3. Worksheet: Basic R

Ford Fishman; Z620: Quantitative Biodiversity, Indiana University

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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. This 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()) # step 1
getwd() # step 2
```

```
## [1] "/Users/ffishman/GitHub/QB2021_Fishman/2.Worksheets/3.RStudio"
```

```
setwd('~/GitHub/QB2021_Fishman/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. 45°) and with hypotenuse length sqrt(2) (remember: sin(theta) = opposite/hypotenuse).
4) the log (base e) of your favorite number.

```
# 1 volume of cube
5^3
```

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

```
# 2 area of circle
pi*2^2
```

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

```
# 3 side of right triangle
sin(pi/4)*sqrt(2)
```

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

```
# 4 ln
log(4)
```

```
## [1] 1.386294
```

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.

```
# 1 vector
x <- c(1,2,3,4,5)

# 2 scalar multiplication
w <- x*14

# 3 vector addition
(x + w)/15
```

```
## [1] 1 2 3 4 5
```

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`.

```
# 1 initialize k
k <- c(6,7,8,9,10)

# 2 vector multiplication
k*x # assuming you meant element-wise multiplication, and not dot-product (k %*% x)
```

```
## [1]  6 14 24 36 50
```

```
# 3 combine
c(sample(w, 3), sample(k, 4)) # not sure if this was what you meant
```

```
## [1] 14 70 56 10  8  6  7
```

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)

w <- na.omit(v) # omit NA in vector

max(w)
```

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

```
min(w)
```

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

```
sum(w)
```

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

```
mean(w)
```

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

```
median(w)
```

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

```
var(w)
```

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

```
sd(w)
```

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

```
sd(w)/sqrt(length(w)) # omitted NA doesn't count for SE estimate
```

```
## [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.

```
matrix(
  c(
    rnorm(5,8,2),
    rnorm(5,25,10)
  ),
  ncol=2, nrow=5
)
```

```
##          [,1]     [,2]
## [1,] 8.711473 39.82566
## [2,] 6.295181 16.41572
## [3,] 8.948864 12.02394
## [4,] 7.505516 29.95317
## [5,] 7.945535 18.90930
```

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` returns a vector of specified length where each value is drawn from a normal distribution of specified 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.

```
# 1 read table
m <- read.table('data/matrix.txt')

# 2 transpose
m.t <- t(m)

# 3 dimensions
dim(m.t)
```

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

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

> Answer 2: 5 x 10: 5 rows, 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`.

```
# 1 index
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
```

```
# 2 drop last row
m[1:(nrow(m)-1),]
```

```
##   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.

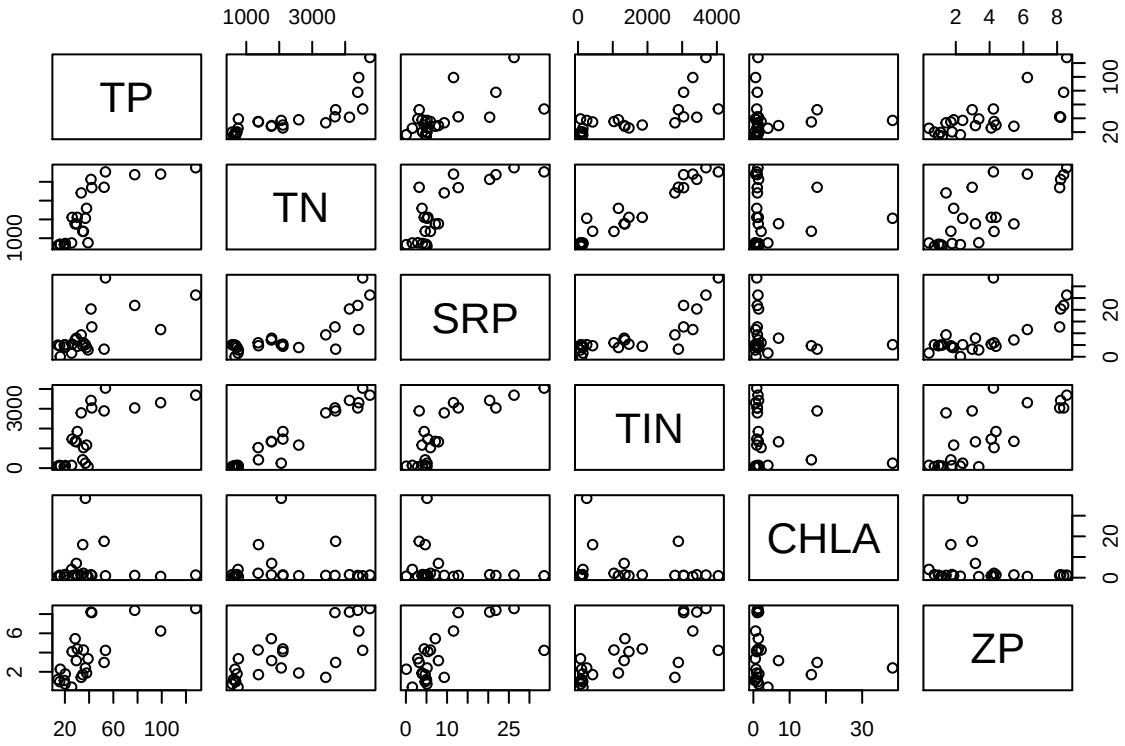
```
meso <- read.table('data/zoop_nuts.txt', header = TRUE)
str(meso)
```

