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title: '3Worksheet' author: "Herbert Sizek; Z620: Quantitative Biodiversity, Indiana University" date: "25 March, 2021" geometry: margin=2.54cm —s ## 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. In the Markdown version of this document in your cloned repo, 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 (color may vary if you changed the editor theme).
5. Before you leave the classroom today, it is *imperative* that you **push** this file to your GitHub repo, at whatever stage you are. Ths will enable you to pull your work onto your own computer.
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, March 24th, 2021 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. Next to the `Knit` button in the RStudio scripting panel there is a spell checker button (`ABC`) button.

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.

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

```
## [1] "D:/GitHub/QB2021_Sizek/2.Worksheets/3.RStudio"
```

```
setwd("D:/GitHub/QB2021_Sizek/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)

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

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

2) the area of a circle with radius, r, = 2 (area = pi * r^2).

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

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

3) the length of the opposite side of a right-triangle given that the angle, theta, = pi/4. (radians, a.k.a. 45°) and with hypotenuse length sqrt(2) (remember: sin(theta) = opposite/hypotenuse).

```
theta = pi/4
hypot = sqrt(2)
sin(theta)*hypot
```

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

4) the log (base e) of your favorite number.

```
log(0)
```

```
## [1] -Inf
```

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.

```
x <- c(0,1,2,3,4)
```

2) Create a new vector `w` by multiplying `x` by 14 (i.e., "scalar").

```
w <-x*14
```

3) Add `x` and `w` and divide by 15.

```
(x+w)/15
```

```
## [1] 0 1 2 3 4
```

Now, do the following: 1) Create another vector (`k`) that is the same length as `w`.

```
k <- runif(length(w))
```

2) Multiply `k` by `x`.

```
k*x
```

```
## [1] 0.0000000 0.8055621 0.8374349 1.6089582 0.8778889
```

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`.

```
d <- c(w[0:3],k[0:4])
```

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)
v <- na.omit(v)
max(v)
```

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

```
min(v)
```

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

```
mean(v)
```

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

```r
median(v)
```

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

```r
var(v)
```

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

```r
sd(v)
```

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

```r
sd(v)/sqrt(length(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.

```r
m <- matrix(c(rnorm(5,8,2),rnorm(5,25,10)),nrow=5,ncol=2)
```

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: The `rnorm` function produces a series of `n` random numbers drawn from a random distribution, with a mean of zero and a sd of 1 by default.

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.

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

```
## [1]  5 10
```

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

> Answer 2: 5 rows by 10 columns

###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`.

```
n <- m[1:4,c(seq(0,2,1),seq(4,10,1))]
```

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.

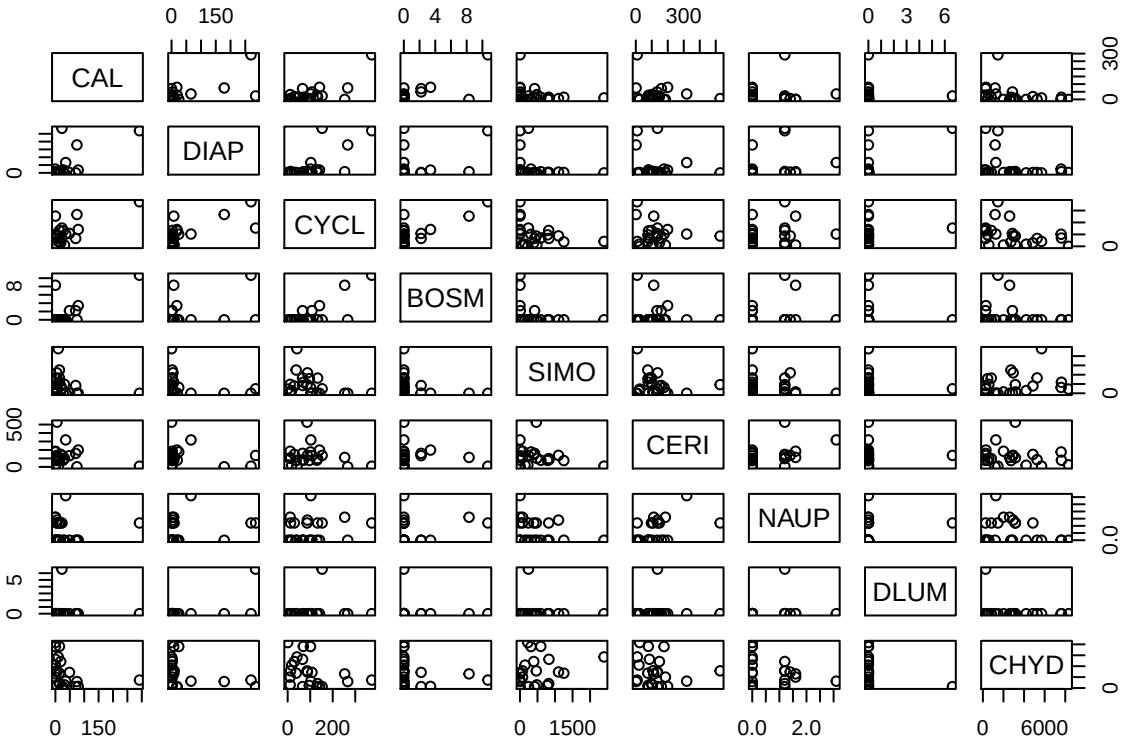
```
zoops <- read.table("data/zoops.txt",sep = "\t", header = TRUE)
str(zoops)
```

