

Designing and Analyzing Statistical Models

EES 4891-06/5891-01

Bayesian Statistical Methods

Jonathan Magnolia Gilligan

Class #8: Monday February 9, 2026

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

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

$$I_A + I_B + I_C = 1$$

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

$$\mu = \alpha + \beta_A I_A + \beta_B I_B + \beta_C (1 - (I_A + I_B))$$

$$= \alpha + (\beta_A - \beta_C) I_A + (\beta_B - \beta_C) I_B + \beta_C$$

$$= (\alpha + \beta_C) + (\beta_A - \beta_C) I_A + (\beta_B - \beta_C) I_B$$

- Now pick any number δ and let

$$\alpha' = \alpha - \delta$$

$$\beta'_A = \beta_A + \delta$$

$$\beta'_B = \beta_B + \delta$$

$$\beta'_C = \beta_C + \delta$$

And

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

Non-Identifiability (cont.)

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

$$= (\alpha + \beta_C) + (\beta_A - \beta_C) I_A + (\beta_B - \beta_C) I_B$$

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

$$= (\alpha' + \beta_C) + (\beta'_A - \beta'_C) I_A + (\beta'_B - \beta'_C) I_B$$

$$= [(\alpha - \delta) + (\beta_C + \delta)] + [(\beta_A + \delta) - (\beta_C + \delta)] I_A + [(\beta_B + \delta) - (\beta_C + \delta)] I_B$$

$$= [(\alpha - \delta') + (\beta_C + \delta')] + [(\beta_A + \delta') - (\beta_C + \delta')] I_A + [(\beta_B + \delta') - (\beta_C + \delta')] I_B$$

$$= (\alpha + \beta_C) + (\beta_A - \beta_C) I_A + (\beta_B - \beta_C) I_B$$

$$= \mu$$

- 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: $\alpha' = 0.5, \beta_A = 2.5, \beta_B = 3.5, \beta_C = 4.5$

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

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

Multicollinearity

Multicollinearity

- Height versus length of legs:

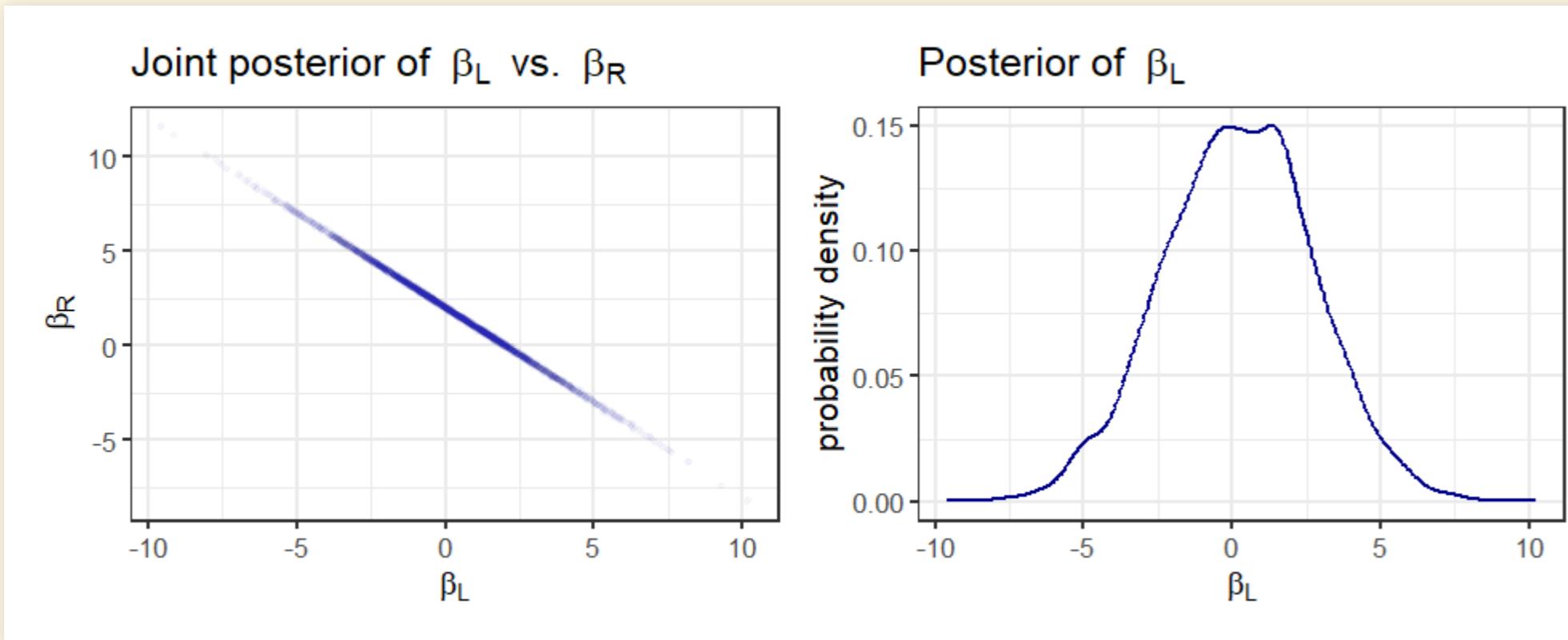
$$H \sim \text{Normal}(\mu, \sigma)$$
$$\mu = \alpha + \beta_R R + \beta_L L,$$

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.

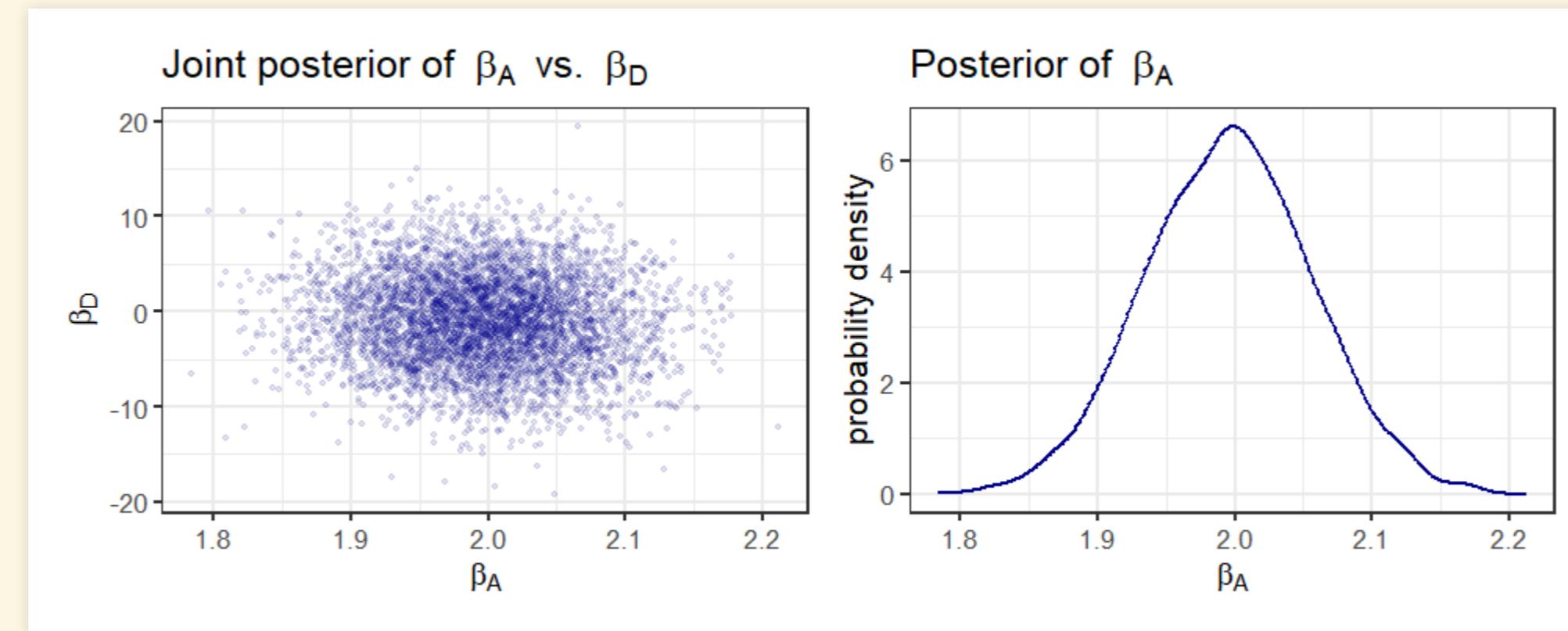
Does Multicollinearity Matter?

