

3. Worksheet: Basic R

Student Name; 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, 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.

```
getwd()

## [1] "/cloud/project/QB2025_Vaidya/Week1-RStudio"

setwd("/cloud/project/QB2025_Vaidya/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, θ , = $\pi/4$. (radians, a.k.a. 45°) and with hypotenuse length $\sqrt{2}$ (remember: $\sin(\theta) = \text{opposite}/\text{hypotenuse}$).
- 4) the log (base e) of your favorite number.

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

## [1] 125

r<-2
area<-pi*r^2
area

## [1] 12.56637

sin(45)

## [1] 0.8509035

hypotenuse <- sqrt(2)
opposite <- hypotenuse * sin(45 * pi /4)
opposite

## [1] -1

log10(1000)

## [1] 3
```

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(2,5,7,8,11)
w <- x*14
w

## [1] 28 70 98 112 154
```

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

```
## [1] 2 5 7 8 11
```

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(21,24,15,78,66)
k*x
```

```
## [1] 42 120 105 624 726
```

```
rm(w)
rm(k)
w<-c(28,70,112)
k<-c(21,24,78,66)
d<-c(w)[c(k)]
d
```

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

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)
maximum <- max(v, na.rm = TRUE)
maximum
```

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

```
minimum <- min(v, na.rm = TRUE)
minimum
```

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

```
sum(v, na.rm = TRUE)
```

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

```
mean(v, na.rm = TRUE)
```

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

```
median(v, na.rm = TRUE)
```

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

```
variance <- var(v, na.rm = TRUE)
variance
```

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

```
sd(v, na.rm = TRUE)
```

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

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

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

5) WORKING WITH MATRICES

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

```
column1 <- rnorm(5, mean = 8, sd = 2)
column2 <- rnorm(5, mean = 25, sd = 10)
my_matrix <- matrix(c(column1, column2), nrow = 5, ncol = 2)
my_matrix
```

```
##           [,1]      [,2]
## [1,]  6.320444 13.103556
## [2,]  9.437913 11.444591
## [3,]  7.404074  4.518692
## [4,]  7.127828 21.531344
## [5,]  7.886291 27.350258
```

This isn't code and it can be inside a code chunk as long as there is a # in front

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` `rnorm` function is used to create random numbers from a normal distribution for a specified mean and standard deviation. Arguments in this function like `n` specify the spread of random numbers (i.e. number of observations), `mean` specifies the mean of the data (vector of means), `sd` i.e. standard deviation specifies the standard deviation in adherence to which the random numbers generated. It also specifies vector of quantiles by typing `x`, `q` and vector of probabilities by typing `p`. `log`, `log.p` suggests that probabilities `p` are written as `log(p)`. Otherwise it also gives a range where lower.tail when true is written as $P[X < x]$ else the opposite holds true. Thus this allows `rnorm` allows one to control `sd` and `mean` while predicting the rest.

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.

```
setwd("/cloud/project/QB2025_Vaidya/Week1-RStudio/data")
data <- read.table("/cloud/project/QB2025_Vaidya/Week1-RStudio/data/matrix.txt")
data <- read.table("data/matrix.txt")
m <- as.matrix(read.table("/cloud/project/QB2025_Vaidya/Week1-RStudio/data/matrix.txt", sep = "\t", header = TRUE))
n <- t(m)
dim(n)
```

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

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

Answer 2: 5 10

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[, -3]
n <- m[1:4, ]
```

```
n<- c( m[1:4, ], m[ , -3])
n
```

```
## [1] 8 5 2 3 1 5 5 2 7 2 4 5 6 4 3 1 1 1 3 4 8 5 2 3 9
## [26] 11 2 3 5 6 1 5 5 2 9 8 2 3 5 5 6 4 3 1 1 8 8 7 3 2
## [51] 1 1 3 4 2 8 5 6 6 2
```

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("/cloud/project/QB2025_Vaidya/Week1-RStudio/data/zoop_nuts.txt" , sep = "\t" , header = TRUE)
str(meso)
```

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

