3. Worksheet: Basic R

Emmi Mueller; Z620: Quantitative Biodiversity, Indiana University

13 January, 2019

OVERVIEW

This worksheet introduces some of the basic features of the R computing environment (http://www.r-project.org). It is designed to be used along side the **3. RStudio** handout in your binder. You will not be able to complete the exercises without the corresponding handout.

Directions:

1. Change "Student Name" on line 3 (above) with your name.
2. Complete as much of the worksheet as possible during class.
3. Use the handout as a guide; it contains a more complete description of data sets along with examples of proper scripting needed to carry out the exercises.
4. Answer questions in the worksheet. Space for your answers is provided in this document and is indicated by the ">" character. If you need a second paragraph be sure to start the first line with ">". You should notice that the answer is highlighted in green by RStudio.
5. Before you leave the classroom today, it is *imperative* that you **push** this file to your GitHub repo.
6. When you have completed the worksheet, **Knit** the text and code into a single PDF file by pressing the `Knit` button in the RStudio scripting panel. This will save the PDF output in your '3.RStudio' folder.
7. After Knitting, please submit the worksheet by making a **push** to your GitHub repo and then create a **pull request** via GitHub. Your pull request should include this file (**3.RStudio_Worksheet.Rmd**) with all code blocks filled out and questions answered) and the PDF output of `Knitr` (**3.RStudio_Worksheet.pdf**).

The completed exercise is due on **Wednesday, January 16th, 2019 before 12:00 PM (noon)**.

1) HOW WE WILL BE USING R AND OTHER TOOLS

You are working in an RMarkdown (.Rmd) file. This allows you to integrate text and R code into a single document. There are two major features to this document: 1) Markdown formatted text and 2) "chunks" of R code. Anything in an R code chunk will be interpreted by R when you *Knit* the document.

When you are done, you will *knit* your document together. However, if there are errors in the R code contained in your Markdown document, you will not be able to knit a PDF file. If this happens, you will need to review your code, locate the source of the error(s), and make the appropriate changes. Even if you are able to knit without issue, you should review the knitted document for correctness and completeness before you submit the Worksheet.

2) SETTING YOUR WORKING DIRECTORY

In the R code chunk below, please provide the code to: 1) clear your R environment, 2) print your current working directory, and 3) set your working directory to your '3.RStudio' folder.

```r
rm(list=ls())
getwd()
```

```
## [1] "C:/Users/emmim/GitHub/QB2019_Mueller/2.Worksheets/3.RStudio"
```

```r
setwd("~/GitHub/QB2019_Mueller/2.Worksheets/3.Rstudio")
```

3) USING R AS A CALCULATOR

To follow up on the pre-class exercises, please calculate the following in the R code chunk below. Feel free to reference the **1. Introduction to version control and computing tools** handout.

1) the volume of a cube with length, l, = 5 (volume = l^3)
2) the area of a circle with radius, r, = 2 (area = pi * r^2).
3) the length of the opposite side of a right-triangle given that the angle, theta, = pi/4. (radians, a.k.a. 45Â°) and with hypotenuse length sqrt(2) (remember: sin(theta) = opposite/hypotenuse).
4) the log (base e) of your favorite number.

```
l <- 5
l^3
```

```
## [1] 125
```

```
r <- 2
pi * r^2
```

```
## [1] 12.56637
```

```
theta <- pi/4
hypotenuse <- sqrt(2)
sin(theta)*hypotenuse
```

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

```
log(12)
```

```
## [1] 2.484907
```

4) WORKING WITH VECTORS

To follow up on the pre-class exercises, please perform the requested operations in the R-code chunks below.

Basic Features Of Vectors

In the R-code chunk below, do the following: 1) Create a vector `x` consisting of any five numbers. 2) Create a new vector `w` by multiplying `x` by 14 (i.e., "scalar"). 3) Add `x` and `w` and divide by 15.

```
x <- c(12, 5, 83, 44, 6)
w <- x * 14
(x + w) /15
```

```
## [1] 12  5 83 44  6
```

Now, do the following: 1) Create another vector (`k`) that is the same length as `w`. 2) Multiply `k` by `x`. 3) Use the combine function to create one more vector, `d` that consists of any three elements from `w` and any four elements of `k`.

```
k <- c(5, 7, 33, 51, 444)
k *x
```

```
## [1]   60   35 2739 2244 2664
```

```
d <- c(w[1:3],k[1:4])
d
```

```
## [1]  168   70 1162    5    7   33   51
```

Summary Statistics of Vectors

In the R-code chunk below, calculate the **summary statistics** (i.e., maximum, minimum, sum, mean, median, variance, standard deviation, and standard error of the mean) for the vector (`v`) provided.

```
v <- c(16.4, 16.0, 10.1, 16.8, 20.5, NA, 20.2, 13.1, 24.8, 20.2, 25.0, 20.5, 30.5, 31.4, 27.1)

sem <-function(x){
  sd(na.omit(x))/sqrt(length(na.omit(x)))
}
max(na.omit(v))
```

```
## [1] 31.4
```

```
min(na.omit(v))
```

```
## [1] 10.1
```

```
sum(na.omit(v))
```

```
## [1] 292.6
```

```
mean(na.omit(v))
```

```
## [1] 20.9
```

```
median(na.omit(v))
```

```
## [1] 20.35
```

```
var(na.omit(v))
```

```
## [1] 39.44
```

```
sd(na.omit(v))
```

```
## [1] 6.280127
```

```
sem(v)
```

```
## [1] 1.678435
```

5) WORKING WITH MATRICES

In the R-code chunk below, do the following: Using a mixture of Approach 1 and 2 from the **3. RStudio** handout, create a matrix with two columns and five rows. Both columns should consist of random numbers. Make the mean of the first column equal to 8 with a standard deviation of 2 and the mean of the second column equal to 25 with a standard deviation of 10.

```
j <- c(rnorm(5,mean = 8,sd = 2))
z <- c(rnorm(5,mean = 25, sd = 10))
col1 <- matrix(j, nrow = 5, ncol = 1, byrow = FALSE)
col2 <- matrix(z, nrow = 5, ncol = 1, byrow = FALSE)
k <- cbind(col1, col2)
```

Question 1: What does the `rnorm` function do? What do the arguments in this function specify? Remember to use `help()` or type `?rnorm`.