- 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.



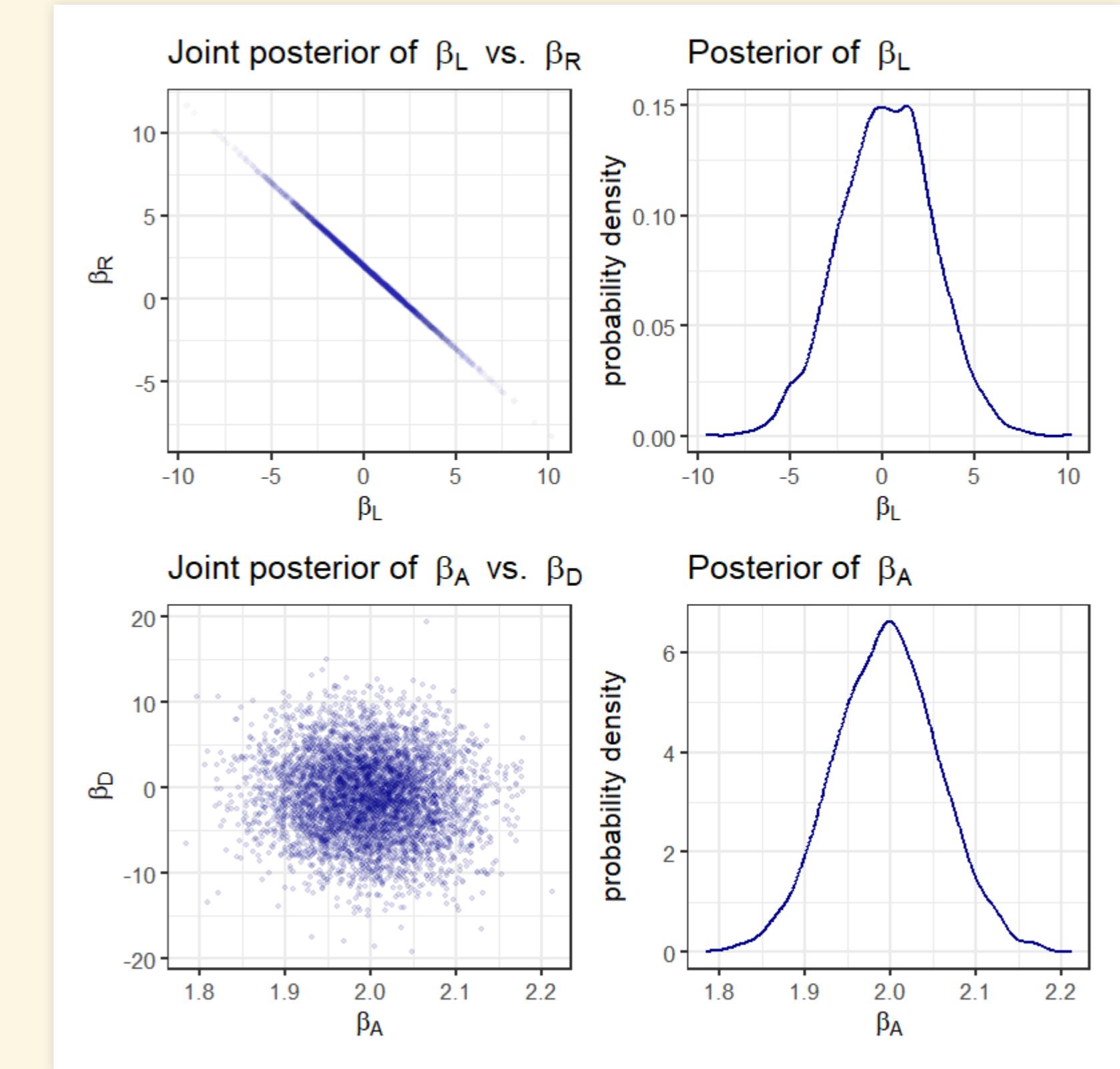
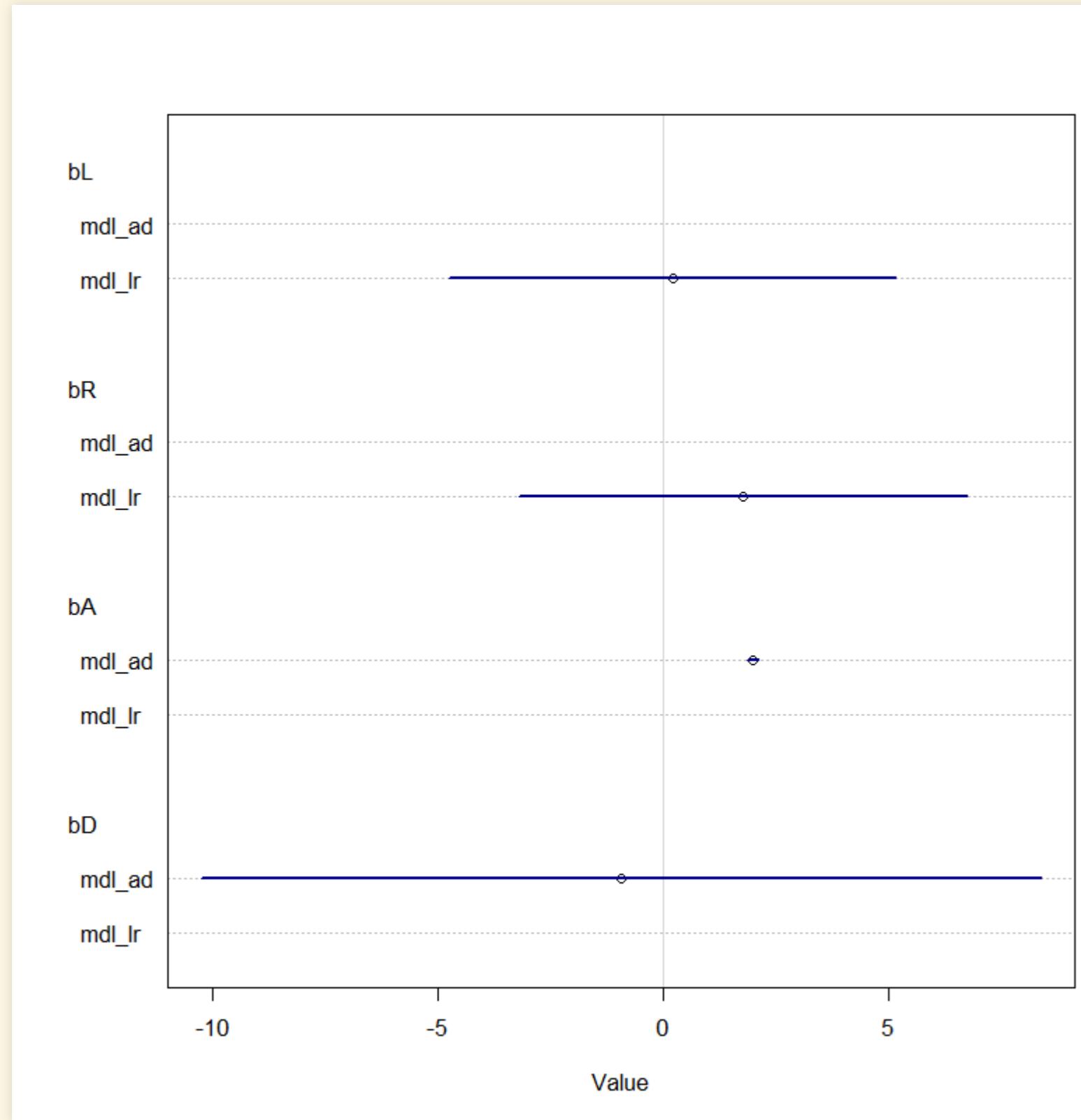
Another perspective