```
##      TP      TN      SRP      TIN      CHLA      ZP
## 1  20.31  720.1  4.02  131.62  1.52  1.7808
## 2  25.55  750.5  1.56  141.10  4.00  0.4090
## 3  14.22  610.1  4.97  107.70  0.61  1.2014
## 4  39.11  760.9  2.89   71.28  0.53  3.3598
## 5  20.09  570.4  5.11   80.40  1.44  0.7332
## 6  15.75  680.5  4.68  135.77  1.19  0.9773
## 7  19.55  665.5  5.00   79.40  0.37  1.0999
## 8  16.19  660.8  0.10  100.91  0.72  2.2714
## 9  29.46 1770.4  7.90 1329.26  6.93  3.1633
## 10 37.88 2590.3  3.92 1163.64  0.94  1.8747
## 11 30.26 2110.9  4.45 1850.18  1.36  4.3802
## 12 36.94 2060.9  5.14  249.93 38.38  2.4051
## 13 34.73 1370.1  4.69  420.01 15.99  1.7079
## 14 26.00 2110.3  5.35 1466.70  0.95  4.0999
## 15 28.50 1760.4  7.15 1351.83  1.36  5.4430
## 16 35.33 1360.8  5.96 1036.27  2.13  4.2677
## 17 41.56 4130.1 20.34 3421.43  1.44  8.2084
## 18 53.50 4530.4 33.57 4042.10  0.93  4.2273
## 19 99.07 4410.9 11.57 3307.05  0.61  6.2381
## 20 128.04 4750.4 26.27 3686.17  1.27  8.5713
```

```
## 21 33.47 3410.4 9.32 2791.52 1.11 1.4240
## 22 52.41 3710.3 3.23 2890.73 17.59 2.9714
## 23 42.21 3690.4 12.71 3041.75 1.08 8.1509
## 24 77.65 4380.6 21.86 3041.75 1.08 8.3868
```

```
cor1 <- cor(meso.num)
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: Except for CHLA, All other groups have a positive pearson's correlation with each other. Of the groups, correlation of TN with TIN has a strong positive correlation of 0.969, suggesting the presence of TIN positively reinforces TN. CHLA is negatively correlated to all the other variables within the dataset.

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.

```
require(psych)
```

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

```
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
```

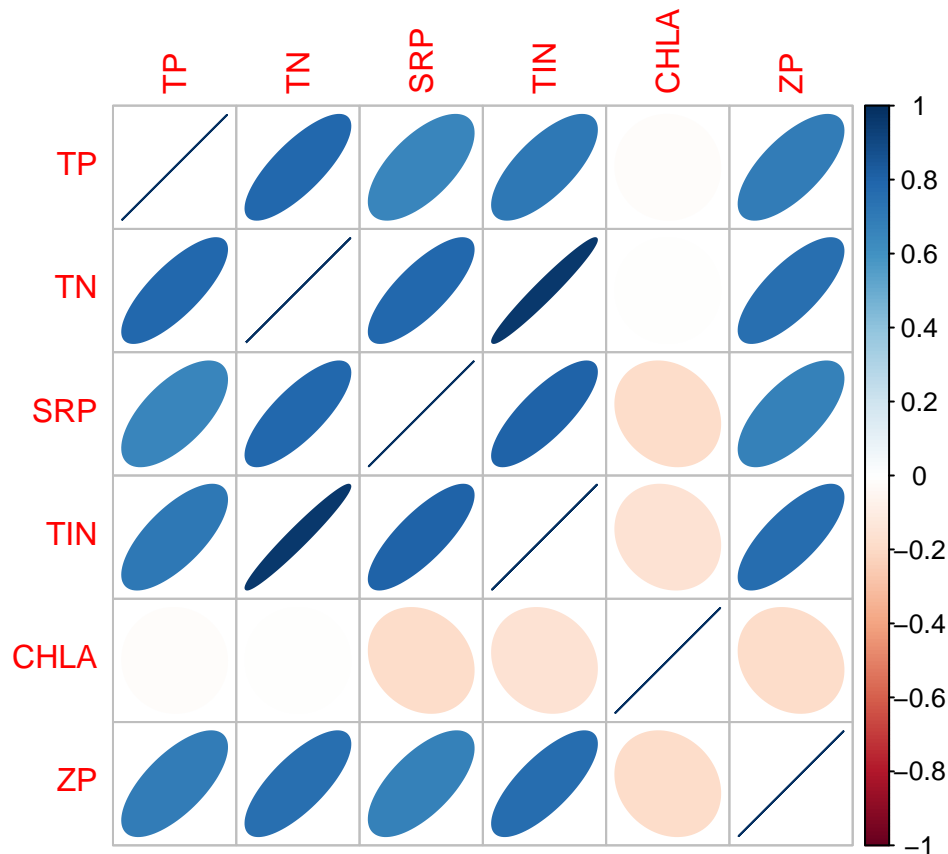
```

cor2 <- corr.test(meso.num, method = "spearman", adjust = "BH")
print(cor2, 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
require(corrplot)

## Loading required package: corrplot
## corrplot 0.95 loaded
corrplot(cor1, method = "ellipse")

