Designing and Analyzing Statistical Models

EES 4891-06/5891-01

Bayesian Statistical Methods

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More Categories of Confounding

General Principle: Identifiability

- **Identifiable Models:** Each set of *model parameters* makes different predictions
- **Non-Identifiable Models:** For any set of parameters, there are many other sets of parameters that make the same prediction
- Example: Categorical variables
  - *x* has three possible values: **Architect**, **Baker**, or **Carpenter**, and your regression will connect profession to income.
  - Represent *x* with two variables I_A and I_B, which are 1 if *x* has that value, and 0 otherwise.

$$\text{Income} \sim \text{Normal}(\mu, \sigma)$$

$$\mu = \alpha + \beta_A I_A + \beta_B I_B$$

  - Why don't we have I_C?

Non-Identifiability

$$\mu = \alpha + \beta_A I_A + \beta_B I_B + \beta_C I_C$$

$$I_A + I_B + I_C = 1$$

$$I_C = 1 - (I_A + I_B)$$

$$\begin{aligned}\mu &= \alpha + \beta_A I_A + \beta_B I_B + \beta_C (1 - (I_A + I_B)) \\ &= \alpha + (\beta_A - \beta_C) I_A + (\beta_B - \beta_C) I_B + \beta_C \\ &= (\alpha + \beta_C) + (\beta_A - \beta_C) I_A + (\beta_B - \beta_C) I_B\end{aligned}$$

- Now pick any number δ and let

$$\begin{aligned}\alpha' &= \alpha - \delta \\ \beta'_A &= \beta_A + \delta \\ \beta'_B &= \beta_B + \delta \\ \beta'_C &= \beta_C + \delta\end{aligned}$$

And

$$\mu' = \alpha' + \beta'_A I_A + \beta'_B I_B + \beta'_C I_C$$

Non-Identifiability (cont.)

$$
\begin{aligned}
\mu &= \alpha + \beta_A I_A + \beta_B I_B + \beta_C I_C \\
&= (\alpha + \beta_C) + (\beta_A - \beta_C) I_A + (\beta_B - \beta_C) I_B \\
\mu' &= \alpha' + \beta'_A I_A + \beta'_B I_B + \beta'_C I_C \\
&= (\alpha' + \beta_C) + (\beta'_A - \beta'_C) I_A + (\beta'_B - \beta'_C) I_B \\
&= [(\alpha - \delta) + (\beta_C + \delta)] + [(\beta_A + \delta) - (\beta_C + \delta)] I_A + [(\beta_B + \delta) - (\beta_C + \delta)] I_B \\
&= [(\alpha - \cancel{\delta}) + (\beta_C + \cancel{\delta})] + [(\beta_A + \cancel{\delta}) - (\beta_C + \cancel{\delta})] I_A + [(\beta_B + \cancel{\delta}) - (\beta_C + \cancel{\delta})] I_B \\
&= (\alpha + \beta_C) + (\beta_A - \beta_C) I_A + (\beta_B - \beta_C) I_B \\
&= \mu
\end{aligned}
$$

- So for any δ, $\mu' = \mu$.
  - This means that there isn't a **best** set of values for α, β_A, β_B, and β_C.
  - The problem is if you know I_A and I_B, then you also know I_C.
  - If you don't have an I_C variable, then this problem doesn't come up.
- There should be one fewer indicator variables than there are levels of the category variable.

Worked Example

- Pick values: $\alpha = 1$, $\beta_A = 2$, $\beta_B = 3$, $\beta_C = 4$
- $\delta = 0.5$
- Alternate values: $\alpha' = 0.5$, $\beta_A = 2.5$, $\beta_B = 3.5$, $\beta_C = 4.5$

$$
\begin{aligned}
\mu &= 1 + 2I_A + 3I_B + 4I_C \\
&= (1 + 4) + (2 - 4)I_A + (3 - 4)I_B \\
&= 5 - 2I_A - 1I_B \\
\mu' &= 0.5 + 2.5I_A + 3.5I_B + 4.5I_C \\
&= (0.5 + 4.5) + (2.5 - 4.5)I_A + (3.5 - 4.5)I_B \\
&= 5 - 2I_A - 1I_B \\
&= \mu
\end{aligned}
$$

Multicollinearity

Multicollinearity

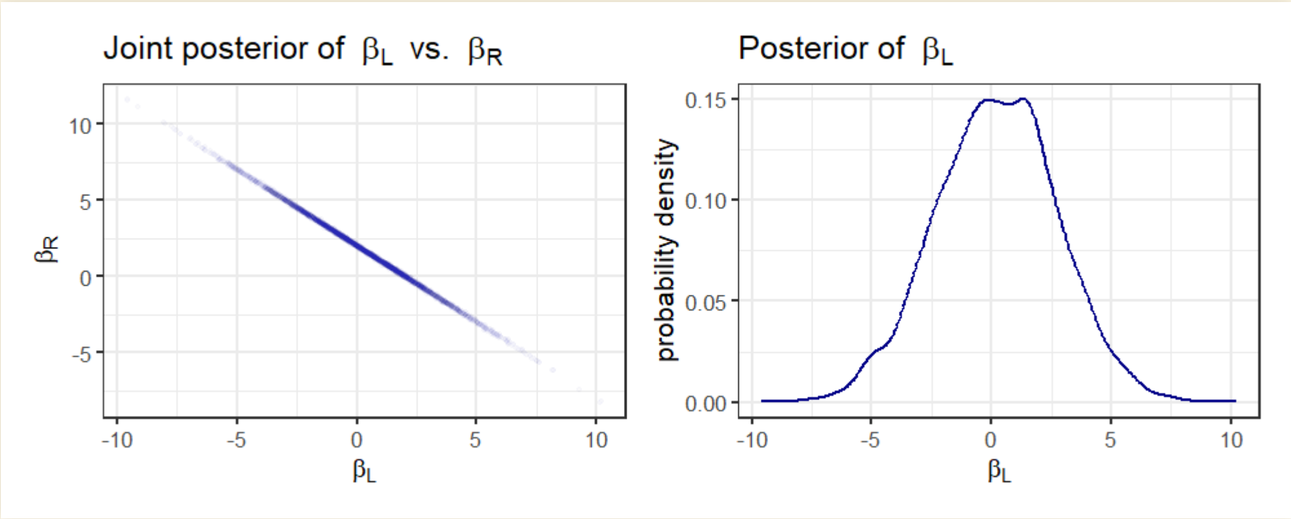
- Height versus length of legs:

$$H \sim \text{Normal}(\mu, \sigma)$$
$$\mu = \alpha + \beta_R R + \beta_L L,$$

  where
  - H is the person's height,
  - R is the length of the right leg,
  - L is the length of the left leg.
- The legs don't have identical length, but they are highly correlated.
- This creates a problem of identifiability:
  - Start with β_L and β_R,
    - then for some number δ, consider
      - $\beta'_L = \beta_L + \delta$
      - $\beta'_R = \beta_R - \delta$
  - On average $L = R$, so $\mu' = \mu$.
    - β_L and β_R are not identifiable.

