3. Worksheet: Basic R

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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, you must **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, January 22nd, 2025 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] "/cloud/project/QB2025_Huang/Week1-RStudio"
```

```
#setwd( "/cloud/project/QB2025_Huang/Week1-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.

```
l <- 5
V_cube <- l^3
print(V_cube)
```

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

```
r <- 2
A_circle <- pi * r^2
print(A_circle)
```

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

```
theta <- pi/4
hypo <- sqrt(2)
l_opst <- theta*hypo
print(l_opst)
```

```
## [1] 1.110721
```

```
fav_num <- 25
fav_log <- log(fav_num)
print(fav_log)
```

```
## [1] 3.218876
```

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(1,2,3,4,5)
w <- x*14
final <- (x + w)/15
```

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(3,5,7,2)
filler <- k*x
```

```
## Warning in k * x: longer object length is not a multiple of shorter object
## length
```

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

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)
```

```
max <- max(v)
min <- min(v)
sum <- sum(v)
mean <- mean(v)
median <- median(v)
var <- var(v)
sd <- sd(v)
sem <- sd/(sqrt(length(v)))
```

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.

```
n_r <- 5
n_c <- 2
mtx <- matrix(c(rnorm(n_r, mean = 8, sd = 2), rnorm(n_r, mean = 25, sd = 10)), nrow = n_r, ncol = n_c, 
```

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' function randomly generate a normal distribution of n numbers with the mean and standard deviation specified by the user. The basic fomular for 'rnorm' is rnorm(n, mean = , **sd** =), in which n stands for how many numbers you want it to generates, mean and sd stands for mean and standard deviation of the distribution that you also need to put in.

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 = "", header = FALSE))
n <- t(m)
dim(n)
```

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

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

> Answer 2: The matrix is 5x10 (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`.

```
m_mod <- m[, c(1:2,4:5)]
m_mod2 <- m[1:9, ]
```

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 = "", 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.

```
meso.num <- meso[, 3:8]
pairs(meso.num)
```
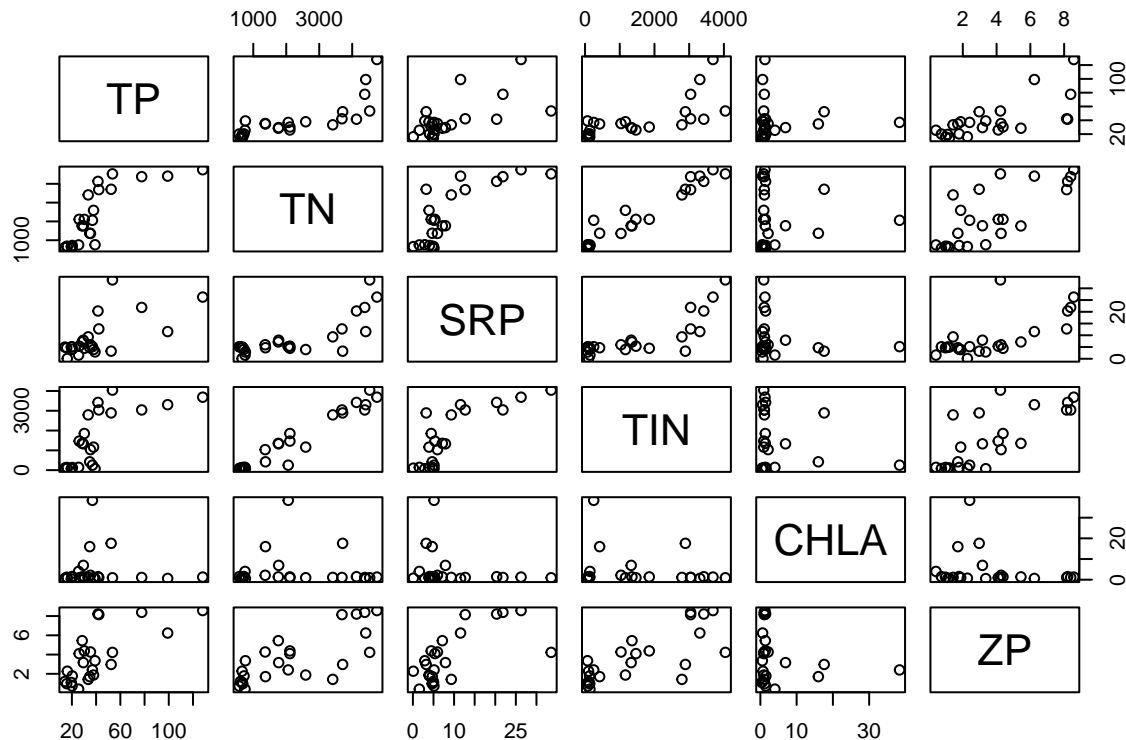
```r
cor1 <- cor(meso.num)
print(cor1)
```

```
##                   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: Algal biamass seems to have a weak negative correlation with all other variables (total phosphorus concentration, total nitrogen concentration, soluable reactive phosphorus concentration, total inorganic nutrient concentration, and zooplankton biomass). The total nitrogen concentration and the total inorganic nutrient concentration has the strongest correlation with the coefficient of 0.969. The zooplankton biomass is positively and somewhat strongly correlated the concentration of total phosphorus (0.6974), total nitrogen (0.7562), soluable reactive phosphorus (0.6762), and total inorganic nutrient (0.7605).

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 = "spearman", adjust = "BH")
print(cor3, digits = 3)
```

```
## Call:corr.test(x = meso.num, method = "spearman", adjust = "BH")
## Correlation matrix
##          TP    TN    SRP   TIN   CHLA     ZP
## TP    1.000 0.895  0.539 0.761  0.040  0.741
## TN    0.895 1.000  0.647 0.942  0.021  0.748
## SRP   0.539 0.647  1.000 0.726 -0.064  0.627
## TIN   0.761 0.942  0.726 1.000  0.088  0.738
## CHLA 0.040 0.021 -0.064 0.088  1.000 -0.072
## ZP    0.741 0.748  0.627 0.738 -0.072  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 0.010 0.000 0.914 0.000
## TN    0.000 0.000 0.001 0.000 0.923 0.000
## SRP   0.007 0.001 0.000 0.000 0.884 0.002
## TIN   0.000 0.000 0.000 0.000 0.884 0.000
## CHLA 0.853 0.923 0.767 0.683 0.000 0.884
## ZP    0.000 0.000 0.001 0.000 0.737 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: While the cor() function in base R generate the correlation coefficient matrix for the pairwise comparsion of selected variables, corr.test() in psych package can generate another the P-value matrix, which represents the probability of each pairwise comparison of variables having zero coefficient in the population. "BH" stands for the Benjamini & Hochberg correction, which

avoids false discovery rate. Comparing between using parametric and non-parametric methods, the results of the p-value are not sensitive. Correlation between chlorophyll a concentration (algal biomass) and any of the other variables are not significantly different from zero using both parametric and non-parametric test, which means there is nearly no correlation between algal biomass and all other factors. However, p-value for coefficient in all other pairwise comparison are significant regardless of the test used. Generally speaking, non-parametric tests are used when the data is ranked, or if the data is not normally distributed or have a relatively small sample size. False discovery rate measures the false rejection of null hypothesis (the amount of false significance that are supposed to be not significant). False discovery rate will arise when we perform multiple tests at the same time (like in this example, each pairs are tested twice). The role of the false discovery rate is to control the chance of making Type I error and count less insignificant as significant.

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, "g/L)")),
     ylab = "Zooplankton Biomass (mg/L)", las = 1)
text(x = meso$TN, y = meso$ZP, labels = 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, type = "response")
matlines(newTN, conf95[, c("lwr", "upr")], type = "l", lty = 2, lwd = 1, col = "black")
```
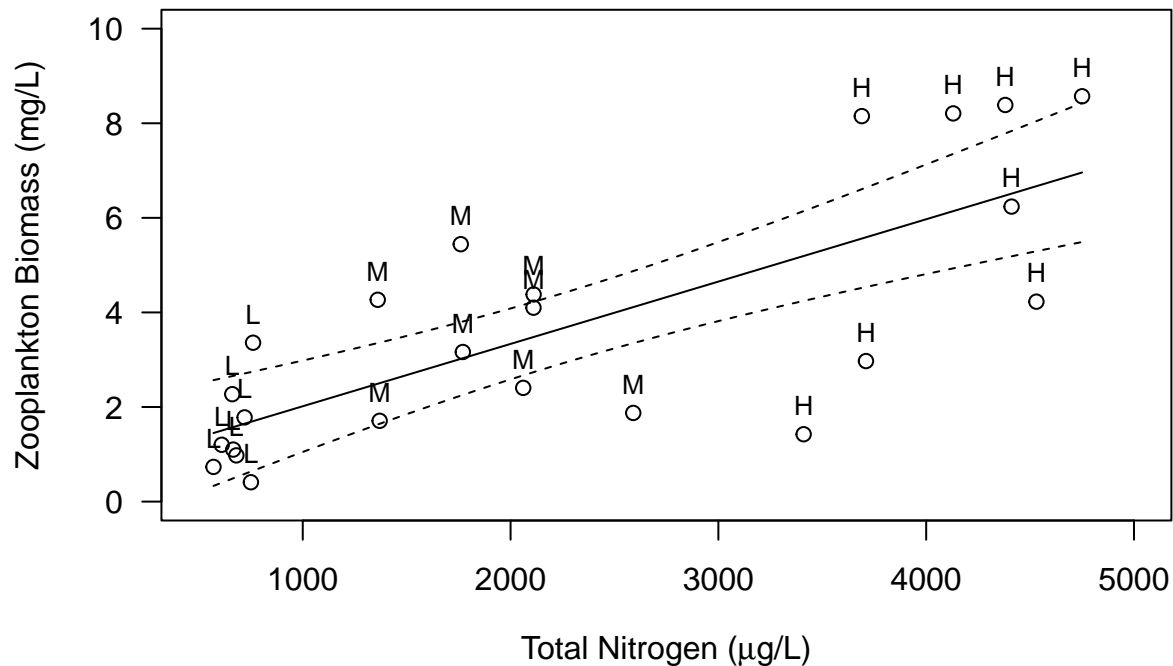
Question 5: Interpret the results from the regression model

