Multiple Regression

FW8051 Statistics for Ecologists

Department of Fisheries, Wildlife and Conservation Biology

Learning Goals

1. Understand regression analysis with **matrix notation**.
2. Become familiar with creating **dummy variables** for categorical regressors
3. **Interpret** the results of regression analyses with categorical and quantitative variables

Matrix Notation for Regression

Recall: $Y_i = \beta_0 + \beta_1 X_i + \epsilon_i \quad (i = 1, \ldots, n)$

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- This implies:

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- We can extract this set of equations with matrices.

Matrix Notation for Regression

$$
\begin{aligned}
Y_1 &= \beta_0 + \beta_1 X_1 + \epsilon_1 \\
Y_2 &= \beta_0 + \beta_1 X_2 + \epsilon_2 \\
&\vdots \\
Y_n &= \beta_0 + \beta_1 X_n + \epsilon_n
\end{aligned}
$$

$$
Y_{n\times 1} = \begin{bmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{bmatrix} \quad X_{n\times 2} = \begin{bmatrix} 1 & X_1 \\ 1 & X_2 \\ \vdots & \vdots \\ 1 & X_n \end{bmatrix} \quad \beta_{2\times 1} = \begin{bmatrix} \beta_0 \\ \beta_1 \end{bmatrix} \quad \epsilon_{n\times 1} = \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \vdots \\ \epsilon_n \end{bmatrix}
$$

Matrix Notation for Regression

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&\vdots \\
Y_n &= \beta_0 + \beta_1 X_n + \epsilon_n
\end{aligned}
$$

$$
\begin{bmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{bmatrix} = \begin{bmatrix} 1 & X_1 \\ 1 & X_2 \\ \vdots & \vdots \\ 1 & X_n \end{bmatrix} \times \begin{bmatrix} \beta_0 \\ \beta_1 \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \vdots \\ \epsilon_n \end{bmatrix}
$$

Matrix Notation for Regression

Also, recall that $\epsilon \sim \mathrm{N}(0, \sigma^2)$.

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- The assumption of independence can be shown with the variance covariance matrix for ϵ:

$$\sigma^2_{\epsilon_{n\times n}} = \begin{bmatrix} \sigma^2 & 0 & 0 & \cdots & 0 \\ 0 & \sigma^2 & 0 & \cdots & 0 \\ 0 & 0 & \sigma^2 & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & \sigma^2 \end{bmatrix}$$

- The (i, i) entry = $\mathrm{var}(y_i)$
- The (i, j) entry = $\mathrm{cov}(y_i, y_j)$

Matrix Notation for Regression

Think-Pair-Share

Simple linear regression (i.e., 1 regressor):

$$\begin{bmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{bmatrix} = \begin{bmatrix} 1 & X_1 \\ 1 & X_2 \\ \vdots & \vdots \\ 1 & X_n \end{bmatrix} \times \begin{bmatrix} \beta_0 \\ \beta_1 \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \vdots \\ \epsilon_n \end{bmatrix}$$

If we have **two** regressors (i.e., multiple linear regression), what would the X and β matrices look like?

Matrix Notation for Regression

We can generalize this matrix notation for any number $(p-1)$ of regressors:

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$$\begin{bmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{bmatrix} = \begin{bmatrix} 1 & X_{11} & X_{12} & \cdots & X_{1,p-1} \\ 1 & X_{21} & X_{22} & \cdots & X_{2,p-1} \\ \vdots & \vdots & \vdots & & \vdots \\ 1 & X_{n1} & X_{n2} & \cdots & X_{n,p-1} \end{bmatrix} \times \begin{bmatrix} \beta_0 \\ \beta_1 \\ \vdots \\ \beta_{p-1} \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \vdots \\ \epsilon_n \end{bmatrix}$$

Note, I am using 2 subscripts (the first indexes each observation; the second indexes each variable in the model).

Multiple linear regression

With multiple ($p-1$) explanatory variables, the multiple linear regression model is:

$$Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \cdots + \beta_{p-1} X_{i,p-1} + \epsilon_i$$

$$\epsilon \sim \mathrm{N}(0, \sigma^2)$$

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Or,

$$Y_i \sim \mathrm{N}(\mu_i, \sigma^2)$$

$$\mu_i = \beta_0 + \beta_1 X_{i1} + \cdots + \beta_{p-1} X_{i,p-1} + \epsilon_i$$

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$$\mu_i = \beta_0 + \beta_1 X_{i1} + \cdots + \beta_{p-1} X_{i,p-1} + \epsilon_i$$

We can use `lm` to find estimates of intercept (β_0) and slope parameters ($\beta_1, \beta_2, \ldots$) that minimize SSE:

$$SSE = \sum_i^n (Y_i - \hat{Y}_i)^2 = \sum_i^n (Y_i - [\beta_0 + \beta_1 X_{1,i} + \ldots + \beta_{p-1} X_{i,p-1}])^2$$

Multiple Linear Regression

We have the same assumptions (HILE Gauss) and can use the same diagnostic plots.

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The Coefficient of Determination (R^2) is calculated the same way ($R^2 = SSR/SST$), with:

- $SST_{df=n-1} = \sum_i^n (Y_i - \bar{Y})^2$
- $SSE_{df=n-p} = \sum_i^n (Y_i - \hat{Y})^2$
- $SSR_{df=p-1} = SST - SSE = \sum_i^n (\hat{Y}_i - \bar{Y})^2$

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In section 8, we will discuss an adjusted R^2 which is more useful when comparing models.

Mutliple Predictors and RIKZ data

Recall the RIKZ data.

- Assuming, naively, that observations are independent, we already established the relationship between Richness (R) and relative elevation (NAP):

$$\hat{\mathrm{R}}_i = 6.886 - 2.867\mathrm{NAP}_i$$

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What if we also hypothesized that **humus** (H, amount of organic material) would affect Richness *in addition to* NAP?

- The multiple linear regression model would look like:

$$\hat{\mathrm{R}}_i = \beta_0 + \beta_1\mathrm{NAP}_i + \beta_2\mathrm{H}_i + \epsilon_i$$

$$R_i = \beta_0 + \beta_1 NAP_i + \beta_2 H_i + \epsilon_i$$

```
lmfit3<-lm(Richness~NAP+humus, data=RIKZ)
summary(lmfit3)
```

```
Call:
lm(formula = Richness ~ NAP + humus, data = RIKZ)

Residuals:
   Min     1Q Median     3Q    Max
-4.767 -2.464 -0.891  1.389 15.277

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   5.4592     0.8304   6.575 5.92e-08 ***
NAP          -2.5123     0.6227  -4.035 0.000226 ***
humus        21.9424     9.7098   2.260 0.029080 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.974 on 42 degrees of freedom
Multiple R-squared:  0.3978,    Adjusted R-squared:  0.3691
F-statistic: 13.87 on 2 and 42 DF,  p-value: 2.372e-05
```

Model Comparison

We can compare models:

$$\begin{aligned}\hat{\mathrm{R}}_i &= 6.886 - 2.867\mathrm{NAP}_i \\ \hat{\mathrm{R}}_i &= 5.459 - 2.512\mathrm{NAP}_i + 21.942\mathrm{H}_i\end{aligned}$$

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Interpretations:

- β_1:

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Interpretations:

- β_1: the change in Richness for every 1 unit increase in NAP *while holding Humus constant*.