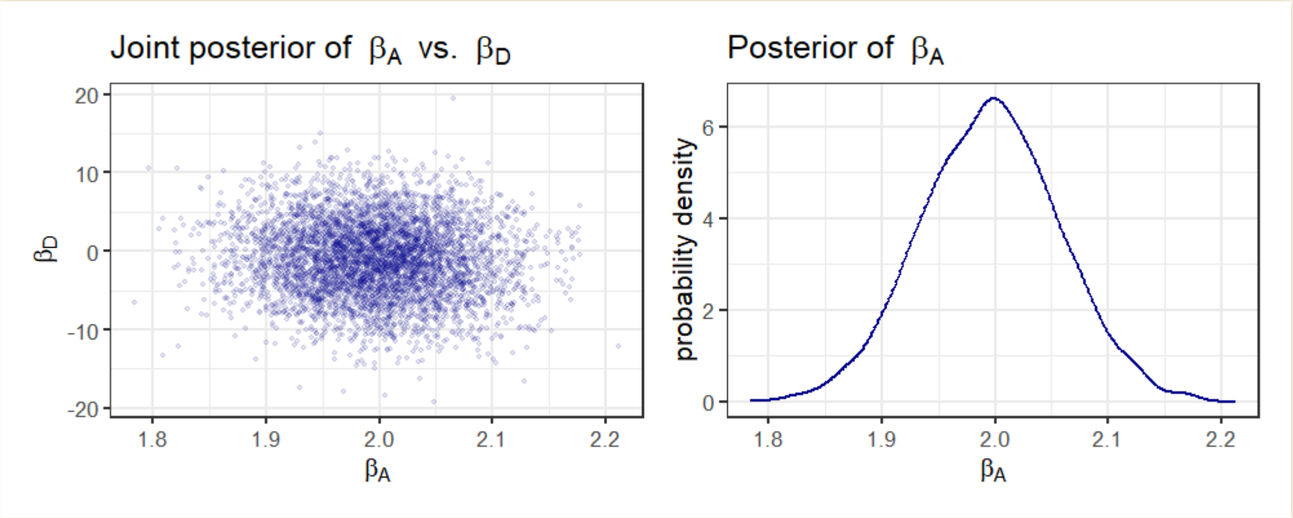
Does Multicollinearity Matter?

- McElreath says it doesn't matter for model predictions
  - Only matters for interpreting model.
  - Large uncertainty in posteriors for parameters when considered,
    - Because many values of β_L and β_R are just as probable.
  - The *joint posterior* for β_L and β_R is very narrow.



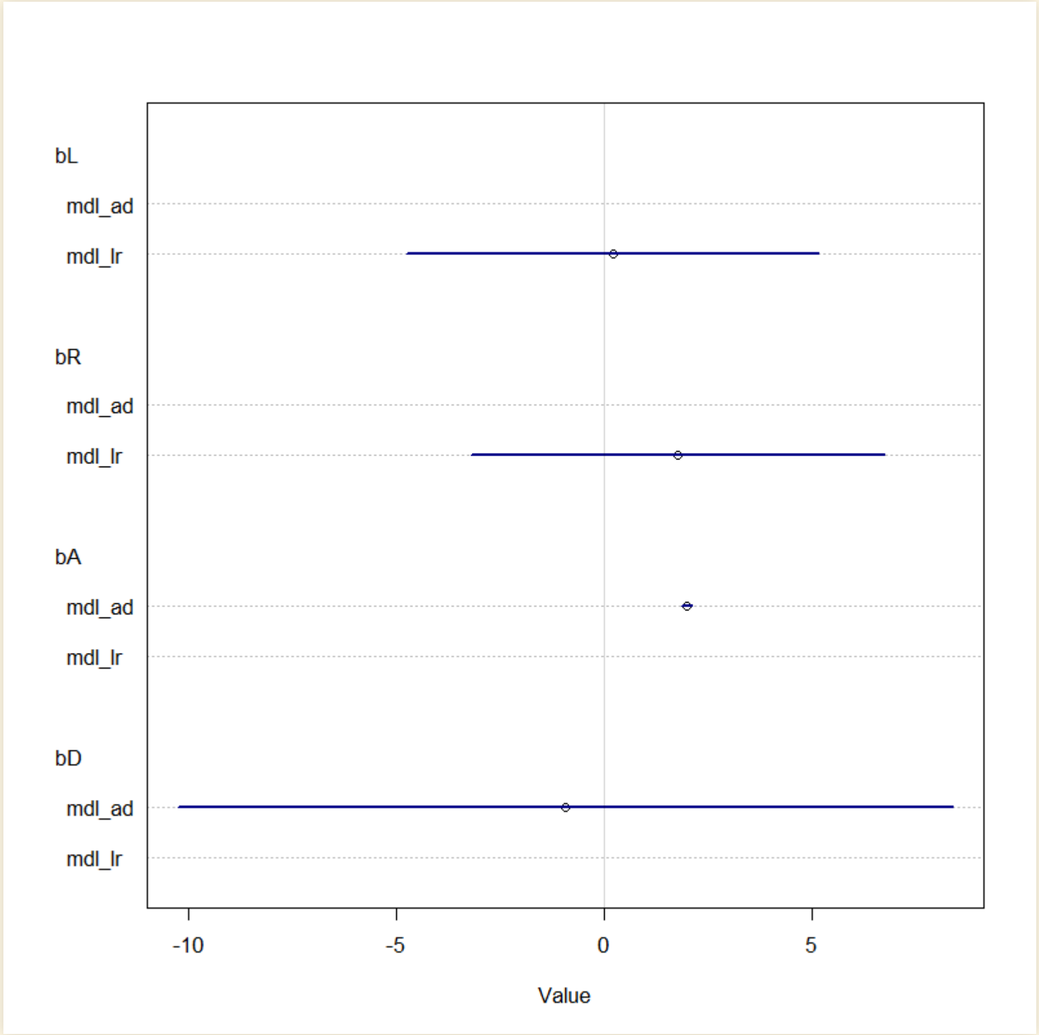
Another perspective

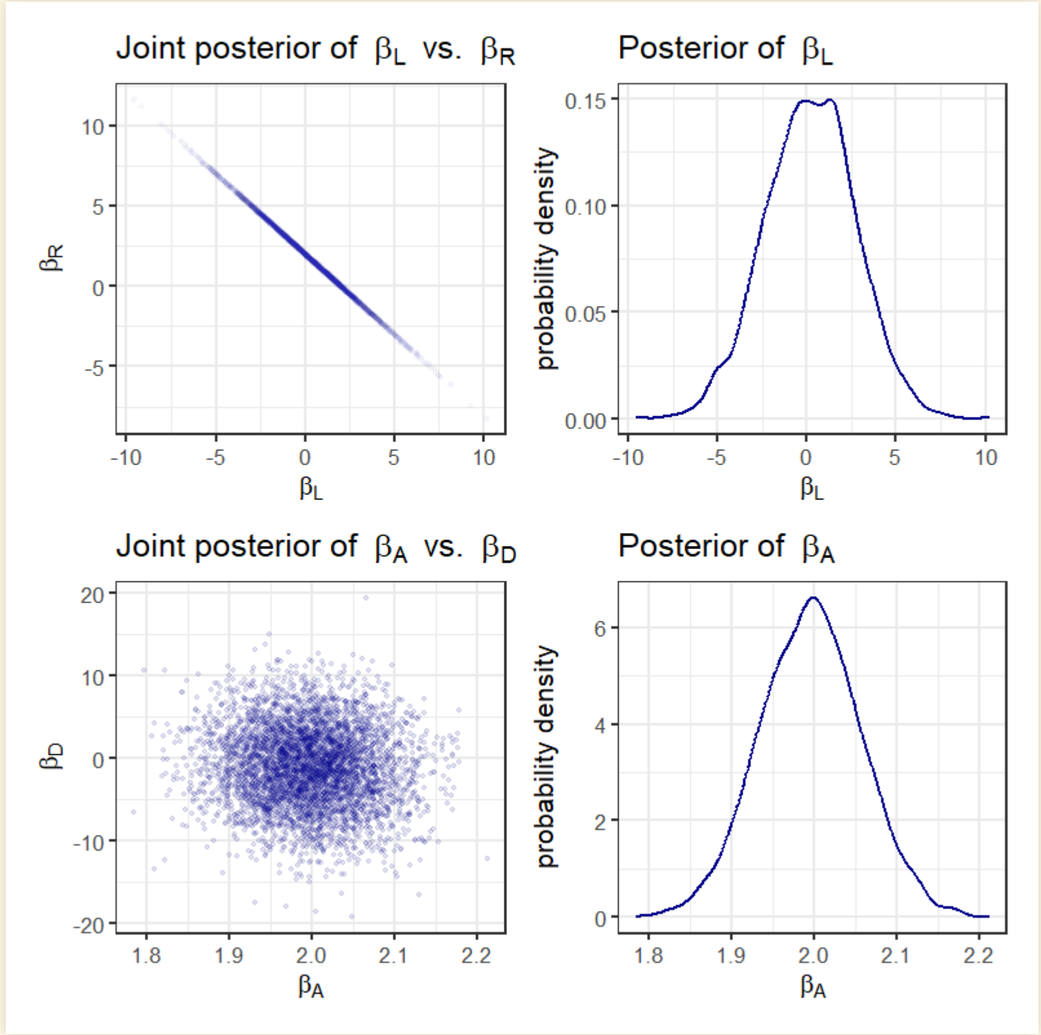
- Multicollinearity can make computational analysis difficult
- One response:
  - Define new variables:
    - $A = \text{average} = (L + R)/2$
    - $D = \text{difference} = (L - R)/2$
    - $L = A + D, R = A - D.$



