

SR HW 8

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8e1.

1. The third variable linking dough to rising would be heat.
2. A third variable linking education to income could be connections made while in school.
3. A third variable between gas and a car driving could be whether or not the tires are flat.

8e2.

1. The interaction would be between heat and dryness of the onions.
2. There is no interaction these are just different variables.
3. The interaction is between parents beliefs and friends beliefs that interact to predict an individuals beliefs
4. How social someone is and having manipulative appendages interact to predict intelligence.

8e3.

1. $u_i = \alpha + (\beta_{HH_i}) + (\beta_{DD_i}) + (\beta_{DH_i} H_i D_i)$ H is heat and D is dryness
2. $u_i = \alpha + (\beta_{CC_i}) + (\beta_{FF_i})$ C is cylinders F is fuel injectors
3. $u_i = \alpha + (\beta_{XPT_i} P_i) + (\beta_{XFX_i} F_i)$ X is one's belief, P is Parent's belief, and F is Friend's belief
4. $u_i = \alpha + (\beta_{SS_i}) + (\beta_{AA_i}) + (\beta_{SAS_i} S_i A_i)$ S is socialness and A is Appendages

8m1.

Water and shade interact with temperature. Temperature has an interaction effect on water and shade. Additionally, water has an impact on temperature and shade. Lastly, shade impacts temperature and water. There essentially one interaction between water, shade, and temperature. Finally, there are three two-way interactions between water/temperature, shade/temperature, and water/shade.

8m2.

water= W/temperature=T/shade=S/ bloom =B

Can you invent a regression equation that would make the bloom size zero, whenever the temperature is hot?

$$u_i = \alpha + \beta_W * W + \beta_S * S + \beta_T * T + \beta_{WS} * W * S + \beta_{WT} * W * T + \beta_{ST} * S * T + \beta_{WST} * W * S * T$$

original model

Temperature should be an indicator variable in which zero is hot. So what's left of the equation after anything multiplied by 0 would be...

$$u_i = \alpha + \beta_W * W + \beta_S * S + \beta_{WS} * W * S$$

so to get the bloom size to zero

$$\beta_{WS} = -(\alpha + \beta_W + \beta_S)$$

8m3.

In parts of North America, ravens depend upon wolves for their food. This is because ravens are carnivorous but cannot usually kill or open carcasses of prey. Wolves however can and do kill and tear open animals, and they tolerate ravens co-feeding at their kills. This species relationship is generally described as a “species interaction.” Can you invent a hypothetical set of data on raven population size in which this relationship would manifest as a statistical interaction? Do you think the biological interaction could be linear? Why or why not?

Raven = α + $\beta_{\text{Prey}} \text{Prey}$ + $\beta_{\text{Wolf}} \text{Wolf}$ + $\beta_{\text{WolfPrey}} \text{WolfPrey}$

```
library(rethinking)
```

```
## Loading required package: rstan
```

```
## Loading required package: StanHeaders
```

```
## Loading required package: ggplot2
```

```
## rstan (Version 2.21.5, GitRev: 2e1f913d3ca3)
```

```
## For execution on a local, multicore CPU with excess RAM we recommend calling
## options(mc.cores = parallel::detectCores()).
## To avoid recompilation of unchanged Stan programs, we recommend calling
## rstan_options(auto_write = TRUE)
```

```
## Loading required package: cmdstanr
```

```
## This is cmdstanr version 0.5.3
```

```
## - CmdStanR documentation and vignettes: mc-stan.org/cmdstanr
```

```
## - Use set_cmdstan_path() to set the path to CmdStan
```

```
## - Use install_cmdstan() to install CmdStan
```

```
## Loading required package: parallel
```

```
## rethinking (Version 2.23)
```

```
##
## Attaching package: 'rethinking'
```

```
## The following object is masked from 'package:rstan':
##
##   stan
```

```
## The following object is masked from 'package:stats':
##
##   rstudent
```

```
library(tidyverse)
```

```
## — Attaching packages
## _____
## tidyverse 1.3.2 —
```

```
## ✓ tibble  3.1.8      ✓ dplyr   1.0.10
## ✓ tidyr   1.2.0      ✓ stringr 1.4.1
## ✓ readr   2.1.2      ✓ forcats 0.5.2
## ✓ purrr   0.3.4
## — Conflicts ————— tidyverse_conflicts() —
## X tidyr::extract() masks rstan::extract()
## X dplyr::filter()  masks stats::filter()
## X dplyr::lag()     masks stats::lag()
## X purrr::map()     masks rethinking::map()
```

```
N <- 5000
```

```
β_Prey <- .3
β_Wolf <- .4
β_WolfPrey <- .6
```