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- β_2:

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- β_1: the change in Richness for every 1 unit increase in NAP *while holding Humus constant*.
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- β_0:

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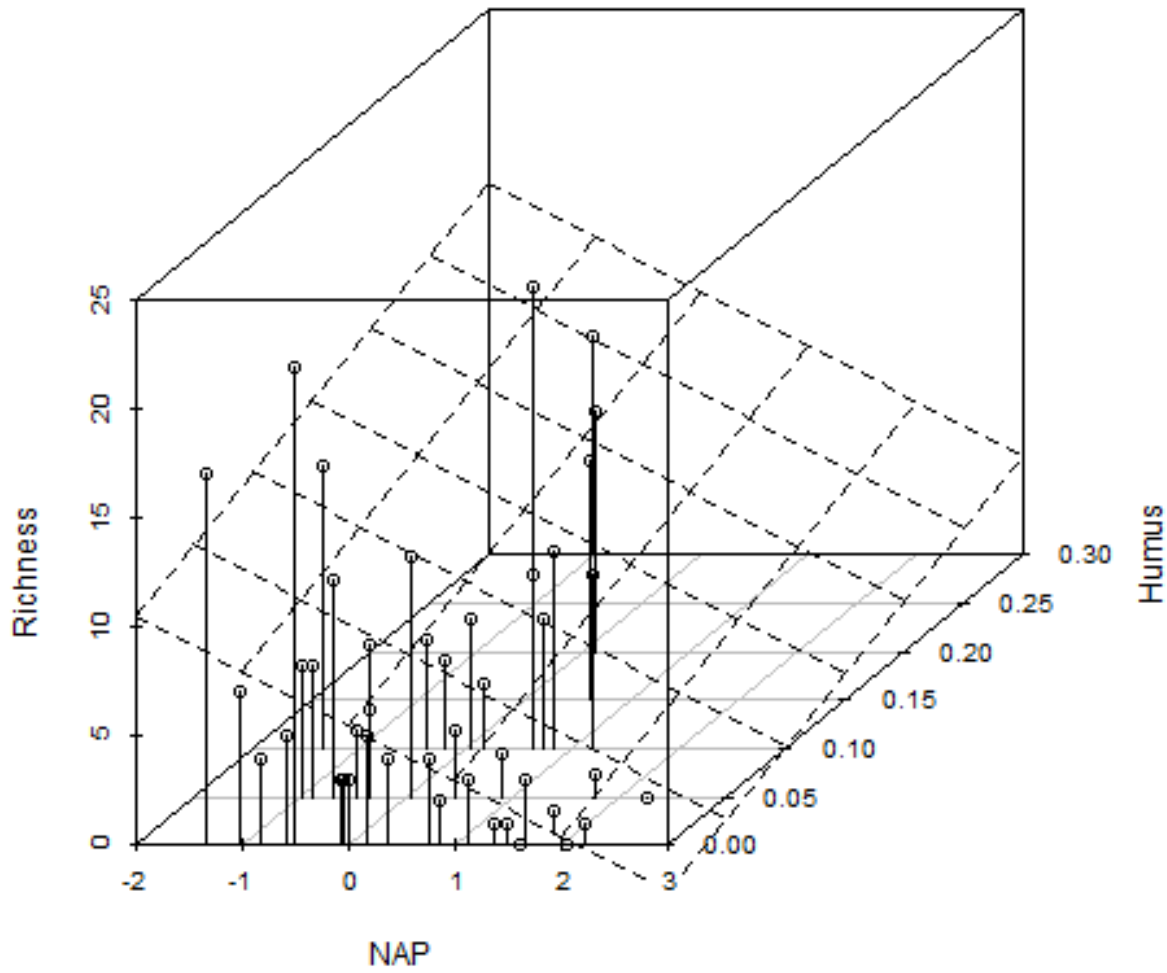
Interpretations:

- β_1: the change in Richness for every 1 unit increase in NAP *while holding Humus constant*.
- β_2: the change in Richness for every 1 unit increase in Humus *while holding NAP constant*.
- β_0: the level of Richness if Humus and NAP both equal 0.


Richness
0
5
10
15
20
25
-2
-1
0
1
2
3
NAP
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Humus

T-test as a regression

Mandible lengths in mm:

- 10 male and 10 female golden jackals
- From British Museum (Manly 1991)

```
males<-c(120, 107, 110, 116, 114, 111, 113, 117, 114, 112)
females<-c(110, 111, 107, 108, 110, 105, 107, 106, 111, 111)
```

Do males and females have, on average, different mandible lengths?

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```

Do males and females have, on average, different mandible lengths?

$$H_0 : \mu_m = \mu_f \text{ versus } H_a : \mu_m \neq \mu_f$$

T-test

```r
t.test(males, females, var.equal=T)
```

```
    Two Sample t-test

data:  males and females
t = 3.4843, df = 18, p-value = 0.002647
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 1.905773 7.694227
sample estimates:
mean of x mean of y
    113.4     108.6
```

Categorical Variables

We can also test the effect of jackal sex on mandible lengths with a regression model.