```
## 'data.frame':    24 obs. of  11 variables:
##  $ TANK: int  5 14 16 21 23 25 27 34 12 15 ...
##  $ NUTS: Factor w/ 3 levels "H","L","M": 2 2 2 2 2 2 2 2 3 3 ...
##  $ CAL : num  70.5 27.1 5.3 79.2 31.4 22.7 0 35.7 74.8 5.3 ...
##  $ DIAP: num  0 19.2 8.8 17.9 0 ...
##  $ CYCL: num  66.1 129.6 12.7 141.3 11 ...
##  $ BOSM: num  2.2 0 0 3.4 0 0 0 0 0 0 ...
##  $ SIMO: num  417.8 0 73.1 0 482 ...
##  $ CERI: num  159.8 79.4 107.5 199 101.9 ...
##  $ NAUP: num  0 0 1.2 0 0 1.2 1.6 3.1 0 1.4 ...
##  $ DLUM: num  0 0 0 0 0 6.6 0 0 0 0 ...
##  $ CHYD: num  267 159 3158 298 580 ...
```

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.

```
zoops.num <- zoops[,3:11]
pairs(zoops.num)
```




```
cor1 <-cor(zoops.num)
print(cor1, digits= 3)
```

```
##          CAL   DIAP   CYCL    BOSM    SIMO    CERI    NAUP    DLUM   CHYD
## CAL   1.0000  0.643  0.712  0.7281 -0.2715 -0.1912  0.0577 -0.0335 -0.322
## DIAP  0.6426  1.000  0.694  0.3811 -0.2865 -0.1723  0.2168  0.6367 -0.314
## CYCL  0.7119  0.694  1.000  0.7467 -0.3248 -0.1322  0.1856  0.1252 -0.369
## BOSM  0.7281  0.381  0.747  1.0000 -0.3083 -0.1414  0.1789 -0.0863 -0.206
## SIMO -0.2715 -0.287 -0.325 -0.3083  1.0000 -0.1825 -0.2368 -0.0766  0.262
## CERI -0.1912 -0.172 -0.132 -0.1414 -0.1825  1.0000  0.4745  0.0202 -0.135
## NAUP  0.0577  0.217  0.186  0.1789 -0.2368  0.4745  1.0000  0.1475 -0.238
## DLUM -0.0335  0.637  0.125 -0.0863 -0.0766  0.0202  0.1475  1.0000 -0.224
## CHYD -0.3217 -0.314 -0.369 -0.2062  0.2624 -0.1354 -0.2377 -0.2240  1.000
```

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

> Answer 3: DLUM has alot of zero values. NAUP has three values. There are quite a few near zero values. Most of the negative correlations are not too strong consisting really of situations where there are not high-high values. The positive correlations are harder to tease out but appear to be drawn from a small subset of high-high values. More analysis would be needed.

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.

```
# install.packages("psych")
require("psych")
```

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

```
## Warning: package 'psych' was built under R version 3.6.3
```

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