Answer 5: The regression model above shows that the total nitrogen concentration (ug/L) has a significantly strong effect on the zooplankton biomass (mg/L), since the p-value is small enough (p = 1.91e-05). Higher total nitrogen concentration in the environment, larger the zooplankton biomass is. The 95% confidence interval represents the region where, with 95% confidence, the actual regression between the total nitrogen concentration in the environment and the biomass of the zooplankton will fall between. Since the R-squared is 0.5719, the regression model is moderatel fit as the model captures 57.19% of the variance in zooplankton biomass.

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)

#bar plot
bp <- barplot(zp.means, ylim = c(0, round(max(meso$ZP))), digits = 0, pch = 15,
              cex = 1.25, las = 1, cex.lab = 1.4, cex.axis = 1.25,
              xlab = "nutrient supply", ylab = "zooplankton biomass (mg/L)",
              names.arg = c("low", "medium,", "high"))
```

```
## Warning in plot.window(xlim, ylim, log = log, ...): "digits" is not a graphical
## parameter
```

```
## Warning in axis(if (horiz) 2 else 1, at = at.l, labels = names.arg, lty =
```

```
## axis.lty, : "digits" is not a graphical parameter

## Warning in title(main = main, sub = sub, xlab = xlab, ylab = ylab, ...):
## "digits" is not a graphical parameter

## Warning in axis(if (horiz) 1 else 2, cex.axis = cex.axis, ...): "digits" is not
## a graphical parameter
```

```r
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)
```
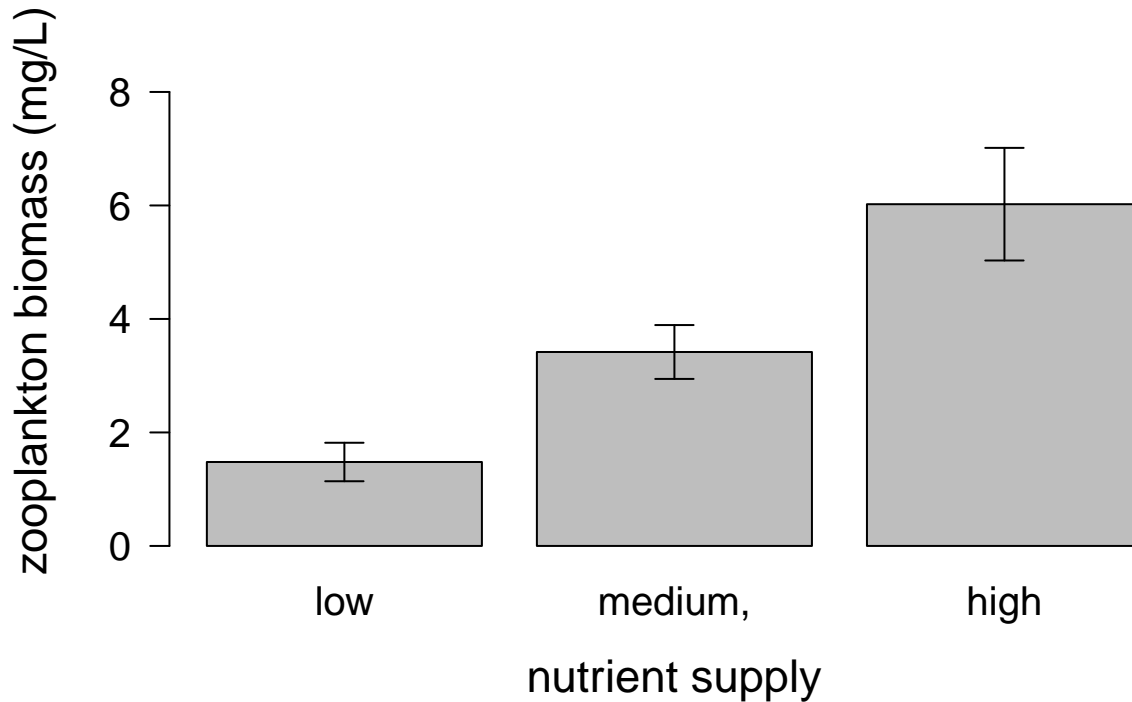


```r
#ANOVA
fitanova <- aov(ZP ~ NUTS, data = meso)
summary(fitanova)
```

```
##             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
```

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.

> Answer 6: I used a stacked bar plot and two-way ANOVA in order to assess whether different zooplankton taxa contribute differently to the total biomass reponse to nutrient. In another word, I compared the biomass of different zooplankton taxa under different nutrient treatment. I found that among the nine taxa, CHYD (*Chydorus* sp.) is the taxon that contribute the most to the total biomass of zooplankton in all three treatment groups, and SIMO (*Simocephallus* sp.) being the second biggest contributor in medium and high nutrient groups. The result of the ANOVA shows that threatment groups, taxon of the zooplankton, and the interaction of taxon and zooplankton all have a significant effect on zooplankton biomass, showing that there is a difference between each taxon in biomass contribution.