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- We have to create a data.frame with mandible lengths (quantitative) and sex (categorical)

```
jawdat <- data.frame(jaws = c(males, females),
                     sex = c(rep("M",10), rep("F", 10)))
head(jawdat)
```

```
  jaws sex
1  120   M
2  107   M
3  110   M
4  116   M
5  114   M
6  111   M
```

Linear Model

```
lmfit2<-lm(jaws~sex, data=jawdat)
summary(lmfit2)
```

```
Call:
lm(formula = jaws ~ sex, data = jawdat)

Residuals:
   Min     1Q Median     3Q    Max
  -6.4   -1.8    0.1    2.4    6.6

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 108.6000     0.9741 111.486  < 2e-16 ***
sexM          4.8000     1.3776   3.484  0.00265 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.08 on 18 degrees of freedom
Multiple R-squared:  0.4028,    Adjusted R-squared:  0.3696
F-statistic: 12.14 on 1 and 18 DF,  p-value: 0.002647
```

Dummy Variables

This is easier to understand if we use the matrix form of the regression model to view our data.

```
# sort by jaw size to mix the sexes and see the dummy variable
head(jawdat[order(jawdat$jaws),])
```

```
   jaws sex
16  105   F
18  106   F
2   107   M
13  107   F
17  107   F
14  108   F
```

$$\begin{bmatrix} 105 \\ 106 \\ 107 \\ 107 \\ \vdots \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ 1 & 0 \\ 1 & 1 \\ 1 & 0 \\ \vdots & \vdots \end{bmatrix} \times \begin{bmatrix} \beta_0 \\ \beta_1 \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \epsilon_3 \\ \epsilon_4 \\ \vdots \end{bmatrix}$$

Dummy Variables

- For k groups of categorical variables, we need to have $k - 1$ dummy variables.
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Dummy Variables

- For k groups of categorical variables, we need to have $k - 1$ dummy variables.
- How many dummy variables do we need for the jackals example? 1
- Each dummy variable is used as an indicator variable in the model for one group.
- In this case, the dummy variable will indicate (i.e., equal 1) for the male jackal observations.

Look at confidence intervals

```
confint(lmfit2)
```

```
                  2.5 %      97.5 %
(Intercept) 106.553472 110.646528
sexM          1.905773   7.694227
```

Understanding Model Parameters

Think-Pair-Share

How do we interpret the results?

$$
\begin{aligned}
Y_i &= \beta_0 + \beta_1 X_{mi} + \epsilon_i \\
&\quad \text{where } X_{mi} \text{ is 1 if male and 0 if female} \\
\hat{Y}_i &= 108.6 + 4.8 X_{mi}
\end{aligned}
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- So, if male:

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\end{aligned}
$$

- So, if male:

$$\hat{Y}_i = 108.6 + 4.8(1)$$

- And if female:

$$\hat{Y}_i = 108.6 + 4.8(0) = 108.6$$

Note: This parameterization is called "reference" or "effects" coding

Understanding Model Parameters

Alternatively, we can use the "cell-means" or "means" coding:

$$
\begin{aligned}
Y_i &= \beta_m X_{mi} + \beta_f X_{fi} + \epsilon_i \\
&\quad \text{where } X_{mi} = 1 \text{ if male and 0 if female} \\
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Understanding Model Parameters

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\end{aligned}
$$

In R: lm(jaws~sex-1, data=jawdat)

Cell Means Coding

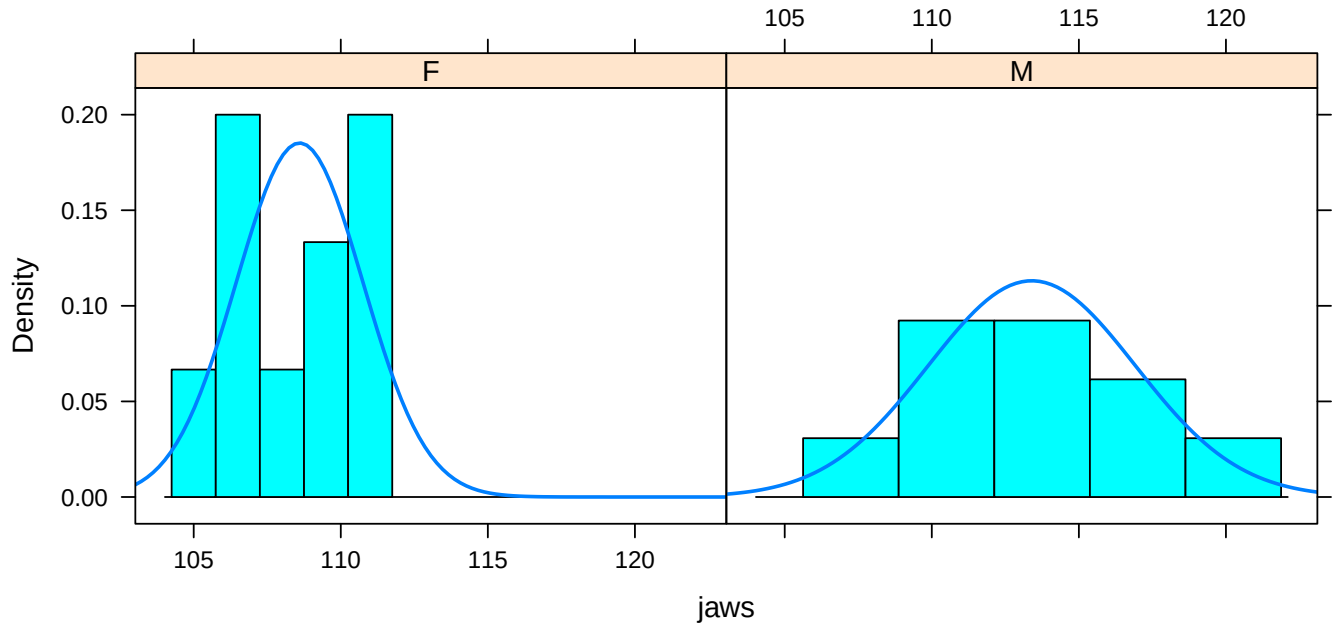
```
lmfit2b<-lm(jaws~sex-1, data=jawdat)
summary(lmfit2b)
```

```
Call:
lm(formula = jaws ~ sex - 1, data = jawdat)

Residuals:
   Min     1Q Median     3Q    Max
  -6.4   -1.8    0.1    2.4    6.6

Coefficients:
     Estimate Std. Error t value Pr(>|t|)
sexF 108.6000     0.9741   111.5   <2e-16 ***
sexM 113.4000     0.9741   116.4   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.08 on 18 degrees of freedom
Multiple R-squared:  0.9993,    Adjusted R-squared:  0.9992
F-statistic: 1.299e+04 on 2 and 18 DF,  p-value: < 2.2e-16
```

Assumptions?

