

SR 2025 Week 3 Solutions (Chapter 5)

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5E1

Only (2) and (4) are multiple linear regressions. Both have more than one predictor variable and corresponding coefficients in the linear model. The model (1) has only a single predictor variable, x . The model (3) has two predictor variables, but only their difference for each case enters the model, so effectively this is a univariate regression, with a single slope parameter.

5E2

When we say model definition we mean mathy form. While these statements can seem ambiguous, a common interpretation of this would be:

$$A_i \sim \text{Normal}(\mu_i, \sigma)$$

.

$$\mu_i = \alpha + \beta_L L_i + \beta_P P_i$$

.

Here A is animal diversity, L is latitude, and P is plant diversity. This linear model “controls” for plant diversity, while estimating a linear relationship between latitude and animal diversity.

5E3

Define T as time to PhD degree, the outcome variable implied by the problem. Define F as amount of funding and S as laboratory size, the implied predictor variables. Then the model (ignoring priors) might be:

$$T_i \sim \text{Normal}(\mu_i, \sigma)$$

.

$$\mu_i = \alpha + \beta_F F_i + \beta_S S_i$$

.

The slopes (β_F and β_S) should be positive. How can both be positively associated with the outcome in a multiple regression, but neither by itself? If they are negatively correlated with one another, then considering each alone may miss the positive relationships with the outcome. For example, large labs have less funding per student. Small labs have more funding per student, but poorer intellectual environments. So both could be positive influences on time to degree, but be negatively associated in nature.

5E4

This question is tricky, and the answer depends on how you fit the model. First, the answer will actually depend upon the priors, which aren't mentioned in the problem. Assuming weakly informative or flat priors, the answer is that (1), (3), (4), and (5) are inferentially equivalent. They'll make the same predictions, and

you can convert among them after model fitting. (2) stands out because it has a redundant parameter, the intercept α .

5M4

It is worth finding and entering the values yourself, for the practice at data management. I entered old data from wikipedia, and scraped current from Wikipedia and merged both into the original data:

[illegible]

We could fit as regressions:

```
## it would be better to match up the other covariates as they likely changed, but i wanted to show you
m_5M4 <- quap(
  alist(
    D ~ dnorm(mu,sigma),
    mu <- a + bM*M + bA*A + bL*L,
    a ~ dnorm(0,0.2),
    c(bA,bM,bL) ~ dnorm(0,0.5),
    sigma ~ dexp(1)
  ), data=d )

precis( m_5M4 )
```

##	mean	sd	5.5%	94.5%
## a	-1.954402e-09	0.09615207	-0.1536696	0.15366958
## bA	-6.155496e-01	0.14930372	-0.8541658	-0.37693346
## bM	-1.291620e-02	0.15669373	-0.2633430	0.23751064

```
## bL      -1.315079e-01 0.11859098 -0.3210392  0.05802338
## sigma   7.753849e-01 0.07686543  0.6525391  0.89823069
```

```
m_5M4o <- quap(
  alist(
    D ~ dnorm(mu,sigma),
    mu <- a + bM*M + bA*A + bL*L0,
    a ~ dnorm(0,0.2),
    c(bA,bM,bL) ~ dnorm(0,0.5),
    sigma ~ dexp(1)
  ), data=d )
```

```
precis( m_5M4o )
```

```
##              mean          sd        5.5%        94.5%
## a      -3.606387e-08 0.09195197 -0.1469570  0.1469570
## bA     -6.890159e-01 0.14440778 -0.9198074 -0.4582244
## bM       3.541040e-02 0.14741676 -0.2001900  0.2710109
## bL     -3.131974e-01 0.11946706 -0.5041288 -0.1222659
## sigma   7.321700e-01 0.07270049  0.6159805  0.8483594
```

```
coeftab(m_5M4o,m_5M4)
```

```
##      m_5M4o  m_5M4
## a           0      0
## bA        -0.69   -0.62
## bM         0.04   -0.01
## bL        -0.31   -0.13
## sigma      0.73    0.78
## nobs        50     50
```