```
## Call:corr.test(x = zoops.num, method = "pearson", adjust = "BH")
## Correlation matrix
##         CAL   DIAP   CYCL   BOSM   SIMO   CERI   NAUP   DLUM   CHYD
## CAL   1.000  0.643  0.712  0.728 -0.271 -0.191  0.058 -0.034 -0.322
## DIAP  0.643  1.000  0.694  0.381 -0.287 -0.172  0.217  0.637 -0.314
## CYCL  0.712  0.694  1.000  0.747 -0.325 -0.132  0.186  0.125 -0.369
## BOSM  0.728  0.381  0.747  1.000 -0.308 -0.141  0.179 -0.086 -0.206
## SIMO -0.271 -0.287 -0.325 -0.308  1.000 -0.183 -0.237 -0.077  0.262
## CERI -0.191 -0.172 -0.132 -0.141 -0.183  1.000  0.475  0.020 -0.135
## NAUP  0.058  0.217  0.186  0.179 -0.237  0.475  1.000  0.148 -0.238
## DLUM -0.034  0.637  0.125 -0.086 -0.077  0.020  0.148  1.000 -0.224
## CHYD -0.322 -0.314 -0.369 -0.206  0.262 -0.135 -0.238 -0.224  1.000
## Sample Size
## [1] 24
## Probability values (Entries above the diagonal are adjusted for multiple tests.)
##        CAL  DIAP  CYCL  BOSM  SIMO  CERI  NAUP  DLUM  CHYD
## CAL  0.000 0.005 0.001 0.001 0.479 0.580 0.835 0.901 0.395
## DIAP 0.001 0.000 0.002 0.298 0.449 0.582 0.556 0.005 0.395
## CYCL 0.000 0.000 0.000 0.001 0.395 0.646 0.580 0.650 0.306
## BOSM 0.000 0.066 0.000 0.000 0.395 0.646 0.580 0.774 0.572
## SIMO 0.199 0.175 0.122 0.143 0.000 0.580 0.531 0.788 0.485
## CERI 0.371 0.421 0.538 0.510 0.393 0.000 0.098 0.925 0.646
## NAUP 0.789 0.309 0.385 0.403 0.265 0.019 0.000 0.646 0.531
## DLUM 0.876 0.001 0.560 0.688 0.722 0.925 0.491 0.000 0.554
## CHYD 0.125 0.136 0.076 0.334 0.216 0.528 0.263 0.293 0.000
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

```
cor4 <- corr.test(zoops.num, method = "kendall", adjust = "BH")
print(cor4,digits=3)
```

```
## Call:corr.test(x = zoops.num, method = "kendall", adjust = "BH")
## Correlation matrix
##         CAL   DIAP   CYCL   BOSM   SIMO   CERI   NAUP   DLUM   CHYD
## CAL   1.000  0.225  0.343  0.377 -0.242  0.023 -0.107  0.092 -0.394
## DIAP  0.225  1.000  0.498  0.127 -0.423  0.043  0.225  0.312 -0.176
## CYCL  0.343  0.498  1.000  0.409 -0.292  0.007  0.130  0.214 -0.313
## BOSM  0.377  0.127  0.409  1.000 -0.401  0.083  0.038 -0.102 -0.224
## SIMO -0.242 -0.423 -0.292 -0.401  1.000 -0.112 -0.181 -0.013  0.254
```

```
## CERI  0.023  0.043  0.007  0.083 -0.112  1.000  0.375  0.088 -0.094
## NAUP -0.107  0.225  0.130  0.038 -0.181  0.375  1.000  0.160 -0.097
## DLUM  0.092  0.312  0.214 -0.102 -0.013  0.088  0.160  1.000 -0.264
## CHYD -0.394 -0.176 -0.313 -0.224  0.254 -0.094 -0.097 -0.264  1.000
## Sample Size
## [1] 24
## Probability values (Entries above the diagonal are adjusted for multiple tests.)
##        CAL  DIAP  CYCL  BOSM  SIMO  CERI  NAUP  DLUM  CHYD
## CAL  0.000 0.618 0.456 0.365 0.618 0.970 0.814 0.814 0.365
## DIAP 0.290 0.000 0.365 0.814 0.365 0.939 0.618 0.498 0.740
## CYCL 0.101 0.013 0.000 0.365 0.543 0.973 0.814 0.630 0.498
## BOSM 0.070 0.553 0.047 0.000 0.365 0.814 0.939 0.814 0.618
## SIMO 0.254 0.039 0.166 0.052 0.000 0.814 0.740 0.973 0.618
## CERI 0.916 0.842 0.973 0.701 0.602 0.000 0.365 0.814 0.814
## NAUP 0.620 0.291 0.545 0.861 0.397 0.071 0.000 0.778 0.814
## DLUM 0.669 0.138 0.315 0.635 0.952 0.683 0.454 0.000 0.618
## CHYD 0.057 0.411 0.137 0.292 0.231 0.662 0.651 0.213 0.000
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

```
cor3 <- corr.test(zoops.num, method = "spearman", adjust = "BH")
print(cor3,digits=3)
```

```
## Call:corr.test(x = zoops.num, method = "spearman", adjust = "BH")
## Correlation matrix
##         CAL   DIAP   CYCL   BOSM   SIMO   CERI   NAUP   DLUM   CHYD
## CAL   1.000  0.307  0.474  0.419 -0.329 -0.007 -0.116  0.107 -0.590
## DIAP  0.307  1.000  0.663  0.151 -0.571  0.019  0.271  0.355 -0.239
## CYCL  0.474  0.663  1.000  0.478 -0.433  0.003  0.164  0.256 -0.479
## BOSM  0.419  0.151  0.478  1.000 -0.472  0.099  0.048 -0.106 -0.279
## SIMO -0.329 -0.571 -0.433 -0.472  1.000 -0.127 -0.223 -0.015  0.320
## CERI -0.007  0.019  0.003  0.099 -0.127  1.000  0.465  0.105 -0.154
## NAUP -0.116  0.271  0.164  0.048 -0.223  0.465  1.000  0.170 -0.092
## DLUM  0.107  0.355  0.256 -0.106 -0.015  0.105  0.170  1.000 -0.316
## CHYD -0.590 -0.239 -0.479 -0.279  0.320 -0.154 -0.092 -0.316  1.000
## Sample Size
## [1] 24
## Probability values (Entries above the diagonal are adjusted for multiple tests.)
##        CAL  DIAP  CYCL  BOSM  SIMO  CERI  NAUP  DLUM  CHYD
## CAL  0.000 0.347 0.100 0.151 0.340 0.990 0.774 0.774 0.043
## DIAP 0.144 0.000 0.015 0.720 0.043 0.990 0.422 0.292 0.492
## CYCL 0.019 0.000 0.000 0.100 0.138 0.990 0.720 0.454 0.100
## BOSM 0.042 0.480 0.018 0.000 0.100 0.774 0.925 0.774 0.421
## SIMO 0.117 0.004 0.035 0.020 0.000 0.774 0.532 0.990 0.340
## CERI 0.976 0.929 0.990 0.645 0.555 0.000 0.100 0.774 0.720
## NAUP 0.590 0.199 0.444 0.823 0.296 0.022 0.000 0.720 0.776
## DLUM 0.620 0.089 0.227 0.622 0.944 0.624 0.428 0.000 0.340
## CHYD 0.002 0.260 0.018 0.187 0.128 0.473 0.668 0.132 0.000
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