> Answer 1: rnorm generates n observations of a normal distrubtion given a mean and standard deviation.

In the R code chunk below, do the following: 1) Load `matrix.txt` from the **3.RStudio** data folder as matrix `m`. 2) Transpose this matrix. 3) Determine the dimensions of the transposed matrix.

```
m <- as.matrix(read.table("data/matrix.txt", sep = "\t", header = FALSE))
n <-t(m)
n
```

```
##    [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
## V1    8    5    2    3    9   11    2    3    5     6
## V2    1    5    5    2    9    8    2    3    5     5
## V3    7    2    4    5    1    1    5    6    1     9
## V4    6    4    3    1    1    8    8    7    3     2
## V5    1    1    3    4    2    8    5    6    6     2
```

Question 2: What are the dimensions of the matrix you just transposed?

> Answer 2: The dimension of the matrix are 5x10.

Indexing a Matrix

In the R code chunk below, do the following: 1) Index matrix `m` by selecting all but the third column. 2) Remove the last row of matrix `m`.

```
m[,c(1:2,4:5)]
```

```
##       V1 V2 V4 V5
##  [1,]  8  1  6  1
##  [2,]  5  5  4  1
##  [3,]  2  5  3  3
##  [4,]  3  2  1  4
##  [5,]  9  9  1  2
##  [6,] 11  8  8  8
##  [7,]  2  2  8  5
##  [8,]  3  3  7  6
##  [9,]  5  5  3  6
## [10,]  6  5  2  2
```

```
m[c(1:9),]
```

```
##       V1 V2 V3 V4 V5
##  [1,]  8  1  7  6  1
##  [2,]  5  5  2  4  1
##  [3,]  2  5  4  3  3
##  [4,]  3  2  5  1  4
##  [5,]  9  9  1  1  2
##  [6,] 11  8  1  8  8
##  [7,]  2  2  5  8  5
##  [8,]  3  3  6  7  6
##  [9,]  5  5  1  3  6
```

6) BASIC DATA VISUALIZATION AND STATISTICAL ANALYSIS

Load Zooplankton Data Set

In the R code chunk below, do the following: 1) Load the zooplankton data set from the **3.RStudio** data folder. 2) Display the structure of this data set.

```
meso <-read.table("data/zoop_nuts.txt", sep = "\t", header = TRUE)
str(meso)
```

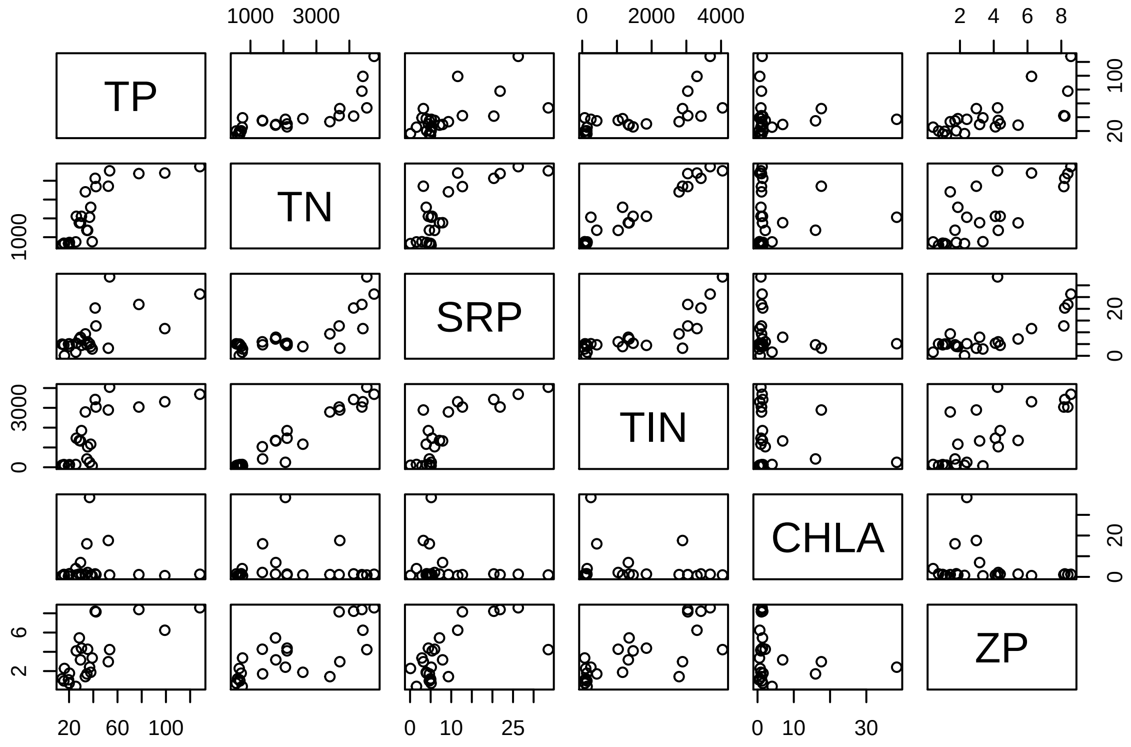
```
## 'data.frame':    24 obs. of  8 variables:
```

```
##  $ TANK: int  34 14 23 16 21 5 25 27 30 28 ...
##  $ NUTS: Factor w/ 3 levels "H","L","M": 2 2 2 2 2 2 2 2 3 3 ...
##  $ TP  : num  20.3 25.6 14.2 39.1 20.1 ...
##  $ TN  : num  720 750 610 761 570 ...
##  $ SRP : num  4.02 1.56 4.97 2.89 5.11 4.68 5 0.1 7.9 3.92 ...
##  $ TIN : num  131.6 141.1 107.7 71.3 80.4 ...
##  $ CHLA: num  1.52 4 0.61 0.53 1.44 1.19 0.37 0.72 6.93 0.94 ...
##  $ ZP  : num  1.781 0.409 1.201 3.36 0.733 ...
```

Correlation

In the R-code chunk below, do the following: 1) Create a matrix with the numerical data in the `meso` dataframe. 2) Visualize the pairwise **bi-plots** of the six numerical variables. 3) Conduct a simple **Pearson's correlation** analysis.

```r
meso.num <- meso[,3:8]
pairs(meso.num)
```



```r
cor1 <- cor(meso.num)
```

Question 3: Describe some of the general features based on the visualization and correlation analysis above?