Summary

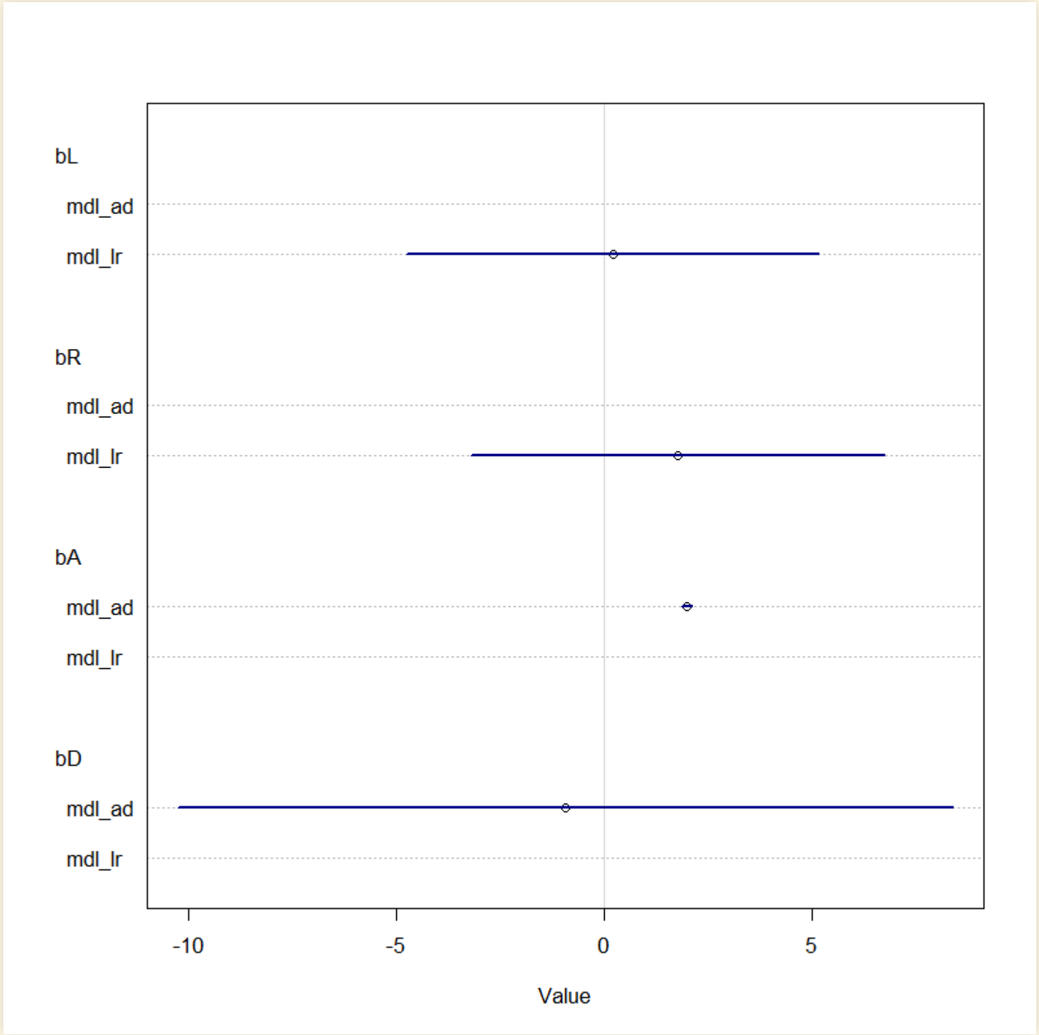
- Note how different the scales are for β_A vs. β_L.