```
## 'data.frame':    24 obs. of  8 variables:
##  $ TANK: int  34 14 23 16 21 5 25 27 30 28 ...
##  $ NUTS: chr  "L" "L" "L" "L" ...
##  $ 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.

```
# 1 numerical matrix
meso.num <- meso[,3:ncol(meso)]

# 2 biplots
pairs(meso.num)
```




```
# 3 correlation
cor(meso.num)
```

```
##                TP           TN        SRP        TIN         CHLA         ZP
## TP    1.00000000  0.786510407  0.6540957  0.7171143 -0.016659593  0.6974765
## TN    0.78651041  1.000000000  0.7841904  0.9689999 -0.004470263  0.7562474
## SRP   0.65409569  0.784190400  1.0000000  0.8009033 -0.189148017  0.6762947
## TIN   0.71711434  0.968999866  0.8009033  1.0000000 -0.156881463  0.7605629
## CHLA -0.01665959 -0.004470263 -0.1891480 -0.1568815  1.000000000 -0.1825999
## ZP    0.69747649  0.756247384  0.6762947  0.7605629 -0.182599904  1.0000000
```

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

> Answer 3: Most of the features are correlated. The main exception is `CHLA`, which is not correlated with any other feature. `TN` and `TIN` are the most highly correlated.

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.

```
suppressPackageStartupMessages(library('psych'))

corr.pearson <- corr.test(meso.num, method = 'pearson', adjust = 'BH')

corr.kendall <- corr.test(meso.num, method = 'kendall', adjust = 'BH')

print(corr.pearson, 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
```

```
print(corr.kendall, 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
```

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: The results appear to somewhat sensitive to which correlation method is used. The non-parametric correlations in general are smaller than the parametric methods, and after p-value correction, the Kendall approach considers several correlations to not be significant that the Pearson approach does. The Pearson approach alone does not suggest false-discovery from multiple testing, but the Kendall method does. The Kendall approach appears to be more conservative and limit false positives. False discovery is important because you might conclude that a trend exists when in reality there is none.

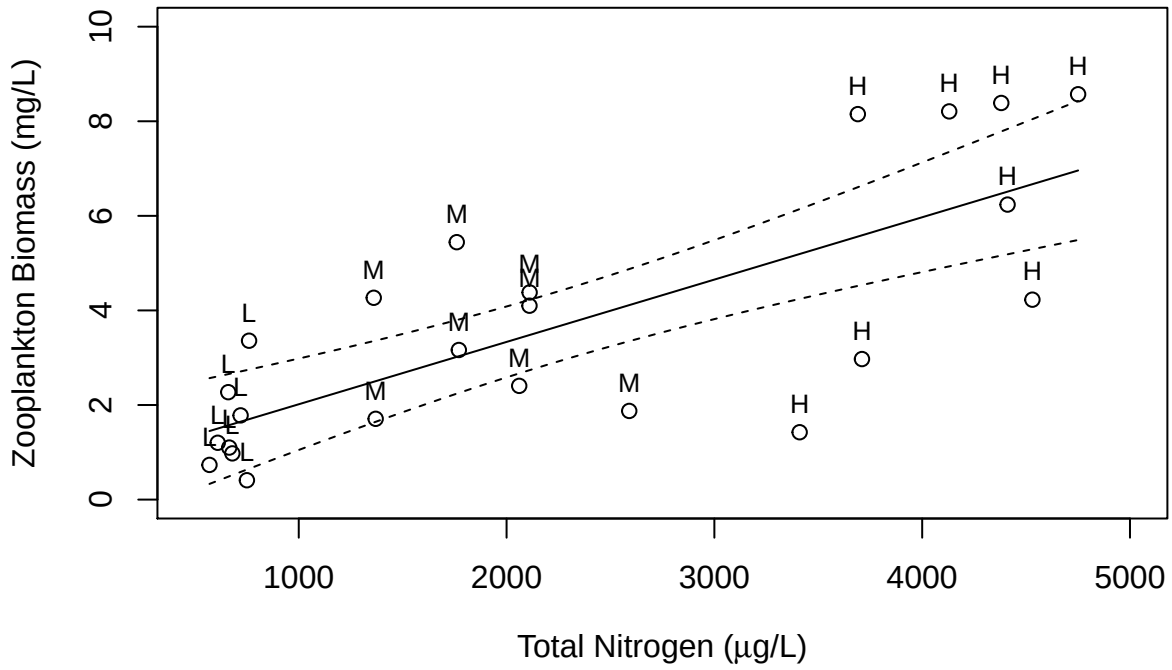
Linear Regression

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.

```
# 1 run regression
lm1 <- lm(data=meso, ZP~TN)

# 2 summary
summary(lm1)
```

```
##
## 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
```

```
# 3 plot
ZP <- meso$ZP; TN <- meso$TN
x <- seq(min(TN), max(TN),10)
y <- predict(lm1, newdata = data.frame(TN=x))
conf <- predict(lm1, newdata = data.frame(TN=x), interval = c("confidence"),level= 0.95, type='response

plot(
  y=ZP, x=TN,
  xlab = expression(paste("Total Nitrogen (",mu,"g/L)")),
  ylab="Zooplankton Biomass (mg/L)",
  ylim=c(0,10), xlim=c(500,5000)
  )
text(TN, ZP, meso$NUTS, pos=3, cex=0.8)
lines(x,y)
matlines(x,conf[,c("lwr","upr")], typ="l", lty=2, col = "black")
```