> Answer 3:The strongest positive correlation is between TIN and TN. Most other pairs also have positive correlations. CHLA does not seem to be correlated with any of the other variables.

In the R code chunk below, do the following: 1) Redo the correlation analysis using the `corr.test()` function in the `psych` package with the following options: method = "pearson", adjust = "BH". 2) Now, redo this correlation analysis using a non-parametric method. 3) Use the print command from the handout to see the results of each correlation analysis.

```r
require("psych")
```

```
## Loading required package: psych
```

```r
cor2 <- corr.test(meso.num, method = "pearson", adjust = "BH")
print(cor2, digits = 3)
```

```
## Call:corr.test(x = meso.num, method = "pearson", adjust = "BH")
## Correlation matrix
##          TP     TN    SRP    TIN   CHLA     ZP
## TP    1.000  0.787  0.654  0.717 -0.017  0.697
## TN    0.787  1.000  0.784  0.969 -0.004  0.756
## SRP   0.654  0.784  1.000  0.801 -0.189  0.676
## TIN   0.717  0.969  0.801  1.000 -0.157  0.761
## CHLA -0.017 -0.004 -0.189 -0.157  1.000 -0.183
## ZP    0.697  0.756  0.676  0.761 -0.183  1.000
## Sample Size
## [1] 24
## Probability values (Entries above the diagonal are adjusted for multiple tests.)
##         TP    TN   SRP   TIN  CHLA    ZP
## TP   0.000 0.000 0.001 0.000 0.983 0.000
## TN   0.000 0.000 0.000 0.000 0.983 0.000
## SRP  0.001 0.000 0.000 0.000 0.491 0.000
## TIN  0.000 0.000 0.000 0.000 0.536 0.000
## CHLA 0.938 0.983 0.376 0.464 0.000 0.491
## ZP   0.000 0.000 0.000 0.000 0.393 0.000
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

```r
cor3 <- corr.test(meso.num, method = "kendall", adjust = "BH")
print(cor3, digits = 3)
```

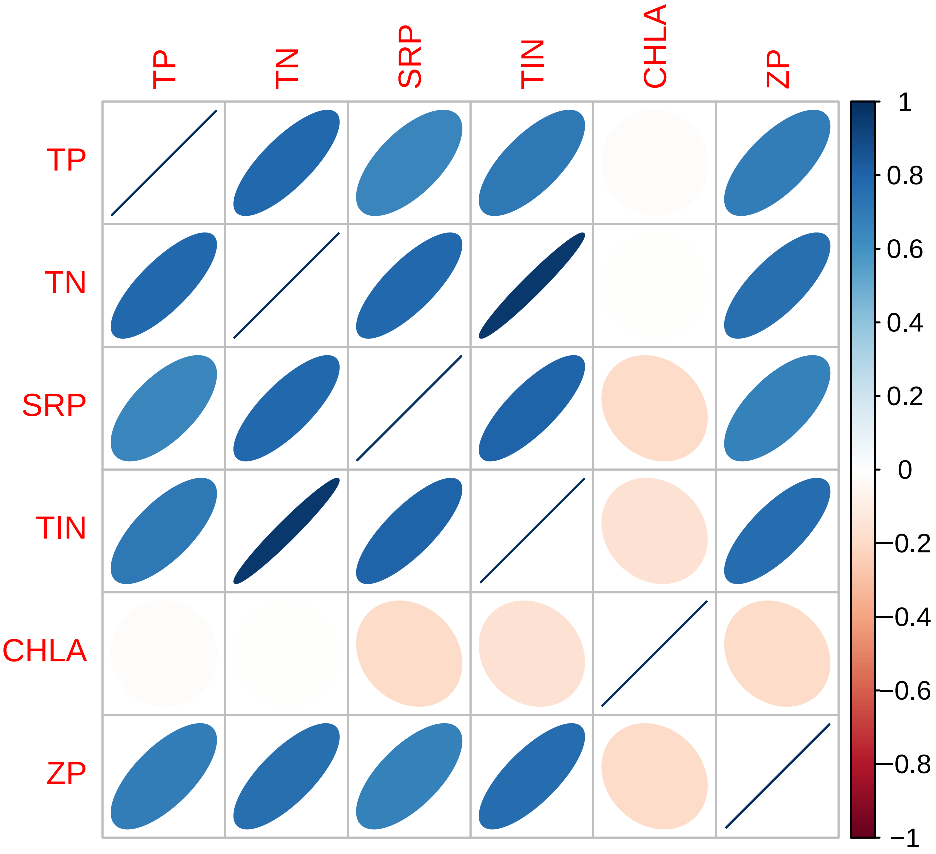
```
## Call:corr.test(x = meso.num, method = "kendall", adjust = "BH")
## Correlation matrix
##         TP    TN    SRP   TIN   CHLA     ZP
## TP   1.000 0.739  0.391 0.577  0.044  0.536
## TN   0.739 1.000  0.478 0.809  0.015  0.551
## SRP  0.391 0.478  1.000 0.563 -0.066  0.449
## TIN  0.577 0.809  0.563 1.000  0.044  0.548
## CHLA 0.044 0.015 -0.066 0.044  1.000 -0.051
## ZP   0.536 0.551  0.449 0.548 -0.051  1.000
## Sample Size
## [1] 24
## Probability values (Entries above the diagonal are adjusted for multiple tests.)
##         TP    TN   SRP   TIN  CHLA    ZP
## TP   0.000 0.000 0.088 0.014 0.899 0.015
## TN   0.000 0.000 0.034 0.000 0.946 0.014
## SRP  0.059 0.018 0.000 0.014 0.899 0.046
## TIN  0.003 0.000 0.004 0.000 0.899 0.014
## CHLA 0.839 0.946 0.760 0.839 0.000 0.899
## ZP   0.007 0.005 0.028 0.006 0.813 0.000
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

```
require("corrplot")
```

```
## Loading required package: corrplot
```

```
## corrplot 0.84 loaded
```

```
corrplot(cor1, method = "ellipse")
```



```
dev.off()
```

```
## null device
##           1
```

Question 4: Describe what you learned from `corr.test`. Specifically, are the results sensitive to whether you use parametric (i.e., Pearson's) or non-parametric methods? When should one use non-parametric methods instead of parametric methods? With the Pearson's method, is there evidence for false discovery rate due to multiple comparisons? Why is false discovery rate important?