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



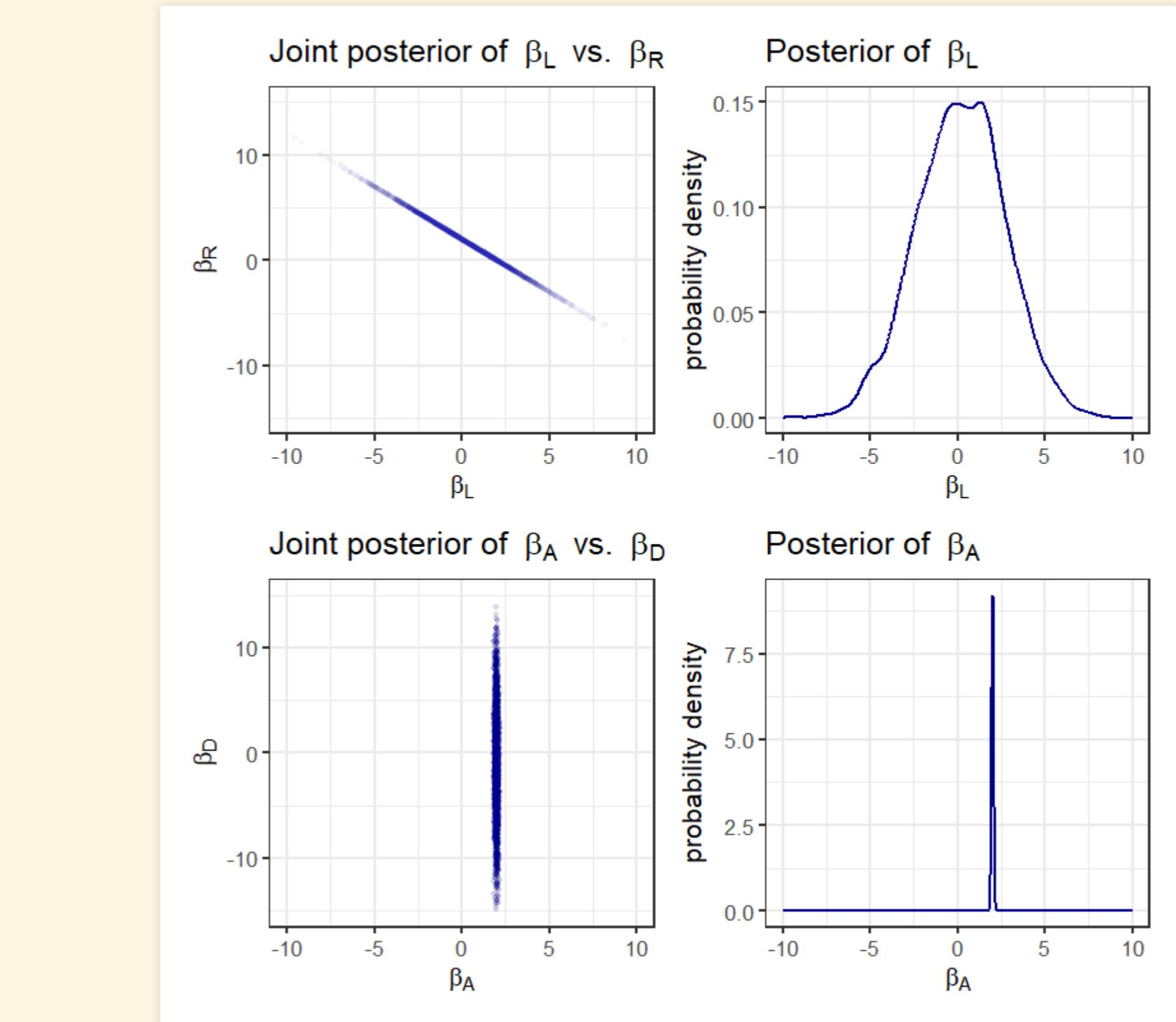
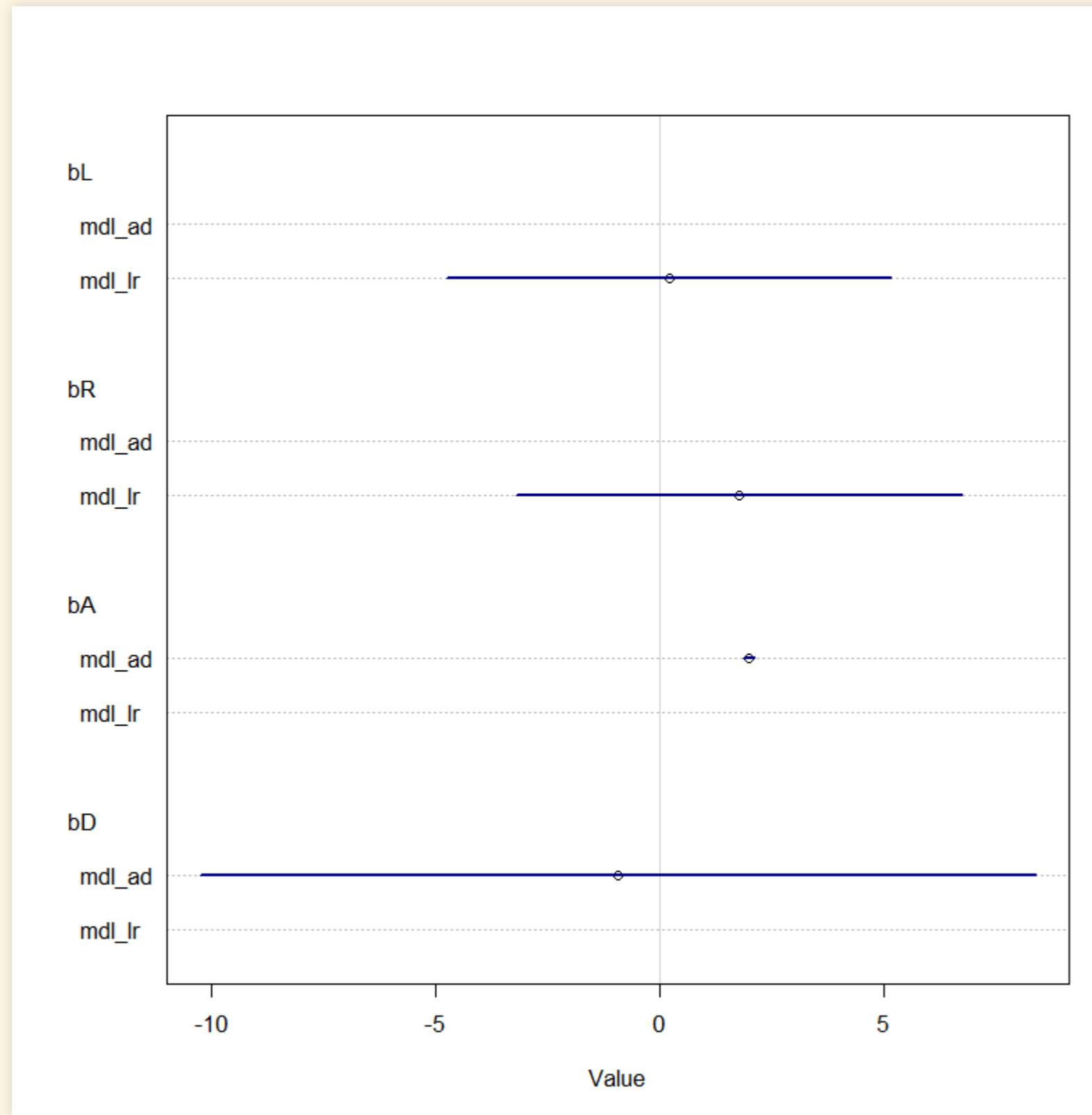
Summary