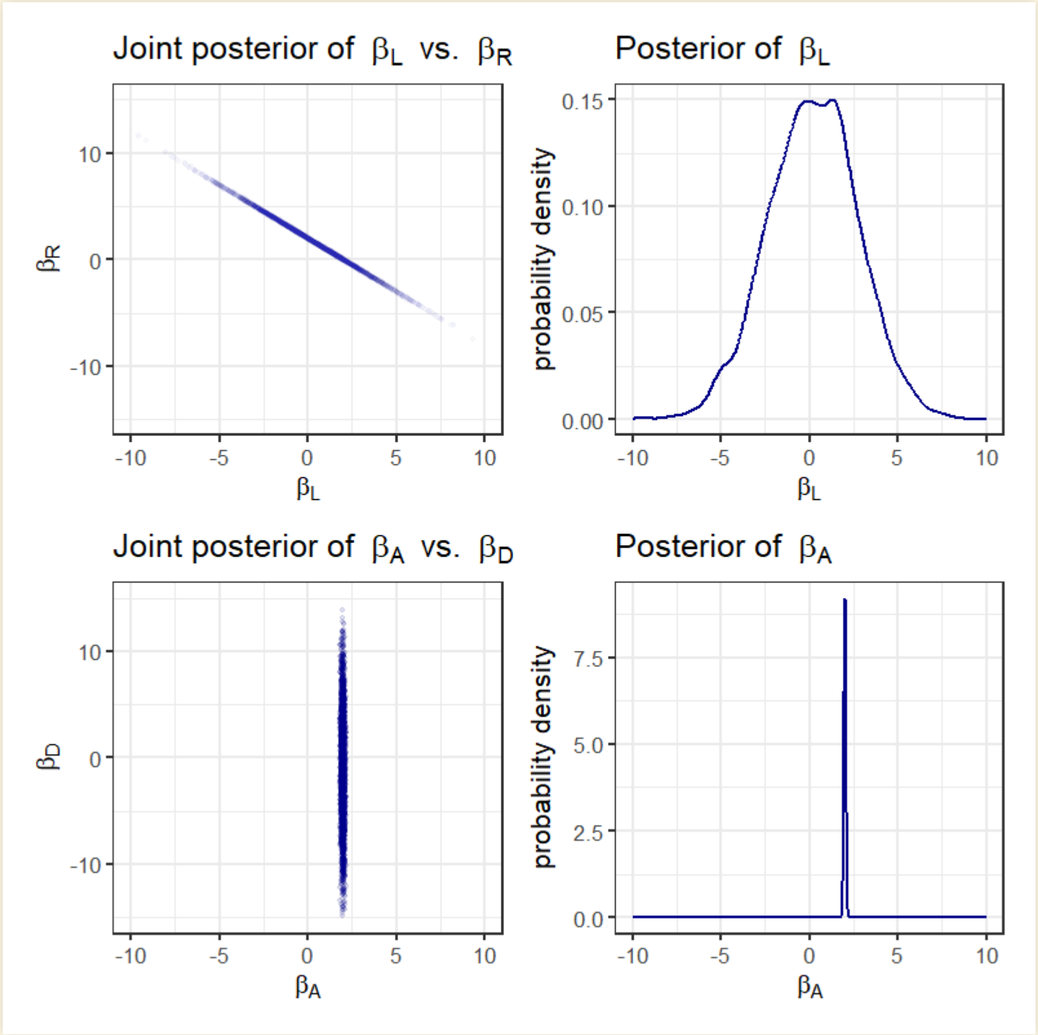




Summary

- Replotted with equal scales





Multicollinearity with Milk Data

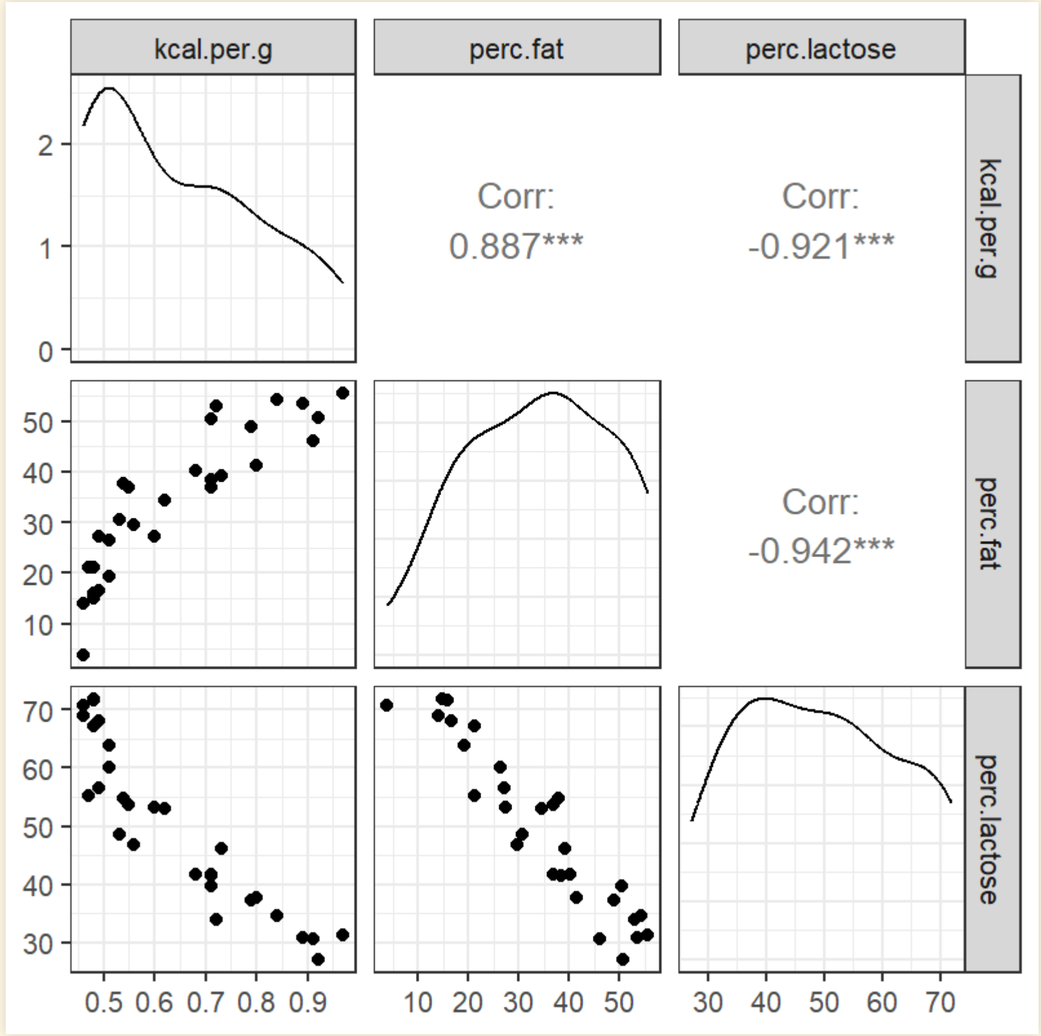
Multicollinearity with Milk Data

- Calories come from fat and sugar (lactose):

```
data(milk)
d <- milk
d$K <- standardize(d$kcal.per.g)
d$F <- standardize(d$perc.fat)
d$L <- standardize(d$perc.lactose)
```

- Make a pairwise correlation plot

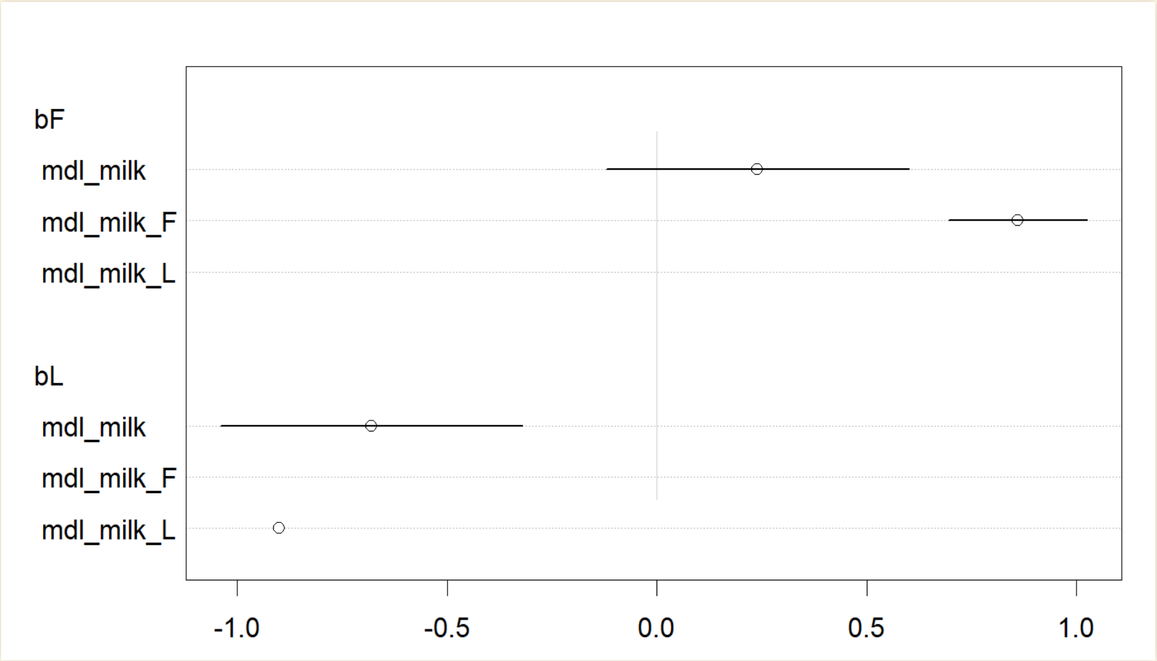
```
library(tidyverse)
library(GGally)

d %>% select(kcal.per.g, perc.fat, perc.lactose) %>%
  ggpairs()
```



