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
- 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

- Make predictions using the model on the cloned data sets
- Calculate the estimate you want, e.g. mean(x_1) - 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	у	
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

greek_model <- lm(y ~ a + 1, data = greek_data)</pre>

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

name	l	a	у
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

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

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Zeus	0	1	1
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3. Set the value of a to a single value for each cloned data set

name	l	a	у
Rheia	0	0	0
Kronos	0	0	1
Demeter	0	0	0
Hades	0	0	0
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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(</pre>
 predicted untreated,
 predicted treated
```

5. Calculate the estimate you want

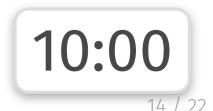
1

0.5

0.5

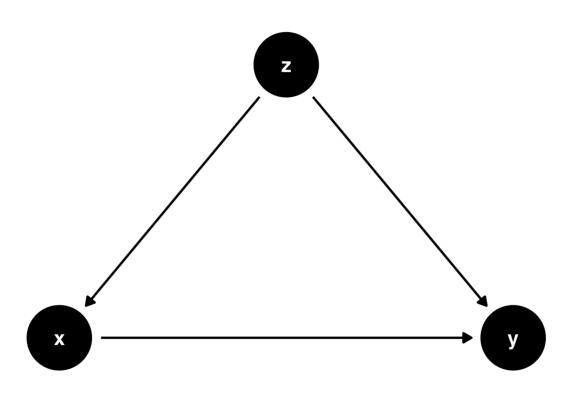
Your Turn

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

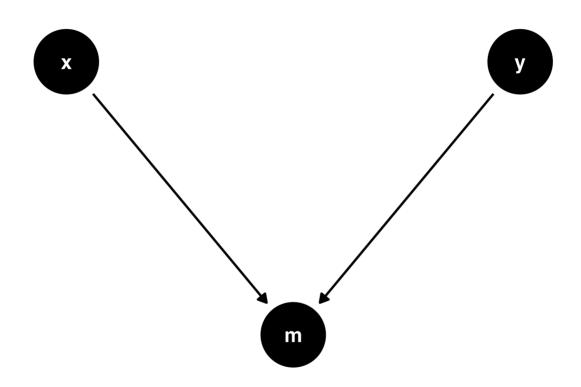


Detour: Colliders, selection bias, and loss to follow-up

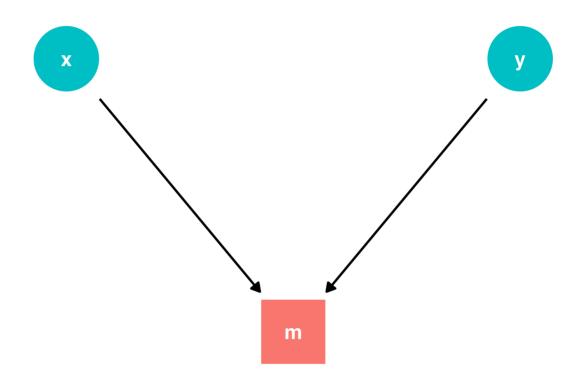
Confounders and chains



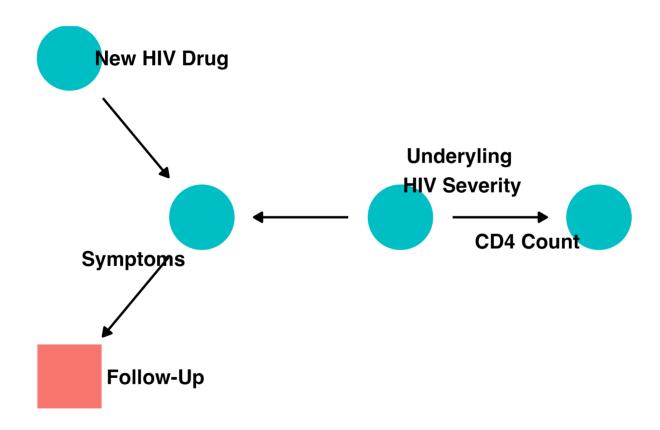
Colliders



Colliders



Loss to follow-up



Adjusting for selection bias

- Fit a probability of censoring model, e.g. glm(censoring ~ predictors, family = binomial())
- Create weights using inverse probability strategy
- 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-computationexercises.Rmd