- 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

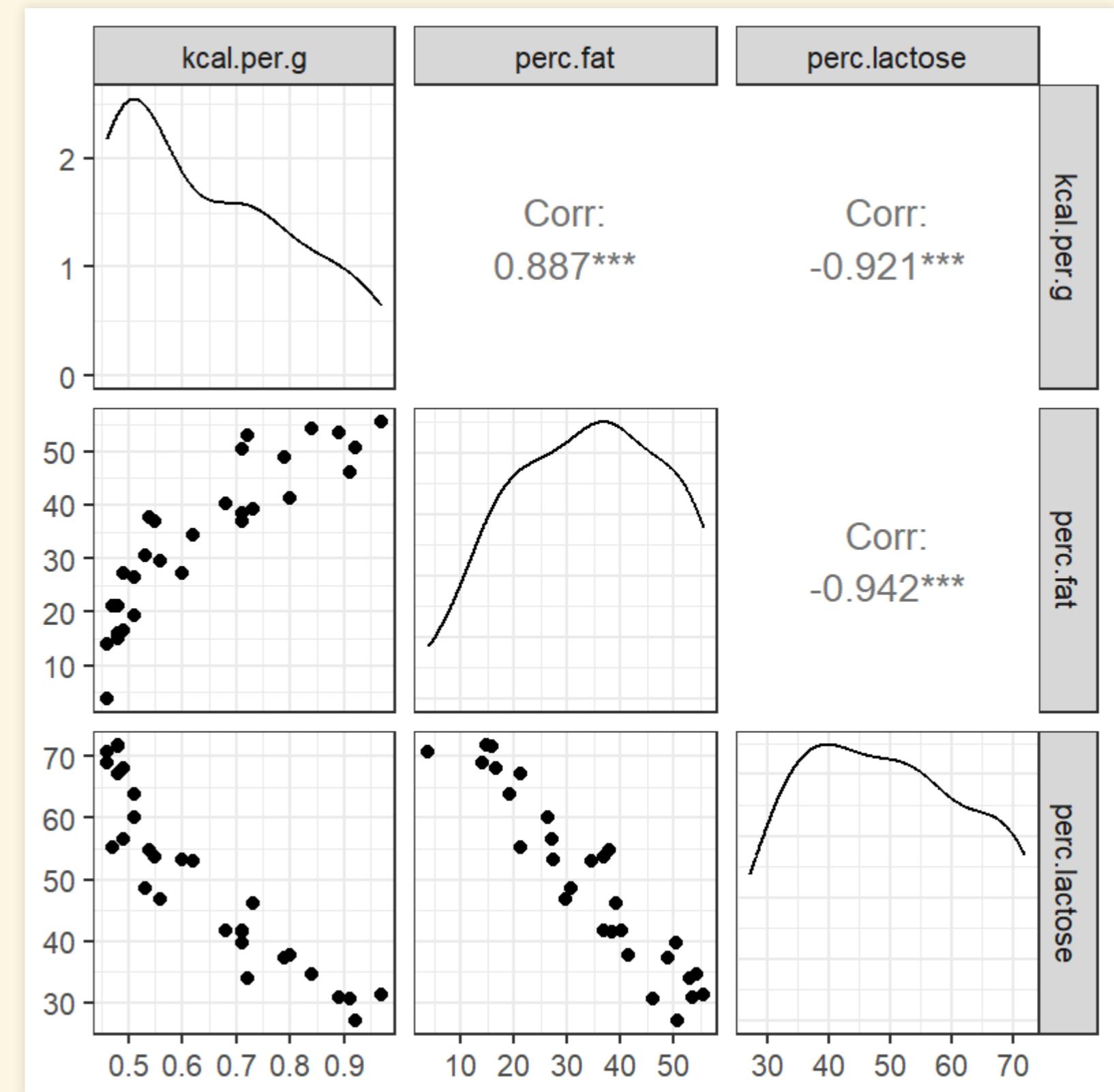
- Calories come from fat and sugar (lactose):

```
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)

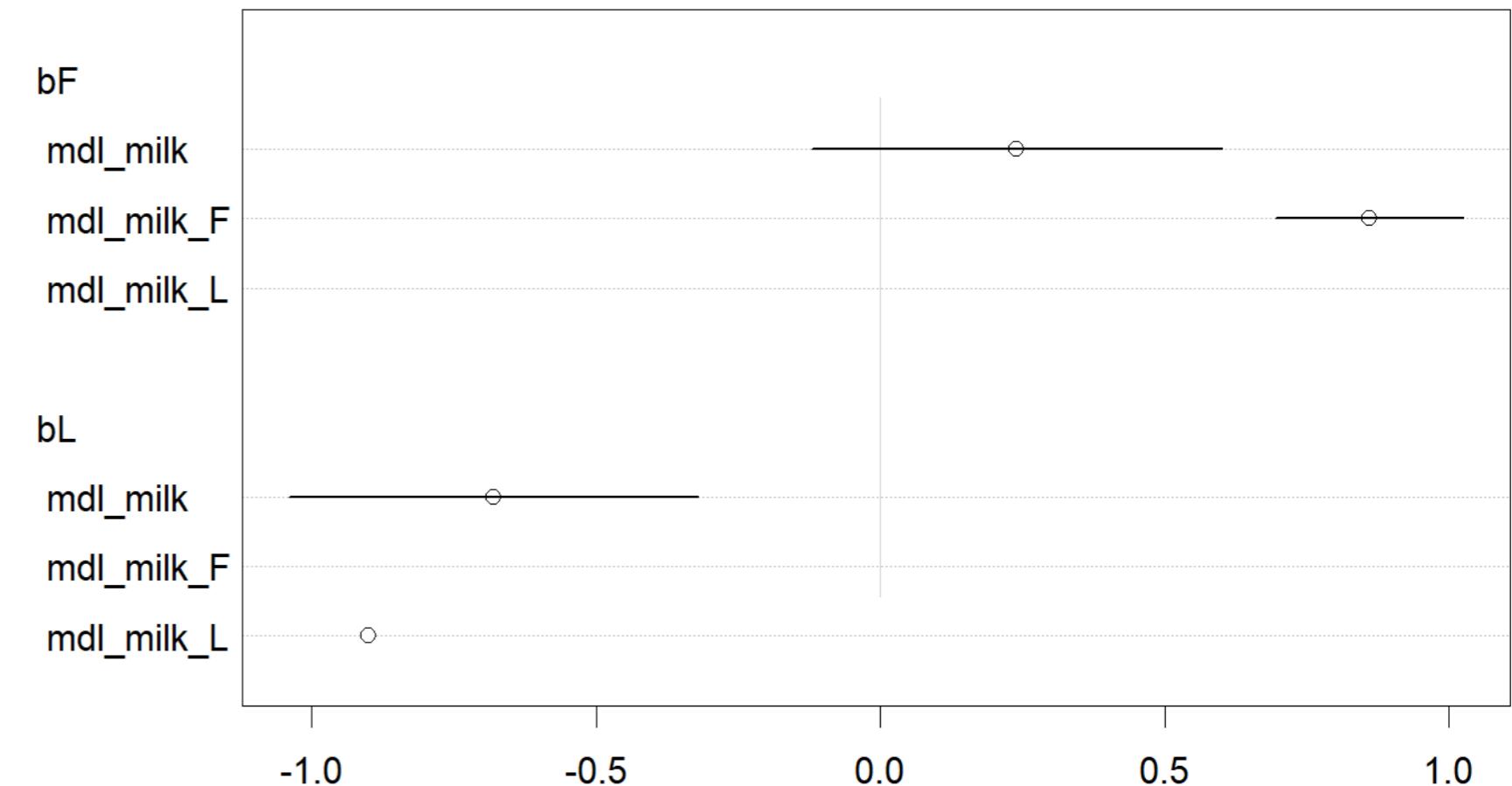
d %>% select(kcal.per.g, perc.fat, perc.lactose) %>%
  ggpairs()
```