Making a model

```
mdl_milk_F <- quap(
    alist(
        K ~ dnorm(mu, sigma),
        mu <- a + bF * F,
        a ~ dnorm(0, 0.2),
        bF ~ dnorm(0, 0.5),
        sigma ~ dexp(1)
    ), data = d)

mdl_milk_L <- quap(
    alist(
        K ~ dnorm(mu, sigma),
        mu <- a + bL * L,
        a ~ dnorm(0, 0.2),
        bL ~ dnorm(0, 0.5),
        sigma ~ dexp(1)
    ), data = d)
```

```
mdl_milk <- quap(
    alist(
        K ~ dnorm(mu, sigma),
        mu <- a + bF * F + bL *
         L,
        a ~ dnorm(0, 0.2),
        bF ~ dnorm(0, 0.5),
        bL ~ dnorm(0, 0.5),
        sigma ~ dexp(1)
    ), data = d)
```




```
precis_show(precis(mdl_milk_F, digits = 2))
```

```
##       mean   sd  5.5% 94.5%
## a     0.00 0.08 -0.12  0.12
## bF    0.86 0.08  0.73  1.00
## sigma 0.45 0.06  0.36  0.54
```

```
precis_show(precis(mdl_milk_L, digits = 2))
```

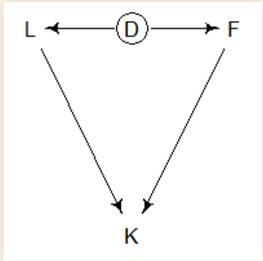
```
##         mean   sd  5.5% 94.5%
## a       0.00 0.07 -0.11  0.11
## bL     -0.90 0.07 -1.02 -0.79
## sigma   0.38 0.05  0.30  0.46
```

```
precis_show(precis(mdl_milk, digits = 2))
```

```
##         mean   sd  5.5% 94.5%
## a       0.00 0.07 -0.11  0.11
## bF      0.24 0.18 -0.05  0.54
## bL     -0.68 0.18 -0.97 -0.38
## sigma   0.38 0.05  0.30  0.46
```

Explaining the multicollinearity

- Knowledge of biology



- Density D is important
  - Frequent nursing: watery, low-energy milk, high in sugar (lactose)
  - Infrequent nursing: rich, dense, high-energy milk, high in fat

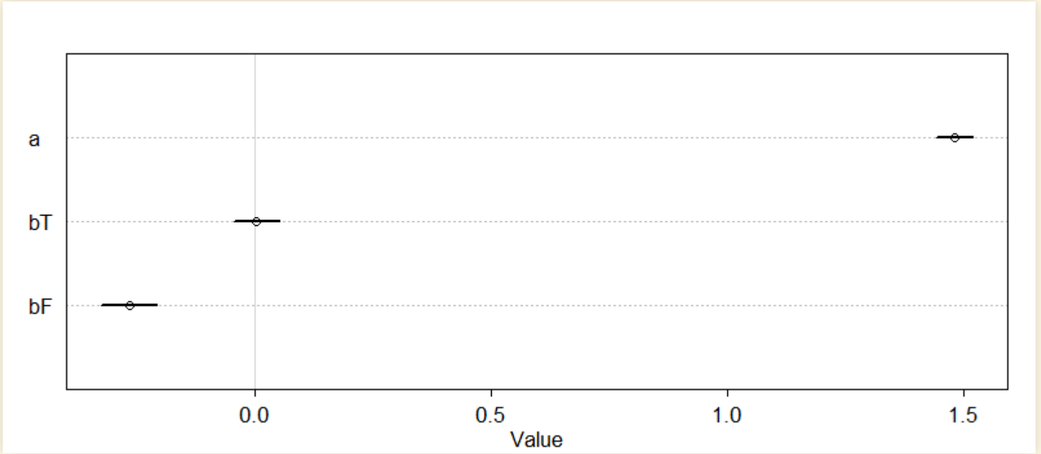
Post-Treatment Bias

Anti-Fungal Treatment Experiment

- You do an experiment
  - Divide plants in 2 groups
    - Apply anti-fungal treatment to one group ($T = 1$)
    - The other is a control ($T = 0$)
    - Observe whether there is fungus after treatment (F)
    - Compare height before treatment (H_0) to height some time after treatment (H_1).
      - Growth rate $p \geq 0$ unless fungus is very bad.
- Why doesn't the treatment have an effect?
  - `mean(bT)` = 0.

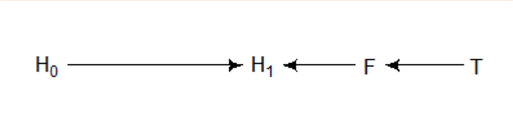
```
mdl_fungus <- quap(
    alist(
        H1 ~ dnorm(mu, sigma),
        mu <- H0 * p,
        # p is growth rate
        p <- a + bT * T + bF * F,
        a ~ dlnorm(0, 0.2),
        bT ~ dnorm(0, 0.5),
        bF ~ dnorm(0, 0.5),
        sigma ~ dexp(1)
    ), data = d)

precis_show(precis(mdl_fungus, digits = 2))
```

```
##         mean   sd  5.5% 94.5%
## a       1.48 0.02  1.44  1.52
## bT      0.00 0.03 -0.05  0.05
## bF     -0.27 0.04 -0.33 -0.21
## sigma   1.41 0.10  1.25  1.57
```



Understanding the problem

- Fungus is the big thing that affects the plants' growth
- Treatment affects fungus.
  - Doesn't affect plants directly
  - Doesn't always eliminate all fungus
- Fungus is a better predictor
  - But we don't know how bad fungus will be until *after* we treat.
- DAG



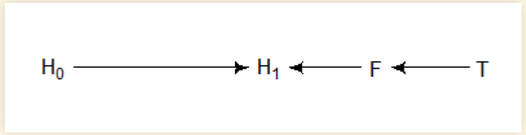

```
## Implied Conditional Independencies
```

```
## F _||_ H_0
## H_0 _||_ T
## H_1 _||_ T | F
```

```
mdl_fungus <- quap(
    alist(
        H1 ~ dnorm(mu, sigma),
        mu <- H0 * p,
        # p is growth rate
        p <- a + bT * T + bF * F,
        a ~ dlnorm(0, 0.2),
        bT ~ dnorm(0, 0.5),
        bF ~ dnorm(0, 0.5),
        sigma ~ dexp(1)
    ), data = d)
```

A Better Model

- DAG



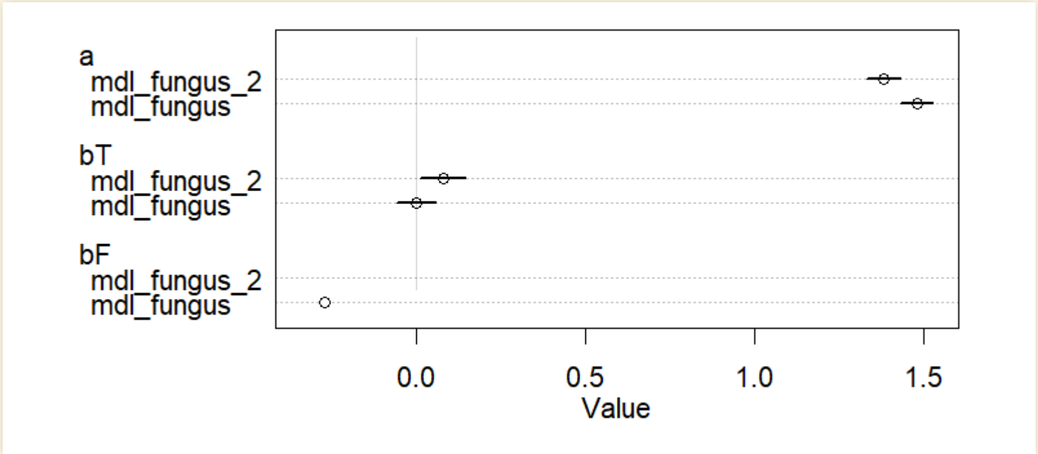

```
## Implied Conditional Independencies
```

```
## F _||_ H_0
## H_0 _||_ T
## H_1 _||_ T | F
```

- Conditioning on *F* induces a *D-separation* (*directional* separation) between *T* and *H1*.
- Remove fungus data from the model.