> Answer 4: Non-parametric tests should be used when the data is not normally distributed. The results of the correlation test are sensitive to whether you use parametric or non-parametric methods. For Pearson's method, the probability values corrected for multiple comparisons are slightly different than the uncorrected values which is important because as you do more comparison, the more likely errors are to occur.

Linear Regression

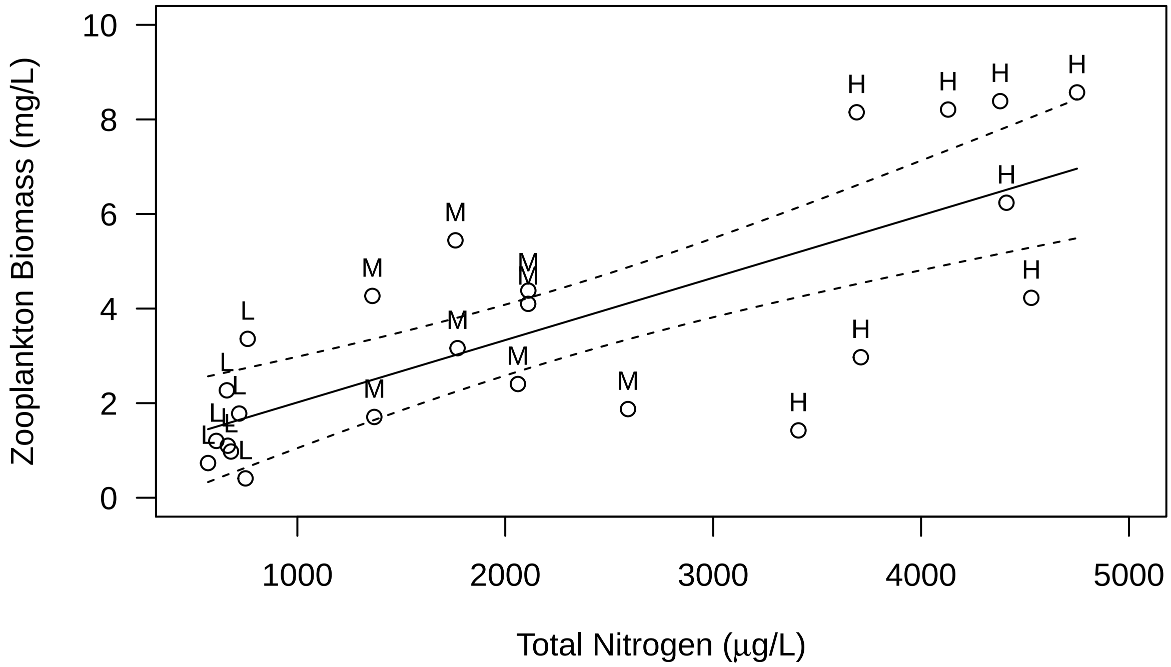
In the R code chunk below, do the following: 1) Conduct a linear regression analysis to test the relationship between total nitrogen (TN) and zooplankton biomass (ZP). 2) Examine the output of the regression analysis.

3) Produce a plot of this regression analysis including the following: categorically labeled points, the predicted regression line with 95% confidence intervals, and the appropriate axis labels.

```
fitreg <-lm(ZP~TN, data = meso)
summary(fitreg)
```

```
## 
## Call:
## lm(formula = ZP ~ TN, data = meso)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -3.7690 -0.8491 -0.0709  1.6238  2.5888 
## 
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 0.6977712  0.6496312   1.074    0.294    
## TN          0.0013181  0.0002431   5.421 1.91e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.75 on 22 degrees of freedom
## Multiple R-squared:  0.5719, Adjusted R-squared:  0.5525 
## F-statistic: 29.39 on 1 and 22 DF,  p-value: 1.911e-05
```