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))
```

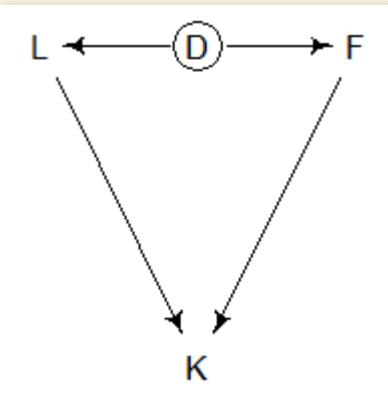
```
##          mean     sd  5.5% 94.5%  
## a      0.00  0.07 -0.11  0.11  
## bL    -0.90  0.07 -1.02 -0.79  
## sigma  0.38  0.05  0.30  0.46
```

```
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

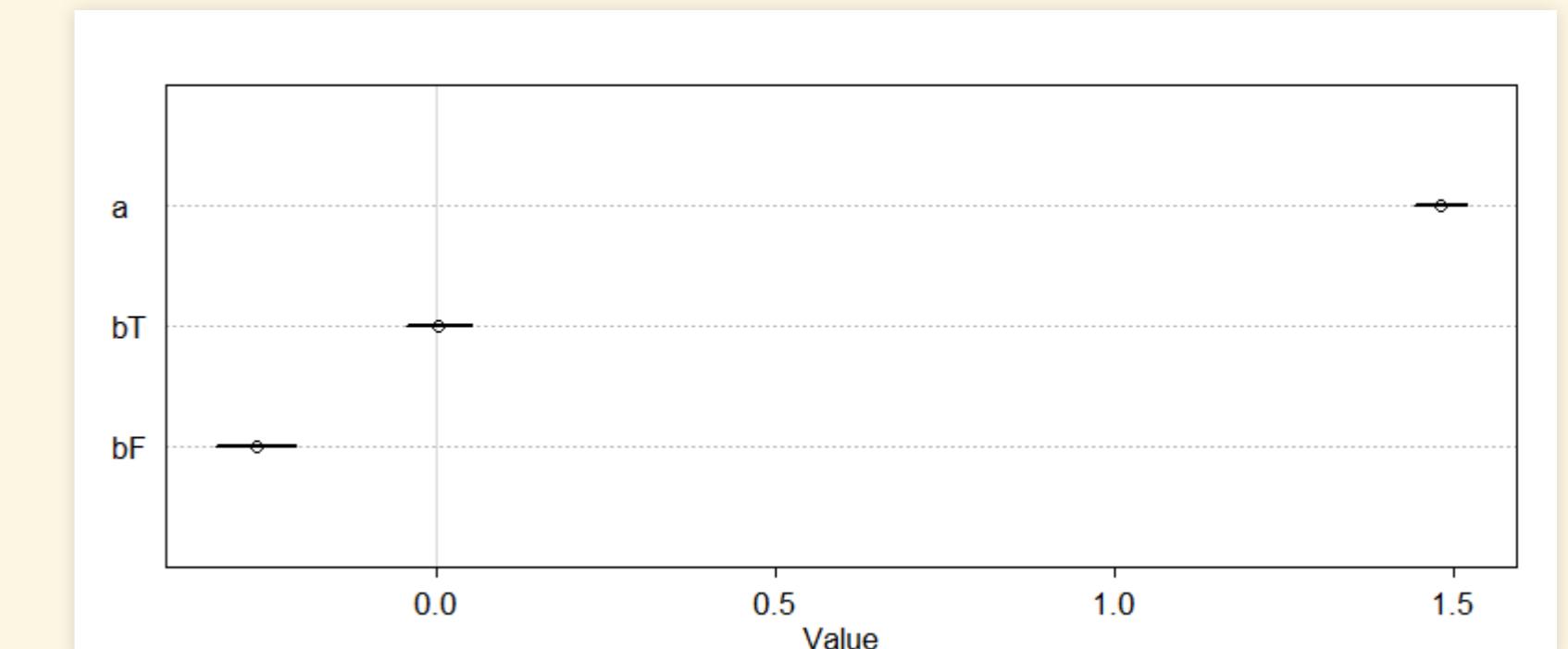
Post-Treatment Bias

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?
 - $\text{mean}(bT) = 0$.

```
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))
```

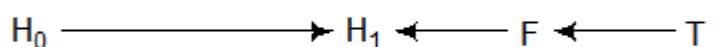
```
##          mean     sd  5.5% 94.5%
## a       1.48  0.02  1.44  1.52
## bT      0.00  0.03 -0.05  0.05
## bF     -0.27  0.04 -0.33 -0.21
## sigma   1.41  0.10  1.25  1.57
```



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

```
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)
```

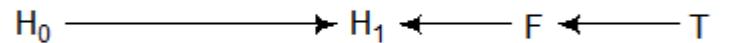


```
## Implied Conditional Independencies
```

```
## F ⊥⊥ H_0  
## H_0 ⊥⊥ T  
## H_1 ⊥⊥ T | F
```

A Better Model

- DAG



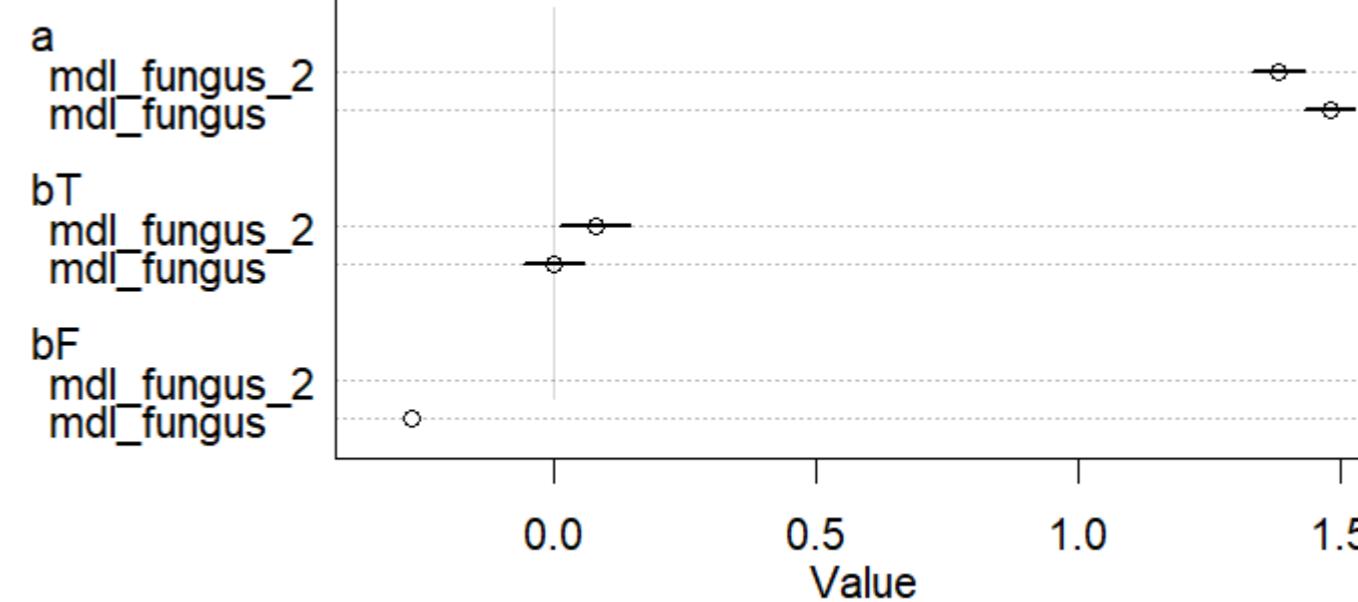
```
## Implied Conditional Independencies
```

```
## 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.

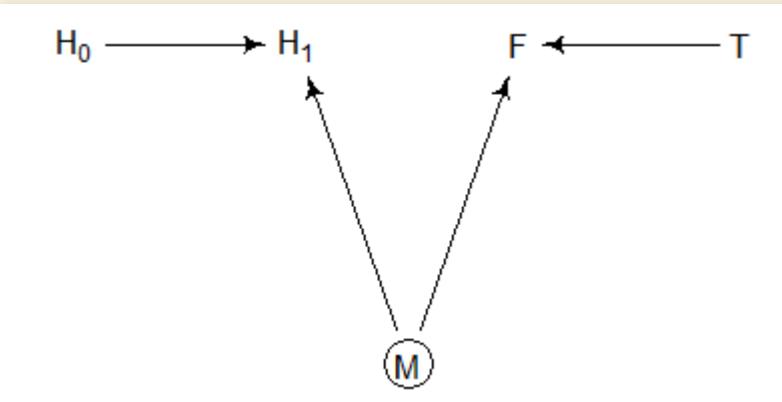
```
mdl_fungus_2 <- quap(  
  alist(  
    h1 ~ dnorm(mu, sigma),  
    mu <- h0 * p,  
    p <- a + bT * T,  
    a ~ dlnorm(0, 0.2),  
    bT ~ dnorm(0, 0.5),  
    sigma ~ dexp(1)  
  ), data = d)  
precis_show(precis(mdl_fungus_2, digits = 2))
```