```
zoops <- read.table("data/zoops.txt", sep = "", header = TRUE)
sbs <- zoops[, 3:11] #create site by species matrix
print(sbs)
```

```
##        CAL  DIAP  CYCL BOSM   SIMO  CERI NAUP DLUM   CHYD
## 1     70.5   0.0  66.1  2.2  417.8 159.8  0.0  0.0  266.9
## 2     27.1  19.2 129.6  0.0    0.0  79.4  0.0  0.0  158.7
## 3      5.3   8.8  12.7  0.0   73.1 107.5  1.2  0.0 3158.2
## 4     79.2  17.9 141.3  3.4    0.0 199.0  0.0  0.0  298.5
## 5     31.4   0.0  11.0  0.0  482.0 101.9  0.0  0.0  580.2
## 6     22.7 285.1 153.0  0.0  241.5 135.5  1.2  6.6  262.4
## 7      0.0   2.3  11.0  0.0   73.1 185.0  1.6  0.0 2004.4
## 8     35.7  65.9 102.9  0.0    0.0 318.5  3.1  0.0 1260.7
## 9     74.8 178.7 266.5  0.0    0.0   1.9  0.0  0.0 1190.9
## 10     5.3   4.9  87.8  0.0 1099.2 136.4  1.4  0.0 2939.6
## 11    18.4   2.3  29.4  0.0  393.8 147.6  1.2  0.0 4857.3
## 12    14.0   2.3  37.7  0.0 1251.5  74.8  0.0  0.0 2725.5
## 13    14.0   2.3 132.9  0.0  818.6  98.1  1.2  0.0  814.5
## 14    48.8   2.3 107.9  2.2    9.0 132.7  0.0  0.0 2867.5
```

```
## 15    0.0    0.0   17.7  0.0  145.3   19.7  0.0  0.0 4201.6
## 16  292.0  269.5  373.4 10.7    0.0    8.5  1.2  0.0 1456.8
## 17    9.7    0.0   41.1  0.0 2397.8    9.4  0.0  0.0 5697.9
## 18    0.0    2.3    0.0  0.0  225.5   24.3  0.0  0.0 8323.2
## 19    5.3    0.0   86.2  0.0  465.9  527.7  1.2  0.0 3146.9
## 20   14.0    7.5   69.5  0.0  594.2   78.5  0.0  0.0 7629.2
## 21    0.0   24.4  101.2  0.0  313.6  176.6  0.0  0.0 7597.6
## 22    0.0    7.5  253.2  8.3    0.0  112.1  1.6  0.0 2594.8
## 23    5.3    2.3   96.2  0.0  786.6   76.6  0.0  0.0  463.0
## 24    0.0    2.3   66.1  0.0  826.7   85.1  0.0  0.0 5263.0
```

```r
zoops$total.biomass <- zoops$CAL + zoops$DIAP + zoops$CYCL + zoops$BOSM +
  zoops$SIMO + zoops$CERI + zoops$NAUP + zoops$DLUM + zoops$CHYD


NUTS <- factor(zoops$NUTS, levels = c('L', 'M', 'H'))
total.mean <- tapply(zoops$total.biomass, NUTS, mean)
cal.mean <- tapply(zoops$CAL, NUTS, mean)
diap.mean <- tapply(zoops$DIAP, NUTS, mean)
cycl.mean <- tapply(zoops$CYCL, NUTS, mean)
bosm.mean <- tapply(zoops$BOSM, NUTS, mean)
simo.mean <- tapply(zoops$SIMO, NUTS, mean)
ceri.mean <- tapply(zoops$CERI, NUTS, mean)
naup.mean <- tapply(zoops$NAUP, NUTS, mean)
dlum.mean <- tapply(zoops$DLUM, NUTS, mean)
chyd.mean <- tapply(zoops$CHYD, NUTS, mean)

#Create matrix for bar plot
species_by_treatment <- rbind(cal.mean, diap.mean, cycl.mean, bosm.mean,
                              simo.mean, ceri.mean, naup.mean, dlum.mean,
                              chyd.mean)
colnames(species_by_treatment) <- c("Low", "Medium", "High")
rownames(species_by_treatment) <- c("CAL", "DIAP", "CYCL", "BOSM", "SIMO",
                                    "CERI", "NAUP", "DLUM", "CHYD")
species_by_treatment <- as.matrix(species_by_treatment)

#Stacked bar plot
library(RColorBrewer)
color <- brewer.pal(9, "Paired")
barplot(species_by_treatment, col = color , border = "white", space= 0.04,
        font.axis=2, ylim = c(0,round(max(total.mean))),
        legend = rownames(species_by_treatment),
        args.legend = list(x = "topright", inset = c(-0.1, 0), bty = "n", cex = 0.5),
        xlab = "categorical nutrient treatment",
        ylab = "zooplankton biomass (mg/L)")
```
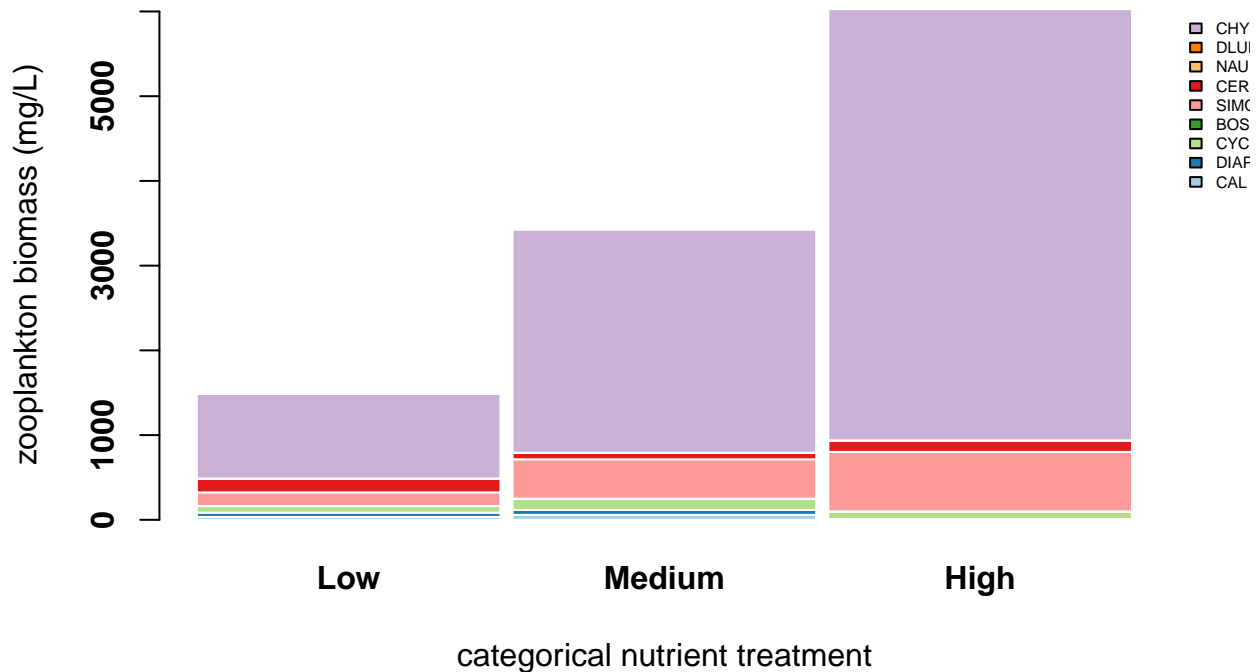
Legend: CHY, DLU, NAU, CER, SIMO, BOS, CYC, DIAP, CAL

x-axis: Low, Medium, High

y-axis: zooplankton biomass (mg/L)

categorical nutrient treatment

```r
#Create new data set for ANOVA
stacked <- stack(zoops[, 3:11])
anova_frame <- data.frame(NUTS = rep(zoops$NUTS, times = 9),
                          taxon = stacked$ind,
                          biomass = stacked$values)


species_anova <- aov(biomass ~ NUTS * taxon, data = anova_frame)
summary(species_anova)
```

```
##              Df    Sum Sq  Mean Sq F value   Pr(>F)
## NUTS          2   9235972  4617986  10.368 5.34e-05 ***
## taxon         8 172690808 21586351  48.466  < 2e-16 ***
## NUTS:taxon   16  59846623  3740414   8.398 3.86e-15 ***
## Residuals   189  84179134   445392
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
TukeyHSD(species_anova)
```