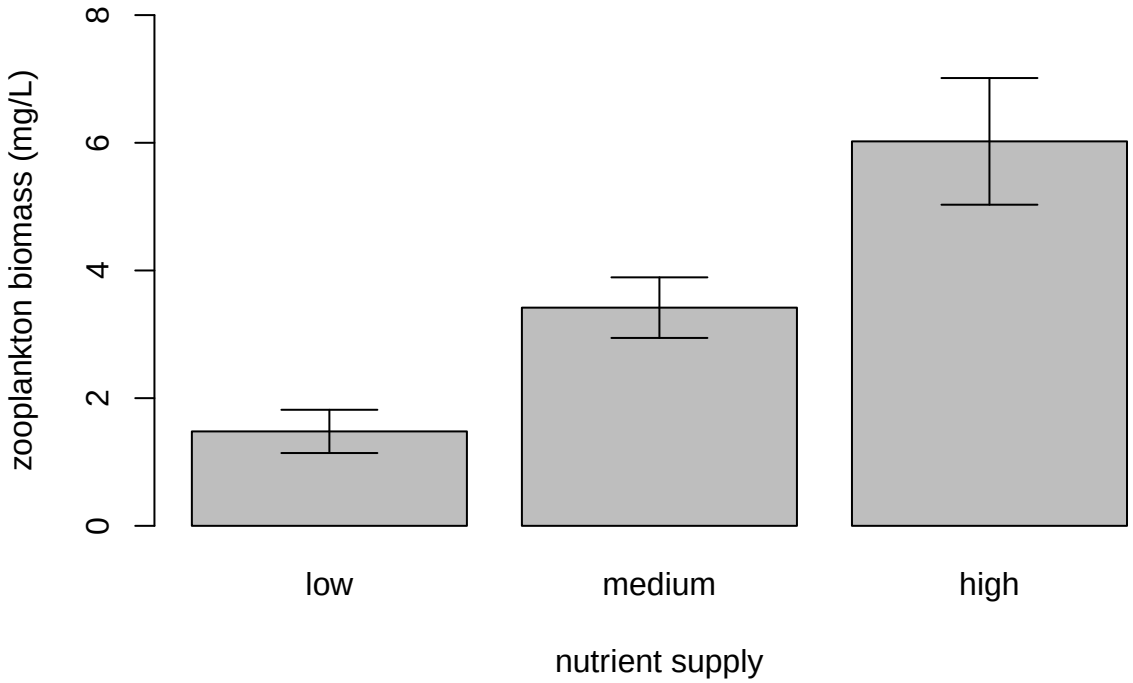
Question 5: Interpret the results from the regression model

> Answer 5: There is a significant ($p < 0.001$) positive linear relationship between TN and ZP. The higher the nutrient concentration, the larger the zooplankton biomass. However, within each labeled group, there is a lot of variance. For instance, it is unclear if there is a linear relationship within `M` between the two features.

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.

```r
# 1 reorder treatments
NUTS <- factor(meso$NUTS, levels = c("L","M","H"))

# 2+3 bar plot
zp.means <- tapply(meso$ZP, NUTS, mean) # get treatment means

sem <- function(x){ # define sem function
  v <- na.omit(x)
  return(sd(v)/sqrt(length(v)))
}

zp.sem <- tapply(meso$ZP, NUTS, sem) # get sem

# make plot
bp <- barplot(zp.means, ylim=c(0,8), xlab = "nutrient supply", ylab="zooplankton biomass (mg/L)", names
# add error bars
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 anova
anova1 <- aov(ZP ~ NUTS, data = meso)
summary(anova1)
```

```
##             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
```

```
TukeyHSD(anova1)
```

```
##   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
```

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. 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.

```
# read in data
zoo <- read.table("~/GitHub/QB2021_Fishman/2.Worksheets/3.RStudio/data/zoops.txt", header = TRUE)

sbs <- zoo[,3:ncol(zoo)] # make site by species matrix

summary(sbs) # summarize
```