- Equal (constant) variance for the two groups
- Data are normally distributed

```
library(mosaic)
histogram(~jaws|sex, data=jawdat, cex=1, fit="normal")
```



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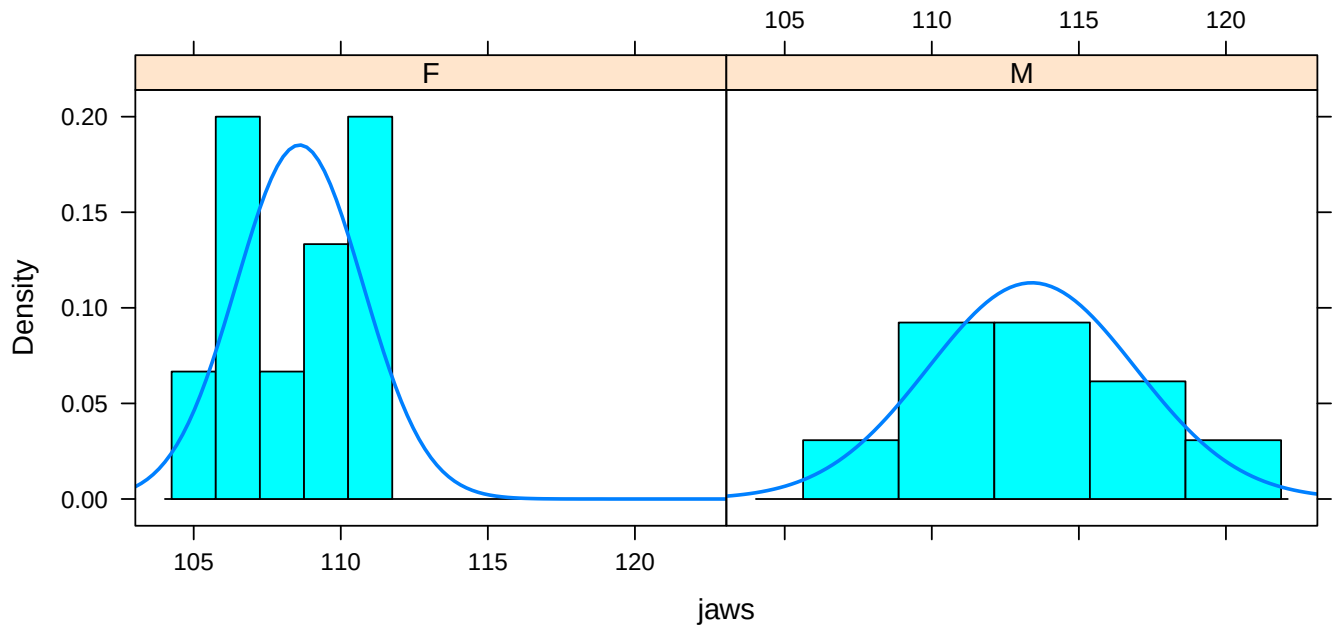

Later, we will see how we can relax these assumptions (using either JAGS or `gls` in the `nlme` package).

Categorical variables

Recall the RIKZ data.

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- Week could be considered continuous, but probably better to analyze it as a nominal variable with 4 categories.

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- How many dummy variables will we need to have in order to analyze the effect of Week? 3!

In R, use `as.factor(week)` to convert to a nominal variable.

Analysis of Covariance Model

```
lmfit4<-lm(Richness~NAP+as.factor(week), data=RIKZ)
summary(lmfit4)
```

```
Call:
lm(formula = Richness ~ NAP + as.factor(week), data = RIKZ)

Residuals:
    Min      1Q  Median      3Q     Max
-5.0788 -1.4014 -0.3633  0.6500 12.0845

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)        11.3677     0.9459  12.017 7.48e-15 ***
NAP                -2.2708     0.4678  -4.854 1.88e-05 ***
as.factor(week)2   -7.6251     1.2491  -6.105 3.37e-07 ***
as.factor(week)3   -6.1780     1.2453  -4.961 1.34e-05 ***
as.factor(week)4   -2.5943     1.6694  -1.554    0.128
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.987 on 40 degrees of freedom
Multiple R-squared:  0.6759,    Adjusted R-squared:  0.6435
F-statistic: 20.86 on 4 and 40 DF,  p-value: 2.369e-09
```

Dummy Variables

$$Y_i = \beta_0 + \beta_1 X_{NAP,i} + \beta_2 X_{W2,i} + \beta_3 X_{W3,i} + \beta_4 X_{W4,i} + \epsilon_i$$

- where $X_{W2,i}$, $X_{W3,i}$, and $X_{W4,i}$ are indicator variables for Week 2, 3, and 4, respectively.

Dummy Variables

$$Y_i = \beta_0 + \beta_1 X_{NAP,i} + \beta_2 X_{W2,i} + \beta_3 X_{W3,i} + \beta_4 X_{W4,i} + \epsilon_i$$

- where $X_{W2,i}$, $X_{W3,i}$, and $X_{W4,i}$ are indicator variables for Week 2, 3, and 4, respectively.

In matrix form, the data with dummy variables would look like this (try to identify which weeks each observation comes from!):

$$\begin{bmatrix} 11 \\ 10 \\ 13 \\ 11 \\ \vdots \end{bmatrix} = \begin{bmatrix} 1 & 0.045 & 0 & 0 & 1 \\ 1 & -1.036 & 0 & 1 & 0 \\ 1 & -1.336 & 0 & 1 & 0 \\ 1 & 0.616 & 1 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots \end{bmatrix} \times \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \\ \beta_3 \\ \beta_4 \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \epsilon_3 \\ \epsilon_4 \\ \vdots \end{bmatrix}$$

Use `model.matrix` in R to see full dataset . . .

Analysis of Covariance (ANCOVA model)

The model is:

$$Y_i = \beta_0 + \beta_1 X_{NAP,i} + \beta_2 X_{W2,i} + \beta_3 X_{W3,i} + \beta_4 X_{W4,i} + \epsilon_i$$

There is one slope (β_1) relating to the effect of NAP on Richness. In addition, each Week gets its own intercept:

- Week 1: $Y_i = \beta_0 + \beta_1 X_{NAP,i} + \epsilon_i$

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There is one slope (β_1) relating to the effect of NAP on Richness. In addition, each Week gets its own intercept:

- Week 1: $Y_i = \beta_0 + \beta_1 X_{NAP,i} + \epsilon_i$
- Week 2: $Y_i = [\beta_0 + \beta_2(1)] + \beta_1 X_{NAP,i} + \epsilon_i$

Analysis of Covariance (ANCOVA model)

The model is:

$$Y_i = \beta_0 + \beta_1 X_{NAP,i} + \beta_2 X_{W2,i} + \beta_3 X_{W3,i} + \beta_4 X_{W4,i} + \epsilon_i$$

There is one slope (β_1) relating to the effect of NAP on Richness. In addition, each Week gets its own intercept:

- Week 1: $Y_i = \beta_0 + \beta_1 X_{NAP,i} + \epsilon_i$
- Week 2: $Y_i = [\beta_0 + \beta_2(1)] + \beta_1 X_{NAP,i} + \epsilon_i$
- Week 3: $Y_i = [\beta_0 + \beta_3(1)] + \beta_1 X_{NAP,i} + \epsilon_i$