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: Looks like the non-parametric methods didn't find as much correlation in the data. I would use the non-parametric methods when looking at where rank is more important (spearmans, where x is ranked, kendall when both items are ranked.) Dependent on the threshold for discovery, yes. False discovery rate is somewhat important, because the p-value is a calculation that uses a base null model to see the probability of an event occurring by random given the data and the number of tests. I would just use it as a earmark/intuition check, other properties could be more important like effect size.

Linear Regression

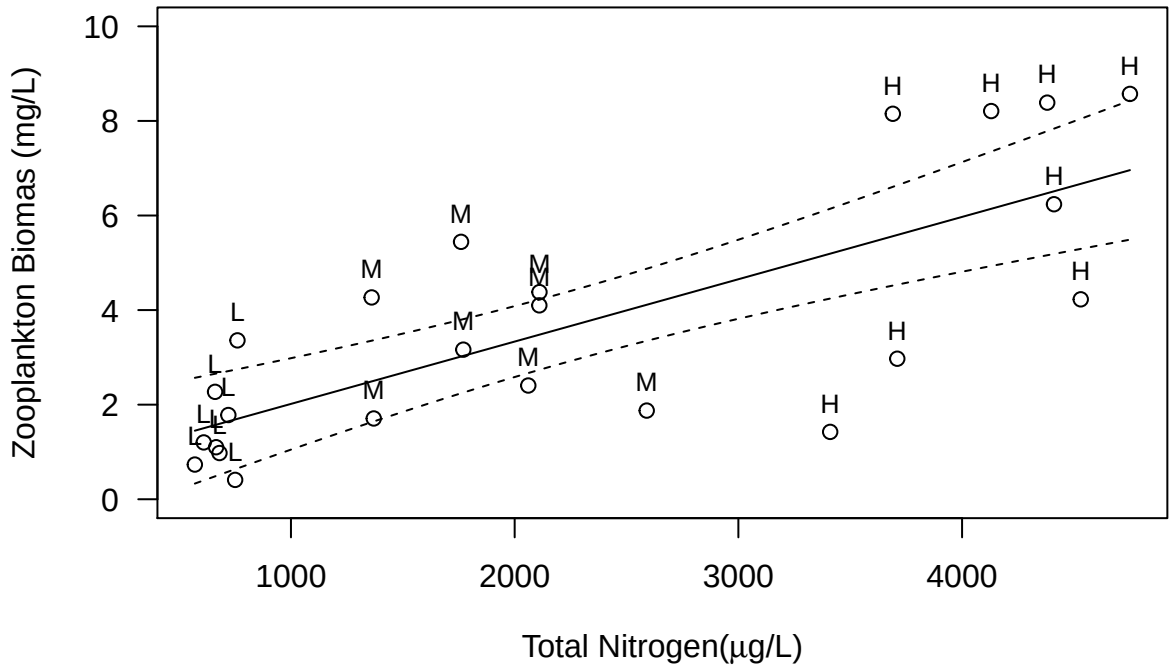
In the R code chunk below, do the following: 1) Conduct a linear regression analysis to test the relationship between total nitrogen (TN) and zooplankton biomass (ZP). 2) Examine the output of the regression analysis. 3) Produce a plot of this regression analysis including the following: categorically labeled points, the predicted regression line with 95% confidence intervals, and the appropriate axis labels.