```
##    Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = biomass ~ NUTS * taxon, data = anova_frame)
##
## $NUTS
##          diff        lwr        upr      p adj
## L-H -504.7125 -767.47293 -241.95207 0.0000300
## M-H -289.3028 -552.06321  -26.54235 0.0269885
## M-L  215.4097  -47.35071  478.17015 0.1312885
##
## $taxon
##                   diff        lwr       upr      p adj
## DIAP-CAL     5.5958333  -598.9761  610.1678 1.0000000
```

```
## CYCL-CAL      67.5375000  -537.0344   672.1094 0.9999933
## BOSM-CAL     -31.1125000  -635.6844   573.4594 1.0000000
## SIMO-CAL     410.0708333  -194.5011  1014.6428 0.4571928
## CERI-CAL      92.6291667  -511.9428   697.2011 0.9999229
## NAUP-CAL     -31.6083333  -636.1803   572.9636 1.0000000
## DLUM-CAL     -31.9541667  -636.5261   572.6178 1.0000000
## CHYD-CAL    2874.4083333  2269.8364  3478.9803 0.0000000
## CYCL-DIAP     61.9416667  -542.6303   666.5136 0.9999966
## BOSM-DIAP    -36.7083333  -641.2803   567.8636 0.9999999
## SIMO-DIAP    404.4750000  -200.0969  1009.0469 0.4768330
## CERI-DIAP     87.0333333  -517.5386   691.6053 0.9999521
## NAUP-DIAP    -37.2041667  -641.7761   567.3678 0.9999999
## DLUM-DIAP    -37.5500000  -642.1219   567.0219 0.9999999
## CHYD-DIAP   2868.8125000  2264.2406  3473.3844 0.0000000
## BOSM-CYCL    -98.6500000  -703.2219   505.9219 0.9998757
## SIMO-CYCL    342.5333333  -262.0386   947.1053 0.6966197
## CERI-CYCL     25.0916667  -579.4803   629.6636 1.0000000
## NAUP-CYCL    -99.1458333  -703.7178   505.4261 0.9998709
## DLUM-CYCL    -99.4916667  -704.0636   505.0803 0.9998674
## CHYD-CYCL   2806.8708333  2202.2989  3411.4428 0.0000000
## SIMO-BOSM    441.1833333  -163.3886  1045.7553 0.3534776
## CERI-BOSM    123.7416667  -480.8303   728.3136 0.9993272
## NAUP-BOSM     -0.4958333  -605.0678   604.0761 1.0000000
## DLUM-BOSM     -0.8416667  -605.4136   603.7303 1.0000000
## CHYD-BOSM   2905.5208333  2300.9489  3510.0928 0.0000000
## CERI-SIMO   -317.4416667  -922.0136   287.1303 0.7770066
## NAUP-SIMO   -441.6791667 -1046.2511   162.8928 0.3519191
## DLUM-SIMO   -442.0250000 -1046.5969   162.5469 0.3508341
## CHYD-SIMO   2464.3375000  1859.7656  3068.9094 0.0000000
## NAUP-CERI   -124.2375000  -728.8094   480.3344 0.9993072
## DLUM-CERI   -124.5833333  -729.1553   479.9886 0.9992930
## CHYD-CERI   2781.7791667  2177.2072  3386.3511 0.0000000
## DLUM-NAUP     -0.3458333  -604.9178   604.2261 1.0000000
## CHYD-NAUP   2906.0166667  2301.4447  3510.5886 0.0000000
## CHYD-DLUM   2906.3625000  2301.7906  3510.9344 0.0000000
##
## $`NUTS:taxon`
##                        diff        lwr       upr     p adj
## L:CAL-H:CAL    2.970000e+01 -1222.8421  1282.2421 1.0000000
## M:CAL-H:CAL    5.412500e+01 -1198.4171  1306.6671 1.0000000
## H:DIAP-H:CAL   1.500000e+00 -1251.0421  1254.0421 1.0000000
## L:DIAP-H:CAL   4.561250e+01 -1206.9296  1298.1546 1.0000000
## M:DIAP-H:CAL   5.350000e+01 -1199.0421  1306.0421 1.0000000
## H:CYCL-H:CAL   8.490000e+01 -1167.6421  1337.4421 1.0000000
## L:CYCL-H:CAL   7.416250e+01 -1178.3796  1326.7046 1.0000000
## M:CYCL-H:CAL   1.273750e+02 -1125.1671  1379.9171 1.0000000
## H:BOSM-H:CAL  -3.250000e+00 -1255.7921  1249.2921 1.0000000
## L:BOSM-H:CAL  -3.587500e+00 -1256.1296  1248.9546 1.0000000
## M:BOSM-H:CAL  -2.675000e+00 -1255.2171  1249.8671 1.0000000
## H:SIMO-H:CAL   6.970000e+02  -555.5421  1949.5421 0.9403521
## L:SIMO-H:CAL   1.566500e+02 -1095.8921  1409.1921 1.0000000
## M:SIMO-H:CAL   4.603875e+02  -792.1546  1712.9296 0.9998308
## H:CERI-H:CAL   1.320000e+02 -1120.5421  1384.5421 1.0000000
## L:CERI-H:CAL   1.565375e+02 -1096.0046  1409.0796 1.0000000
```

```
## M:CERI-H:CAL    7.317500e+01 -1179.3671   1325.7171 1.0000000
## H:NAUP-H:CAL   -3.937500e+00 -1256.4796   1248.6046 1.0000000
## L:NAUP-H:CAL   -3.400000e+00 -1255.9421   1249.1421 1.0000000
## M:NAUP-H:CAL   -3.662500e+00 -1256.2046   1248.8796 1.0000000
## H:DLUM-H:CAL   -4.287500e+00 -1256.8296   1248.2546 1.0000000
## L:DLUM-H:CAL   -3.462500e+00 -1256.0046   1249.0796 1.0000000
## M:DLUM-H:CAL   -4.287500e+00 -1256.8296   1248.2546 1.0000000
## H:CHYD-H:CAL    5.085162e+03  3832.6204   6337.7046 0.0000000
## L:CHYD-H:CAL    9.944625e+02  -258.0796   2247.0046 0.3646085
## M:CHYD-H:CAL    2.627425e+03  1374.8829   3879.9671 0.0000000
## M:CAL-L:CAL     2.442500e+01 -1228.1171   1276.9671 1.0000000
## H:DIAP-L:CAL   -2.820000e+01 -1280.7421   1224.3421 1.0000000
## L:DIAP-L:CAL    1.591250e+01 -1236.6296   1268.4546 1.0000000
## M:DIAP-L:CAL    2.380000e+01 -1228.7421   1276.3421 1.0000000
## H:CYCL-L:CAL    5.520000e+01 -1197.3421   1307.7421 1.0000000
## L:CYCL-L:CAL    4.446250e+01 -1208.0796   1297.0046 1.0000000
## M:CYCL-L:CAL    9.767500e+01 -1154.8671   1350.2171 1.0000000
## H:BOSM-L:CAL   -3.295000e+01 -1285.4921   1219.5921 1.0000000
## L:BOSM-L:CAL   -3.328750e+01 -1285.8296   1219.2546 1.0000000
## M:BOSM-L:CAL   -3.237500e+01 -1284.9171   1220.1671 1.0000000
## H:SIMO-L:CAL    6.673000e+02  -585.2421   1919.8421 0.9625903
## L:SIMO-L:CAL    1.269500e+02 -1125.5921   1379.4921 1.0000000
## M:SIMO-L:CAL    4.306875e+02  -821.8546   1683.2296 0.9999491
## H:CERI-L:CAL    1.023000e+02 -1150.2421   1354.8421 1.0000000
## L:CERI-L:CAL    1.268375e+02 -1125.7046   1379.3796 1.0000000
## M:CERI-L:CAL    4.347500e+01 -1209.0671   1296.0171 1.0000000
## H:NAUP-L:CAL   -3.363750e+01 -1286.1796   1218.9046 1.0000000
## L:NAUP-L:CAL   -3.310000e+01 -1285.6421   1219.4421 1.0000000
## M:NAUP-L:CAL   -3.336250e+01 -1285.9046   1219.1796 1.0000000
## H:DLUM-L:CAL   -3.398750e+01 -1286.5296   1218.5546 1.0000000
## L:DLUM-L:CAL   -3.316250e+01 -1285.7046   1219.3796 1.0000000
## M:DLUM-L:CAL   -3.398750e+01 -1286.5296   1218.5546 1.0000000
## H:CHYD-L:CAL    5.055462e+03  3802.9204   6308.0046 0.0000000
## L:CHYD-L:CAL    9.647625e+02  -287.7796   2217.3046 0.4289484
## M:CHYD-L:CAL    2.597725e+03  1345.1829   3850.2671 0.0000000
## H:DIAP-M:CAL   -5.262500e+01 -1305.1671   1199.9171 1.0000000
## L:DIAP-M:CAL   -8.512500e+00 -1261.0546   1244.0296 1.0000000
## M:DIAP-M:CAL   -6.250000e-01 -1253.1671   1251.9171 1.0000000
## H:CYCL-M:CAL    3.077500e+01 -1221.7671   1283.3171 1.0000000
## L:CYCL-M:CAL    2.003750e+01 -1232.5046   1272.5796 1.0000000
## M:CYCL-M:CAL    7.325000e+01 -1179.2921   1325.7921 1.0000000
## H:BOSM-M:CAL   -5.737500e+01 -1309.9171   1195.1671 1.0000000
## L:BOSM-M:CAL   -5.771250e+01 -1310.2546   1194.8296 1.0000000
## M:BOSM-M:CAL   -5.680000e+01 -1309.3421   1195.7421 1.0000000
## H:SIMO-M:CAL    6.428750e+02  -609.6671   1895.4171 0.9756575
## L:SIMO-M:CAL    1.025250e+02 -1150.0171   1355.0671 1.0000000
## M:SIMO-M:CAL    4.062625e+02  -846.2796   1658.8046 0.9999830
## H:CERI-M:CAL    7.787500e+01 -1174.6671   1330.4171 1.0000000
## L:CERI-M:CAL    1.024125e+02 -1150.1296   1354.9546 1.0000000
## M:CERI-M:CAL    1.905000e+01 -1233.4921   1271.5921 1.0000000
## H:NAUP-M:CAL   -5.806250e+01 -1310.6046   1194.4796 1.0000000
## L:NAUP-M:CAL   -5.752500e+01 -1310.0671   1195.0171 1.0000000
## M:NAUP-M:CAL   -5.778750e+01 -1310.3296   1194.7546 1.0000000
## H:DLUM-M:CAL   -5.841250e+01 -1310.9546   1194.1296 1.0000000
```