correlation between prey and wolf

```
rPreyWolf <- .8
```

```
Prey <- rnorm(n = N, mean = 0, sd = 1)
```

```
Wolf <- rnorm(n = N, mean = rPreyWolf*Prey, sd = sqrt(1-rPreyWolf^2))
```

```
Raven <- rnorm(n = N, mean = β_Prey*Prey + β_Wolf*Wolf + β_WolfPrey*Prey*Wolf, sd = 1)
```

```
Data <- data.frame(Raven, Prey, Wolf)
```

```
model <- map( alist( Raven ~ dnorm(mu, sigma), mu <- alpha +  $\beta_{PreyPrey}$  +  $\beta_{WolfWolf}$  +  $\beta_{WolfPreyPreyWolf}$ ,
alpha ~ dnorm(0, 1),  $\beta_{Wolf}$  ~ dnorm(0, 1),  $\beta_{Prey}$  ~ dnorm(0, 1),  $\beta_{WolfPrey}$  ~ dnorm(0, 1), sigma ~ dunif(0, 5) ),
data=Data, start = list(alpha=0,  $\beta_{Prey}$ =0,  $\beta_{Wolf}$ =0,  $\beta_{WolfPrey}$ =0, sigma=1) ) precis(model)
```

The model shows that a linear connection does exist.