```



```
dev.off()
```

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

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

Answer 4:1. Yes we can certainly see differences. Since spearman is a non-parametric test, it is far more stringent than the parametric test, thus the pearson test shows a stronger correlation with most variables than the spearman, as the spearman also considers any outliers unlike the pearson test that is less sensitive. p values between them are also different when comparing variables like TPN and SRP has a pvalue of 0.01 for spearman test while 0.001 for pearson's test. 2. If the data is normally distributed then pearson's test (parametric) would be more apt, while when the data are not normally distributed with the presence of significant outliers, then one will consider non-parametric test like spearman. False discovery rate strikes the right balance between the very stringent tests like Bonferroni that sometimes prevents true detectable difference and also prevents the other extreme Type I errors which are created due to false detection of a significant difference as a result of many variables being tested at the same time. False discovery rate limits Type I error while preventing a true significant difference from being unnoticed.

Linear Regression

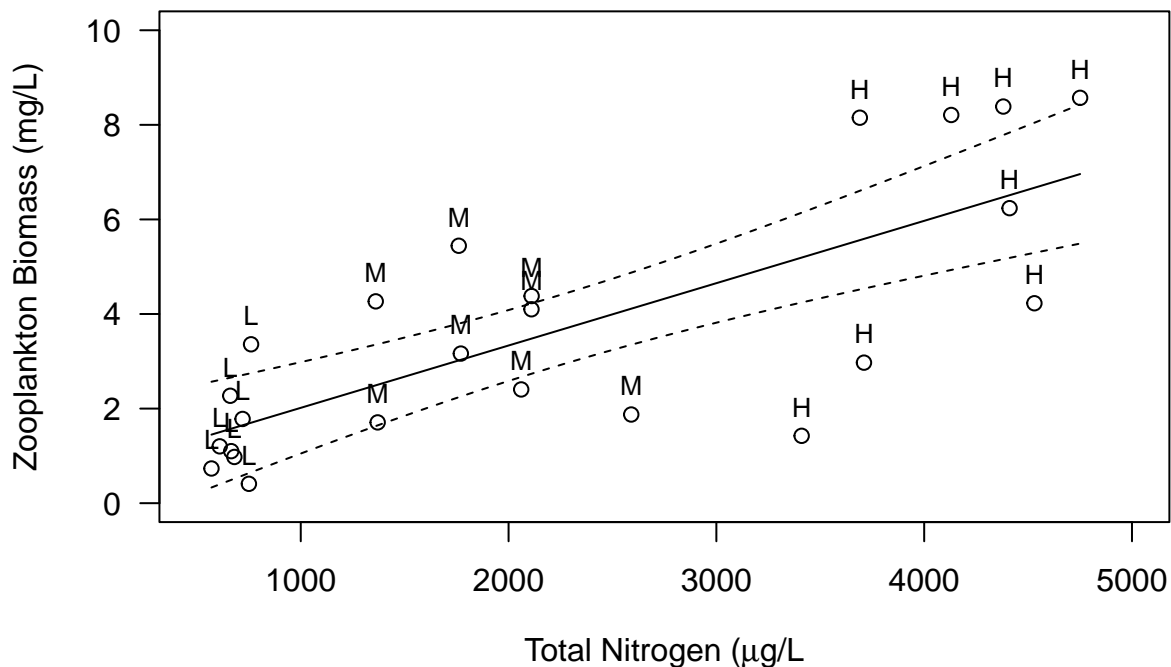
In the R code chunk below, do the following: 1) Conduct a linear regression analysis to test the relationship between total nitrogen (TN) and zooplankton biomass (ZP). 2) Examine the output of the regression analysis. 3) Produce a plot of this regression analysis including the following: categorically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