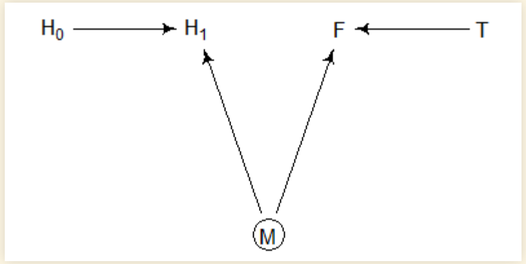
```
mdl_fungus_2 <- quap(
    alist(
        h1 ~ dnorm(mu, sigma),
        mu <- h0 * p,
        p <- a + bT * T,
        a ~ dlnorm(0, 0.2),
        bT ~ dnorm(0, 0.5),
        sigma ~ dexp(1)
    ), data = d)
precis_show(precis(mdl_fungus_2, digits = 2))
```

```
##       mean   sd 5.5% 94.5%
## a     1.38 0.03 1.34  1.42
## bT    0.08 0.03 0.03  0.14
## sigma 1.75 0.12 1.55  1.94
```



Other Post-Treatment Bias Problems

- Suppose we have this DAG:

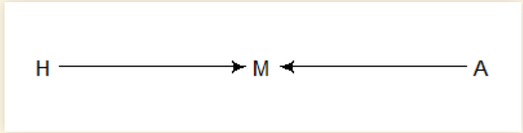


- Fungus *F* does not influence plant growth.
- Moisture *M* influences both plant growth *H1* and fungus *F*
- Fitting our original model falsely implies that treatment benefits plants.
- This is a kind of *collider* effect.

Collider Bias

Happiness and Age

- Do people get happier as they get older?
- Suppose:
  - Everyone’s happiness is something they are born with and it doesn’t change.
  - Happier people are more likely to get married
  - Older people are more likely to be married.
  - DAG:



This diagram is a **collider**: Causal paths from *H* and *A collide* at *M*

Analyze Happiness Data

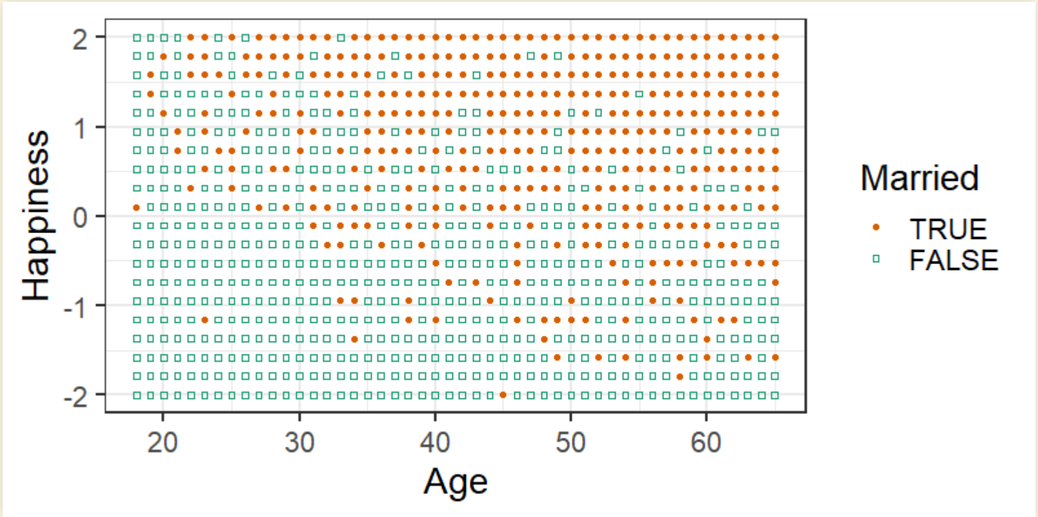
- Generate simulated data

```
# sim_happiness is a function in the rethinking package
d <- sim_happiness(seed=1977, N_years=1000)
```

- Look for an association between *age* and *happiness*.
  - We suspect that the relationship between age and happiness may be different for married people, so we include marriage as a variable.
- Clean the data: Select adults and convert age to a variable that goes from 0 to 1, and create a marriage index:

```
d2 <- filter(d, age > 17) |> # only adults
  mutate(A = (age - 18) / (65 - 18),
         m_id = married + 1,
         married = as.logical(married))
```

- The model says that people become unhappy as they get older




```
mdl_happy <- quap(
  alist(
    happiness ~ dnorm(mu, sigma),
    mu <- a[m_id] + bA * A,
    a[m_id] ~ dnorm(0, 1),
    bA ~ dnorm(0, 2),
    sigma ~ dexp(1)
  ), data = d2)
precis_show(precis(mdl_happy, depth = 2, digits = 2))
```

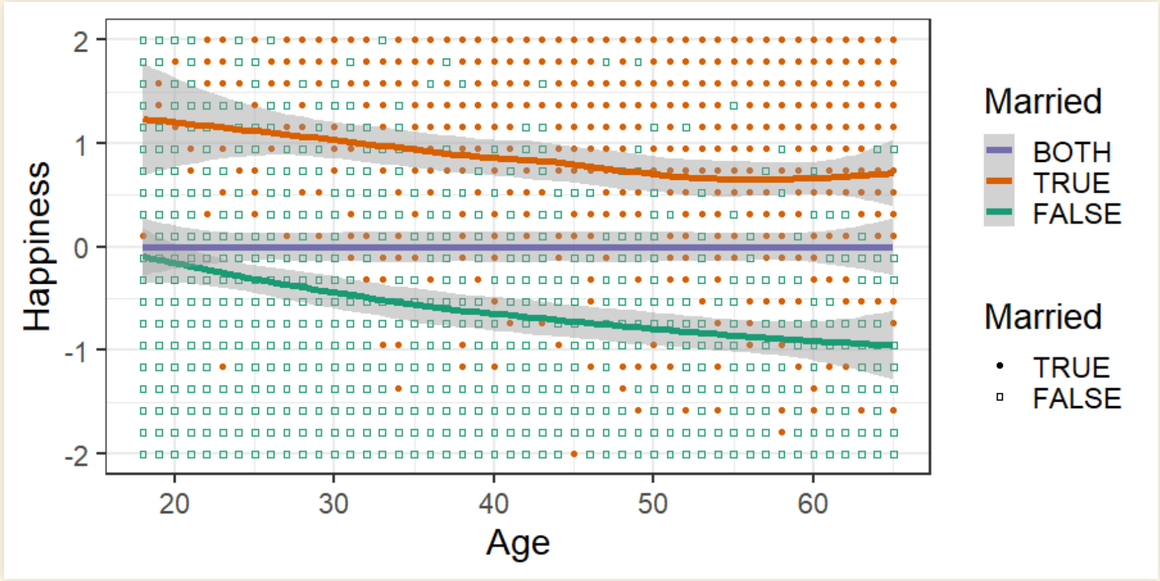
```
##          mean   sd  5.5% 94.5%
## a[1]   -0.24 0.06 -0.34 -0.13
## a[2]    1.26 0.08  1.12  1.39
## bA     -0.75 0.11 -0.93 -0.57
## sigma   0.99 0.02  0.95  1.03
```

A Different Model

- Try a different model that does not control for marriage.
- This model shows no association between age and happiness.
- What happened?
- Consider married people:
  - Older people are more likely to get married
  - Happier people are more likely to get married
  - Happy people get married younger
  - Unhappy people get married older
  - Thus, among married people, younger people are happier, and older ones are unhappier.
- Consider single people
  - As people age, happier ones marry,
  - So the older someone is, if they are still single, they're more likely to be unhappy.