Analysis of Covariance (ANCOVA model)

The model is:

$$Y_i = \beta_0 + \beta_1 X_{NAP,i} + \beta_2 X_{W2,i} + \beta_3 X_{W3,i} + \beta_4 X_{W4,i} + \epsilon_i$$

There is one slope (β_1) relating to the effect of NAP on Richness. In addition, each Week gets its own intercept:

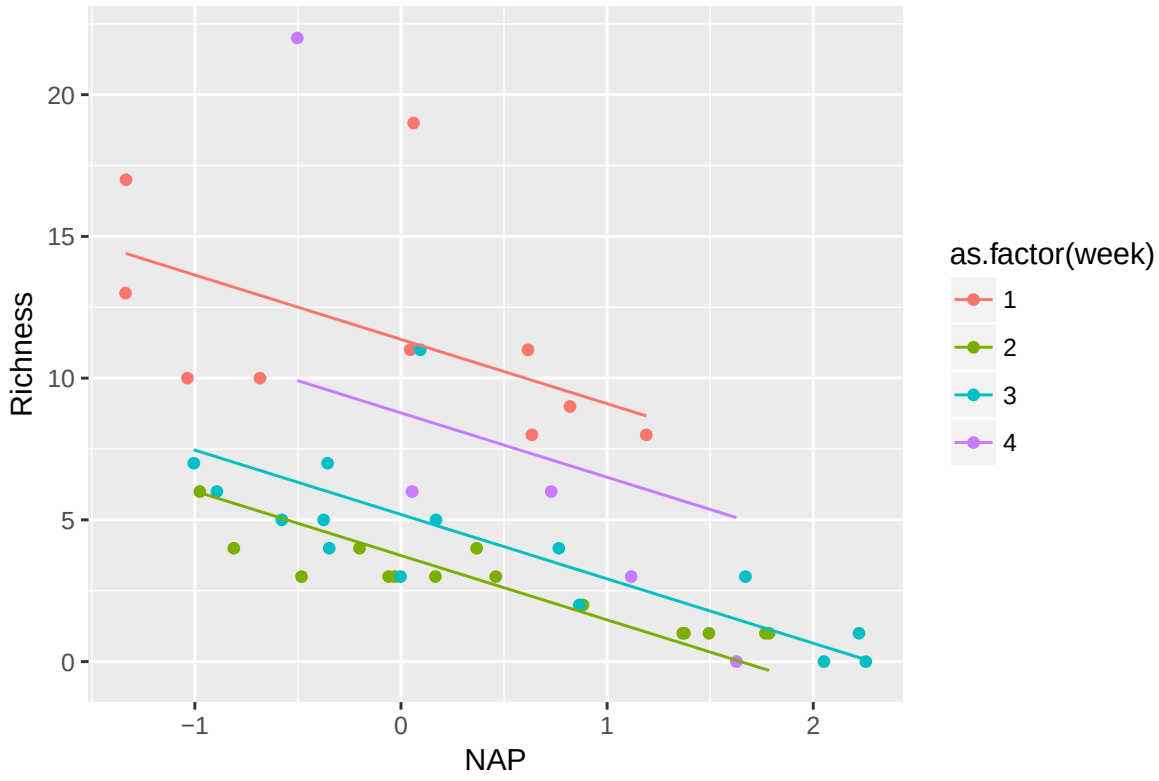
- Week 1: $Y_i = \beta_0 + \beta_1 X_{NAP,i} + \epsilon_i$
- Week 2: $Y_i = [\beta_0 + \beta_2(1)] + \beta_1 X_{NAP,i} + \epsilon_i$
- Week 3: $Y_i = [\beta_0 + \beta_3(1)] + \beta_1 X_{NAP,i} + \epsilon_i$
- Week 4: $Y_i = [\beta_0 + \beta_4(1)] + \beta_1 X_{NAP,i} + \epsilon_i$

```r
lmfit.ancova <- lm(Richness ~ NAP + as.factor(week), data = RIKZ)

summary(lmfit.ancova)
```

```
Call:
lm(formula = Richness ~ NAP + as.factor(week), data = RIKZ)

Residuals:
    Min      1Q  Median      3Q     Max
-5.0788 -1.4014 -0.3633  0.6500 12.0845

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)        11.3677     0.9459  12.017 7.48e-15 ***
NAP                -2.2708     0.4678  -4.854 1.88e-05 ***
as.factor(week)2   -7.6251     1.2491  -6.105 3.37e-07 ***
as.factor(week)3   -6.1780     1.2453  -4.961 1.34e-05 ***
as.factor(week)4   -2.5943     1.6694  -1.554    0.128
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.987 on 40 degrees of freedom
Multiple R-squared:  0.6759,    Adjusted R-squared:  0.6435
F-statistic: 20.86 on 4 and 40 DF,  p-value: 2.369e-09
```

ANCOVA

```
library(ggplot2)
p <- ggplot(data = cbind(RIKZ, pred = predict(lmfit.ancova)),
aes(x = NAP, y = Richness, color = as.factor(week)))
p + geom_point() + geom_line(aes(y = pred))
```