regression line with 95% confidence intervals, and the appropriate axis labels.

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

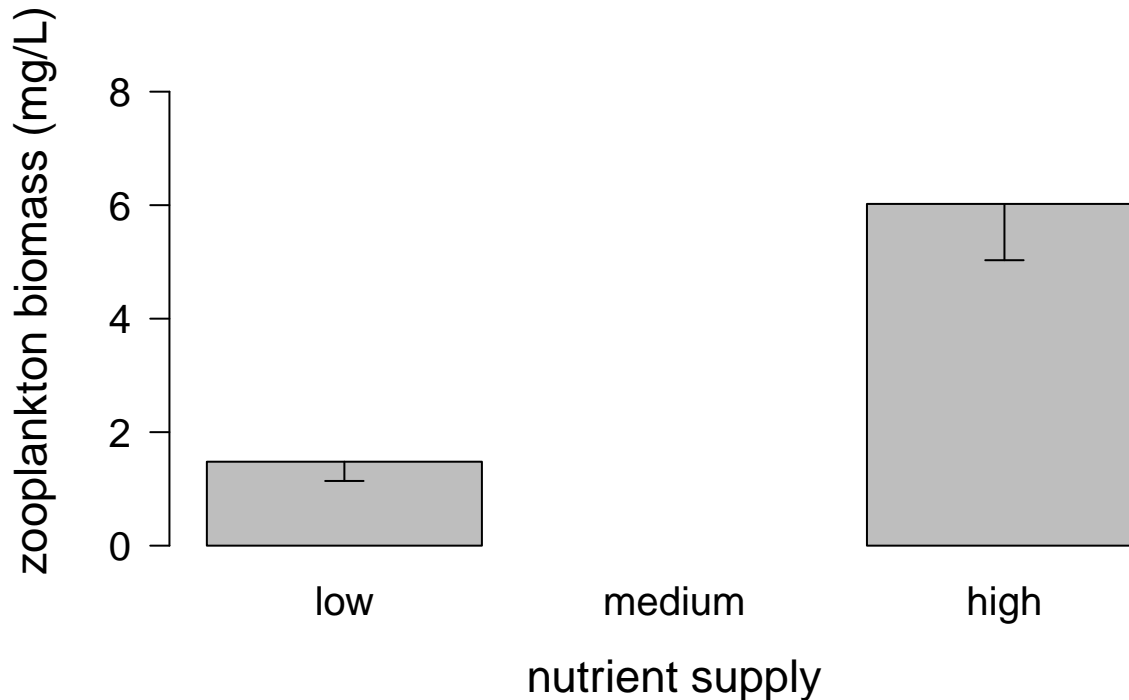
##
## Call:
## lm(formula = ZP ~ TN, data = meso)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.7690 -0.8491 -0.0709  1.6238  2.5888
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.6977712  0.6496312   1.074   0.294
## TN           0.0013181  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 (",
text(meso$TN, meso$ZP, meso$NUTS, pos = 3, cex = 0.8)
newTN <- seq(min(meso$TN), max(meso$TN), 10)
regline <- predict(fitreg, newdata = data.frame(TN = newTN))
lines(newTN, regline)
conf95 <- predict(fitreg, newdata = data.frame(TN = newTN), interval = c("confidence"), level = 0.95,
matlines(newTN, conf95[, c("lwr", "upr")], type = "l", lty = 2, lwd = 1, col = "black")
```