8m4.

```
library(rethinking)
data(tulips)
d <- tulips
str(d)
```

```
## 'data.frame': 27 obs. of 4 variables:
## $ bed : Factor w/ 3 levels "a","b","c": 1 1 1 1 1 1 1 1 1 2 ...
## $ water : int 1 1 1 2 2 2 3 3 3 1 ...
## $ shade : int 1 2 3 1 2 3 1 2 3 1 ...
## $ blooms: num 0 0 111 183.5 59.2 ...
```

```
d$blooms_std <- d$blooms / max(d$blooms)
d$water_cent <- d$water - mean(d$water)
d$shade_cent <- d$shade - mean(d$shade)
```

```
a <- rnorm( 1e4 , 0.5 , 1 ); sum( a < 0 | a > 1 ) / length( a )
```

```
## [1] 0.6118
```

```
a <- rnorm( 1e4 , 0.5 , 0.25 ); sum( a < 0 | a > 1 ) / length( a )
```

```
## [1] 0.048
```

```

m8.4 <- quap(
  alist(
    blooms_std ~ dnorm( mu , sigma ) ,
    mu <- a + bw*water_cent - bs*shade_cent ,
    a ~ dnorm( 0.5 , 0.25 ) ,
    bw ~ dnorm( 0 , 0.25 ) ,
    bs ~ dnorm( 0 , 0.25 ) ,
    sigma ~ dexp( 1 )
  ) , data=d )

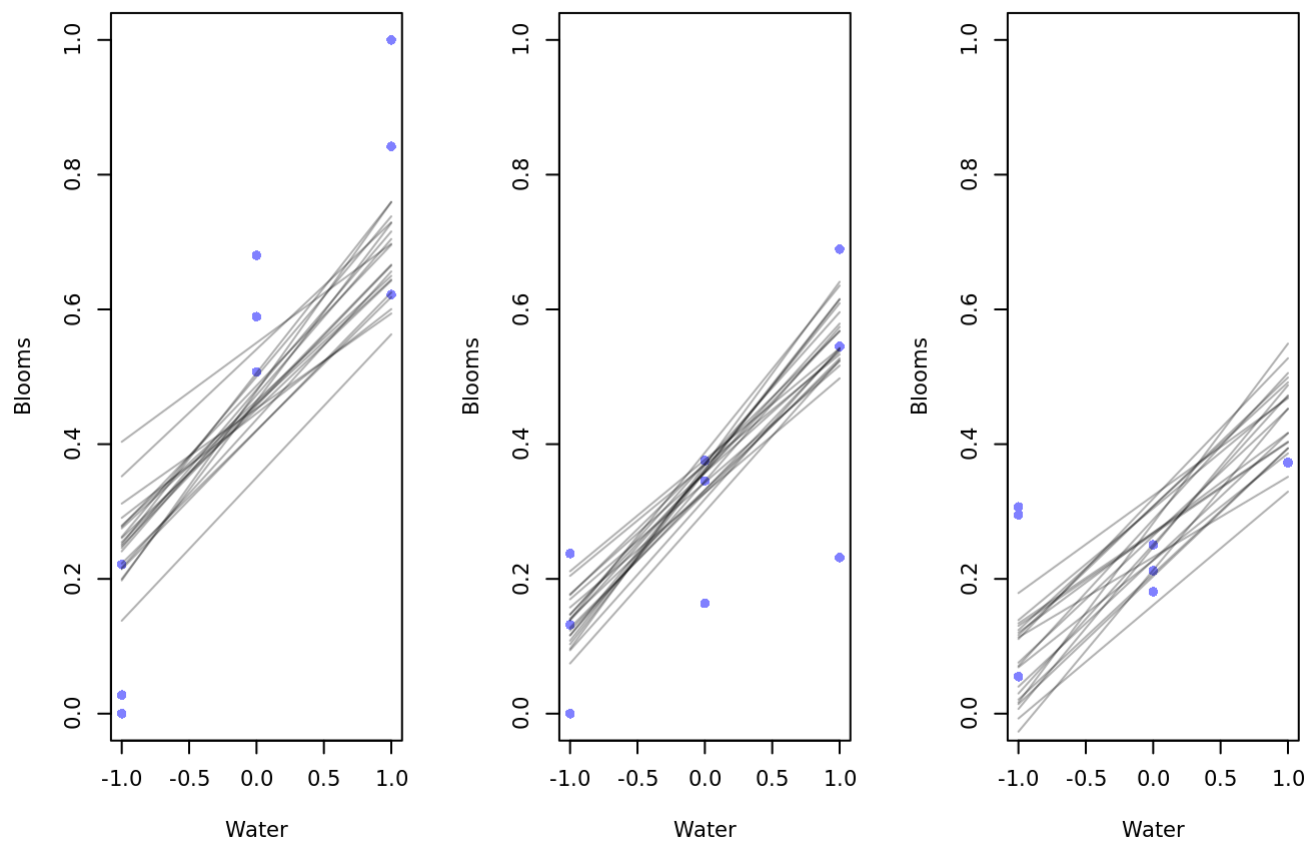
m8.5 <- quap(
  alist(
    blooms_std ~ dnorm( mu , sigma ) ,
    mu <- a + bw*water_cent - bs*shade_cent + bws*water_cent*shade_cent ,
    a ~ dnorm( 0.5 , 0.25 ) ,
    bw ~ dnorm( 0 , 0.25 ) ,
    bs ~ dnorm( 0 , 0.25 ) ,
    bws ~ dnorm( 0 , 0.25 ) ,
    sigma ~ dexp( 1 )
  ) , data=d )

```

```

par(mfrow=c(1,3))
for ( s in -1:1 ) {
  idx <- which( d$shade_cent==s )
  plot( d$water_cent[idx] , d$blooms_std[idx] , xlim=c(-1,1) , ylim=c(0,1) ,
        xlab="Water" , ylab="Blooms" , pch=16 , col=rangi2 )
  mu <- link( m8.4 , data=data.frame( shade_cent=s , water_cent=-1:1 ) )
  for ( i in 1:20 ) lines( -1:1 , mu[i,] , col=col.alpha("black",0.3) )}

```



Water and shade both affect the bloom. Water has a stronger effect when light is strong and less of an effect when the light is weak.