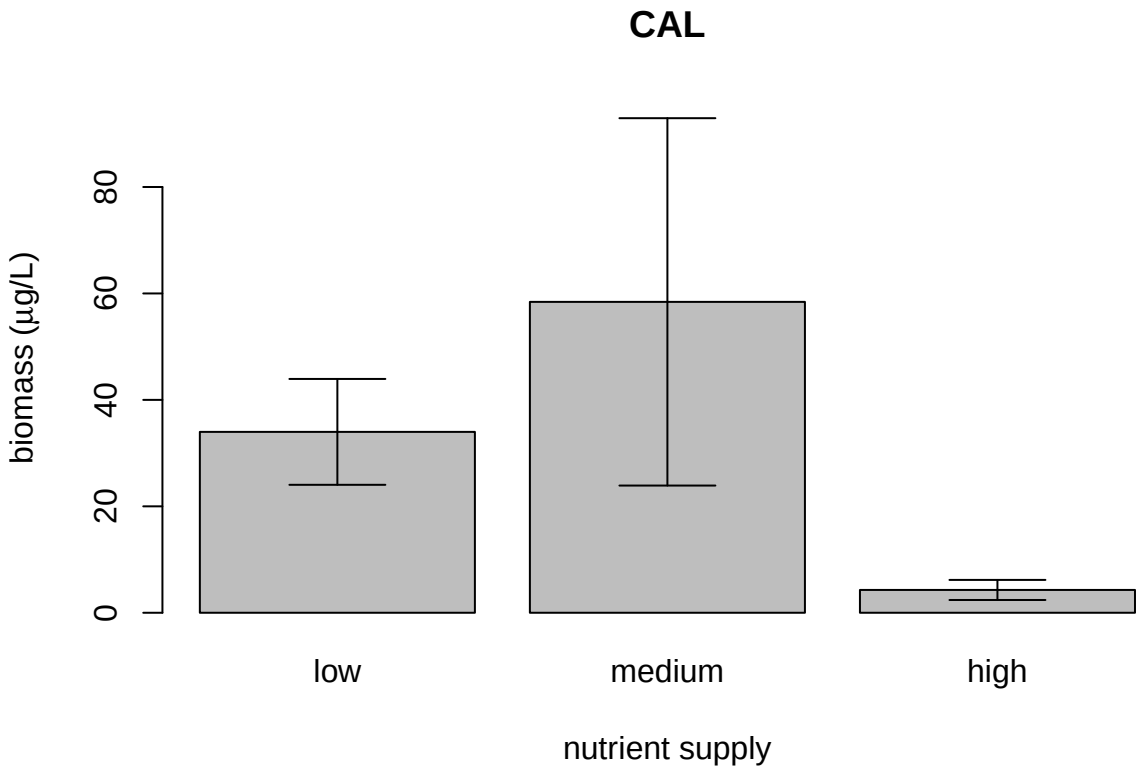
```
##       CAL               DIAP             CYCL             BOSM
##  Min.   :  0.000   Min.   :  0.00   Min.   :  0.00   Min.   : 0.000
##  1st Qu.:  3.975   1st Qu.:  2.30   1st Qu.: 35.62   1st Qu.: 0.000
##  Median : 14.000   Median :  2.30   Median : 87.00   Median : 0.000
##  Mean   : 32.229   Mean   : 37.83   Mean   : 99.77   Mean   : 1.117
##  3rd Qu.: 32.475   3rd Qu.: 18.23   3rd Qu.:130.43   3rd Qu.: 0.000
##  Max.   :292.000   Max.   :285.10   Max.   :373.40   Max.   :10.700
##       SIMO              CERI             NAUP             DLUM
##  Min.   :   0.00   Min.   :  1.90   Min.   :0.0000   Min.   :0.000
##  1st Qu.:   6.75   1st Qu.: 76.15   1st Qu.:0.0000   1st Qu.:0.000
##  Median : 277.55   Median :104.70   Median :0.0000   Median :0.000
##  Mean   : 442.30   Mean   :124.86   Mean   :0.6208   Mean   :0.275
##  3rd Qu.: 642.30   3rd Qu.:150.65   3rd Qu.:1.2000   3rd Qu.:0.000
##  Max.   :2397.80   Max.   :527.70   Max.   :3.1000   Max.   :6.600
##       CHYD
##  Min.   : 158.7
##  1st Qu.: 755.9
##  Median :2660.2
##  Mean   :2906.6
##  3rd Qu.:4365.5
##  Max.   :8323.2
```

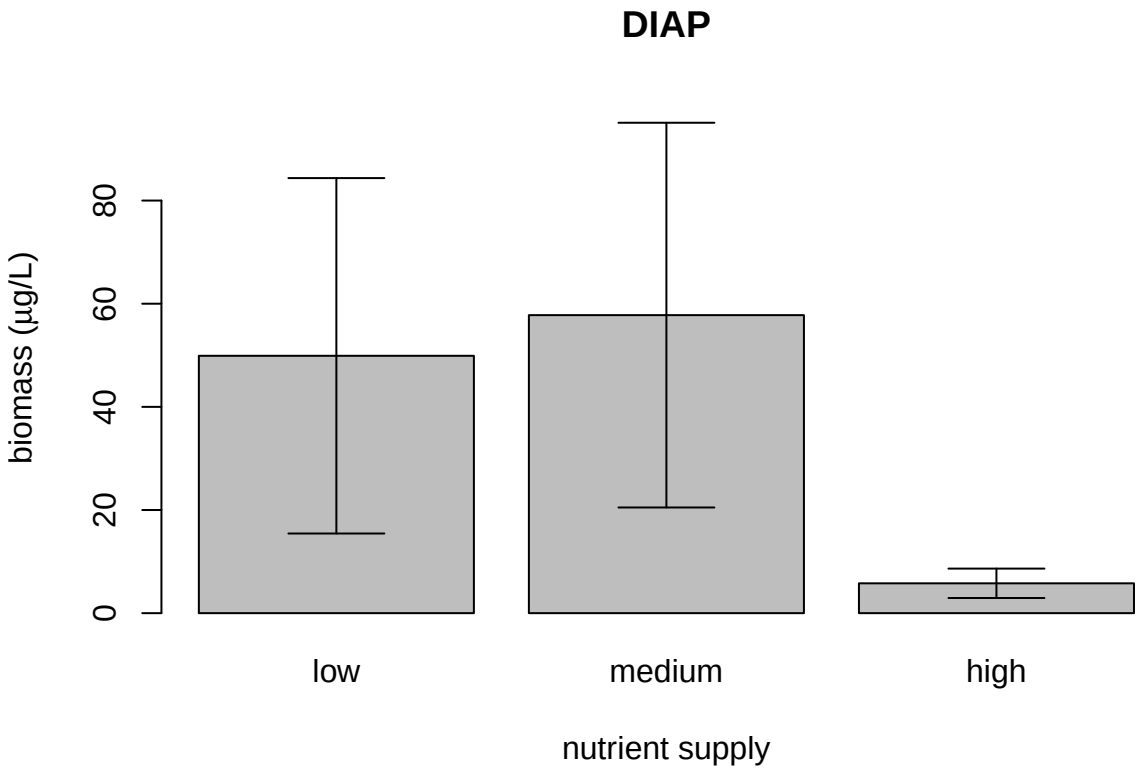
```
cor.zoo <- corr.test(sbs, method="kendall",adjust="BH") # run correlation

print(cor.zoo)
```