```
NUTS <- factor(meso$NUTS, levels = c('L', 'M', 'H'))
zp.means <- tapply(meso$ZP, NUTS, mean)
```

```
sem <- function(x){sd(na.omit(x))/sqrt(length(na.omit(x)))}
zp.sem <- tapply(meso$ZP, NUTS, sem)
bp <- barplot(zp.means, ylim = c(0, round(max(meso$ZP), digits = 0)), pch = 15, cex = 1.25, las = 1, cex.lab = 1.5)
arrows(x0 = bp, y0 = zp.means, y1 = zp.means - zp.sem, angle = 90, length = 0.1, lwd = 1)
```



```
zoops <- read.table("/cloud/project/QB2025_Vaidya/Week1-RStudio/data/zoops.txt", header = TRUE, sep = "\t", as.is = TRUE)
```

```
## 'data.frame': 24 obs. of 11 variables:
## $ TANK: int 5 14 16 21 23 25 27 34 12 15 ...
## $ NUTS: chr "L" "L" "L" "L" ...
## $ 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 ...
## $ 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 ...
```

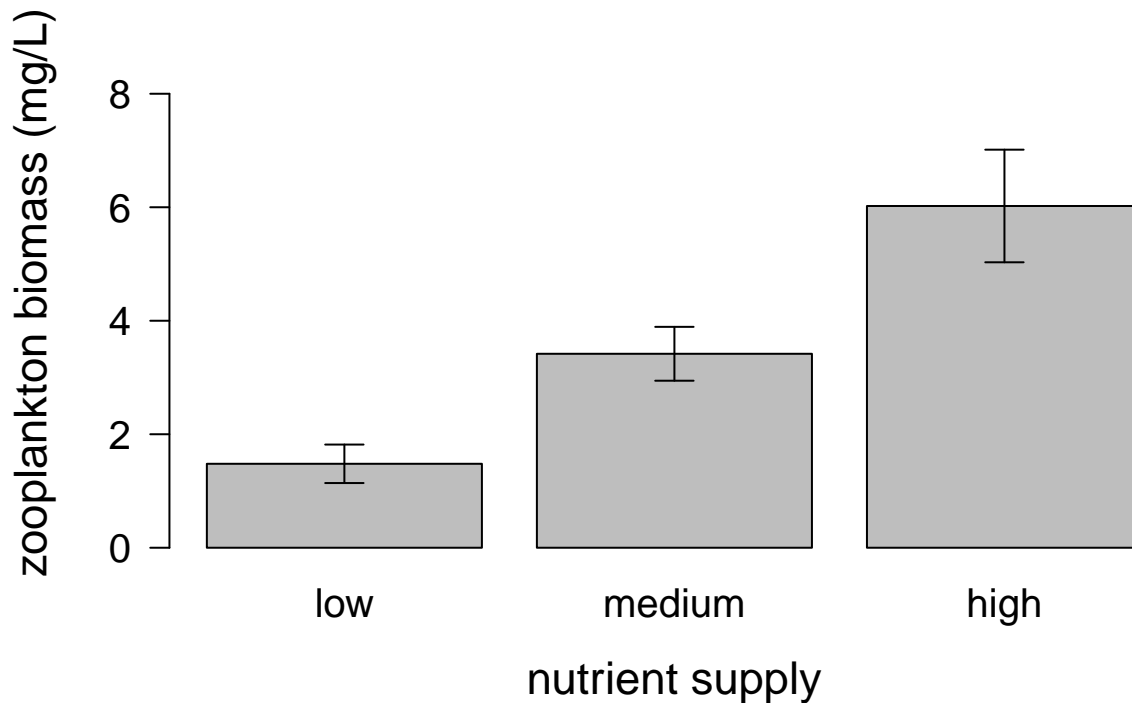
Question 5: Interpret the results from the regression model

Answer 5: Although the regression line roughly follows a straight line, the points are scattered along the fitted regression line, making it a weak relationship. Since the direction of the slope is upwards, i.e. an increase in x increases y, it is a weak positive relationship. Also since some points lie outside the confidence intervals, it suggests greater uncertainty in predictions. Also since the residuals and the points closely follow the reference line and fitted line respectively, the data does follow a normal distribution with a few outliers. Many of these outliers could indicate that they disproportionately influence the model.

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.