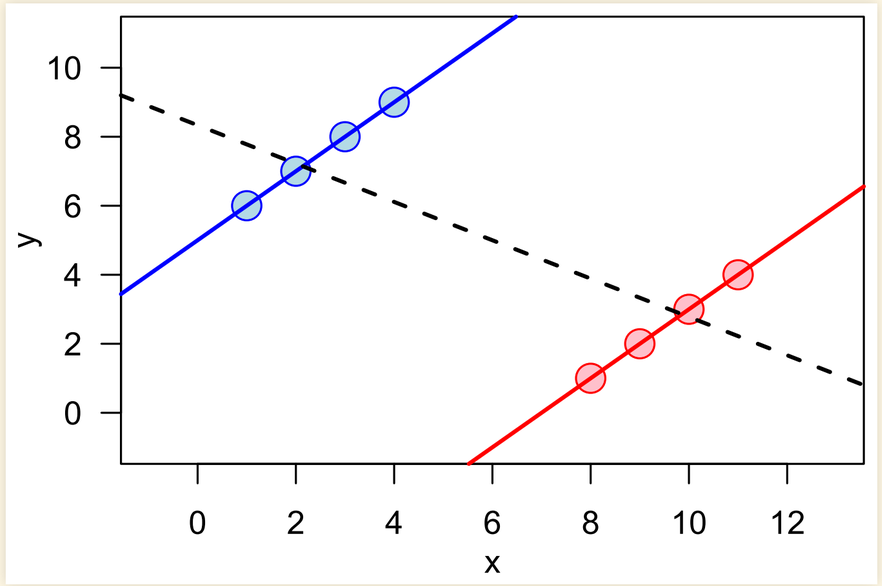
```
mdl_happy_2 <- quap(
    alist(
        happiness ~ dnorm(mu, sigma),
        mu <- a + bA*A,
        a ~ dnorm(0, 1),
        bA ~ dnorm(0, 2),
        sigma ~ dexp(1)
    ), data = d2)

precis_show(precis(mdl_happy_2, digits = 2))
```

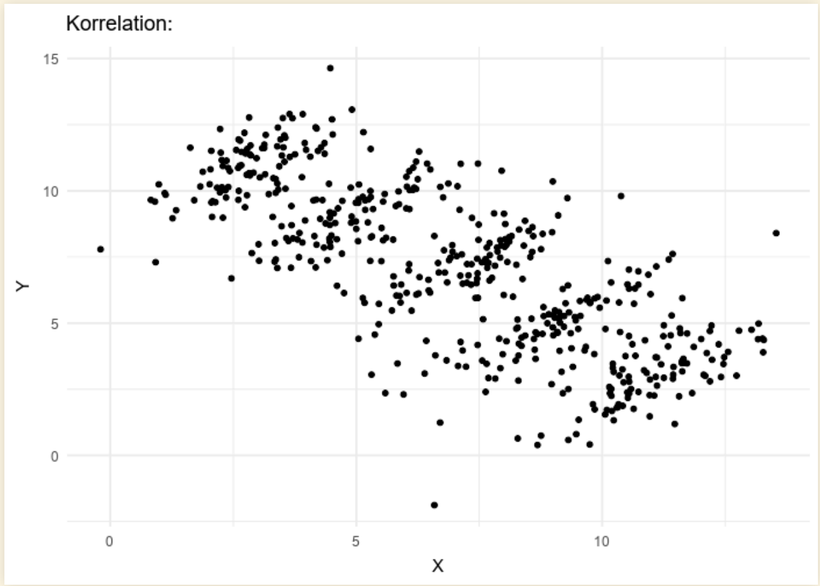
```
##       mean   sd  5.5% 94.5%
## a     0.00 0.08 -0.12  0.12
## bA    0.00 0.13 -0.21  0.21
## sigma 1.21 0.03  1.17  1.26
```



Simpson’s Paradox

- Split data into two groups
  - Each group has one kind of effect.
- When you look at all the data together, it has the opposite effect.





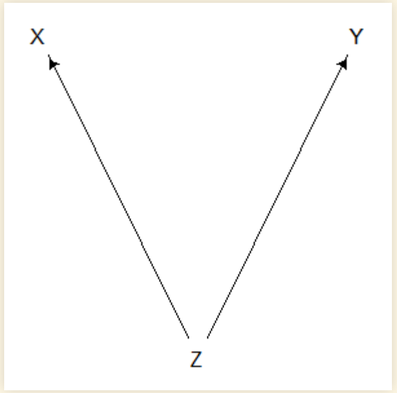
Images: Wikipedia article on Simpson’s Paradox

Categories of Confounding Relationships

Categories of Confounding Relationships

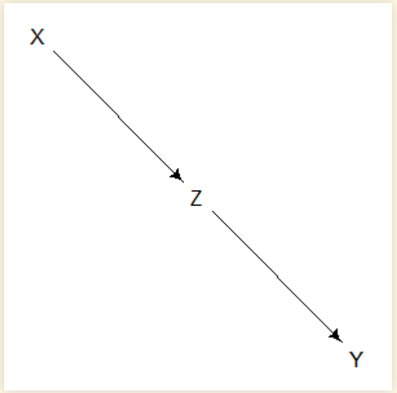
- We want to infer Y from X and Z

1. Fork



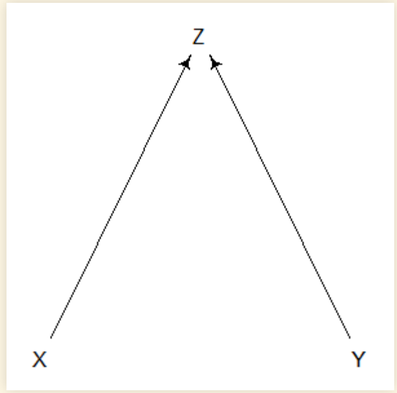
- $X \perp\!\!\!\perp Y | Z$
- Divorce rate
- Post-treatment bias: moisture

2. Pipe



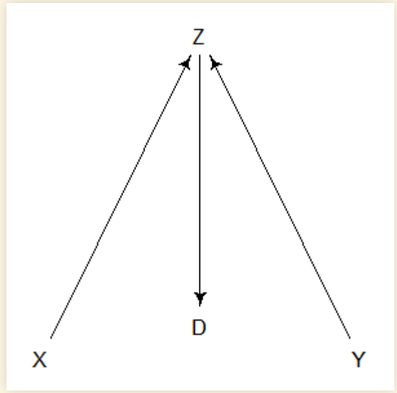
- $X \perp\!\!\!\perp Y | Z$
- Post-treatment bias: fungus & treatment

3. Collider



- $X \not\perp\!\!\!\perp Y | Z$
- Happiness & age
- Trustworthiness vs. newsworthiness

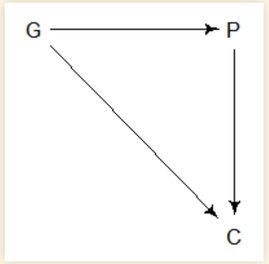
4. Descendant



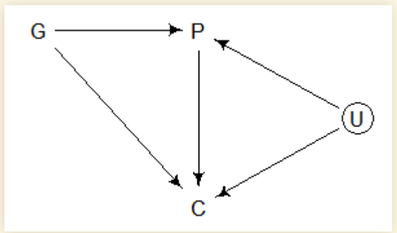
- All causal DAGs are build of combinations of these four patterns.