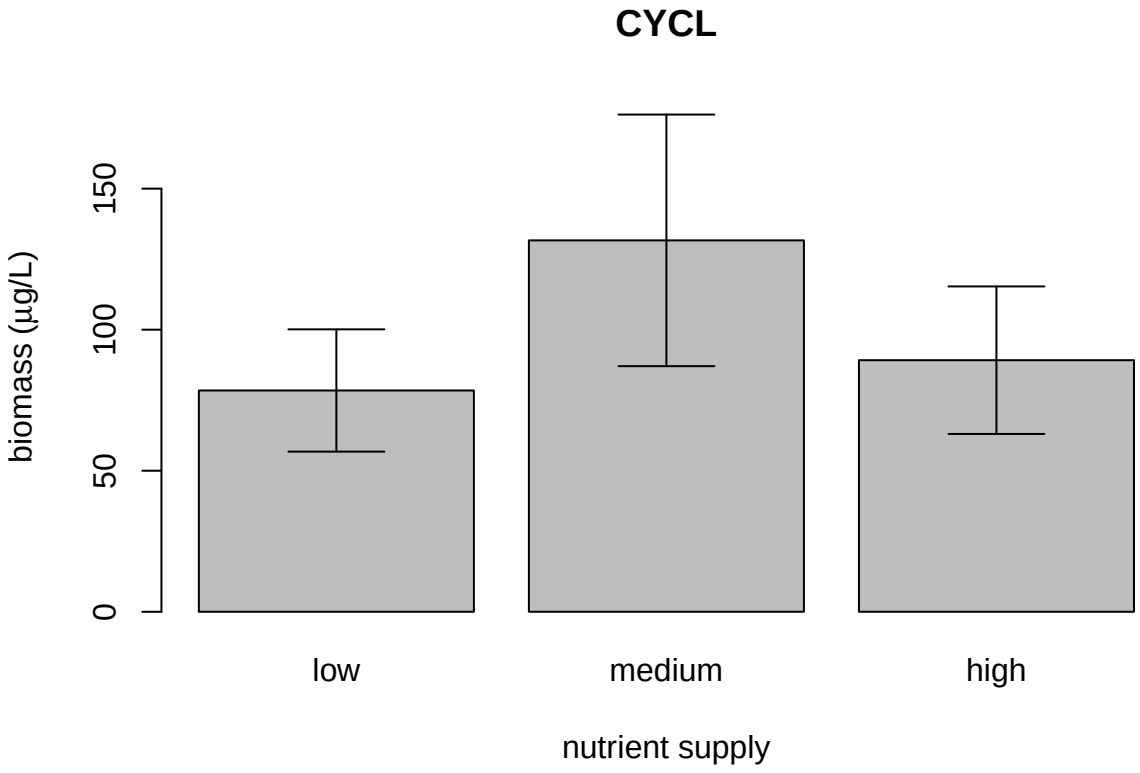
```
## Call:corr.test(x = sbs, method = "kendall", adjust = "BH")
## Correlation matrix
##        CAL  DIAP  CYCL  BOSM  SIMO  CERI  NAUP  DLUM  CHYD
## CAL   1.00  0.23  0.34  0.38 -0.24  0.02 -0.11  0.09 -0.39
## DIAP  0.23  1.00  0.50  0.13 -0.42  0.04  0.22  0.31 -0.18
## CYCL  0.34  0.50  1.00  0.41 -0.29  0.01  0.13  0.21 -0.31
## BOSM  0.38  0.13  0.41  1.00 -0.40  0.08  0.04 -0.10 -0.22
## SIMO -0.24 -0.42 -0.29 -0.40  1.00 -0.11 -0.18 -0.01  0.25
```