```
zoops <- read.table("/cloud/project/QB2025_Vaidya/Week1-RStudio/data/zoops.txt", header = TRUE, sep = "\t")
NUTS <- factor(meso$NUTS, levels = c('L', 'M', 'H'))
zp.means <- tapply(meso$ZP, NUTS, mean)
sem <- function(x){sd(na.omit(x))/sqrt(length(na.omit(x)))}
zp.sem <- tapply(meso$ZP, NUTS, sem)
bp<-barplot(zp.means, ylim = c(0, round(max(meso$ZP), digits = 0)), pch =15, cex = 1.25, las =1, cex.lab=1.5)
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)
```



```
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
```

```
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 ($\mu\text{g/L}$) of different zooplankton taxa:

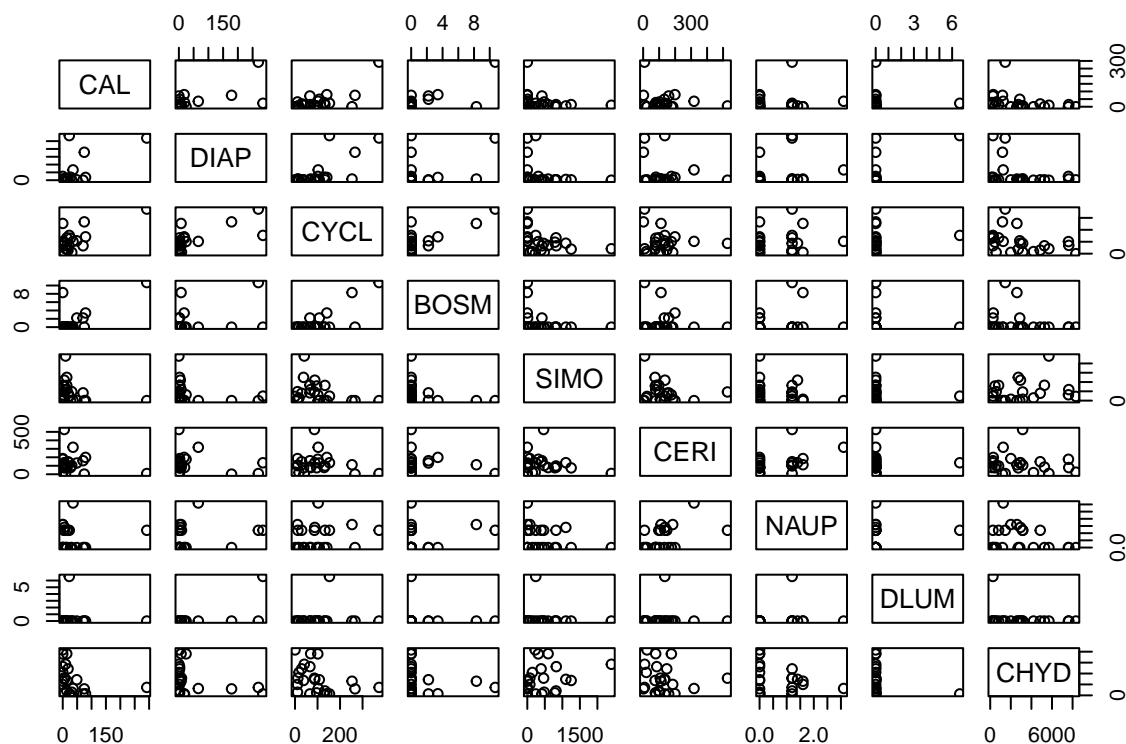
- CAL = calanoid copepods
- DIAP = *Diaphanasoma* sp.
- CYL = cyclopoid copepods
- BOSM = *Bosmina* sp.
- SIMO = *Simocephallus* sp.
- CERI = *Ceriodaphnia* sp.
- NAUP = naupuli (immature copepod)
- DLUM = *Daphnia lumholtzi*
- CHYD = *Chydorus* sp.