```
##          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:

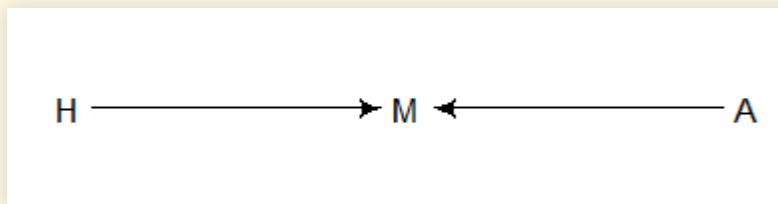


- Fungus F does not influence plant growth.
- Moisture M influences both plant growth H_1 and fungus F
- Fitting our original model falsely implies that treatment benefits plants.
- This is a kind of *collider* effect.

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

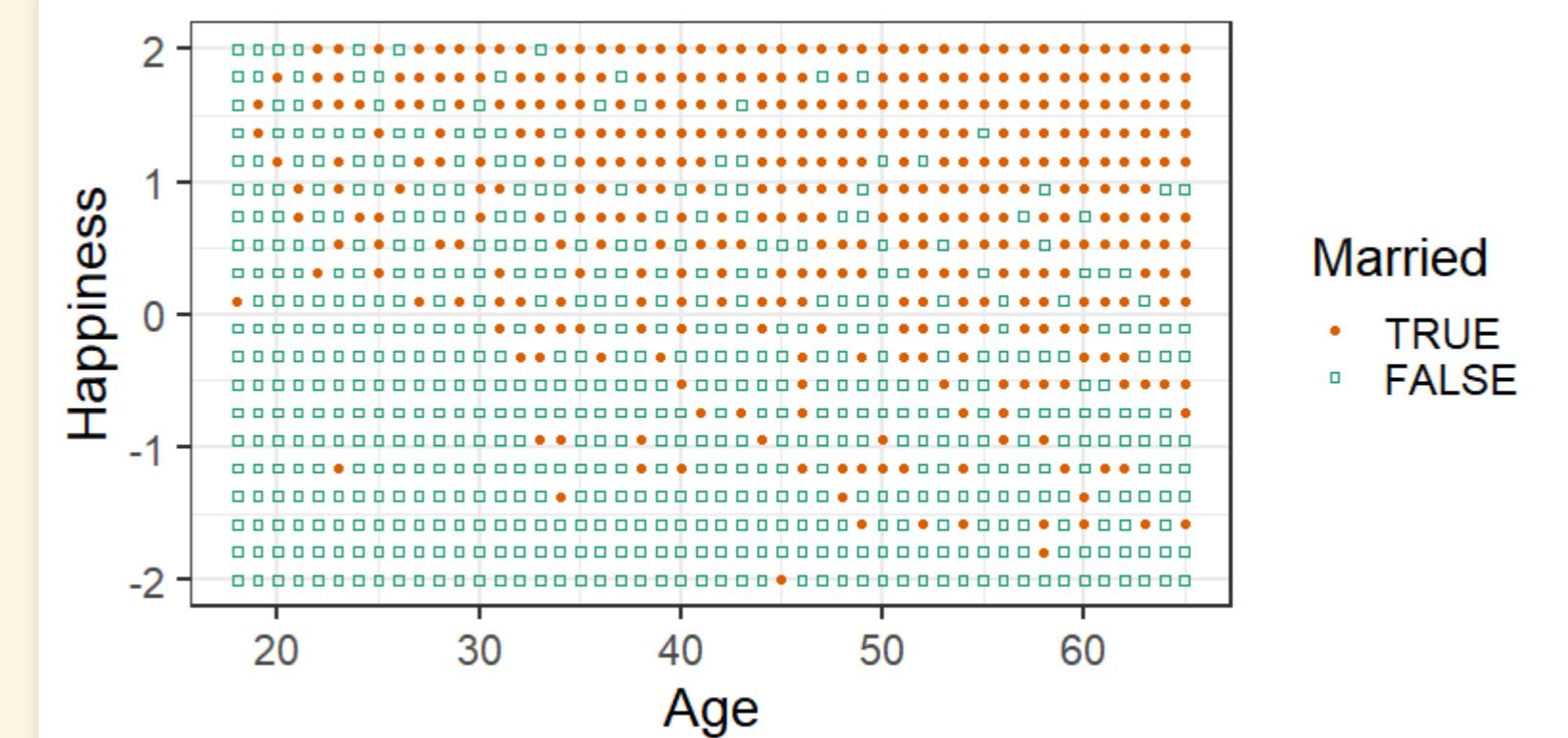
```
# sim_happiness is a function in the rethinking package  
d <- sim_happiness(seed=1977, N_years=1000)
```