As expected from the old data in `m5M4o`, there is a negative association between percent LDS and divorce rate. This model assumes the relationship between divorce rate and percent LDS is linear. This makes sense if the LDS community has a lower divorce rate within itself only, and so as it makes up more of a State's population, that State's divorce rate declines. This is to say that the expected divorce rate of State i is a “convex” mix of two average divorce rates:

$$D_i = (1 - P)D_G + PD_{LDS}$$

where D_i is the divorce rate for State i , P is the proportion of the State's population that is LDS, and the two divorce rates D_G and D_{LDS} are the divorce rates for gentiles (non-LDS) and LDS, respectively. If $D_G > D_{LDS}$, then as P increases, the value of D_i increases linearly as well. But maybe the percent LDS in the population has a secondary impact as a marker of a State-level cultural environment that has lower divorce in more demographic groups than just LDS. In that case, this model will miss that impact. Can you think of a way to address this?

5H1

For the graph $M \rightarrow A \rightarrow D$, the implications are that M is independent of D when conditioning on A . You can check this with `dagitty` if you aren't sure:

```
library(dagitty)
dag_5H1 <- dagitty("dag{M->A->D}")
impliedConditionalIndependencies(dag_5H1)
```

```
## D _||_ M | A
```

We can check these with the data, provided we are willing to make some additional statistical assumptions about the functions that relate each variable to the others. The only functions we've used so far in the book

are linear (additive) functions. The implication above suggests that a regression of D on both M and A should show little association between D and M . You know from the chapter that this is true in the divorce data sample. So the data are consistent with this graph. But can you think of a way that marriage rate M would causally influence median age of marriage A ? If you cannot, then maybe this graph fails on basic scientific grounds. No data are required.

5H2

The first thing to do is outline the full statistical model. If the DAG is $M \rightarrow A \rightarrow D$, then this implies two regressions. The first regresses A on M and the second D on A . That is the model we need to program, in order to compute the counterfactual prediction of intervening on M . The model contains both regressions, and the estimates from both regressions are used to compute the counterfactual prediction, because any intervention on M first influences A which then influences D .

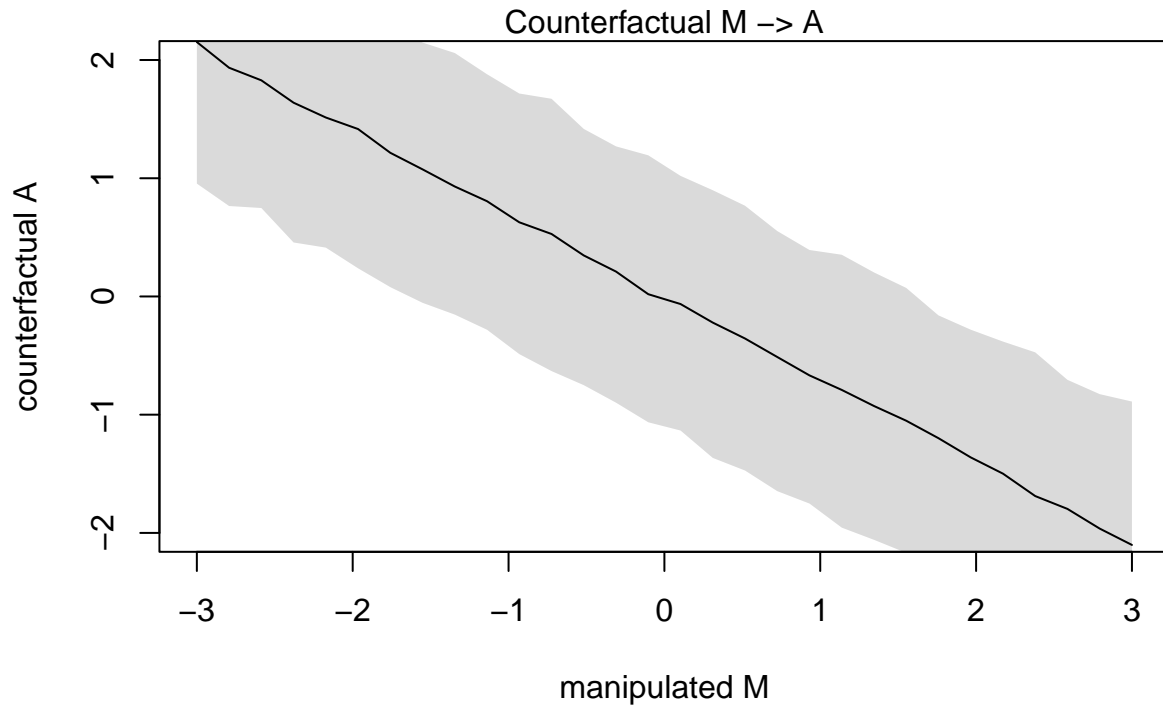
Assume the data is still loaded:

```
m5H2 <- quap(
  alist(
    # A -> D
    D ~ dnorm( muD , sigmaD ),
    muD <- aD + bAD*A,
    # M -> A
    A ~ dnorm( muA , sigmaA ),
    muA <- aA + bMA*M,
    # priors
    c(aD,aA) ~ dnorm(0,0.2),
    c(bAD,bMA) ~ dnorm(0,0.5),
    c(sigmaD,sigmaA) ~ dexp(1)
  ) , data=d )
precis(m5H2)
```