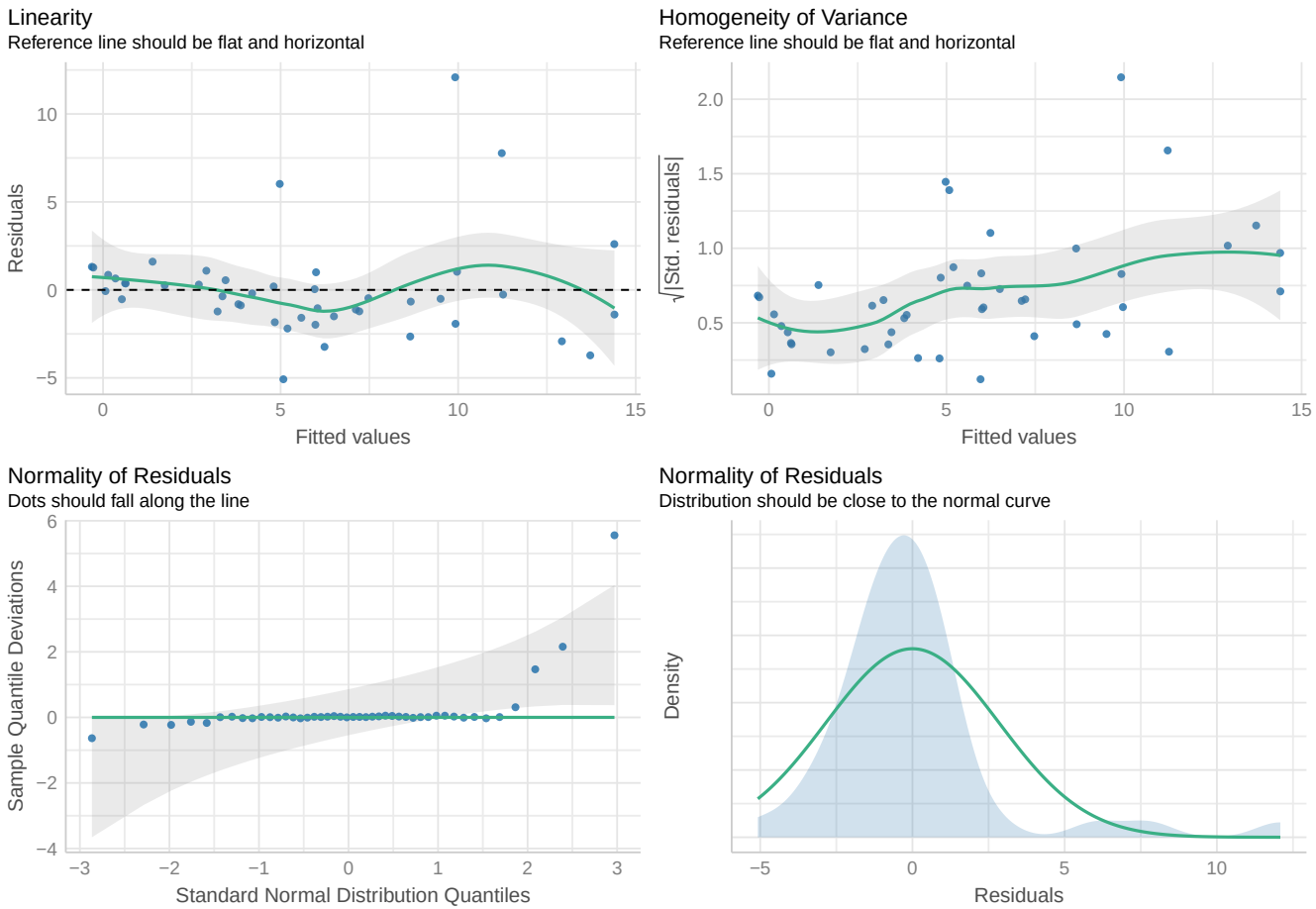
Means coding

```
lmfit.ancova.m <- lm(Richness ~ NAP + as.factor(week)-1, data = RIKZ)

summary(lmfit.ancova.m)
```

```
Call:
lm(formula = Richness ~ NAP + as.factor(week) - 1, data = RIKZ)

Residuals:
    Min      1Q  Median      3Q     Max
-5.0788 -1.4014 -0.3633  0.6500 12.0845

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
NAP                -2.2708     0.4678  -4.854 1.88e-05 ***
as.factor(week)1   11.3677     0.9459  12.017 7.48e-15 ***
as.factor(week)2    3.7426     0.8026   4.663 3.44e-05 ***
as.factor(week)3    5.1897     0.7979   6.505 9.24e-08 ***
as.factor(week)4    8.7734     1.3657   6.424 1.20e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.987 on 40 degrees of freedom
Multiple R-squared:  0.8604,    Adjusted R-squared:  0.843
F-statistic: 49.32 on 5 and 40 DF,  p-value: 4.676e-16
```

Assumptions

```
performance::check_model(lmfit.ancova,
    check = c("linearity", "homogeneity", "qq", "normality"))
```



Interactions

We should be cautious with interactions:

- In experimental data, interactions should **frequently** be examined, and often should be examined **before** testing for main effects.
- In observational studies, data will usually be unbalanced. Interactions should **rarely** be examined unless though to be important a priori.

Interactions

For illustration only, we can naively assume that we think that NAP and Week **interact** in their effects on Richness.

- *Caveat: there's no real biological reason that week and relative elevation should interact, and the researchers did not design this experiment to test for this interaction.*

```r
lmfit.ancovaI <- lm(Richness ~ NAP * as.factor(week), data = RIKZ)
summary(lmfit.ancovaI)
```

```
Call:
lm(formula = Richness ~ NAP * as.factor(week), data = RIKZ)

Residuals:
    Min      1Q  Median      3Q     Max
-6.3022 -0.9442 -0.2946  0.3383  7.7103

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)          11.40561    0.77730  14.673  < 2e-16 ***
NAP                  -1.90016    0.87000  -2.184 0.035369 *
as.factor(week)2     -8.04029    1.05519  -7.620 4.30e-09 ***
as.factor(week)3     -6.37154    1.03168  -6.176 3.63e-07 ***
as.factor(week)4      1.37721    1.60036   0.861 0.395020
NAP:as.factor(week)2  0.42558    1.12008   0.380 0.706152
NAP:as.factor(week)3 -0.01344    1.04246  -0.013 0.989782
NAP:as.factor(week)4 -7.00002    1.68721  -4.149 0.000188 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.442 on 37 degrees of freedom
Multiple R-squared:  0.7997,    Adjusted R-squared:  0.7618
F-statistic: 21.11 on 7 and 37 DF,  p-value: 3.935e-11
```

Interactions

$$
\begin{aligned}
Y_i &= \beta_0 + \beta_1 X_{NAP,i} + \\
&\quad \beta_2 X_{W2,i} + \beta_3 X_{W3,i} + \beta_4 X_{W4,i} + \\
&\quad \beta_5 X_{NAP,i} X_{W2,i} + \beta_6 X_{NAP,i} X_{W3,i} + \beta_7 X_{NAP,i} X_{W4,i} + \\
&\quad \epsilon_i
\end{aligned}
$$

The data in matrix form (again, try to determine which week each observation comes from!):

$$
\begin{bmatrix} 11 \\ 10 \\ 13 \\ 11 \\ \vdots \end{bmatrix} = \begin{bmatrix} 1 & 0.045 & 0 & 0 & 1 & 0 & 0 & 0.045 \\ 1 & -1.036 & 0 & 1 & 0 & 0 & -1.036 & 0 \\ 1 & -1.336 & 0 & 1 & 0 & 0 & -1.336 & 0 \\ 1 & 0.616 & 1 & 0 & 0 & 0.616 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \end{bmatrix} \times \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \\ \beta_3 \\ \beta_4 \\ \beta_5 \\ \beta_6 \\ \beta_7 \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \epsilon_3 \\ \epsilon_4 \\ \vdots \end{bmatrix}
$$