- 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))
```



```
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
```

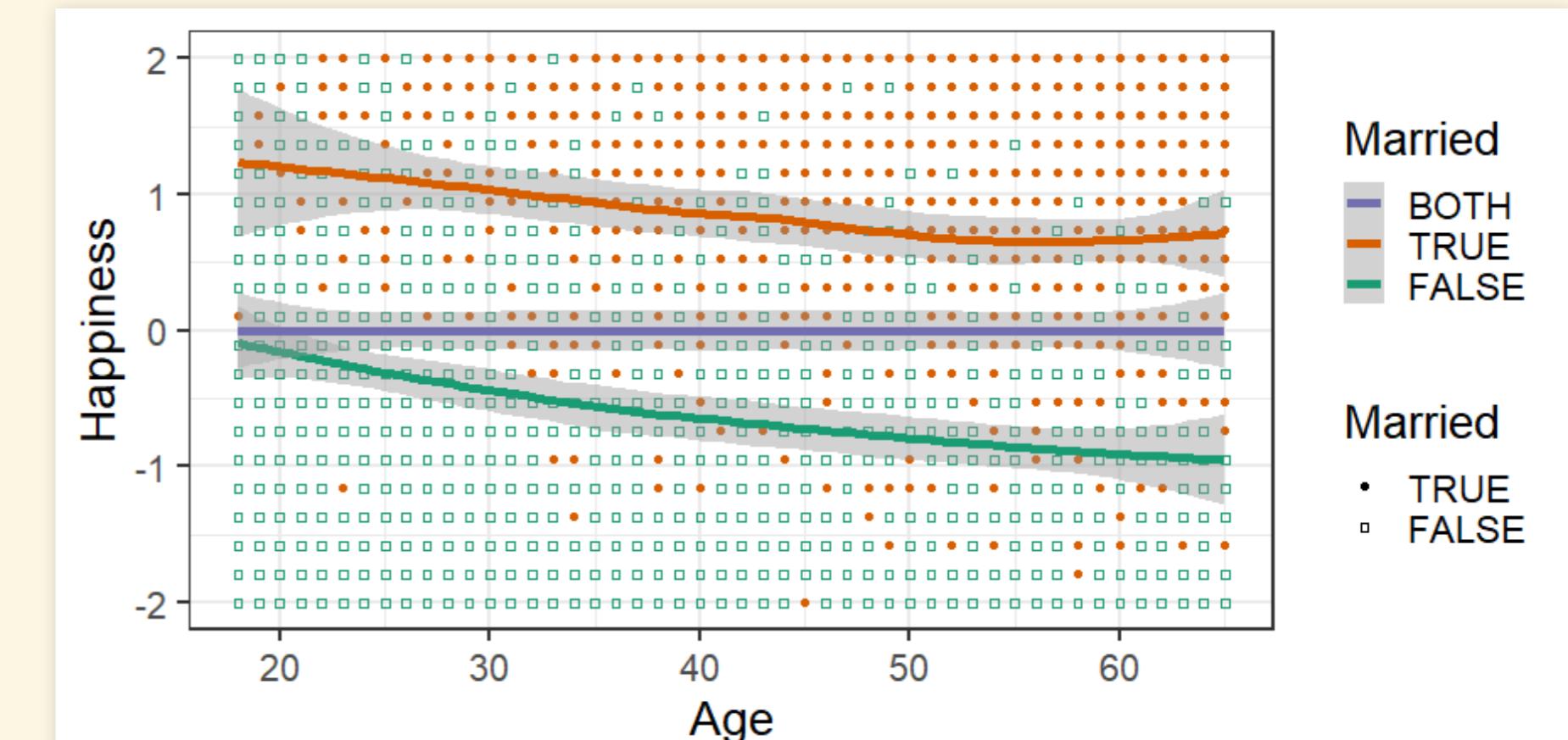
- The model says that people become unhappy as they get older

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
```

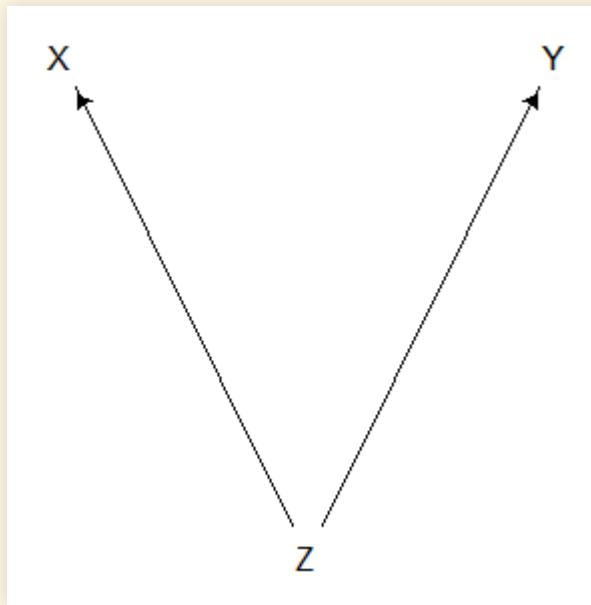


Categories of Confounding Relationships

Categories of Confounding Relationships

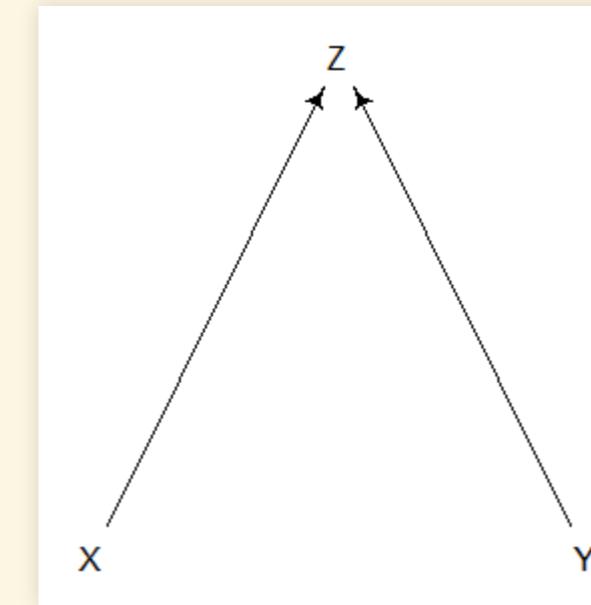
- We want to infer Y from X and Z

1. Fork



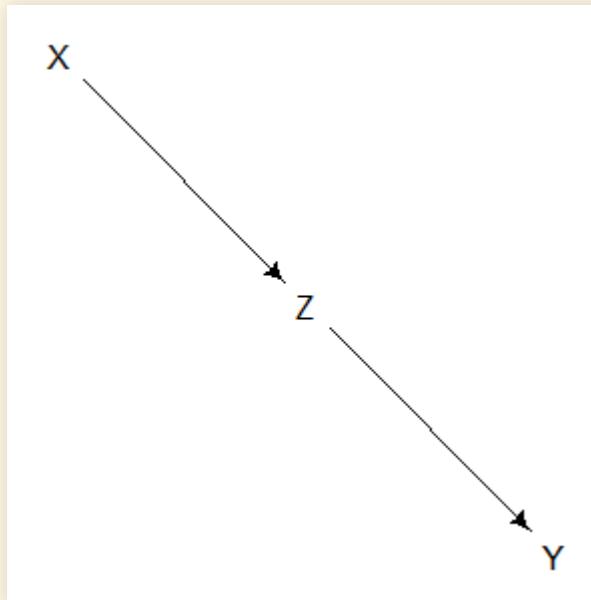
- $X \perp\!\!\!\perp Y|Z$
- Divorce rate
- Post-treatment bias:
moisture

3. Collider



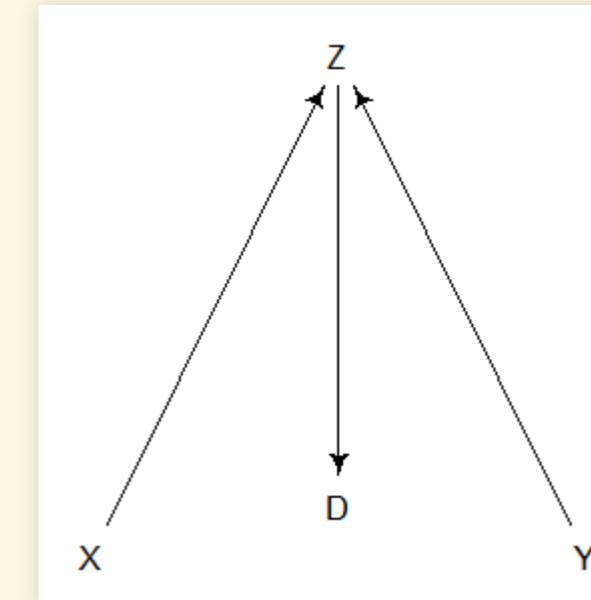
- $X \not\perp\!\!\!\perp Y|Z$
- Happiness & age
- Trustworthiness
vs. newsworthiness