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

lmZN <- lm(ZP ~ TN,data = zoopNuts)
print(lmZN)
```

```
##
## Call:
## lm(formula = ZP ~ TN, data = zoopNuts)
##
## Coefficients:
## (Intercept)           TN
##    0.697771     0.001318
```

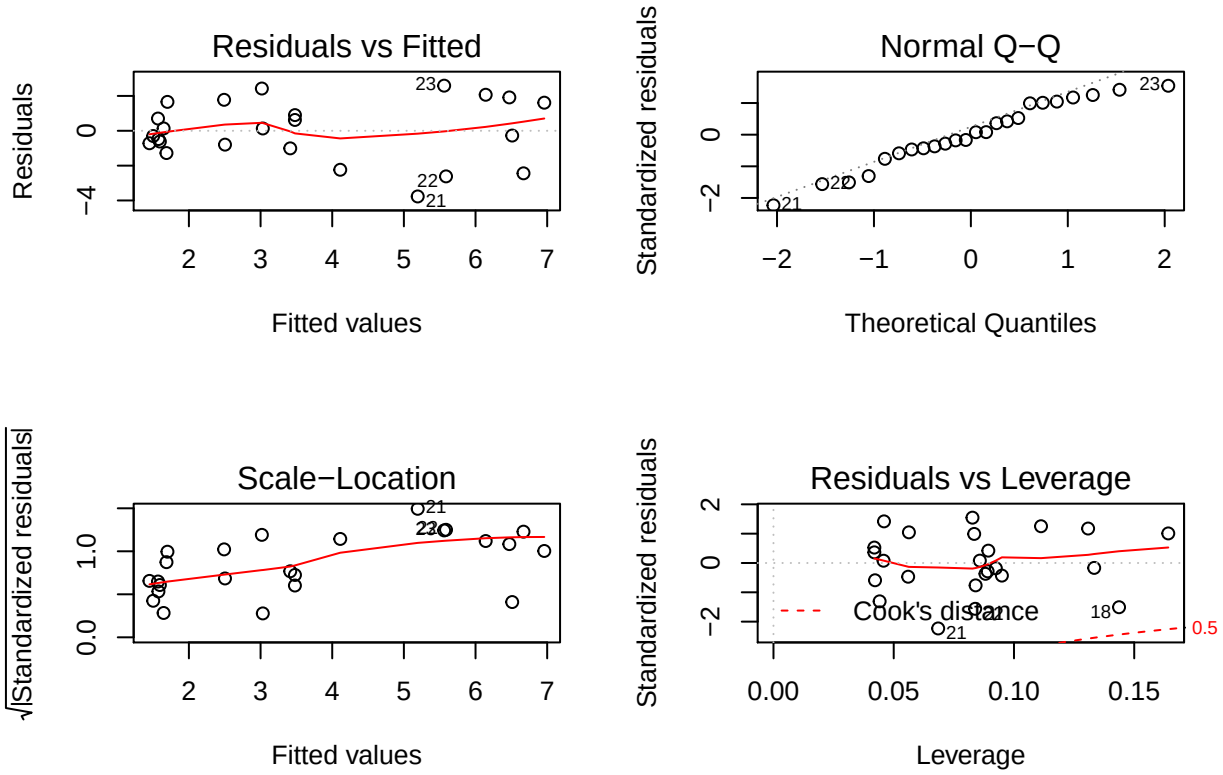
```
plot(zoopNuts$TN,zoopNuts$ZP,
     ylim = c(0,10),
     xlab = expression(paste("Total Nitrogen(", mu,"g/L)")),
     ylab = "Zooplankton Biomas (mg/L)",
     las =1)
xline <- seq(min(zoopNuts$TN),max(zoopNuts$TN),5)
text(zoopNuts$TN,zoopNuts$ZP,zoopNuts$NUTS, pos =3, cex =0.8)
lines(xline,predict(lmZN,newdata = data.frame(TN = xline)))
conf95 <- predict(lmZN,newdata=data.frame(TN=xline), interval = c("confidence"),level = 0.95, type="resp
matlines(xline, conf95[,c("lwr","upr")], type = "l", lty = 2, lwd =1, col="black")
```



Question 5: Interpret the results from the regression model

Answer 5: These results from the residual plots look ok. I don't really get what each plot is actually saying beside the residuals v fitted.

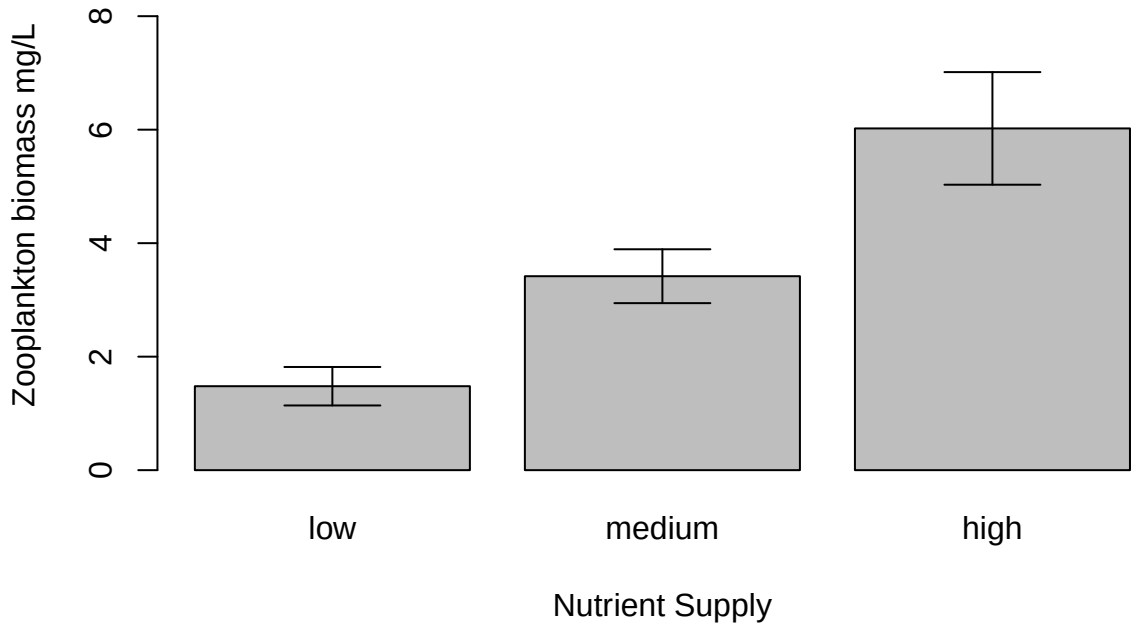
```
par(mfrow= c(2,2),mar = c(5.1,4.1,4.1,2.1))
plot(lmZN)
```



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.

