

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

- We can extract this set of equations with matrices.

Matrix Notation for Regression

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

$$\vdots$$

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

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

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

Matrix Notation for Regression

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

Matrix Notation for Regression

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

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

- The (i, i) entry = $\text{var}(y_i)$
- 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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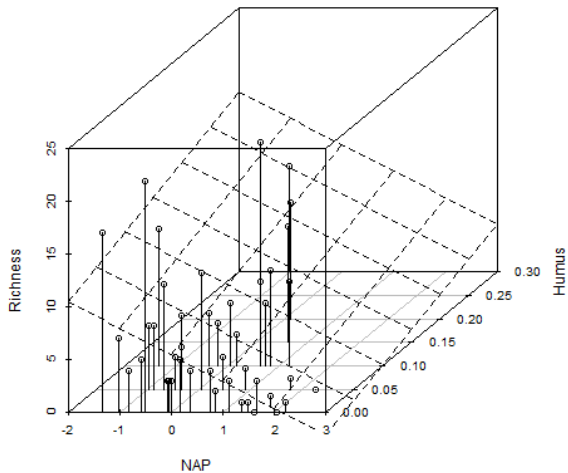
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- β_1 : the change in Richness for every 1 unit increase in NAP *while holding Humus constant*.
- β_2 : the change in Richness for every 1 unit increase in Humus *while holding NAP constant*.
- β_0 : the level of Richness if Humus and NAP both equal 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?

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

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

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

Understanding Model Parameters

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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 ***

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Residual standard error: 3.08 on 18 degrees of freedom

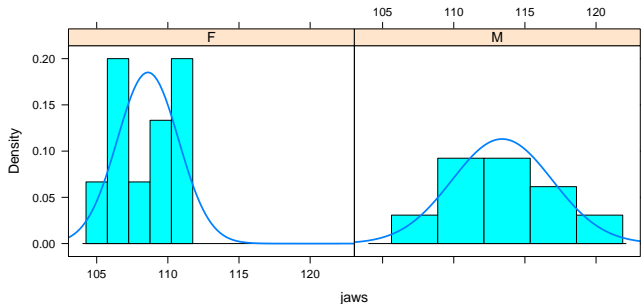
Multiple R-squared: 0.9993, Adjusted R-squared: 0.9992

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

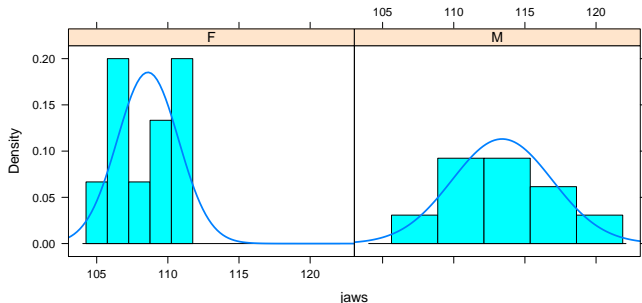
```
library(mosaic)  
histogram(~jaws|sex, data=jawdat, cex=1, fit="normal")
```



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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

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

- 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

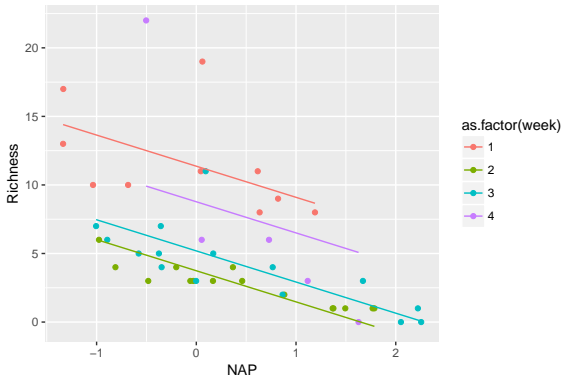
Residual standard error: 2.987 on 40 degrees of freedom

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

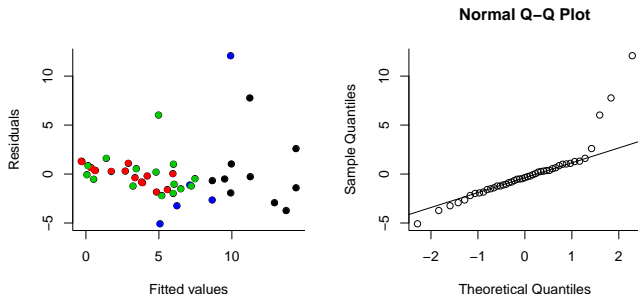
```
library(ggplot2)
p <- ggplot(data = cbind(RIKZ, pred = predict(lmfit.ancova)),
  aes(x = NAP, y = Richness, color = as.factor(week)))
p + geom_point() + geom_line(aes(y = pred))
```



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)
```

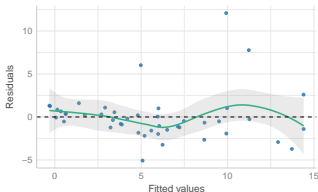


Assumptions

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

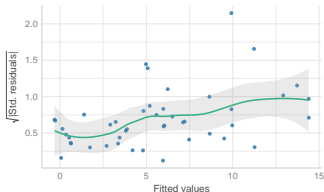
Linearity

Reference line should be flat and horizontal



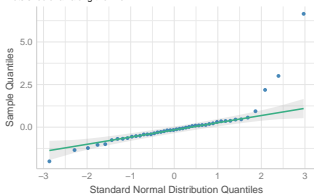
Homogeneity of Variance

Reference line should be flat and horizontal



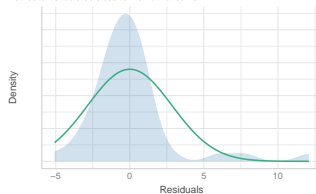
Normality of Residuals

Dots should fall along the line



Normality of Residuals

Distribution should be close to the normal curve



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

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

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: $Y_i = \beta_0 + \beta_1 X_{NAP,i} + \epsilon_i$
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Interactions

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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

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

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

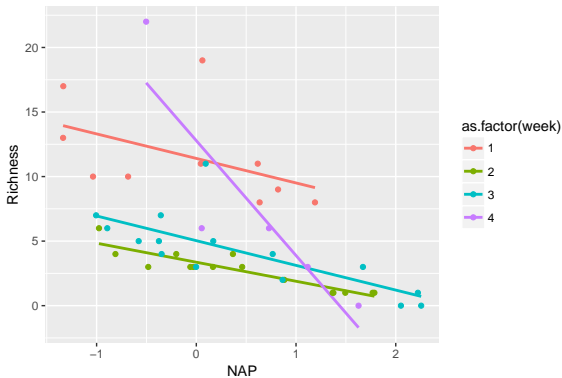
Multiple R-squared: 0.7997, Adjusted R-squared: 0.7618

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

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.