2. Pipe



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

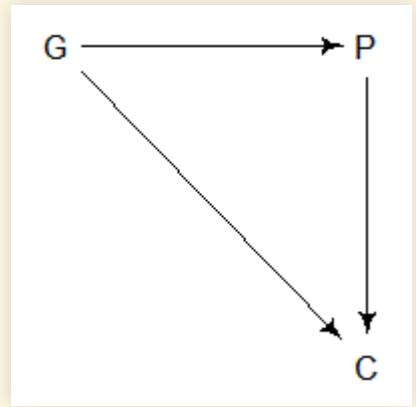
4. Descendant



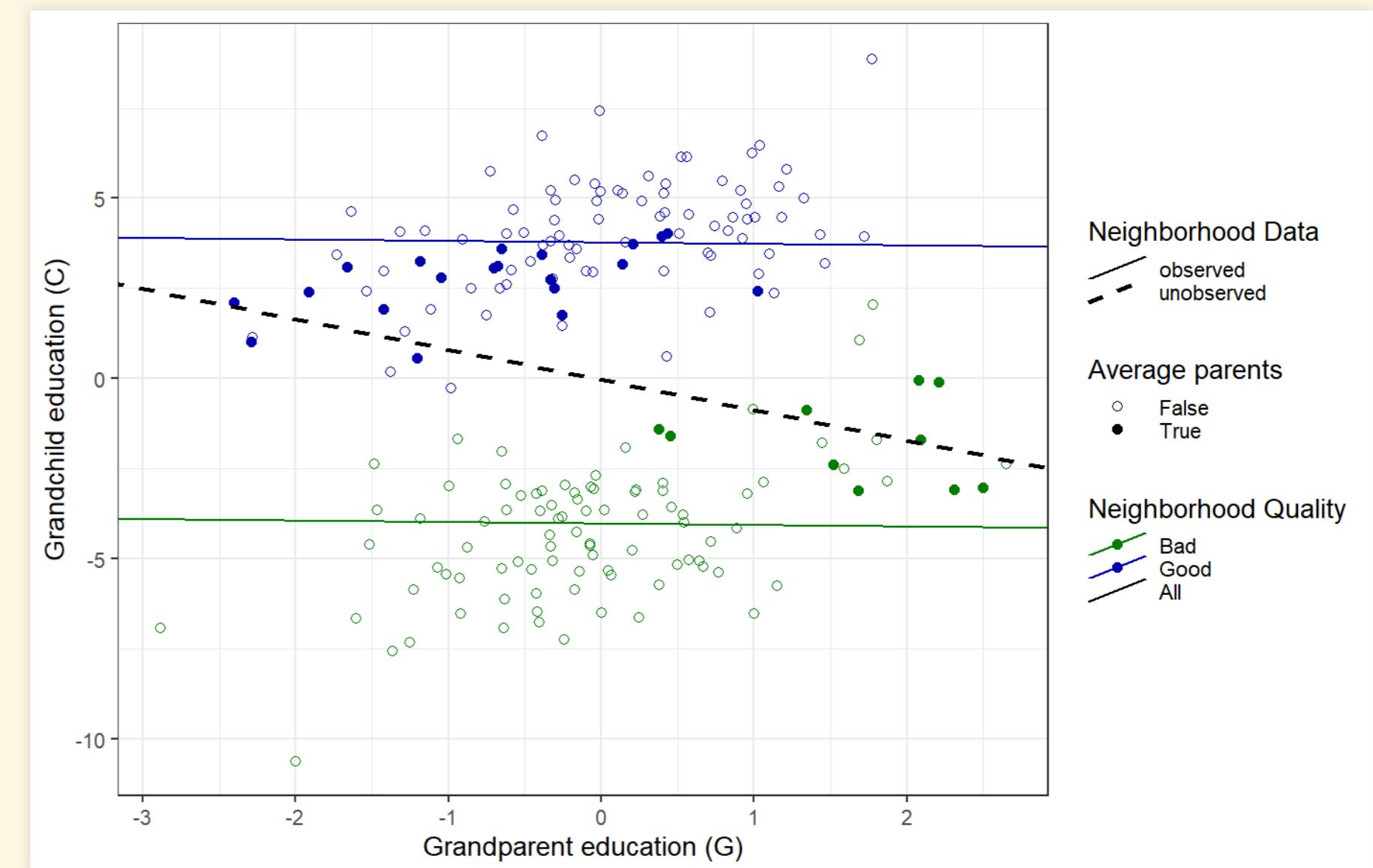
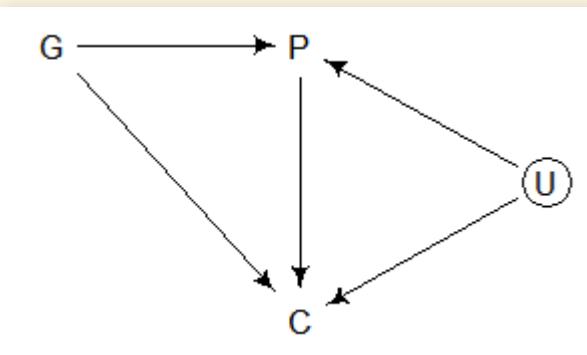
- All causal DAGs are build of combinations of these four patterns.

Example: Haunted DAG

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



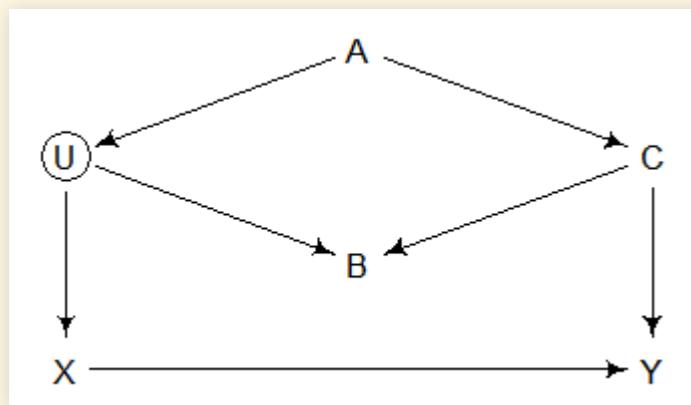
- Problem: there are unmeasured effects here, such as the character of the neighborhood.
 - Grandparents moved into the neighborhood after they finished school,
 - Parents and children grew up in the neighborhood and are affected by it.



- There is 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 .

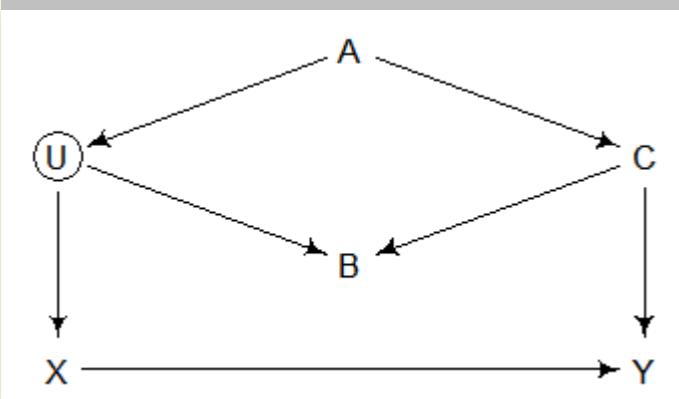
Automated Analysis

- 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

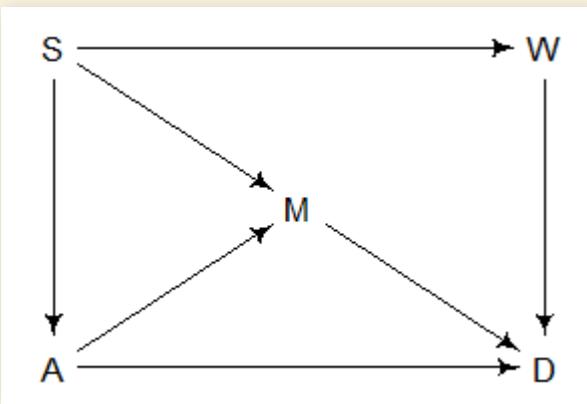
```
adjustmentSets(dag_two_roads, exposure = "X", outcome = "Y")
## { C }
## { A }
```

- 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 .

