

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

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$$\vdots$$

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$$Y_n = \beta_0 + \beta_1 X_n + \epsilon_n$$

- We can extract this set of equations with matrices.

Matrix Notation for Regression

$$Y_1 = \beta_0 + \beta_1 X_1 + \epsilon_1$$

$$Y_2 = \beta_0 + \beta_1 X_2 + \epsilon_2$$

$$\vdots$$

$$Y_n = \beta_0 + \beta_1 X_n + \epsilon_n$$

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

Matrix Notation for Regression

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

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

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

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

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

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

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:

$$Y_{[n \times 1]} = X_{[n \times p]} \beta_{[p \times 1]} + \epsilon_{[n \times 1]}$$

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

Multiple linear regression

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

$$\begin{aligned}y_i &= \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_{p-1} x_{i,p-1} + \epsilon_i \\ \epsilon &\sim \text{N}(0, \sigma^2)\end{aligned}$$

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We can use `lm` to find estimates of intercept (β_0) and slope parameters (β_1, β_2, \dots) that minimize SSE:

$$SSE_{df=n-p} = \sum_i^n (Y_i - \hat{Y})^2 = \sum_i^n (Y_i - [\beta_0 + \beta_1 X_{1,i} + \beta_2 X_{2,i} + \dots])^2$$

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

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 ($R^2 = SSR/SST$).

- However, adding additional covariates *always* increases R^2 , so we can **adjust** R^2 as:

$$R^2_{\text{adj}} = \frac{\frac{SSR}{p-1}}{\frac{SST}{n-1}} = \left(\frac{n-1}{p-1} \right) \frac{SSR}{SST}$$

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):

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

Multiple 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):

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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:

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

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

```
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:

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

$$\hat{R}_i = 5.459 - 2.512\text{NAP}_i + 21.942\text{H}_i$$

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- Adjusted R^2 went from 0.31 to 0.37

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Interpretations:

- β_1 :

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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_2 :

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- 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*.

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- β_2 : the change in Richness for every 1 unit increase in Humus *while holding NAP constant*.
- β_0 :

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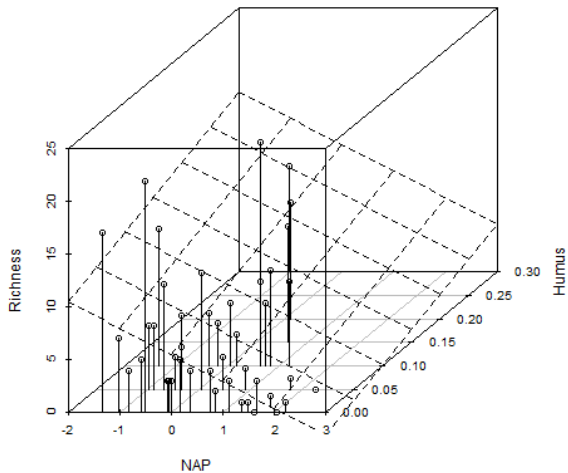
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Interpretations:

- 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.



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?

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

\end{center}

T-test

```
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

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- 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?

$$Y_i = \beta_0 + \beta_1 X_{mi} + \epsilon_i$$

where X_{mi} is 1 if male and 0 if female

$$\hat{Y}_i = 108.6 + 4.8X_{mi}$$

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- So, if **male**:

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where X_{mi} is 1 if male and 0 if female

$$\hat{Y}_i = 108.6 + 4.8X_{mi}$$

- 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:

$$Y_i = \beta_m X_{mi} + \beta_f X_{fi} + \epsilon_i$$

where $X_{mi} = 1$ if male and 0 if female

where $X_{fi} = 1$ if female and 0 if male

Understanding Model Parameters

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

$$Y_i = \beta_m X_{mi} + \beta_f X_{fi} + \epsilon_i$$

where $X_{mi} = 1$ if male and 0 if female

where $X_{fi} = 1$ if female and 0 if male

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

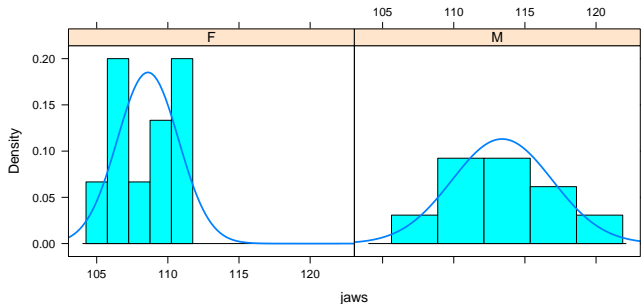
Multiple R-squared: 0.9993, Adjusted R-squared: 0.9992