```
## L:DLUM-M:CAL  -5.758750e+01  -1310.1296  1194.9546 1.0000000
## M:DLUM-M:CAL  -5.841250e+01  -1310.9546  1194.1296 1.0000000
## H:CHYD-M:CAL   5.031038e+03   3778.4954  6283.5796 0.0000000
## L:CHYD-M:CAL   9.403375e+02   -312.2046  2192.8796 0.4847069
## M:CHYD-M:CAL   2.573300e+03   1320.7579  3825.8421 0.0000000
## L:DIAP-H:DIAP  4.411250e+01  -1208.4296  1296.6546 1.0000000
## M:DIAP-H:DIAP  5.200000e+01  -1200.5421  1304.5421 1.0000000
## H:CYCL-H:DIAP  8.340000e+01  -1169.1421  1335.9421 1.0000000
## L:CYCL-H:DIAP  7.266250e+01  -1179.8796  1325.2046 1.0000000
## M:CYCL-H:DIAP  1.258750e+02  -1126.6671  1378.4171 1.0000000
## H:BOSM-H:DIAP -4.750000e+00  -1257.2921  1247.7921 1.0000000
## L:BOSM-H:DIAP -5.087500e+00  -1257.6296  1247.4546 1.0000000
## M:BOSM-H:DIAP -4.175000e+00  -1256.7171  1248.3671 1.0000000
## H:SIMO-H:DIAP  6.955000e+02   -557.0421  1948.0421 0.9416604
## L:SIMO-H:DIAP  1.551500e+02  -1097.3921  1407.6921 1.0000000
## M:SIMO-H:DIAP  4.588875e+02   -793.6546  1711.4296 0.9998403
## H:CERI-H:DIAP  1.305000e+02  -1122.0421  1383.0421 1.0000000
## L:CERI-H:DIAP  1.550375e+02  -1097.5046  1407.5796 1.0000000
## M:CERI-H:DIAP  7.167500e+01  -1180.8671  1324.2171 1.0000000
## H:NAUP-H:DIAP -5.437500e+00  -1257.9796  1247.1046 1.0000000
## L:NAUP-H:DIAP -4.900000e+00  -1257.4421  1247.6421 1.0000000
## M:NAUP-H:DIAP -5.162500e+00  -1257.7046  1247.3796 1.0000000
## H:DLUM-H:DIAP -5.787500e+00  -1258.3296  1246.7546 1.0000000
## L:DLUM-H:DIAP -4.962500e+00  -1257.5046  1247.5796 1.0000000
## M:DLUM-H:DIAP -5.787500e+00  -1258.3296  1246.7546 1.0000000
## H:CHYD-H:DIAP  5.083663e+03   3831.1204  6336.2046 0.0000000
## L:CHYD-H:DIAP  9.929625e+02   -259.5796  2245.5046 0.3677462
## M:CHYD-H:DIAP  2.625925e+03   1373.3829  3878.4671 0.0000000
## M:DIAP-L:DIAP  7.887500e+00  -1244.6546  1260.4296 1.0000000
## H:CYCL-L:DIAP  3.928750e+01  -1213.2546  1291.8296 1.0000000
## L:CYCL-L:DIAP  2.855000e+01  -1223.9921  1281.0921 1.0000000
## M:CYCL-L:DIAP  8.176250e+01  -1170.7796  1334.3046 1.0000000
## H:BOSM-L:DIAP -4.886250e+01  -1301.4046  1203.6796 1.0000000
## L:BOSM-L:DIAP -4.920000e+01  -1301.7421  1203.3421 1.0000000
## M:BOSM-L:DIAP -4.828750e+01  -1300.8296  1204.2546 1.0000000
## H:SIMO-L:DIAP  6.513875e+02   -601.1546  1903.9296 0.9715840
## L:SIMO-L:DIAP  1.110375e+02  -1141.5046  1363.5796 1.0000000
## M:SIMO-L:DIAP  4.147750e+02   -837.7671  1667.3171 0.9999748
## H:CERI-L:DIAP  8.638750e+01  -1166.1546  1338.9296 1.0000000
## L:CERI-L:DIAP  1.109250e+02  -1141.6171  1363.4671 1.0000000
## M:CERI-L:DIAP  2.756250e+01  -1224.9796  1280.1046 1.0000000
## H:NAUP-L:DIAP -4.955000e+01  -1302.0921  1202.9921 1.0000000
## L:NAUP-L:DIAP -4.901250e+01  -1301.5546  1203.5296 1.0000000
## M:NAUP-L:DIAP -4.927500e+01  -1301.8171  1203.2671 1.0000000
## H:DLUM-L:DIAP -4.990000e+01  -1302.4421  1202.6421 1.0000000
## L:DLUM-L:DIAP -4.907500e+01  -1301.6171  1203.4671 1.0000000
## M:DLUM-L:DIAP -4.990000e+01  -1302.4421  1202.6421 1.0000000
## H:CHYD-L:DIAP  5.039550e+03   3787.0079  6292.0921 0.0000000
## L:CHYD-L:DIAP  9.488500e+02   -303.6921  2201.3921 0.4650466
## M:CHYD-L:DIAP  2.581812e+03   1329.2704  3834.3546 0.0000000
## H:CYCL-M:DIAP  3.140000e+01  -1221.1421  1283.9421 1.0000000
## L:CYCL-M:DIAP  2.066250e+01  -1231.8796  1273.2046 1.0000000
## M:CYCL-M:DIAP  7.387500e+01  -1178.6671  1326.4171 1.0000000
## H:BOSM-M:DIAP -5.675000e+01  -1309.2921  1195.7921 1.0000000
```