```
zNuts <- factor(zoopNuts$NUTS, levels = c('L','M','H'))
zp.means<-tapply(zoopNuts$ZP,zNuts,mean)
sem <- function(x){
  sd(na.omit(x))/sqrt(length(na.omit(x)))
}
zp.sem<- tapply(zoopNuts$ZP,zNuts,sem)
bp <- barplot(zp.means,
              ylim = c(0,round(max(zoopNuts$ZP),digits=0)),
              xlab = "Nutrient Supply",
              ylab = "Zooplankton biomass mg/L",
              names.arg = c("low","medium","high"))
arrows(x0=bp,y0=zp.means,y1 = zp.means - zp.sem,angle =90)
arrows(x0=bp,y0=zp.means,y1 = zp.means + zp.sem,angle =90)
```



4) Use a one-way analysis of variance (ANOVA) to test the null hypothesis that zooplankton biomass is affected by the nutrient treatment.

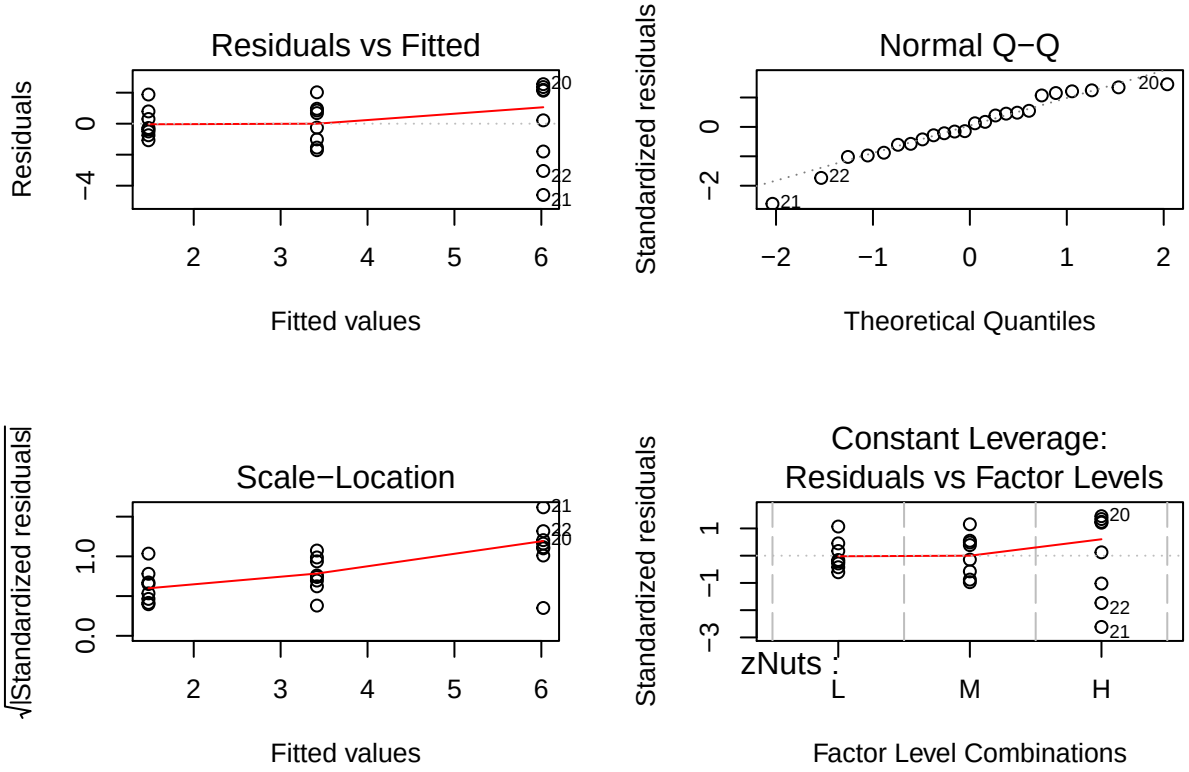
```
fitanova <- aov(ZP ~ zNuts, data=zoopNuts)
summary(fitanova)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## zNuts        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
```

```
TukeyHSD(fitanova)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = ZP ~ zNuts, data = zoopNuts)
##
## $zNuts
##         diff        lwr      upr     p adj
## M-L 1.938625 -0.4297094 4.306959 0.1220246
## H-L 4.543175  2.1748406 6.911509 0.0002512
## H-M 2.604550  0.2362156 4.972884 0.0294932
```

```
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 zoops.txt data set in your **3.RStudio** data folder. Create a site-by-species matrix (or dataframe) that does *not* include TANK or NUTS.

```
zoops <- read.table("data/zoops.txt",sep = "\t", header = TRUE)
zoops.species <- zoops[3:11]
```

The remaining columns of data refer to the biomass (µg/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.