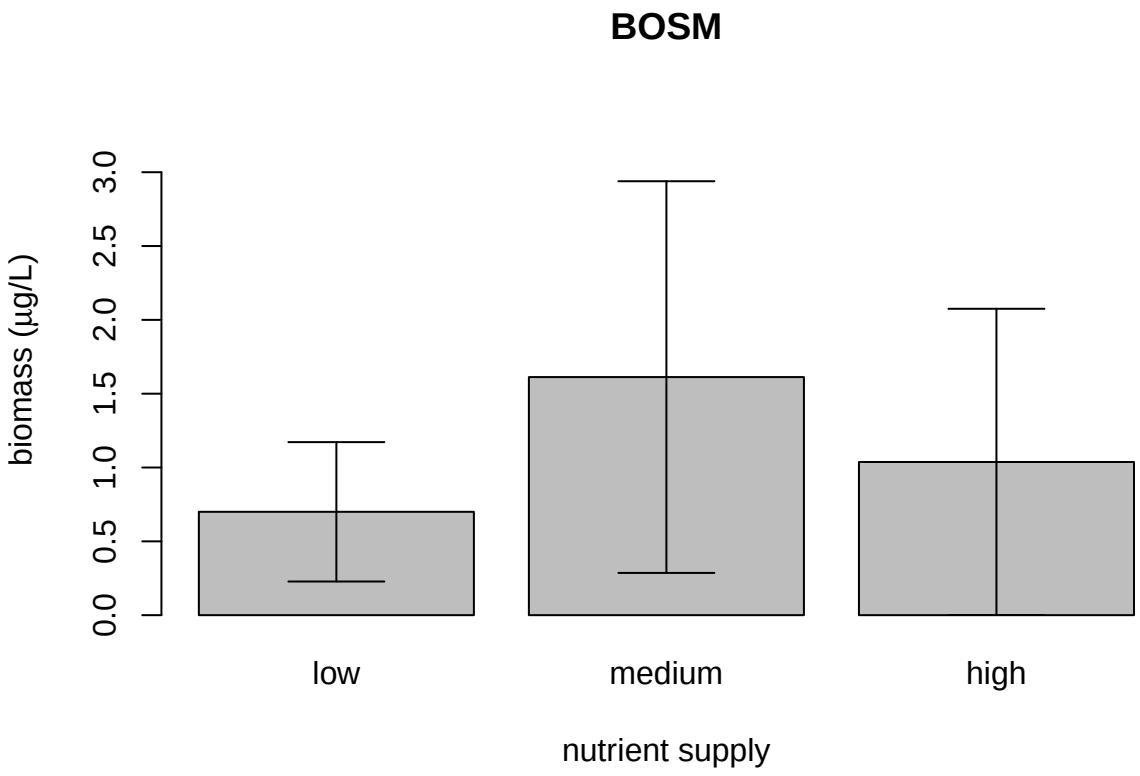
```
## CERI  0.02  0.04  0.01  0.08 -0.11  1.00  0.38  0.09 -0.09
## NAUP -0.11  0.22  0.13  0.04 -0.18  0.38  1.00  0.16 -0.10
## DLUM  0.09  0.31  0.21 -0.10 -0.01  0.09  0.16  1.00 -0.26
## CHYD -0.39 -0.18 -0.31 -0.22  0.25 -0.09 -0.10 -0.26  1.00
## Sample Size
## [1] 24
## Probability values (Entries above the diagonal are adjusted for multiple tests.)
##       CAL DIAP CYCL BOSM SIMO CERI NAUP DLUM CHYD
## CAL  0.00 0.62 0.46 0.36 0.62 0.97 0.81 0.81 0.36
## DIAP 0.29 0.00 0.36 0.81 0.36 0.94 0.62 0.50 0.74
## CYCL 0.10 0.01 0.00 0.36 0.54 0.97 0.81 0.63 0.50
## BOSM 0.07 0.55 0.05 0.00 0.36 0.81 0.94 0.81 0.62
## SIMO 0.25 0.04 0.17 0.05 0.00 0.81 0.74 0.97 0.62
## CERI 0.92 0.84 0.97 0.70 0.60 0.00 0.36 0.81 0.81
## NAUP 0.62 0.29 0.54 0.86 0.40 0.07 0.00 0.78 0.81
## DLUM 0.67 0.14 0.31 0.63 0.95 0.68 0.45 0.00 0.62
## CHYD 0.06 0.41 0.14 0.29 0.23 0.66 0.65 0.21 0.00
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

```
for (name in colnames(sbs)){
  means <- tapply(sbs[,name], NUTS, mean)
  sems <- tapply(sbs[,name], NUTS, sem)