```
## L:BOSM-M:DIAP -5.708750e+01 -1309.6296  1195.4546 1.0000000
## M:BOSM-M:DIAP -5.617500e+01 -1308.7171  1196.3671 1.0000000
## H:SIMO-M:DIAP  6.435000e+02  -609.0421  1896.0421 0.9753748
## L:SIMO-M:DIAP  1.031500e+02 -1149.3921  1355.6921 1.0000000
## M:SIMO-M:DIAP  4.068875e+02  -845.6546  1659.4296 0.9999825
## H:CERI-M:DIAP  7.850000e+01 -1174.0421  1331.0421 1.0000000
## L:CERI-M:DIAP  1.030375e+02 -1149.5046  1355.5796 1.0000000
## M:CERI-M:DIAP  1.967500e+01 -1232.8671  1272.2171 1.0000000
## H:NAUP-M:DIAP -5.743750e+01 -1309.9796  1195.1046 1.0000000
## L:NAUP-M:DIAP -5.690000e+01 -1309.4421  1195.6421 1.0000000
## M:NAUP-M:DIAP -5.716250e+01 -1309.7046  1195.3796 1.0000000
## H:DLUM-M:DIAP -5.778750e+01 -1310.3296  1194.7546 1.0000000
## L:DLUM-M:DIAP -5.696250e+01 -1309.5046  1195.5796 1.0000000
## M:DLUM-M:DIAP -5.778750e+01 -1310.3296  1194.7546 1.0000000
## H:CHYD-M:DIAP  5.031662e+03  3779.1204  6284.2046 0.0000000
## L:CHYD-M:DIAP  9.409625e+02  -311.5796  2193.5046 0.4832565
## M:CHYD-M:DIAP  2.573925e+03  1321.3829  3826.4671 0.0000000
## L:CYCL-H:CYCL -1.073750e+01 -1263.2796  1241.8046 1.0000000
## M:CYCL-H:CYCL  4.247500e+01 -1210.0671  1295.0171 1.0000000
## H:BOSM-H:CYCL -8.815000e+01 -1340.6921  1164.3921 1.0000000
## L:BOSM-H:CYCL -8.848750e+01 -1341.0296  1164.0546 1.0000000
## M:BOSM-H:CYCL -8.757500e+01 -1340.1171  1164.9671 1.0000000
## H:SIMO-H:CYCL  6.121000e+02  -640.4421  1864.6421 0.9867295
## L:SIMO-H:CYCL  7.175000e+01 -1180.7921  1324.2921 1.0000000
## M:SIMO-H:CYCL  3.754875e+02  -877.0546  1628.0296 0.9999964
## H:CERI-H:CYCL  4.710000e+01 -1205.4421  1299.6421 1.0000000
## L:CERI-H:CYCL  7.163750e+01 -1180.9046  1324.1796 1.0000000
## M:CERI-H:CYCL -1.172500e+01 -1264.2671  1240.8171 1.0000000
## H:NAUP-H:CYCL -8.883750e+01 -1341.3796  1163.7046 1.0000000
## L:NAUP-H:CYCL -8.830000e+01 -1340.8421  1164.2421 1.0000000
## M:NAUP-H:CYCL -8.856250e+01 -1341.1046  1163.9796 1.0000000
## H:DLUM-H:CYCL -8.918750e+01 -1341.7296  1163.3546 1.0000000
## L:DLUM-H:CYCL -8.836250e+01 -1340.9046  1164.1796 1.0000000
## M:DLUM-H:CYCL -8.918750e+01 -1341.7296  1163.3546 1.0000000
## H:CHYD-H:CYCL  5.000262e+03  3747.7204  6252.8046 0.0000000
## L:CHYD-H:CYCL  9.095625e+02  -342.9796  2162.1046 0.5570029
## M:CHYD-H:CYCL  2.542525e+03  1289.9829  3795.0671 0.0000000
## M:CYCL-L:CYCL  5.321250e+01 -1199.3296  1305.7546 1.0000000
## H:BOSM-L:CYCL -7.741250e+01 -1329.9546  1175.1296 1.0000000
## L:BOSM-L:CYCL -7.775000e+01 -1330.2921  1174.7921 1.0000000
## M:BOSM-L:CYCL -7.683750e+01 -1329.3796  1175.7046 1.0000000
## H:SIMO-L:CYCL  6.228375e+02  -629.7046  1875.3796 0.9834578
## L:SIMO-L:CYCL  8.248750e+01 -1170.0546  1335.0296 1.0000000
## M:SIMO-L:CYCL  3.862250e+02  -866.3171  1638.7671 0.9999937
## H:CERI-L:CYCL  5.783750e+01 -1194.7046  1310.3796 1.0000000
## L:CERI-L:CYCL  8.237500e+01 -1170.1671  1334.9171 1.0000000
## M:CERI-L:CYCL -9.875000e-01 -1253.5296  1251.5546 1.0000000
## H:NAUP-L:CYCL -7.810000e+01 -1330.6421  1174.4421 1.0000000
## L:NAUP-L:CYCL -7.756250e+01 -1330.1046  1174.9796 1.0000000
## M:NAUP-L:CYCL -7.782500e+01 -1330.3671  1174.7171 1.0000000
## H:DLUM-L:CYCL -7.845000e+01 -1330.9921  1174.0921 1.0000000
## L:DLUM-L:CYCL -7.762500e+01 -1330.1671  1174.9171 1.0000000
## M:DLUM-L:CYCL -7.845000e+01 -1330.9921  1174.0921 1.0000000
## H:CHYD-L:CYCL  5.011000e+03  3758.4579  6263.5421 0.0000000
```