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.

```
zoops <- read.table("/cloud/project/QB2025_Vaidya/Week1-RStudio/data/zoops.txt", header = TRUE, sep = "
str(zoops)
```

```
## 'data.frame': 24 obs. of 11 variables:
## $ TANK: int 5 14 16 21 23 25 27 34 12 15 ...
## $ NUTS: chr "L" "L" "L" "L" ...
## $ 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 ...
```

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

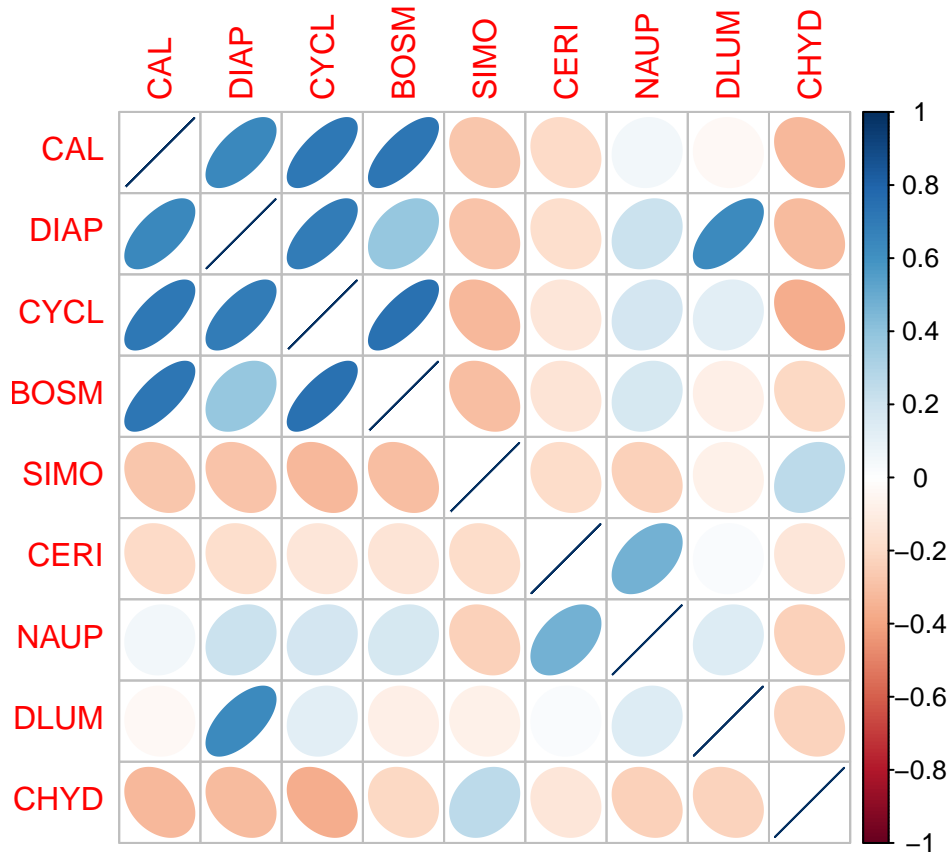


```
cor1<- cor(zoops.num)
require("psych")
cor2 <- corr.test(zoops.num, method = "pearson", adjust = "BH")
print(cor2,digits = 3)
```

```
## 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
```