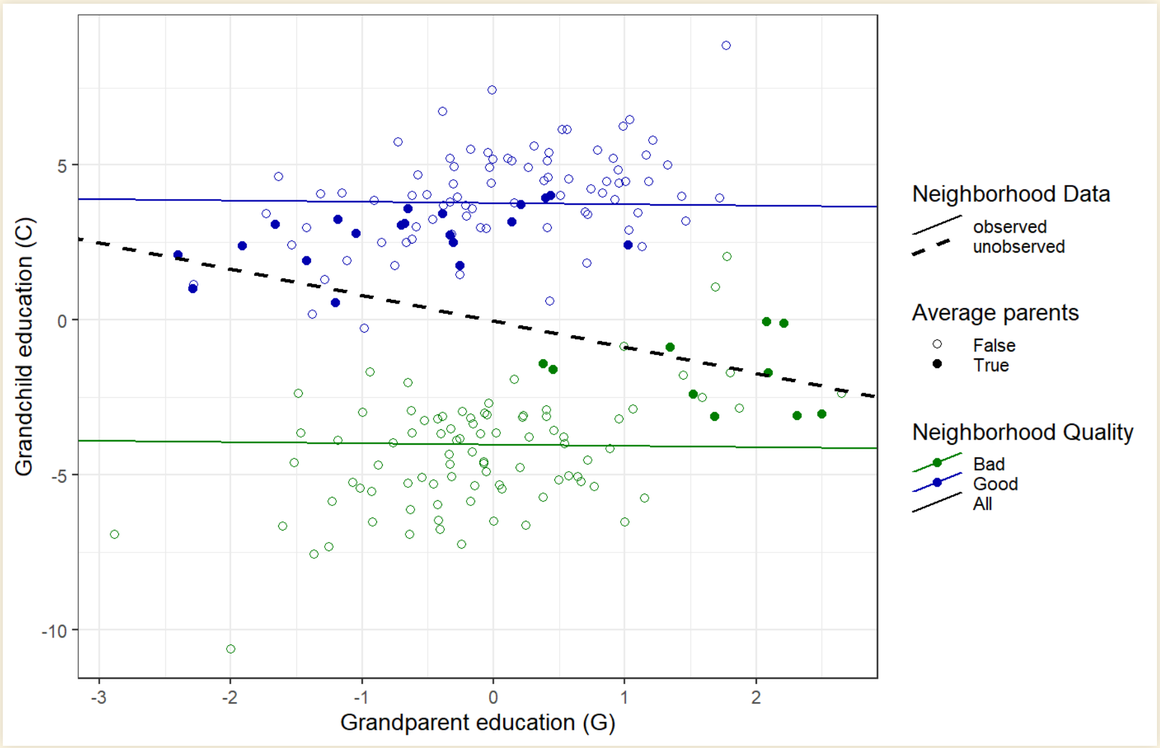
Example: Haunted DAG

- How do parents' *P* and grandparents' *G* educational attainment influence educational attainment of children *C*?



- Problem: there are unmeasured effects here, such as the character of the neighborhood.
  - Grandparents moved into the neighborhood after they finished school,
  - Parents and children grew up in the neighborhood and are affected by it.

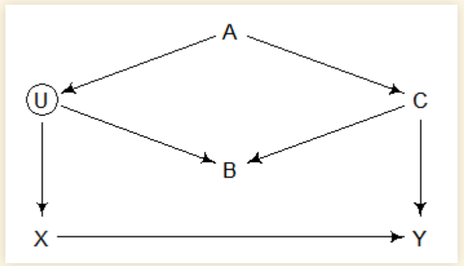




- There is a no correlation between *G* and *C* in each neighborhood
  - This is the correct answer.
- But when we don't account for the neighborhood effect, the collider bias makes it look like there's a negative correlation
  - more educated grandparents have less educated grandchildren

Backdoor Effects

- In the age and happiness example, conditioning on the marriage variable created bias,
- But in the grandparent, parent, and children example, we needed to condition on the neighborhood to avoid bias.
  - How can we tell when to condition on a variable?
- Consider this DAG:



- How does X affect Y?
- Backdoor (non-causal) paths from X to Y:
  1. $X \leftarrow U \leftarrow A \rightarrow C \rightarrow Y$
  2. $X \leftarrow U \rightarrow B \leftarrow C \rightarrow Y$
- Which backdoor path is open?
  1. This backdoor is open because it has no internal collider
     - If we condition on A, C, or U, it will close the backdoor.
  2. This backdoor is closed because B is a collider.
     - If we condition on B, it will open the backdoor and introduce a collider effect.
- Closing backdoors:
  - We don't observe U, so we can't condition on it.
  - To close the backdoor path #1, condition on A or C.

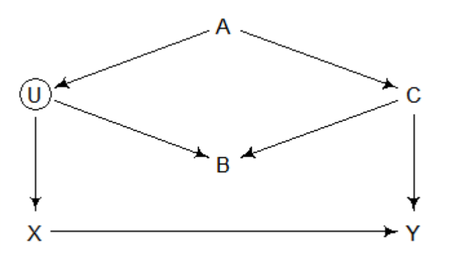
Automated Analysis

- Define the DAG

```
library(dagitty)
dag_two_roads <- dagitty("dag {
U [unobserved]
X -> Y
X <- U <- A -> C -> Y
U -> B <- C
}")
```

- Optionally, draw the DAG diagram

```
coordinates(dag_two_roads) <- list(
x = c(U = 0, X = 0, A = 1, B = 1, C = 2, Y = 2),
y = c(U = 0, X = 1, A = - 0.5, B = 0.5, C = 0, Y = 1)
)
drawdag(dag_two_roads)
```



- Analyze to identify which variables to condition on

```
adjustmentSets(dag_two_roads, exposure = "X", outcome = "Y")
```

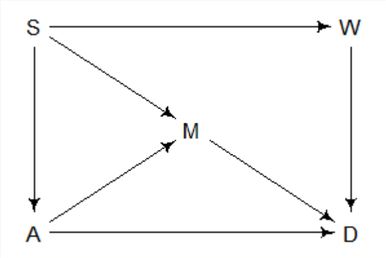
```
## { C }
## { A }
```

  - Condition on *A* or *C*

Backdoors in Waffle-House and Divorce

- Waffle-House and Divorce

```
dag_waffles <- dagitty("dag {
  A -> D
  A -> M -> D
  A <- S -> M
  S -> W -> D
}")
```



S = Southern state, W = waffle-house restaurants, A = median age at marriage, M = marriage rate, and D = divorce rate.

- Identify which variables to condition on

```
adjustmentSets(dag_waffles, exposure="W", outcome="D")
```

```
## { A, M }
## { S }
```

  - What does this mean?

- Backdoors:
  1. $W \leftarrow S \rightarrow M \rightarrow D$
  2. $W \leftarrow S \rightarrow A \rightarrow D$
  3. $W \leftarrow S \rightarrow A \rightarrow M \rightarrow D$
  - All of these pass through S.
  - To close the backdoors, either
    - Condition on S, or
    - Condition on both A and M.

- Further analysis: *conditional independencies*

```
impliedConditionalIndependencies(dag_waffles)
```

```
## A _||_ W | S
## D _||_ S | A, M, W
## M _||_ W | S
```

  - If we condition on S, then A and M should both be independent of W
  - If we simultaneously condition on A, M, and W, then D should be independent of S.