# EEEB UN3005/GR5005 Lab - Week 10 - 01 and 03 April 2019

USE YOUR NAME HERE

### Interactions

## Exercise 1: Multiple Regression with an Interaction

Referencing the *Statistical Rethinking* text (see page 230 and relevant preceding code), reconstruct and fit the model m7.9. More specifically, this model uses the tulips dataset. It models blooms as the outcome variable of interest, with centered versions of water and shade, as well as the interaction between them, as continuous predictor variables.

After fitting the model, use precis() to display the 97% PIs for all model parameters. Double check to make sure your results generally align with what's shown in the book.

Finally, how do you interpret the intercept estimate in the context of this model?

```
data(tulips)
d = tulips
d$shade.c = d$shade - mean(d$shade)
d$water.c = d$water - mean(d$water)
m7.9 = map(
    alist(
        blooms ~ dnorm(mu, sigma),
        mu <- a +
              bW * water.c +
              bS * shade.c +
              bWS * water.c * shade.c,
        bW ~ dnorm(0, 100),
        bS \sim dnorm(0, 100),
        bWS ~ dnorm(0, 100),
        sigma ~ dunif(0, 100)),
    data = d.
    start = list(
        a = mean(d$blooms),
        bW = 0,
        bS = 0,
        bWS = 0.
        sigma = sd(d$blooms)))
precis(m7.9, prob = 0.97)
```

## Mean StdDev 1.5% 98.5%

```
## a
         128.99
                  8.70 110.11 147.88
## bW
          74.96
                 10.60
                        51.95 97.97
## bS
         -41.14
                 10.60 -64.14 -18.14
## bWS
         -51.87
                 12.95 -79.97 -23.77
## sigma
         45.22
                  6.15
                       31.87 58.58
```

Answer:

$$\mu = a + b_W W + b_S S + b_{WS} W S$$

The intercept a is the value of  $\mu$  when both W and S is 0. Since both of these two variables is centered, a is the blooms value of the plants that have water value equals to mean(water) and shade value equals to mean(shade).

## Exercise 2: Triptych Plots for Both Predictor Variables

In the Statistical Rethinking book, Figure 7.7 (page 234), you'll see a series of "triptych" plots. Pay particular attention to the bottom row of the panel, which shows model-based predictions (from model m7.9) for the effect of shade.c on blooms. Because the model includes multiple predictor variables, it makes sense to plot this relationship across multiple values of the other predictor (water.c, hence the series of three plots in the bottom row), and because the model includes an interaction effect, the specific relationship between shade.c and blooms varies across the triptych plots.

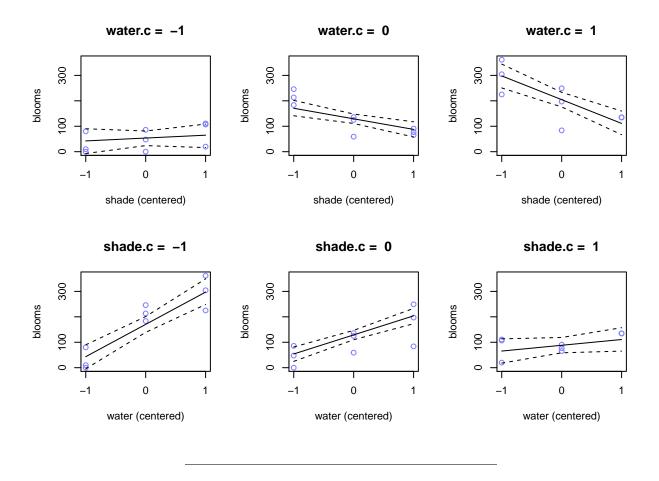
To fully visualize the predictions from model m7.9, create two triptych plots. The first triptych plot should show the effect of water.c on blooms, plotted for three different values of shade.c. The second triptych plot should show the effect of shade.c on blooms, plotted for three different values of water.c (i.e., this second triptych plot should replicate what you see in the bottom row of the book's Figure 7.7). Clearly, modifying the book's code will help you in generating this output. Feel free to visualize the 97% interval of the mean using lines (as in the book code) or using a shaded interval (as has been demonstrated in multiple places throughout the book and lecture code using the shade() function). Also note, you can plot these two triptych plots together neatly with some modification to your plotting window. See the book's R code 7.28 box for a hint as to how...

Using the plots to help with your interpretation, at which value(s) of shade is the effect of water most extreme? At which value(s) of water is the effect of shade most extreme?

```
par(mfrow = c(2, 3))

shade.seq = -1:1
for (w in -1:1){
   dt = d[d$water.c == w,]
   plot(
```

```
blooms ~ shade.c,
        data = dt,
        col = rangi2,
        main = paste("water.c = ", w),
        xaxp = c(-1, 1, 2),
        ylim = c(0, 362),
        xlab = "shade (centered)")
    mu = link(
        m7.9,
        data = data.frame(water.c = w, shade.c = shade.seq))
    mu.mean = apply(mu, 2, mean)
    mu.PI = apply(mu, 2, PI, prob = 0.97)
    lines(shade.seq, mu.mean)
    lines(shade.seq, mu.PI[1,], lty = 2)
    lines(shade.seq, mu.PI[2,], lty = 2)
}
water.seq = -1:1
for (s in -1:1){
    dt = d[d\$shade.c == s,]
    plot(
        blooms ~ water.c,
        data = dt,
        col = rangi2,
        main = paste("shade.c = ", s),
        xaxp = c(-1, 1, 2),
        ylim = c(0, 362),
        xlab = "water (centered)")
    mu = link(
        m7.9,
        data = data.frame(water.c = water.seq, shade.c = s))
    mu.mean = apply(mu, 2, mean)
    mu.PI = apply(mu, 2, PI, prob = 0.97)
    lines(water.seq, mu.mean)
    lines(water.seq, mu.PI[1,], lty = 2)
    lines(water.seq, mu.PI[2,], lty = 2)
}
```



#### Answer:

With water value increasing, the blooms value is more and more negatively related to shade value.

Conversely, with shade value increasing, the blooms value is less and less positively related to water value.