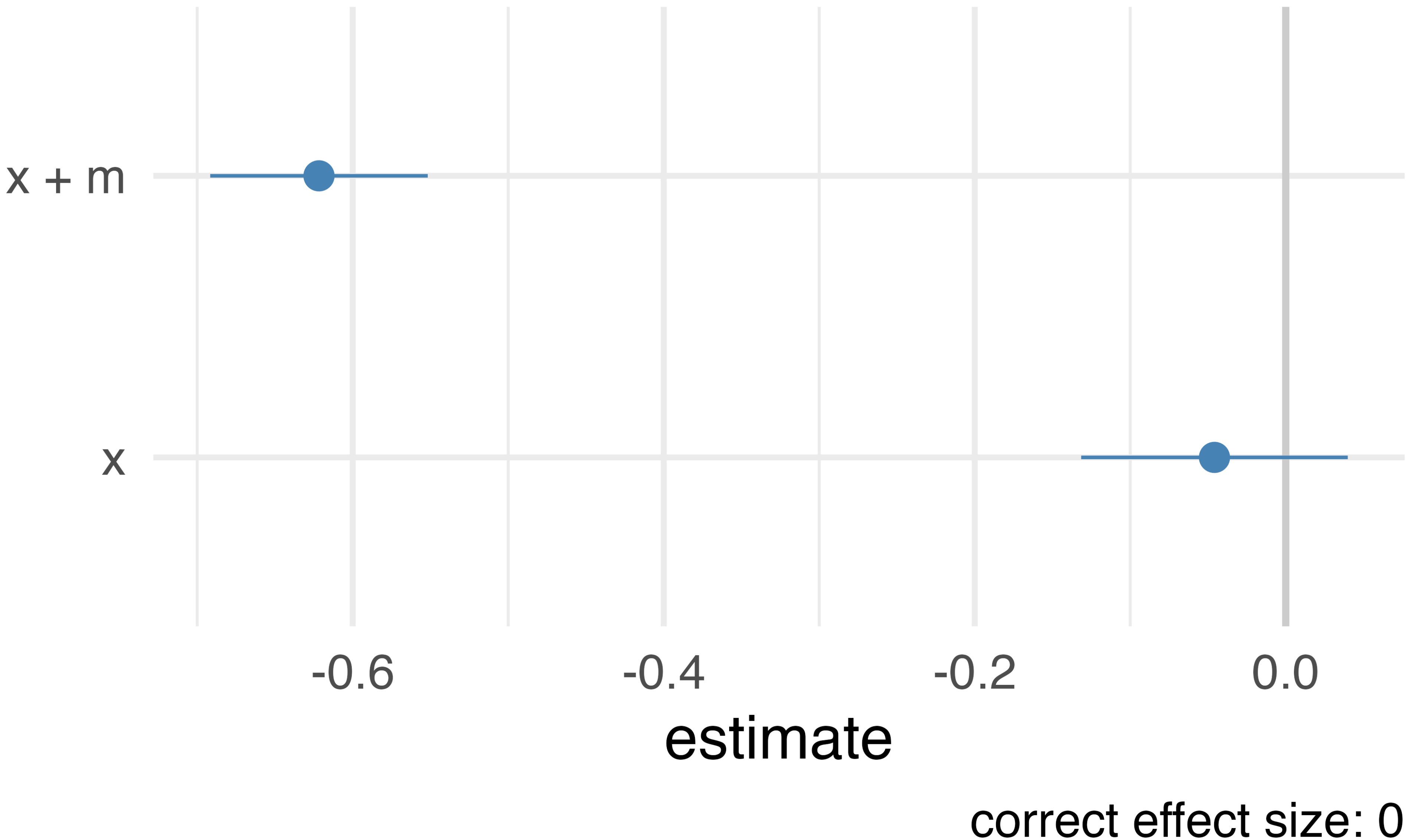
```
set.seed(1234)
collider_data <- collider_triangle() |>
  simulate_data(-.6)
```

Let’s prove it!