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

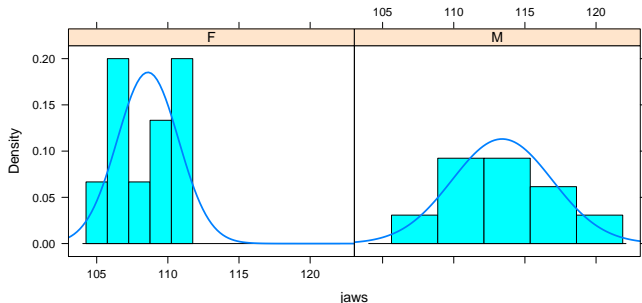
```
library(mosaic)  
histogram(~jaws|sex, data=jawdat, cex=1, fit="normal")
```



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- Equal (constant) variance for the two groups
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```



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

Categorical variables

Recall the RIKZ data.

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

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Now, what if we also suspected that the Week the data were collected might affect Richness in addition to NAP?

- 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?

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Now, what if we also suspected that the Week the data were collected might affect Richness in addition to NAP?

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

The model is:

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

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

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- 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:

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

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

```
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

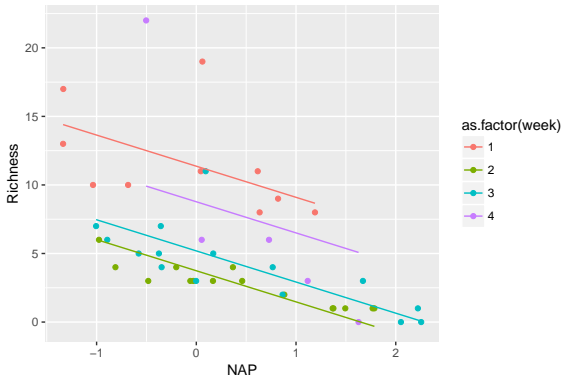
Residual standard error: 2.987 on 40 degrees of freedom

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

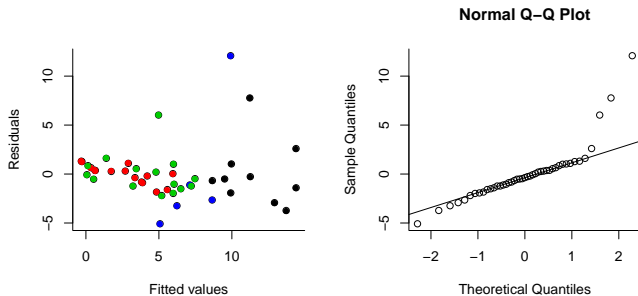
```
library(ggplot2)
p <- ggplot(data = cbind(RIKZ, pred = predict(lmfit.ancova)),
  aes(x = NAP, y = Richness, color = as.factor(week)))
p + geom_point() + geom_line(aes(y = pred))
```



ANCOVA model assumptions

Check assumptions:

```
par(bty="L", mfrow=c(1,2))  
plot(lmfit.ancova$resid ~ lmfit.ancova$fitted,  
     xlab = "Fitted values", ylab = "Residuals")  
points(lmfit.ancova$resid ~ lmfit.ancova$fitted, col=RIKZ$week, pch=16)  
qqnorm(lmfit.ancova$resid)  
qqline(lmfit.ancova$resid)
```



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.*

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

Interactions

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The data in matrix form:

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

Interactions

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

There is one slope and one intercept for each week:

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

Interactions

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

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

Interactions

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

There is one slope and one intercept for each week:

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

Interactions

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

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: $Y_i = [\beta_0 + \beta_4(1)] + [\beta_1 + \beta_7(1)] X_{NAP,i} + \epsilon_i$

```
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

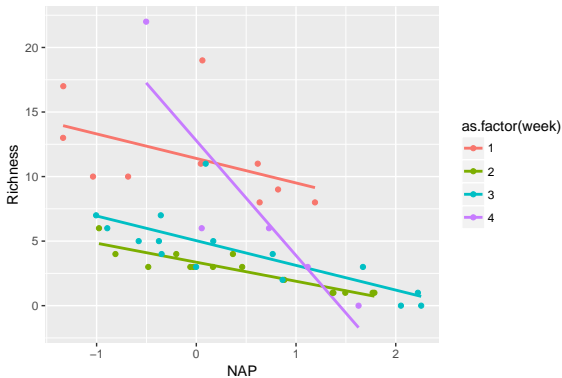
Multiple R-squared: 0.7997, Adjusted R-squared: 0.7618

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'



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!)

```
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

```
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