  bp <- barplot(means, ylim=c(0,round(max(means),digits=0)+max(sems)*1.1), xlab = "nutrient supply", yl
# add error bars
  arrows(x0=bp, y0=means, y1=means-sems, angle = 90)
  arrows(x0=bp, y0=means, y1=means+sems, angle = 90)
}
```

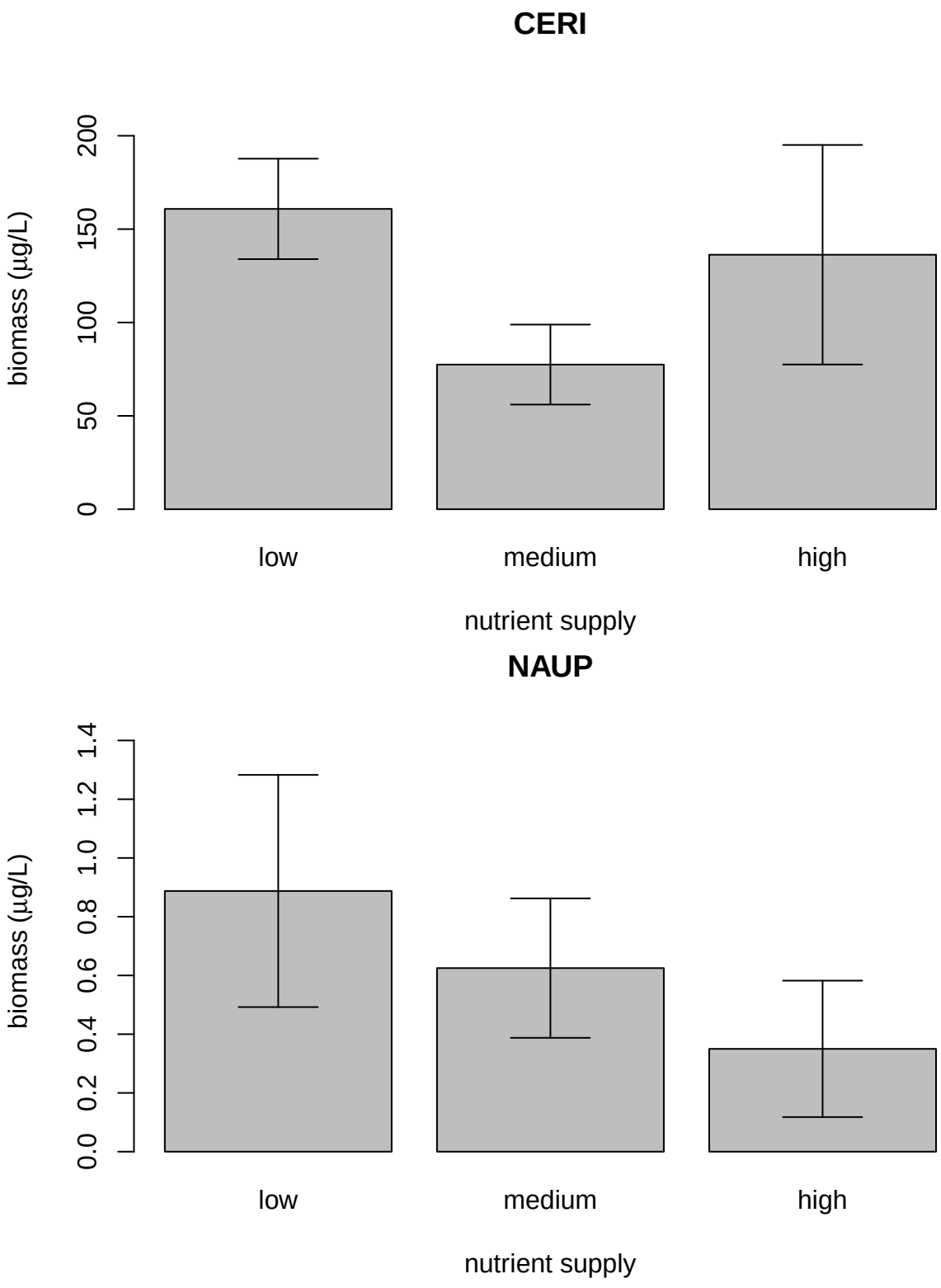



DIAP
biomass (µg/L)
0
20
40
60
80
low
medium
high
nutrient supply


CYCL
biomass (µg/L)
0
50
100
150
low
medium
high
nutrient supply

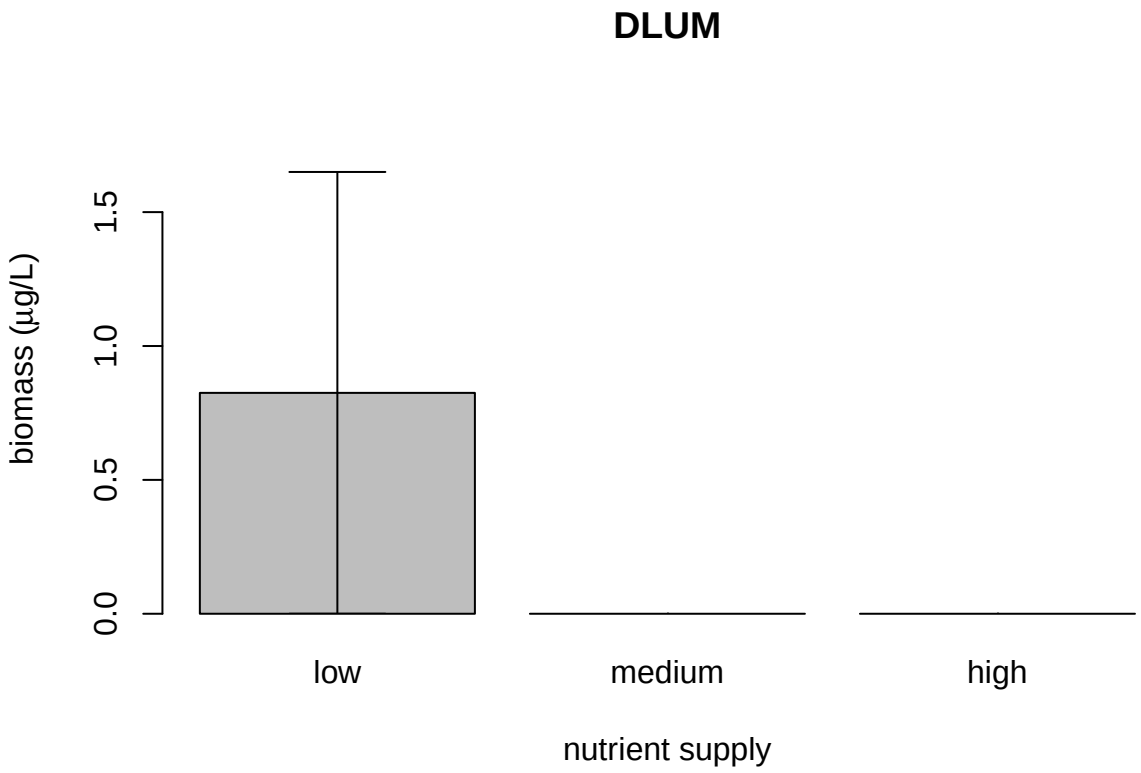

BOSM
biomass (µg/L)
0.0
0.5
1.0
1.5
2.0
2.5
3.0
low
medium
high
nutrient supply

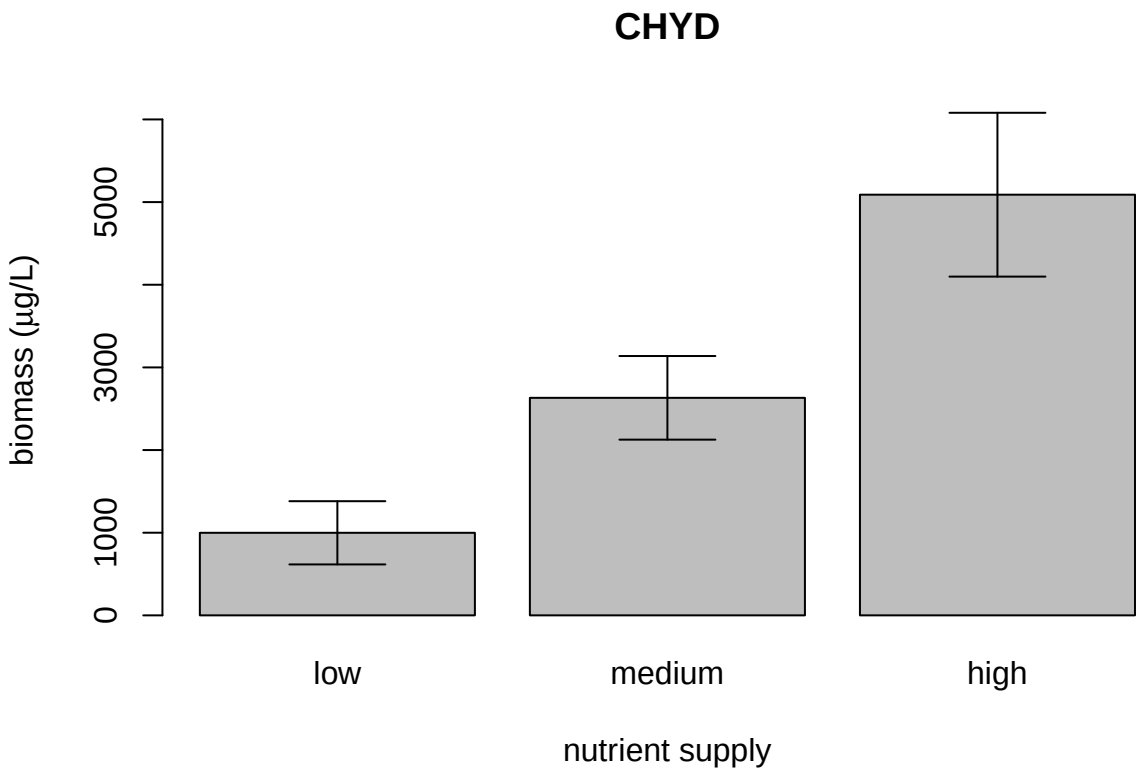

SIMO
biomass (µg/L)
0
200
400
600
800
low
medium
high
nutrient supply




```
## Warning in arrows(x0 = bp, y0 = means, y1 = means - sems, angle = 90): zero-
## length arrow is of indeterminate angle and so skipped

## Warning in arrows(x0 = bp, y0 = means, y1 = means - sems, angle = 90): zero-
## length arrow is of indeterminate angle and so skipped
```

```
## Warning in arrows(x0 = bp, y0 = means, y1 = means + sems, angle = 90): zero-
## length arrow is of indeterminate angle and so skipped

## Warning in arrows(x0 = bp, y0 = means, y1 = means + sems, angle = 90): zero-
## length arrow is of indeterminate angle and so skipped
```





Answer 6: The biomass of the various taxa appear to be uncorrelated, when uses the Kendall approach with BH p-value correction. The massive increase in biomass with high nutrients is almost entirely driven by high concentrations of SIMO and CHYD. CHYD in particular has biomasses orders of magnitude higher than other taxa. BOSM, NAUP, and DLUM are almost at negligible concentration. CAL, DIAP, CYCL, and BOSM all peak at medium nutrient concentrations, while NAUP and DLUM decrease with increasing nutrients.

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)**.