Interactions

$$
\begin{aligned}
Y_i \quad = \quad & \beta_0 + \beta_1 X_{NAP,i} + \\
& \beta_2 X_{W2,i} + \beta_3 X_{W3,i} + \beta_4 X_{W4,i} + \\
& \beta_5 X_{NAP,i} X_{W2,i} + \beta_6 X_{NAP,i} X_{W3,i} + \beta_7 X_{NAP,i} X_{W4,i} + \\
& \epsilon_i
\end{aligned}
$$

There is one slope and one intercept for each week:

- Week 1: $Y_i = \beta_0 + \beta_1 X_{NAP,i} + \epsilon_i$

Interactions

$$
\begin{aligned}
Y_i &= \beta_0 + \beta_1 X_{NAP,i} + \\
&\quad \beta_2 X_{W2,i} + \beta_3 X_{W3,i} + \beta_4 X_{W4,i} + \\
&\quad \beta_5 X_{NAP,i} X_{W2,i} + \beta_6 X_{NAP,i} X_{W3,i} + \beta_7 X_{NAP,i} X_{W4,i} + \\
&\quad \epsilon_i
\end{aligned}
$$

There is one slope and one intercept for each week:

- Week 1: $Y_i = \beta_0 + \beta_1 X_{NAP,i} + \epsilon_i$
- Week 2: $Y_i = [\beta_0 + \beta_2(1)] + [\beta_1 + \beta_5(1)] X_{NAP,i} + \epsilon_i$

Interactions

$$
\begin{aligned}
Y_i &= \beta_0 + \beta_1 X_{NAP,i} + \\
&\quad \beta_2 X_{W2,i} + \beta_3 X_{W3,i} + \beta_4 X_{W4,i} + \\
&\quad \beta_5 X_{NAP,i} X_{W2,i} + \beta_6 X_{NAP,i} X_{W3,i} + \beta_7 X_{NAP,i} X_{W4,i} + \\
&\quad \epsilon_i
\end{aligned}
$$

There is one slope and one intercept for each week:

- Week 1: $Y_i = \beta_0 + \beta_1 X_{NAP,i} + \epsilon_i$
- Week 2: $Y_i = [\beta_0 + \beta_2(1)] + [\beta_1 + \beta_5(1)] X_{NAP,i} + \epsilon_i$
- Week 3: $Y_i = [\beta_0 + \beta_3(1)] + [\beta_1 + \beta_6(1)] X_{NAP,i} + \epsilon_i$

Interactions

$$
\begin{aligned}
Y_i \quad = \quad & \beta_0 + \beta_1 X_{NAP,i} + \\
& \beta_2 X_{W2,i} + \beta_3 X_{W3,i} + \beta_4 X_{W4,i} + \\
& \beta_5 X_{NAP,i} X_{W2,i} + \beta_6 X_{NAP,i} X_{W3,i} + \beta_7 X_{NAP,i} X_{W4,i} + \\
& \epsilon_i
\end{aligned}
$$

There is one slope and one intercept for each week:

- Week 1: $Y_i = \beta_0 + \beta_1 X_{NAP,i} + \epsilon_i$
- Week 2: $Y_i = [\beta_0 + \beta_2(1)] + [\beta_1 + \beta_5(1)] X_{NAP,i} + \epsilon_i$
- Week 3: $Y_i = [\beta_0 + \beta_3(1)] + [\beta_1 + \beta_6(1)] X_{NAP,i} + \epsilon_i$
- Week 4: $Y_i = [\beta_0 + \beta_4(1)] + [\beta_1 + \beta_7(1)] X_{NAP,i} + \epsilon_i$

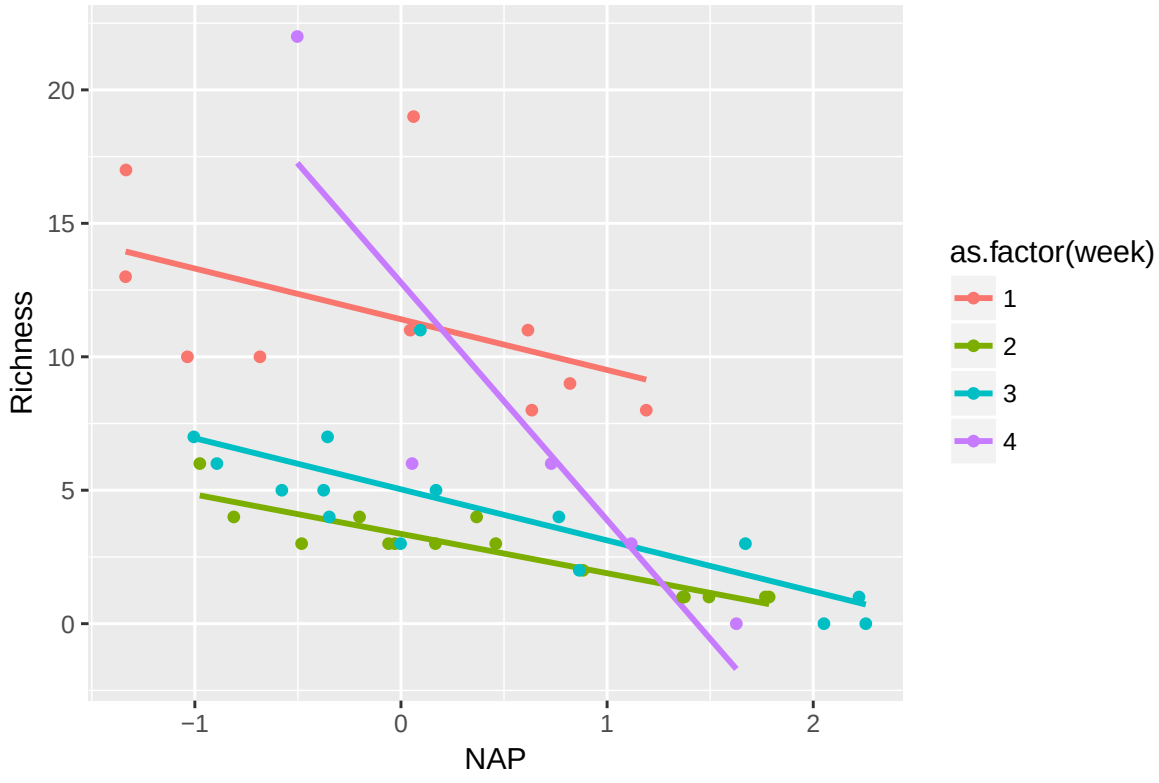
```r
lmfit.ancovaI <- lm(Richness ~ NAP * as.factor(week), data = RIKZ)
summary(lmfit.ancovaI)
```

```
Call:
lm(formula = Richness ~ NAP * as.factor(week), data = RIKZ)

Residuals:
    Min      1Q  Median      3Q     Max
-6.3022 -0.9442 -0.2946  0.3383  7.7103

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)          11.40561    0.77730  14.673  < 2e-16 ***
NAP                  -1.90016    0.87000  -2.184 0.035369 *
as.factor(week)2     -8.04029    1.05519  -7.620 4.30e-09 ***
as.factor(week)3     -6.37154    1.03168  -6.176 3.63e-07 ***
as.factor(week)4      1.37721    1.60036   0.861 0.395020
NAP:as.factor(week)2  0.42558    1.12008   0.380 0.706152
NAP:as.factor(week)3 -0.01344    1.04246  -0.013 0.989782
NAP:as.factor(week)4 -7.00002    1.68721  -4.149 0.000188 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.442 on 37 degrees of freedom
Multiple R-squared:  0.7997,    Adjusted R-squared:  0.7618
F-statistic: 21.11 on 7 and 37 DF,  p-value: 3.935e-11
```