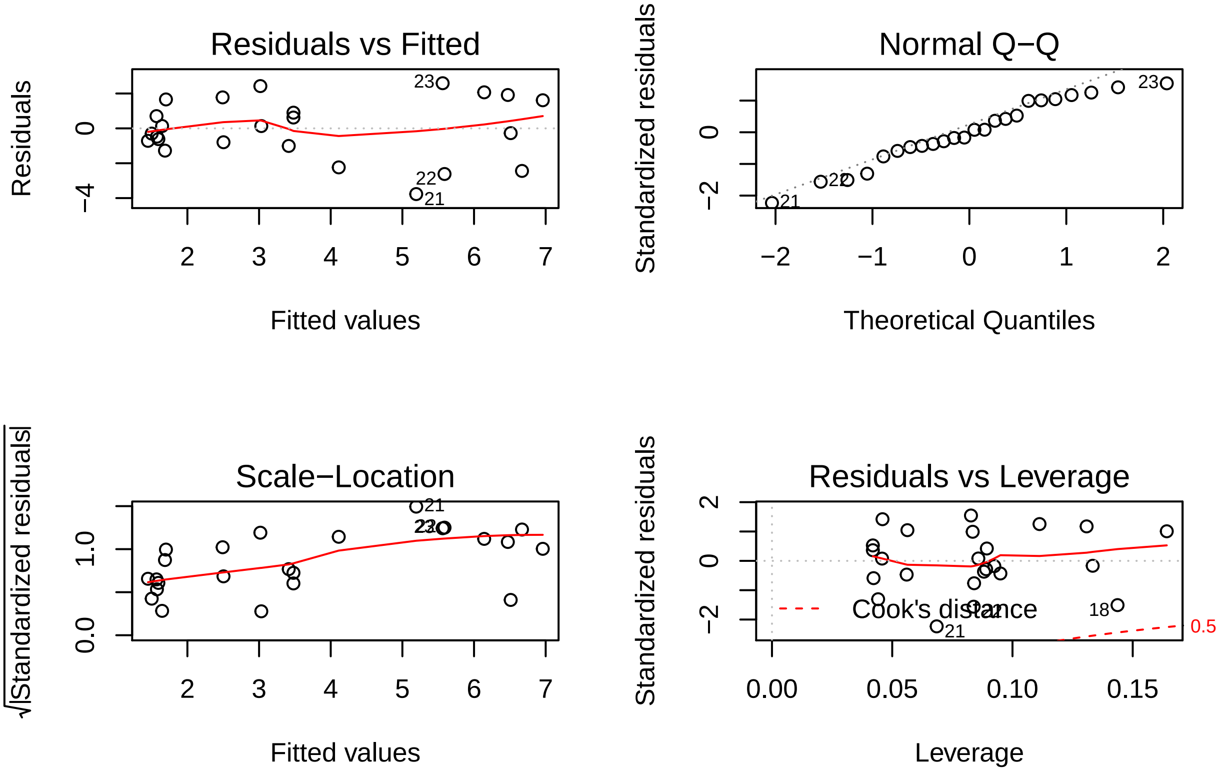
```
plot(meso$TN, meso$ZP, ylim=c(0,10), xlim=c(500,5000), xlab = expression(paste("Total Nitrogen (", mu,
text(meso$TN, meso$ZP, meso$NUTS, pos=3, cex = 0.8)
newTN <- seq(min(meso$TN), max(meso$TN), 10)
regline <- predict(fitreg, newdata = data.frame(TN = newTN))
lines(newTN, regline)
conf95 <- predict(fitreg, newdata=data.frame(TN = newTN), interval = c("confidence"), level = 0.95, typ
matlines(newTN, conf95[,c("lwr","upr")], type ="l", lty = 2, lwd = 1, col = "black")
```



Question 5: Interpret the results from the regression model

Answer 5: Total Nitrogen is a significant predictor of Zooplankton Biomass as shown by the low p-value. Thre residuals appear to be randomly distributed around zero. The Q-Q plot shows a reasonably linear relationship. The square root of the standardized residuals is mostly random and there do not appear to be many stand out cases in the residuals vs. legerage plot.

```
par(mfrow = c(2,2), mar = c(5.1,4.1,4.1,2.1))
plot(fitreg)
```

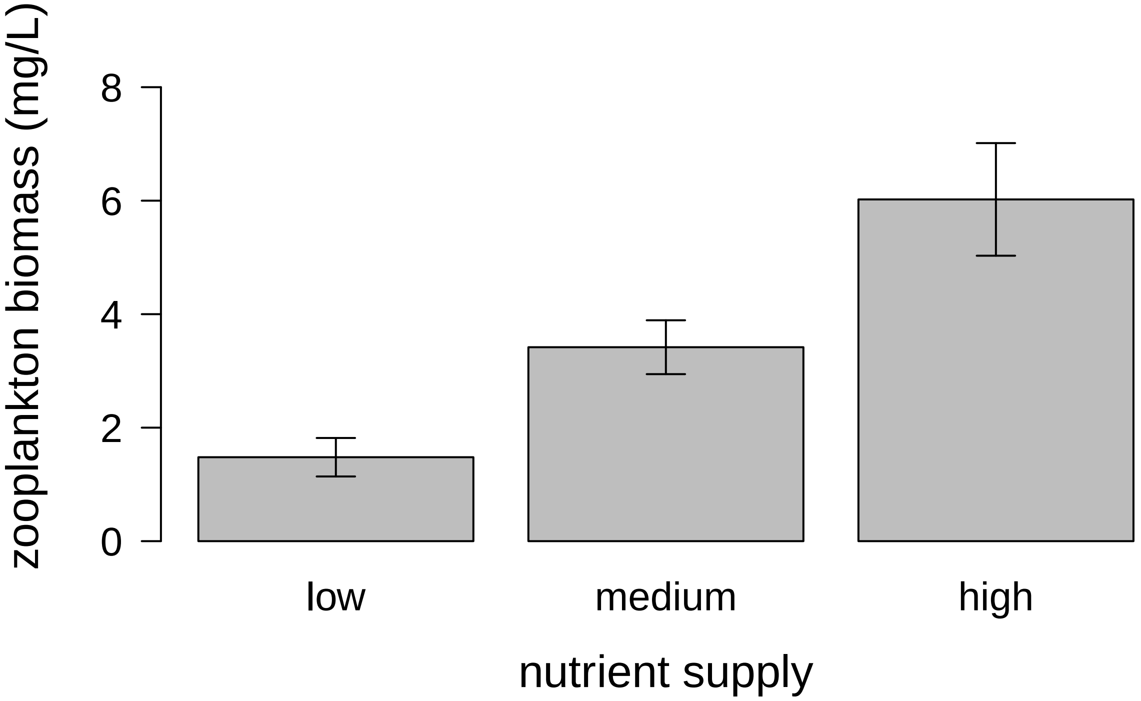


Analysis of Variance (ANOVA)

Using the R code chunk below, do the following: 1) Order the nutrient treatments from low to high (see handout). 2) Produce a barplot to visualize zooplankton biomass in each nutrient treatment. 3) Include error bars (+/- 1 sem) on your plot and label the axes appropriately. 4) Use a one-way analysis of variance (ANOVA) to test the null hypothesis that zooplankton biomass is affected by the nutrient treatment.

```
NUTS <- factor(meso$NUTS, levels = c('L','M','H'))
zp.means <- tapply(meso$ZP, NUTS, mean)
sem <-function(x){
  sd(na.omit(x))/sqrt(length(na.omit(x)))
}
zp.sem <- tapply(meso$ZP, NUTS, sem)

bp <- barplot(zp.means, ylim = c(0, round(max(meso$ZP), digits = 0)), pch = 15, cex = 1.25, las = 1, ce
arrows(x0 = bp, y0 = zp.means, y1 = zp.means - zp.sem, angle = 90, length = 0.1, lwd = 1)
arrows(x0= bp, y0= zp.means, y1 = zp.means + zp.sem, angle = 90, length = 0.1, lwd = 1)
```