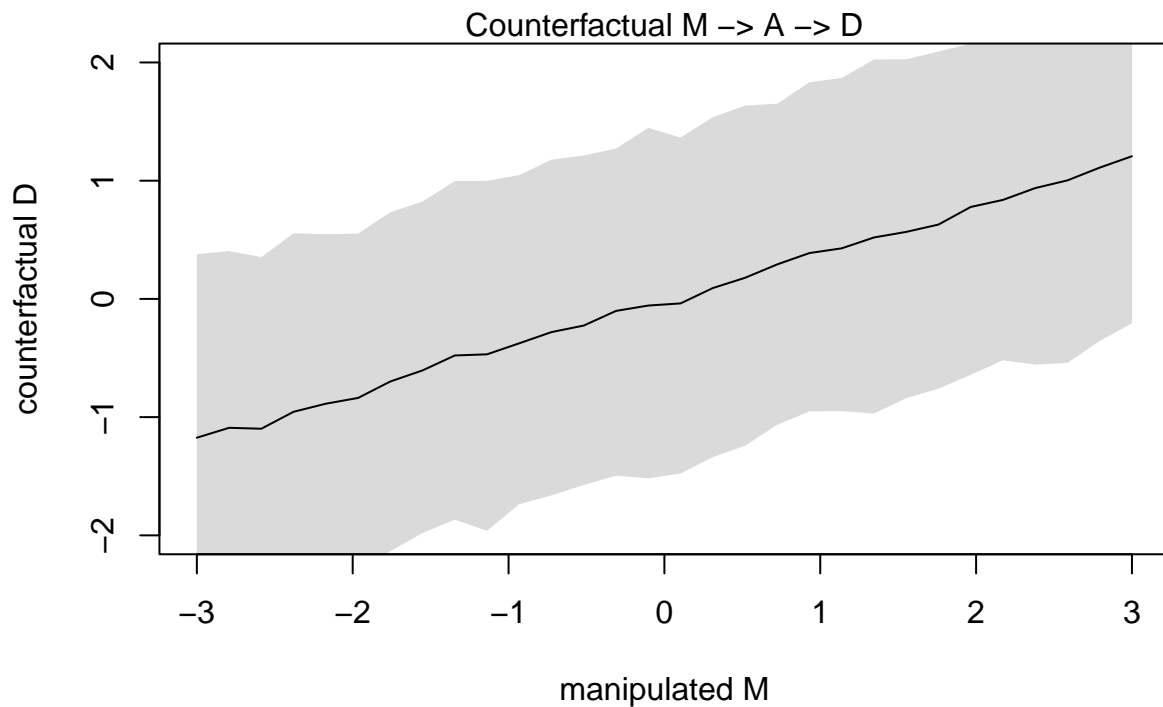
##		mean	sd	5.5%	94.5%
##	aD	1.417657e-07	0.09737870	-0.1556298	0.1556301
##	aA	9.407030e-08	0.08684787	-0.1387996	0.1387998
##	bAD	-5.684033e-01	0.10999971	-0.7442041	-0.3926026
##	bMA	-6.947377e-01	0.09572697	-0.8477279	-0.5417475
##	sigmaD	7.883250e-01	0.07801116	0.6636481	0.9130018
##	sigmaA	6.817372e-01	0.06758013	0.5737311	0.7897433