```
## L:CHYD-L:CYCL  9.203000e+02  -332.2421  2172.8421 0.5316415
## M:CHYD-L:CYCL  2.553263e+03  1300.7204  3805.8046 0.0000000
## H:BOSM-M:CYCL -1.306250e+02 -1383.1671  1121.9171 1.0000000
## L:BOSM-M:CYCL -1.309625e+02 -1383.5046  1121.5796 1.0000000
## M:BOSM-M:CYCL -1.300500e+02 -1382.5921  1122.4921 1.0000000
## H:SIMO-M:CYCL  5.696250e+02  -682.9171  1822.1671 0.9949761
## L:SIMO-M:CYCL  2.927500e+01 -1223.2671  1281.8171 1.0000000
## M:SIMO-M:CYCL  3.330125e+02  -919.5296  1585.5546 0.9999997
## H:CERI-M:CYCL  4.625000e+00 -1247.9171  1257.1671 1.0000000
## L:CERI-M:CYCL  2.916250e+01 -1223.3796  1281.7046 1.0000000
## M:CERI-M:CYCL -5.420000e+01 -1306.7421  1198.3421 1.0000000
## H:NAUP-M:CYCL -1.313125e+02 -1383.8546  1121.2296 1.0000000
## L:NAUP-M:CYCL -1.307750e+02 -1383.3171  1121.7671 1.0000000
## M:NAUP-M:CYCL -1.310375e+02 -1383.5796  1121.5046 1.0000000
## H:DLUM-M:CYCL -1.316625e+02 -1384.2046  1120.8796 1.0000000
## L:DLUM-M:CYCL -1.308375e+02 -1383.3796  1121.7046 1.0000000
## M:DLUM-M:CYCL -1.316625e+02 -1384.2046  1120.8796 1.0000000
## H:CHYD-M:CYCL  4.957787e+03  3705.2454  6210.3296 0.0000000
## L:CHYD-M:CYCL  8.670875e+02  -385.4546  2119.6296 0.6564449
## M:CHYD-M:CYCL  2.500050e+03  1247.5079  3752.5921 0.0000000
## L:BOSM-H:BOSM -3.375000e-01 -1252.8796  1252.2046 1.0000000
## M:BOSM-H:BOSM  5.750000e-01 -1251.9671  1253.1171 1.0000000
## H:SIMO-H:BOSM  7.002500e+02  -552.2921  1952.7921 0.9374466
## L:SIMO-H:BOSM  1.599000e+02 -1092.6421  1412.4421 1.0000000
## M:SIMO-H:BOSM  4.636375e+02  -788.9046  1716.1796 0.9998087
## H:CERI-H:BOSM  1.352500e+02 -1117.2921  1387.7921 1.0000000
## L:CERI-H:BOSM  1.597875e+02 -1092.7546  1412.3296 1.0000000
## M:CERI-H:BOSM  7.642500e+01 -1176.1171  1328.9671 1.0000000
## H:NAUP-H:BOSM -6.875000e-01 -1253.2296  1251.8546 1.0000000
## L:NAUP-H:BOSM -1.500000e-01 -1252.6921  1252.3921 1.0000000
## M:NAUP-H:BOSM -4.125000e-01 -1252.9546  1252.1296 1.0000000
## H:DLUM-H:BOSM -1.037500e+00 -1253.5796  1251.5046 1.0000000
## L:DLUM-H:BOSM -2.125000e-01 -1252.7546  1252.3296 1.0000000
## M:DLUM-H:BOSM -1.037500e+00 -1253.5796  1251.5046 1.0000000
## H:CHYD-H:BOSM  5.088413e+03  3835.8704  6340.9546 0.0000000
## L:CHYD-H:BOSM  9.977125e+02  -254.8296  2250.2546 0.3578551
## M:CHYD-H:BOSM  2.630675e+03  1378.1329  3883.2171 0.0000000
## M:BOSM-L:BOSM  9.125000e-01 -1251.6296  1253.4546 1.0000000
## H:SIMO-L:BOSM  7.005875e+02  -551.9546  1953.1296 0.9371392
## L:SIMO-L:BOSM  1.602375e+02 -1092.3046  1412.7796 1.0000000
## M:SIMO-L:BOSM  4.639750e+02  -788.5671  1716.5171 0.9998062
## H:CERI-L:BOSM  1.355875e+02 -1116.9546  1388.1296 1.0000000
## L:CERI-L:BOSM  1.601250e+02 -1092.4171  1412.6671 1.0000000
## M:CERI-L:BOSM  7.676250e+01 -1175.7796  1329.3046 1.0000000
## H:NAUP-L:BOSM -3.500000e-01 -1252.8921  1252.1921 1.0000000
## L:NAUP-L:BOSM  1.875000e-01 -1252.3546  1252.7296 1.0000000
## M:NAUP-L:BOSM -7.500000e-02 -1252.6171  1252.4671 1.0000000
## H:DLUM-L:BOSM -7.000000e-01 -1253.2421  1251.8421 1.0000000
## L:DLUM-L:BOSM  1.250000e-01 -1252.4171  1252.6671 1.0000000
## M:DLUM-L:BOSM -7.000000e-01 -1253.2421  1251.8421 1.0000000
## H:CHYD-L:BOSM  5.088750e+03  3836.2079  6341.2921 0.0000000
## L:CHYD-L:BOSM  9.980500e+02  -254.4921  2250.5921 0.3571574
## M:CHYD-L:BOSM  2.631013e+03  1378.4704  3883.5546 0.0000000
## H:SIMO-M:BOSM  6.996750e+02  -552.8671  1952.2171 0.9379678
```

```
## L:SIMO-M:BOSM   1.593250e+02  -1093.2171   1411.8671 1.0000000
## M:SIMO-M:BOSM   4.630625e+02   -789.4796   1715.6046 0.9998128
## H:CERI-M:BOSM   1.346750e+02  -1117.8671   1387.2171 1.0000000
## L:CERI-M:BOSM   1.592125e+02  -1093.3296   1411.7546 1.0000000
## M:CERI-M:BOSM   7.585000e+01  -1176.6921   1328.3921 1.0000000
## H:NAUP-M:BOSM  -1.262500e+00  -1253.8046   1251.2796 1.0000000
## L:NAUP-M:BOSM  -7.250000e-01  -1253.2671   1251.8171 1.0000000
## M:NAUP-M:BOSM  -9.875000e-01  -1253.5296   1251.5546 1.0000000
## H:DLUM-M:BOSM  -1.612500e+00  -1254.1546   1250.9296 1.0000000
## L:DLUM-M:BOSM  -7.875000e-01  -1253.3296   1251.7546 1.0000000
## M:DLUM-M:BOSM  -1.612500e+00  -1254.1546   1250.9296 1.0000000
## H:CHYD-M:BOSM   5.087837e+03   3835.2954   6340.3796 0.0000000
## L:CHYD-M:BOSM   9.971375e+02   -255.4046   2249.6796 0.3590454
## M:CHYD-M:BOSM   2.630100e+03   1377.5579   3882.6421 0.0000000
## L:SIMO-H:SIMO  -5.403500e+02  -1792.8921    712.1921 0.9976775
## M:SIMO-H:SIMO  -2.366125e+02  -1489.1546   1015.9296 1.0000000
## H:CERI-H:SIMO  -5.650000e+02  -1817.5421    687.5421 0.9955265
## L:CERI-H:SIMO  -5.404625e+02  -1793.0046    712.0796 0.9976702
## M:CERI-H:SIMO  -6.238250e+02  -1876.3671    628.7171 0.9831272
## H:NAUP-H:SIMO  -7.009375e+02  -1953.4796    551.6046 0.9368194
## L:NAUP-H:SIMO  -7.004000e+02  -1952.9421    552.1421 0.9373101
## M:NAUP-H:SIMO  -7.006625e+02  -1953.2046    551.8796 0.9370708
## H:DLUM-H:SIMO  -7.012875e+02  -1953.8296    551.2546 0.9364984
## L:DLUM-H:SIMO  -7.004625e+02  -1953.0046    552.0796 0.9372532
## M:DLUM-H:SIMO  -7.012875e+02  -1953.8296    551.2546 0.9364984
## H:CHYD-H:SIMO   4.388163e+03   3135.6204   5640.7046 0.0000000
## L:CHYD-H:SIMO   2.974625e+02   -955.0796   1550.0046 1.0000000
## M:CHYD-H:SIMO   1.930425e+03    677.8829   3182.9671 0.0000100
## M:SIMO-L:SIMO   3.037375e+02   -948.8046   1556.2796 1.0000000
## H:CERI-L:SIMO  -2.465000e+01  -1277.1921   1227.8921 1.0000000
## L:CERI-L:SIMO  -1.125000e-01  -1252.6546   1252.4296 1.0000000
## M:CERI-L:SIMO  -8.347500e+01  -1336.0171   1169.0671 1.0000000
## H:NAUP-L:SIMO  -1.605875e+02  -1413.1296   1091.9546 1.0000000
## L:NAUP-L:SIMO  -1.600500e+02  -1412.5921   1092.4921 1.0000000
## M:NAUP-L:SIMO  -1.603125e+02  -1412.8546   1092.2296 1.0000000
## H:DLUM-L:SIMO  -1.609375e+02  -1413.4796   1091.6046 1.0000000
## L:DLUM-L:SIMO  -1.601125e+02  -1412.6546   1092.4296 1.0000000
## M:DLUM-L:SIMO  -1.609375e+02  -1413.4796   1091.6046 1.0000000
## H:CHYD-L:SIMO   4.928512e+03   3675.9704   6181.0546 0.0000000
## L:CHYD-L:SIMO   8.378125e+02   -414.7296   2090.3546 0.7216483
## M:CHYD-L:SIMO   2.470775e+03   1218.2329   3723.3171 0.0000000
## H:CERI-M:SIMO  -3.283875e+02  -1580.9296    924.1546 0.9999998
## L:CERI-M:SIMO  -3.038500e+02  -1556.3921    948.6921 1.0000000
## M:CERI-M:SIMO  -3.872125e+02  -1639.7546    865.3296 0.9999933
## H:NAUP-M:SIMO  -4.643250e+02  -1716.8671    788.2171 0.9998037
## L:NAUP-M:SIMO  -4.637875e+02  -1716.3296    788.7546 0.9998076
## M:NAUP-M:SIMO  -4.640500e+02  -1716.5921    788.4921 0.9998057
## H:DLUM-M:SIMO  -4.646750e+02  -1717.2171    787.8671 0.9998011
## L:DLUM-M:SIMO  -4.638500e+02  -1716.3921    788.6921 0.9998071
## M:DLUM-M:SIMO  -4.646750e+02  -1717.2171    787.8671 0.9998011
## H:CHYD-M:SIMO   4.624775e+03   3372.2329   5877.3171 0.0000000
## L:CHYD-M:SIMO   5.340750e+02   -718.4671   1786.6171 0.9980548
## M:CHYD-M:SIMO   2.167038e+03    914.4954   3419.5796 0.0000002
## L:CERI-H:CERI   2.453750e+01  -1228.0046   1277.0796 1.0000000
```