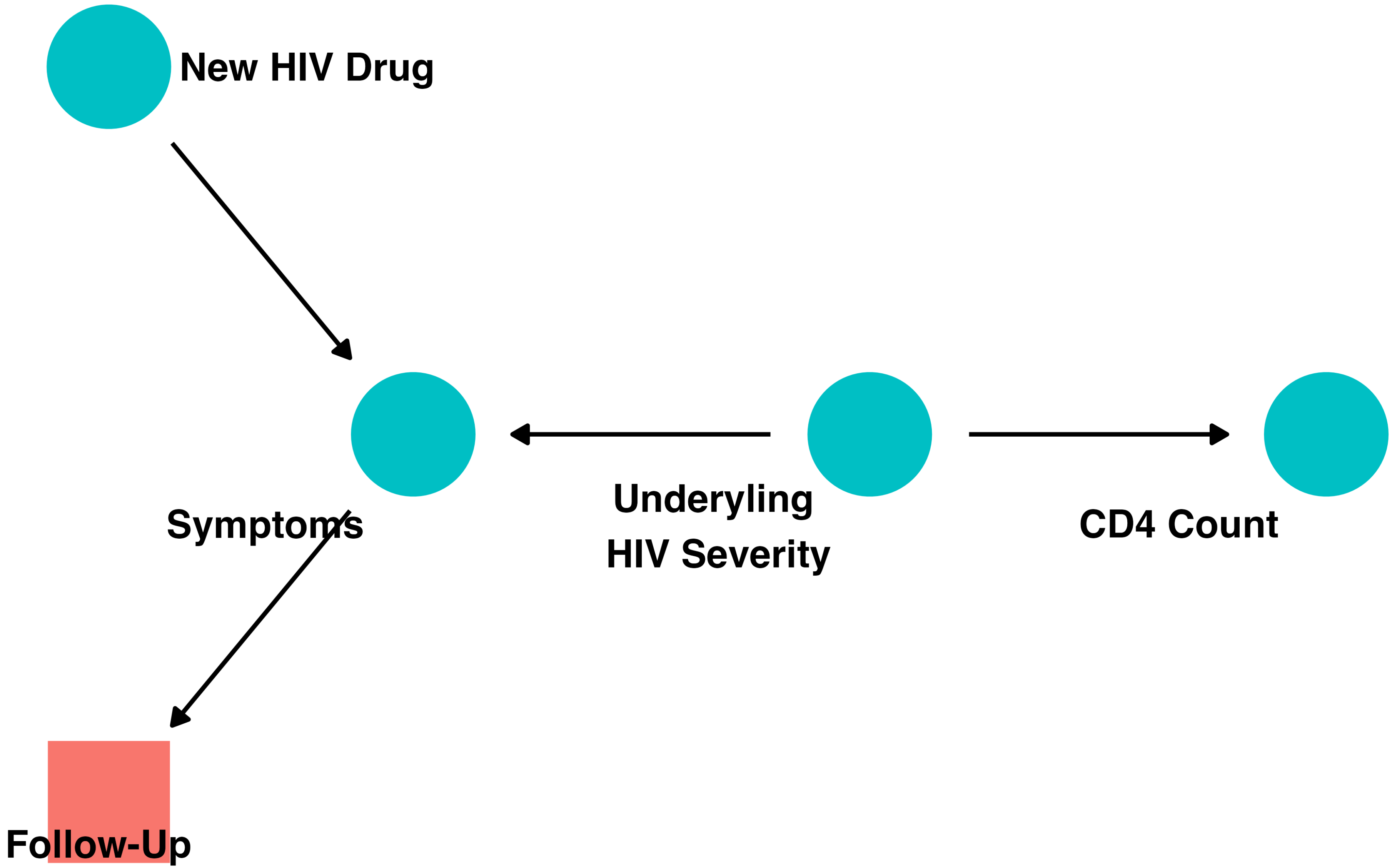
```r
collider_data
```

```
# 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   
```

Let's prove it!



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.qmd`

10:00