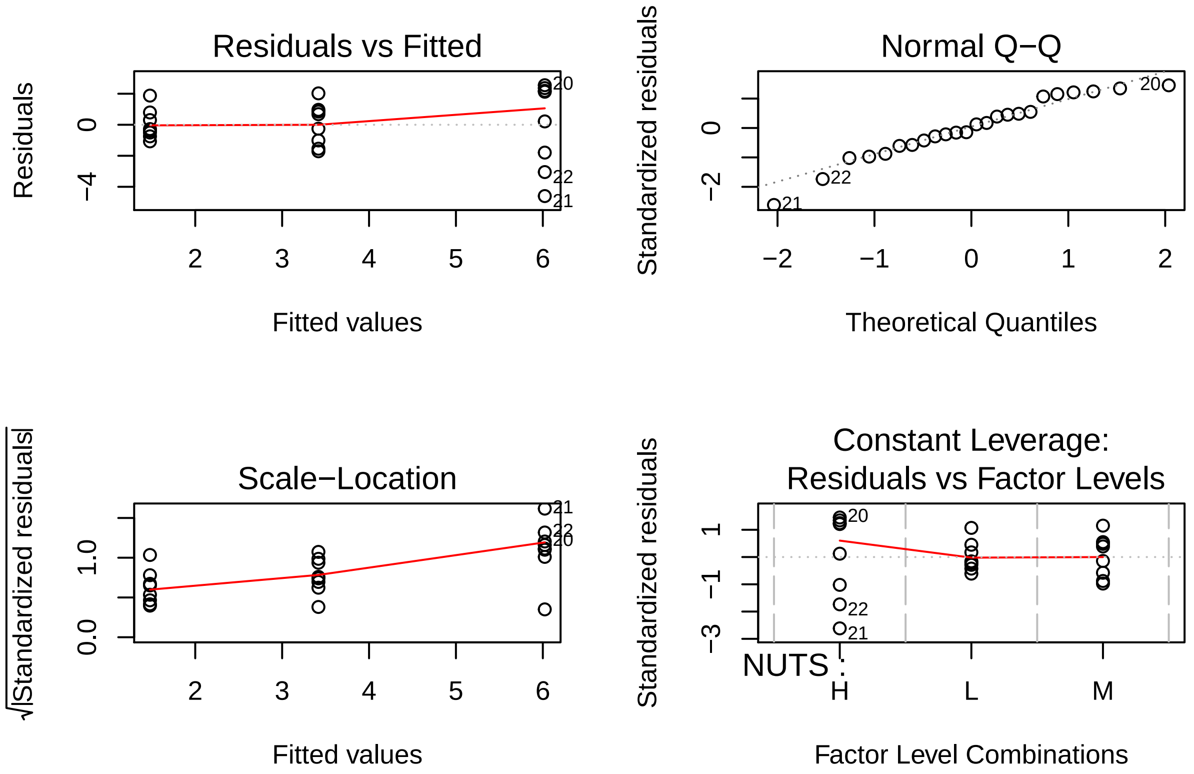
```r
fitanova <- aov(ZP ~NUTS, data = meso)
summary(fitanova)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)    
## NUTS         2  83.15   41.58   11.77 0.000372 ***
## Residuals   21  74.16    3.53                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
TukeyHSD(fitanova)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
## 
## Fit: aov(formula = ZP ~ NUTS, data = meso)
## 
## $NUTS
##          diff        lwr        upr     p adj
## L-H -4.543175 -6.9115094 -2.1748406 0.0002512
## M-H -2.604550 -4.9728844 -0.2362156 0.0294932
## M-L  1.938625 -0.4297094  4.3069594 0.1220246
```

```r
par(mfrow = c(2,2), mar = c(5.1,4.1,4.1,2.1))
plot(fitanova)
```



SYNTHESIS: SITE-BY-SPECIES MATRIX

In the R code chunk below, load the zoop.txt data set in your **3.RStudio** data folder. Create a site-by-species matrix (or dataframe) that does *not* include TANK or NUTS. The remaining columns of data refer to the biomass (Âµg/L) of different zooplankton taxa:

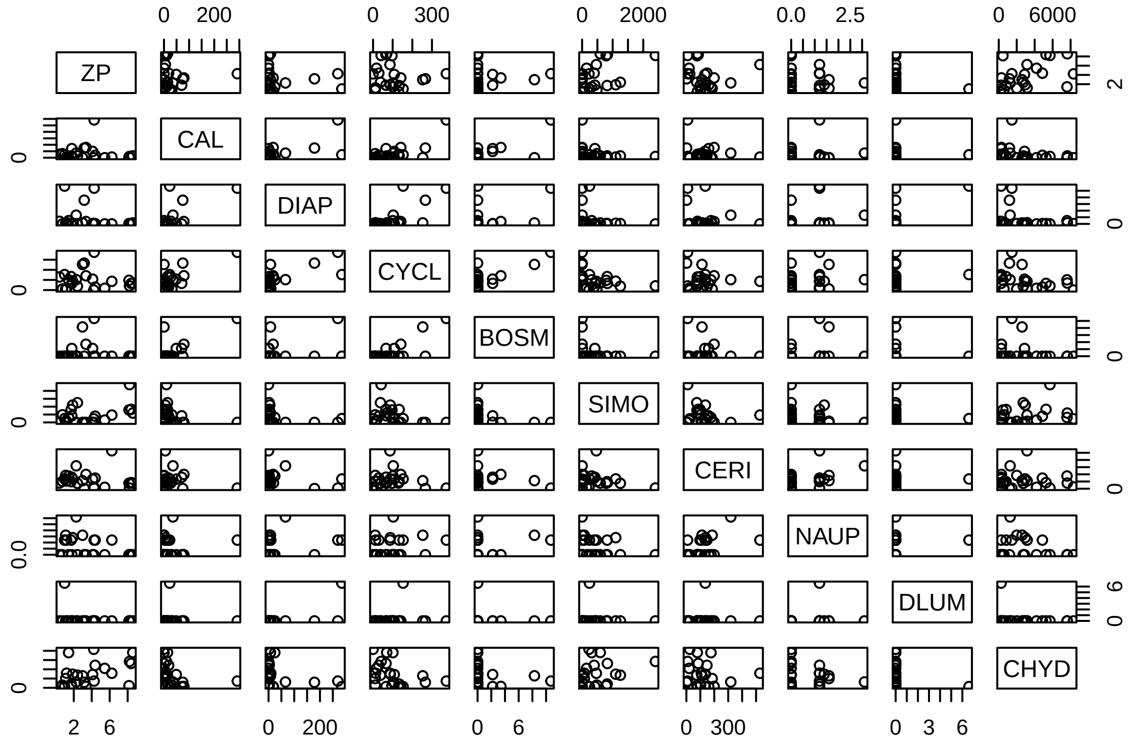
- CAL = calanoid copepods
- DIAP = *Diaphanasoma* sp.
- CYL = cyclopoid copepods
- BOSM = *Bosmina* sp.
- SIMO = *Simocephallus* sp.
- CERI = *Ceriodaphnia* sp.
- NAUP = naupuli (immature copepod)
- DLUM = *Daphnia lumholtzi*
- CHYD = *Chydorus* sp.