This just shows what you already know from the chapter: A and M are negatively associated and A and D are also negatively associated. It's interpreting these associations as having causal directions that makes counterfactual prediction. Now the counterfactual prediction is accomplished by building an input range of values for the interventions on M and then simulating both A and then D . We can use `sim` for this. Or you could do it in raw code just with `rnorm` and samples from the posterior. Here is the `sim` approach, just like in the chapter:

```
M_seq <- seq( from=-3 , to=3 , length.out=30 )
sim_dat <- data.frame( M=M_seq )
s <- sim( m5H2 , data=sim_dat , vars=c("A","D") )
plot( sim_dat$M , colMeans(s$A) , ylim=c(-2,2) , type="l" ,
      xlab="manipulated M" , ylab="counterfactual A" )
shade( apply(s$A,2,PI) , sim_dat$M )
mtext( "Counterfactual M -> A" )
```



```
plot( sim_dat$M , colMeans(s$D) , ylim=c(-2,2) , type="l" ,
      xlab="manipulated M" , ylab="counterfactual D" )
shade( apply(s$D,2,PI) , sim_dat$M )
mtext( "Counterfactual M -> A -> D" )
```



The left plot shows the intermediate $M \rightarrow A$ effect, which comes directly from the coefficient $b_M A$. This effect is negative, with one unit change in M moving A by about -0.7 on average. The right plot shows the full counterfactual effect of M on D . This effect depends upon both coefficients $b_M A$ and $b_A D$. It is not negative, but rather positive. Why? Because both coefficients are negative. If increasing A decreases D , then decreasing A increases D . Since increasing M decreases A , it follows that increasing M increases D . If that is

confusing, that's natural. Luckily the model can get this right without even understanding it. In simple linear models like these, the total causal effect along a path like $M \rightarrow A \rightarrow D$ is given by multiplying the coefficients along the path. In this case that means the product of $b_M A$ and $b_A D$. So that's $(-0.57)(-0.69) \approx 0.4$ at the posterior mean. Okay, but the question asked what would happen if we halved a State's marriage rate. And this is the hard part of the problem. We have to decide what the original marriage rate was, to know what halving it means. And then we have to convert to the standardized scale that the model uses. The average marriage rate in the sample is about 20. So if we halve the rate of an average State, it ends up at 10. What is 10 in the standardized units of the model? We find out by standardizing it!

```
(10 - mean(d$Marriage))/sd(d$Marriage)
```

```
## [1] -2.663047
```

That would be a huge effect! Looking at the righthand plot above, going from $M = 0$ to $M = -2.7$ would take us from about $D = 0$ to $D = -1$. Or we could do this calculation more directly:

```
M_seq <- c( 0 , -2.67 )
sim_dat <- data.frame( M=M_seq )
s <- sim( m5H2 , data=sim_dat , vars=c("A","D") )
diff <- s$D[,2] - s$D[,1]
mean( diff )
```

```
## [1] -1.123478
```

So the causal effect of halving an average State's marriage rate is to decrease divorce by a full standard deviation.

If this causal model is right...