> I don't really get what is being asked here but I'll do my interpretation of the question. We have multiple species whose means are changing across a nutrient level, L,M,H. This makes me think that running an anova by species would be good because we are wanting to know the species response to a nutrient change.

```
for (species in names(zoops.species)){
  fitanova <- aov(eval(as.symbol(species)) ~ NUTS,data=zoops)
  print(species)
  print(TukeyHSD(fitanova))
}
```

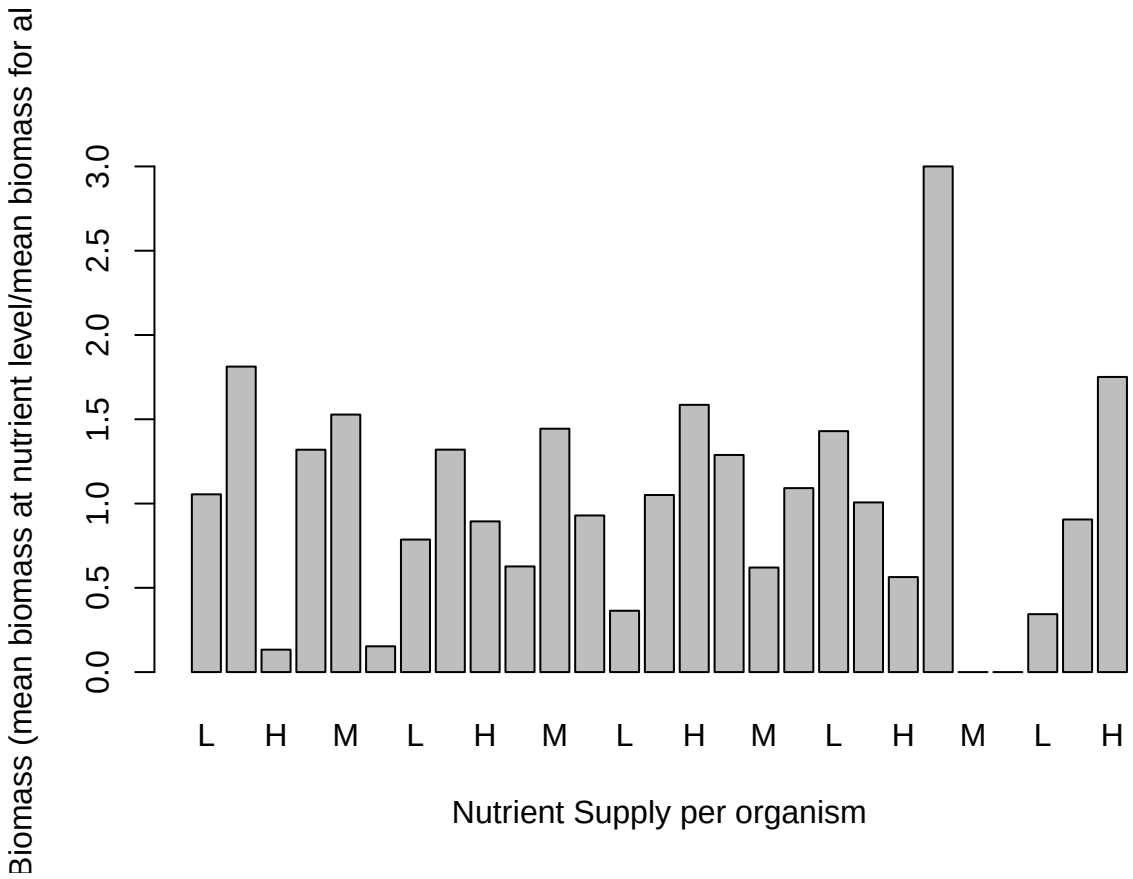
```
## [1] "CAL"
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = eval(as.symbol(species)) ~ NUTS, data = zoops)
##
## $NUTS
##       diff       lwr       upr     p adj
## L-H 29.700 -44.32096 103.72096 0.5780437
## M-H 54.125 -19.89596 128.14596 0.1802941
## M-L 24.425 -49.59596  98.44596 0.6879338
##
## [1] "DIAP"
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = eval(as.symbol(species)) ~ NUTS, data = zoops)
##
## $NUTS
##        diff      lwr      upr     p adj
## L-H 44.1125 -60.5480 148.7730 0.5471211
## M-H 52.0000 -52.6605 156.6605 0.4367980
## M-L  7.8875 -96.7730 112.5480 0.9803227
##
## [1] "CYCL"
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = eval(as.symbol(species)) ~ NUTS, data = zoops)
##
## $NUTS
##         diff        lwr      upr     p adj
## L-H -10.7375 -126.10327 104.6283 0.9701588
## M-H  42.4750  -72.89077 157.8408 0.6290572
## M-L  53.2125  -62.15327 168.5783 0.4877447
```

```
##
## [1] "BOSM"
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = eval(as.symbol(species)) ~ NUTS, data = zoops)
##
## $NUTS
##        diff       lwr      upr     p adj
## L-H -0.3375 -3.936833 3.261833 0.9697197
## M-H  0.5750 -3.024333 4.174333 0.9148629
## M-L  0.9125 -2.686833 4.511833 0.8004781
##
## [1] "SIMO"
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = eval(as.symbol(species)) ~ NUTS, data = zoops)
##
## $NUTS
##          diff        lwr      upr     p adj
## L-H -540.3500 -1213.9270 133.2270 0.1315582
## M-H -236.6125  -910.1895 436.9645 0.6551772
## M-L  303.7375  -369.8395 977.3145 0.5029346
##
## [1] "CERI"
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = eval(as.symbol(species)) ~ NUTS, data = zoops)
##
## $NUTS
##         diff       lwr       upr     p adj
## L-H  24.5375 -115.6261 164.70113 0.8987443
## M-H -58.8250 -198.9886  81.33863 0.5498460
## M-L -83.3625 -223.5261  56.80113 0.3115489
##
## [1] "NAUP"
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = eval(as.symbol(species)) ~ NUTS, data = zoops)
##
## $NUTS
##        diff        lwr       upr     p adj
## L-H  0.5375 -0.5249247 1.5999247 0.4242172
## M-H  0.2750 -0.7874247 1.3374247 0.7930439
## M-L -0.2625 -1.3249247 0.7999247 0.8093697
##
## [1] "DLUM"
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = eval(as.symbol(species)) ~ NUTS, data = zoops)
```

```
##
## $NUTS
##              diff        lwr       upr     p adj
## L-H  8.250000e-01 -0.8728805 2.5228805 0.4522032
## M-H -2.220446e-16 -1.6978805 1.6978805 1.0000000
## M-L -8.250000e-01 -2.5228805 0.8728805 0.4522032
##
## [1] "CHYD"
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = eval(as.symbol(species)) ~ NUTS, data = zoops)
##
## $NUTS
##          diff        lwr         upr     p adj
## L-H -4090.700 -6512.2103 -1669.18972 0.0009809
## M-H -2457.738 -4879.2478   -36.22722 0.0462621
## M-L  1632.962  -788.5478  4054.47278 0.2287067
```