Question 6: With the visualization and statistical tools that we learned about in the **3. RStudio** handout, use the site-by-species matrix to assess whether and how different zooplankton taxa were responsible for the total biomass (ZP) response to nutrient enrichment. Describe what you learned below in the "Answer" section and include appropriate code in the R chunk.

> Answer 6: Both Chydorus and Simocephallus were significant predictors of Zooplankton Biomass. Based on pairs correlations I was able to see that both Chydorus and Simocephallus were the

species that were correlated with ZP. From there I ran linear regressions for each species to see that both are significant predictors of ZP. I then plotted the linear regression and relationship and generated confidence intervals for the relationships.

```
zoopsbys <- read.table("data/zoops.txt", sep = "\t", header = TRUE)
zoopsbys <- zoopsbys[, c(3:11)]
ZP <- meso.num[,6]
zoops <- cbind(ZP, zoopsbys)
pairs(zoops)
```



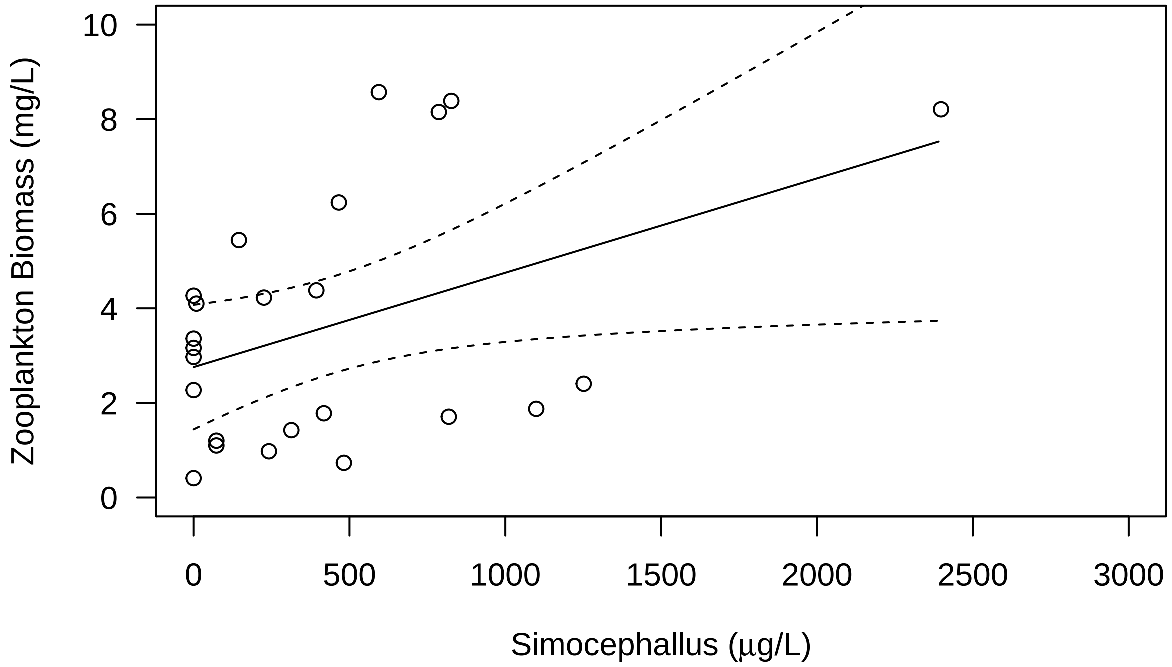
```
corzoo <- cor(zoops)
print(corzoo)
```

```
##               ZP         CAL       DIAP        CYCL        BOSM
## ZP    1.00000000 -0.04755293 -0.1752559 -0.06584517 -0.01722867
## CAL  -0.04755293  1.00000000  0.6425998  0.71189969  0.72809861
## DIAP -0.17525586  0.64259976  1.0000000  0.69436019  0.38105708
## CYCL -0.06584517  0.71189969  0.6943602  1.00000000  0.74669146
## BOSM -0.01722867  0.72809861  0.3810571  0.74669146  1.00000000
## SIMO  0.42610284 -0.27145378 -0.2865365 -0.32477695 -0.30834317
## CERI -0.09599732 -0.19120238 -0.1723296 -0.13215770 -0.14137566
## NAUP -0.30867100  0.05768141  0.2167634  0.18559022  0.17889950
## DLUM -0.21683687 -0.03354653  0.6366939  0.12520183 -0.08630324
## CHYD  0.46255134 -0.32170115 -0.3135602 -0.36853045 -0.20621888
##             SIMO        CERI        NAUP        DLUM       CHYD
## ZP    0.42610284 -0.09599732 -0.30867100 -0.21683687  0.4625513
## CAL  -0.27145378 -0.19120238  0.05768141 -0.03354653 -0.3217012
## DIAP -0.28653648 -0.17232956  0.21676337  0.63669394 -0.3135602
## CYCL -0.32477695 -0.13215770  0.18559022  0.12520183 -0.3685304
## BOSM -0.30834317 -0.14137566  0.17889950 -0.08630324 -0.2062189
## SIMO  1.00000000 -0.18254802 -0.23678921 -0.07658909  0.2623634
## CERI -0.18254802  1.00000000  0.47454001  0.02021705 -0.1354263
## NAUP -0.23678921  0.47454001  1.00000000  0.14753935 -0.2376803
## DLUM -0.07658909  0.02021705  0.14753935  1.00000000 -0.2240296
## CHYD  0.26236337 -0.13542629 -0.23768026 -0.22402962  1.0000000
```

```
fitregsimo <-lm(ZP~SIMO, data = zoops)
summary(fitregsimo)
```

```
##
## Call:
## lm(formula = ZP ~ SIMO, data = zoops)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.0759 -2.0346  0.3103  1.3713  4.6285
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.7570780  0.6351881   4.341 0.000263 ***
## SIMO        0.0019955  0.0009033   2.209 0.037876 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.419 on 22 degrees of freedom
## Multiple R-squared:  0.1816, Adjusted R-squared:  0.1444
## F-statistic: 4.881 on 1 and 22 DF,  p-value: 0.03788
```