```
## M:CERI-H:CERI -5.882500e+01 -1311.3671  1193.7171 1.0000000
## H:NAUP-H:CERI -1.359375e+02 -1388.4796  1116.6046 1.0000000
## L:NAUP-H:CERI -1.354000e+02 -1387.9421  1117.1421 1.0000000
## M:NAUP-H:CERI -1.356625e+02 -1388.2046  1116.8796 1.0000000
## H:DLUM-H:CERI -1.362875e+02 -1388.8296  1116.2546 1.0000000
## L:DLUM-H:CERI -1.354625e+02 -1388.0046  1117.0796 1.0000000
## M:DLUM-H:CERI -1.362875e+02 -1388.8296  1116.2546 1.0000000
## H:CHYD-H:CERI  4.953163e+03  3700.6204  6205.7046 0.0000000
## L:CHYD-H:CERI  8.624625e+02  -390.0796  2115.0046 0.6670046
## M:CHYD-H:CERI  2.495425e+03  1242.8829  3747.9671 0.0000000
## M:CERI-L:CERI -8.336250e+01 -1335.9046  1169.1796 1.0000000
## H:NAUP-L:CERI -1.604750e+02 -1413.0171  1092.0671 1.0000000
## L:NAUP-L:CERI -1.599375e+02 -1412.4796  1092.6046 1.0000000
## M:NAUP-L:CERI -1.602000e+02 -1412.7421  1092.3421 1.0000000
## H:DLUM-L:CERI -1.608250e+02 -1413.3671  1091.7171 1.0000000
## L:DLUM-L:CERI -1.600000e+02 -1412.5421  1092.5421 1.0000000
## M:DLUM-L:CERI -1.608250e+02 -1413.3671  1091.7171 1.0000000
## H:CHYD-L:CERI  4.928625e+03  3676.0829  6181.1671 0.0000000
## L:CHYD-L:CERI  8.379250e+02  -414.6171  2090.4671 0.7214063
## M:CHYD-L:CERI  2.470887e+03  1218.3454  3723.4296 0.0000000
## H:NAUP-M:CERI -7.711250e+01 -1329.6546  1175.4296 1.0000000
## L:NAUP-M:CERI -7.657500e+01 -1329.1171  1175.9671 1.0000000
## M:NAUP-M:CERI -7.683750e+01 -1329.3796  1175.7046 1.0000000
## H:DLUM-M:CERI -7.746250e+01 -1330.0046  1175.0796 1.0000000
## L:DLUM-M:CERI -7.663750e+01 -1329.1796  1175.9046 1.0000000
## M:DLUM-M:CERI -7.746250e+01 -1330.0046  1175.0796 1.0000000
## H:CHYD-M:CERI  5.011988e+03  3759.4454  6264.5296 0.0000000
## L:CHYD-M:CERI  9.212875e+02  -331.2546  2173.8296 0.5293135
## M:CHYD-M:CERI  2.554250e+03  1301.7079  3806.7921 0.0000000
## L:NAUP-H:NAUP  5.375000e-01 -1252.0046  1253.0796 1.0000000
## M:NAUP-H:NAUP  2.750000e-01 -1252.2671  1252.8171 1.0000000
## H:DLUM-H:NAUP -3.500000e-01 -1252.8921  1252.1921 1.0000000
## L:DLUM-H:NAUP  4.750000e-01 -1252.0671  1253.0171 1.0000000
## M:DLUM-H:NAUP -3.500000e-01 -1252.8921  1252.1921 1.0000000
## H:CHYD-H:NAUP  5.089100e+03  3836.5579  6341.6421 0.0000000
## L:CHYD-H:NAUP  9.984000e+02  -254.1421  2250.9421 0.3564345
## M:CHYD-H:NAUP  2.631363e+03  1378.8204  3883.9046 0.0000000
## M:NAUP-L:NAUP -2.625000e-01 -1252.8046  1252.2796 1.0000000
## H:DLUM-L:NAUP -8.875000e-01 -1253.4296  1251.6546 1.0000000
## L:DLUM-L:NAUP -6.250000e-02 -1252.6046  1252.4796 1.0000000
## M:DLUM-L:NAUP -8.875000e-01 -1253.4296  1251.6546 1.0000000
## H:CHYD-L:NAUP  5.088562e+03  3836.0204  6341.1046 0.0000000
## L:CHYD-L:NAUP  9.978625e+02  -254.6796  2250.4046 0.3575449
## M:CHYD-L:NAUP  2.630825e+03  1378.2829  3883.3671 0.0000000
## H:DLUM-M:NAUP -6.250000e-01 -1253.1671  1251.9171 1.0000000
## L:DLUM-M:NAUP  2.000000e-01 -1252.3421  1252.7421 1.0000000
## M:DLUM-M:NAUP -6.250000e-01 -1253.1671  1251.9171 1.0000000
## H:CHYD-M:NAUP  5.088825e+03  3836.2829  6341.3671 0.0000000
## L:CHYD-M:NAUP  9.981250e+02  -254.4171  2250.6671 0.3570024
## M:CHYD-M:NAUP  2.631088e+03  1378.5454  3883.6296 0.0000000
## L:DLUM-H:DLUM  8.250000e-01 -1251.7171  1253.3671 1.0000000
## M:DLUM-H:DLUM  3.588241e-13 -1252.5421  1252.5421 1.0000000
## H:CHYD-H:DLUM  5.089450e+03  3836.9079  6341.9921 0.0000000
## L:CHYD-H:DLUM  9.987500e+02  -253.7921  2251.2921 0.3557123
```

```
## M:CHYD-H:DLUM  2.631713e+03  1379.1704  3884.2546 0.0000000
## M:DLUM-L:DLUM -8.250000e-01 -1253.3671  1251.7171 1.0000000
## H:CHYD-L:DLUM  5.088625e+03  3836.0829  6341.1671 0.0000000
## L:CHYD-L:DLUM  9.979250e+02  -254.6171  2250.4671 0.3574157
## M:CHYD-L:DLUM  2.630888e+03  1378.3454  3883.4296 0.0000000
## H:CHYD-M:DLUM  5.089450e+03  3836.9079  6341.9921 0.0000000
## L:CHYD-M:DLUM  9.987500e+02  -253.7921  2251.2921 0.3557123
## M:CHYD-M:DLUM  2.631713e+03  1379.1704  3884.2546 0.0000000
## L:CHYD-H:CHYD -4.090700e+03 -5343.2421 -2838.1579 0.0000000
## M:CHYD-H:CHYD -2.457737e+03 -3710.2796 -1205.1954 0.0000000
## M:CHYD-L:CHYD  1.632962e+03   380.4204  2885.5046 0.0006556
```

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 22nd, 2025 at 12:00 PM (noon)**.