Interactions

```
ggplot(RIKZ, aes(x=NAP, y=Richness, colour=as.factor(week)))+
  geom_smooth(method = "lm", se = FALSE)+geom_point()
```

```
`geom_smooth()` using formula = 'y ~ x'
```



To specify the same model using means coding, we would use:

```
lmfit.ancovaI.m<-lm(Richness~NAP*as.factor(week)-1-NAP, data=RIKZ)
summary(lmfit.ancovaI.m)
```

```
Call:
lm(formula = Richness ~ NAP * as.factor(week) - 1 - NAP, data = RIKZ)

Residuals:
    Min      1Q  Median      3Q     Max
-6.3022 -0.9442 -0.2946  0.3383  7.7103

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
as.factor(week)1        11.4056     0.7773  14.673  < 2e-16 ***
as.factor(week)2         3.3653     0.7136   4.716 3.38e-05 ***
as.factor(week)3         5.0341     0.6784   7.421 7.85e-09 ***
as.factor(week)4        12.7828     1.3989   9.138 5.05e-11 ***
NAP:as.factor(week)1    -1.9002     0.8700  -2.184  0.03537 *
NAP:as.factor(week)2    -1.4746     0.7055  -2.090  0.04353 *
NAP:as.factor(week)3    -1.9136     0.5743  -3.332  0.00197 **
NAP:as.factor(week)4    -8.9002     1.4456  -6.157 3.85e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.442 on 37 degrees of freedom
Multiple R-squared:  0.9138,    Adjusted R-squared:  0.8951
```

Think-Pair-Share

How could we fit a model where the effect of NAP was the same for all weeks except week 4?

Think-Pair-Share

How could we fit a model where the effect of NAP was the same for all weeks except week 4?

```
lmfit.special <- lm(Richness ~ NAP + as.factor(week) + NAP:I(week==4),
                    data = RIKZ)
summary(lmfit.special)
```

```
Call:
lm(formula = Richness ~ NAP + as.factor(week) + NAP:I(week ==
    4), data = RIKZ)

Residuals:
    Min      1Q  Median      3Q     Max
-6.3022 -0.9762 -0.0838  0.6269  7.6894

Coefficients:
                      Estimate Std. Error t value Pr(>|t|)
(Intercept)            11.4187     0.7558  15.108  < 2e-16 ***
NAP                    -1.7722     0.3875  -4.573 4.77e-05 ***
as.factor(week)2       -7.9124     0.9996  -7.915 1.23e-09 ***
as.factor(week)3       -6.4463     0.9965  -6.469 1.16e-07 ***
as.factor(week)4        1.3641     1.5623   0.873    0.388
NAP:I(week == 4)TRUE   -7.1280     1.4652  -4.865 1.92e-05 ***
---
```

Interactions

Although these results look convincing that there is an interaction between NAP and Week 4, remember:

- this an unbalanced design, with only 5 observations during week 4!

```
table(RIKZ$week)
```

```
 1  2  3  4
10 15 15  5
```

- Hence, this interaction model should be interpreted with caution unless there was an a priori reason to expect the effect of `NAP` to vary by week.

Multiple degree of freedom tests

```
library(car)
lm.RIKZ<-lm(Richness~NAP+exposure+as.factor(week), data=RIKZ)
Anova(lm.RIKZ)
```

```
Anova Table (Type II tests)

Response: Richness
                 Sum Sq Df F value    Pr(>F)
NAP              231.59  1 27.1999 6.335e-06 ***
exposure          24.94  1  2.9289   0.09495 .
as.factor(week)   73.19  3  2.8654   0.04888 *
Residuals        332.07 39
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Multiple df test tests whether all 3 coefficients associated with `as.factor(week)` are 0 versus the alternative hypothesis that at least 1 is non-zero (all weeks are the same vs. at least one of the weeks differs from the others).

Anova versus anova

- For continuous variables, the p-values from `Anova` will be identical to the t-test p-values (see exposure variable).
- These tests for (NAP, exposure, week) are conditional on having the other terms included in the model.
- By contrast the `anova` function which performs "sequential" tests (where, "order of entry" matters!)

```r
anova(lm(Richness~NAP+exposure+as.factor(week), data=RIKZ))
```

```
Analysis of Variance Table

Response: Richness
                Df Sum Sq Mean Sq F value    Pr(>F)
NAP              1 357.53  357.53 41.9907 1.117e-07 ***
exposure         1 338.86  338.86 39.7977 1.931e-07 ***
as.factor(week)  3  73.19   24.40  2.8654   0.04888 *
Residuals       39 332.07    8.51
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
anova(lm(Richness~as.factor(week)+exposure+NAP, data=RIKZ))
```

```
Analysis of Variance Table

Response: Richness
                Df Sum Sq Mean Sq F value    Pr(>F)
as.factor(week)  3 534.31 178.104 20.9177 3.060e-08 ***
exposure         1   3.67   3.675  0.4316    0.5151
NAP              1 231.59 231.593 27.1999 6.335e-06 ***
Residuals       39 332.07   8.514
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Additional Notes

See section 3.8 in the book for information on how to conduct pairwise comparisons (e.g., we have “4 choose 2” = 6 possible comparisons of different weeks).

Additional Notes

See section 3.8 in the book for information on how to conduct pairwise comparisons (e.g., we have "4 choose 2" = 6 possible comparisons of different weeks).

See sections 3.12 and 3.13 for information regarding how to test your own hypotheses using contrasts (formed by taking linear combinations of the regression coefficients).

For example, we could test whether the average richness during weeks 1 and 2 differs from the average richness of weeks 3 and 4.