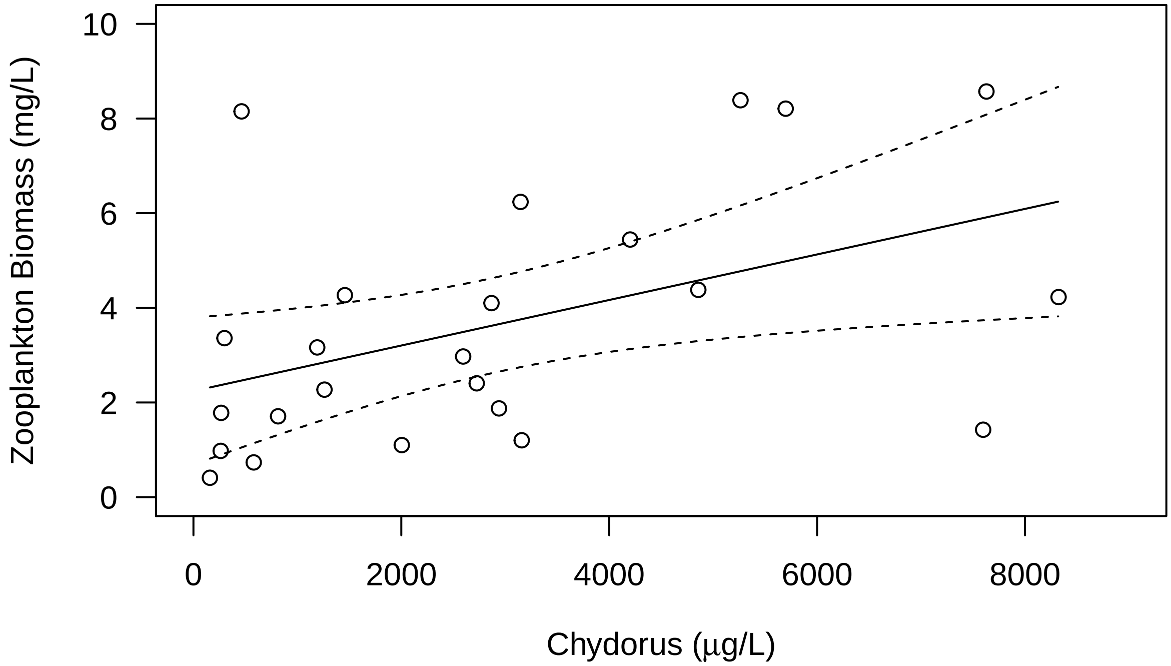
```
plot(zoops$SIMO, zoops$ZP, ylim=c(0,10), xlim=c(0,3000), xlab = expression(paste("Simocephallus (", mu,
newSIMO <- seq(min(zoops$SIMO), max(zoops$SIMO), 10)
reglineSIMO <- predict(fitregsimo, newdata = data.frame(SIMO = newSIMO))
lines(newSIMO, reglineSIMO)
conf95SIMO <- predict(fitregsimo, newdata=data.frame(SIMO = newSIMO), interval = c("confidence"), level
matlines(newSIMO, conf95SIMO[,c("lwr","upr")], type ="l", lty = 2, lwd = 1, col = "black")
```



```
fitregchyd <-lm(ZP~CHYD, data = zoops)
summary(fitregchyd)
```

```
##
## Call:
## lm(formula = ZP ~ CHYD, data = zoops)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.4729 -1.7824 -0.5473  1.2166  5.6870
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.2410921  0.7489034   2.992  0.00671 **
## CHYD        0.0004812  0.0001966   2.447  0.02285 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.371 on 22 degrees of freedom
## Multiple R-squared:  0.214,  Adjusted R-squared:  0.1782
## F-statistic: 5.988 on 1 and 22 DF,  p-value: 0.02285
```

```
plot(zoops$CHYD, zoops$ZP, ylim=c(0,10), xlim=c(0,9000), xlab = expression(paste("Chydorus (", mu, "g/L
newCHYD <- seq(min(zoops$CHYD), max(zoops$CHYD), 10)
reglineCHYD <- predict(fitregchyd, newdata = data.frame(CHYD = newCHYD))
lines(newCHYD, reglineCHYD)
conf95CHYD <- predict(fitregchyd, newdata=data.frame(CHYD = newCHYD), interval = c("confidence"), level
matlines(newCHYD, conf95CHYD[,c("lwr","upr")], type ="l", lty = 2, lwd = 1, col = "black")
```



SUBMITTING YOUR WORKSHEET

Use Knitr to create a PDF of your completed **3.RStudio_Worksheet.Rmd** document, push the repo to GitHub, and create a pull request. Please make sure your updated repo include both the PDF and RMarkdown files.

This assignment is due on **Wednesday, January 16th, 2015 at 12:00 PM (noon)**.