From this it looks like there is a increase in CHYD across environments that is significant. SIMO is also possitively correlated but not to as great of an effect as CHYD. Some species have correlation across environment types. Another way we could analize this data is with a grouped bar plot:

```
#Don't know how to do this any other way:
zpNUTS <- factor(zoops$NUTS, levels = c('L','M','H'))
zspe.means<-c(tapply(zoops$CAL,zpNUTS,mean)/mean(zoops$CAL),
              tapply(zoops$DIAP,zpNUTS,mean)/mean(zoops$DIAP),
              tapply(zoops$CYCL,zpNUTS,mean)/mean(zoops$CYCL),
              tapply(zoops$BOSM,zpNUTS,mean)/mean(zoops$BOSM),
              tapply(zoops$SIMO,zpNUTS,mean)/mean(zoops$SIMO),
              tapply(zoops$CERI,zpNUTS,mean)/mean(zoops$CERI),
              tapply(zoops$NAUP,zpNUTS,mean)/mean(zoops$NAUP),
              tapply(zoops$DLUM,zpNUTS,mean)/mean(zoops$DLUM),
              tapply(zoops$CHYD,zpNUTS,mean)/mean(zoops$CHYD))
sem <- function(x){
  sd(na.omit(x))/sqrt(length(na.omit(x)))
}
zspe.sem<-c(tapply(zoops$CAL,zpNUTS,mean),
              tapply(zoops$DIAP,zpNUTS,sem),
              tapply(zoops$CYCL,zpNUTS,sem),
              tapply(zoops$BOSM,zpNUTS,sem),
              tapply(zoops$SIMO,zpNUTS,sem),
              tapply(zoops$CERI,zpNUTS,sem),
              tapply(zoops$NAUP,zpNUTS,sem),
              tapply(zoops$DLUM,zpNUTS,sem),
              tapply(zoops$CHYD,zpNUTS,sem))
bp <- barplot(zspe.means,
              # ylim = c(0,round(max(zspe.means)+max(zspe.sem),digits=0)),
              xlab = "Nutrient Supply per organism",
              ylab = "Normalized Biomass (mean biomass at nutrient level/mean biomass for all nutrient l
              )
```




```
# arrows(x0=bp,y0=zspe.means,y1 = zspe.means - zspe.sem,angle =90)
# arrows(x0=bp,y0=zspe.means,y1 = zspe.means + zspe.sem,angle =90)
```

I don't know how to organize this better in the coding language to make it prettier, but we can kind of see if you squint that there are two organisms that have a possitive trend pattern, CHYD and SIMO, and the rest are more indeterminant, though a case could be made for decreasing for NAUP and DLUM.

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 24th, 2021 at 12:00 PM (noon)**.