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

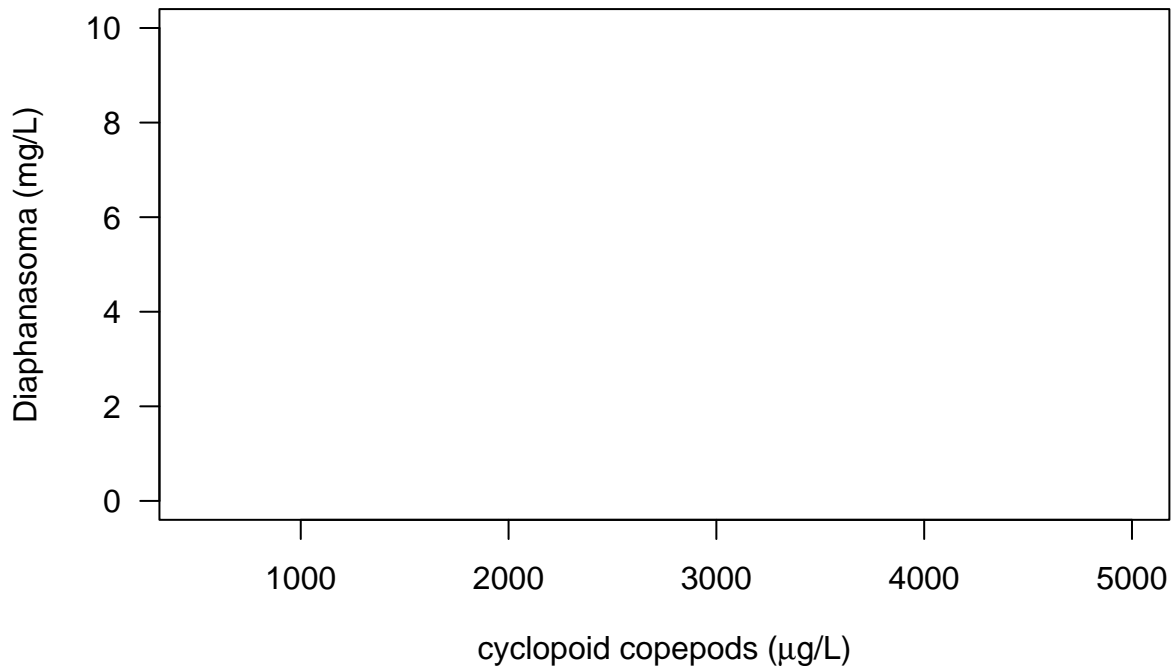


```
fitreg<- lm(CYCL ~ DIAP, data = zoops)
summary(fitreg)
```

```
##
## Call:
## lm(formula = CYCL ~ DIAP, data = zoops)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -134.737  -45.850   -5.788   37.352  176.485
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   71.0134    15.0127   4.730 0.000101 ***
## DIAP           0.7602     0.1680   4.526 0.000167 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 66.64 on 22 degrees of freedom
## Multiple R-squared:  0.4821, Adjusted R-squared:  0.4586
## F-statistic: 20.48 on 1 and 22 DF,  p-value: 0.000167
```

#The above linear regression helps to figure that there is a strong positive correlation between CYCL
#Next, we will be looking at ANOVA to check if individual taxa have an effect on the biomass.

```
plot(zoops$DIAP, zoops$CYCL, ylim = c(0,10), xlim = c(500,5000), xlab = expression(paste("cyclopoid cope", "pods (µg/L)")), ylab = expression(paste("Diaphanasoma (mg/L)")),
text(zoops$DIAP, zoops$CYCL, zoops$NAUP, pos=3, cex = 0.8)
newDIAP<- seq(min(zoops$DIAP), max(zoops$DIAP), 10)
regline <- predict(fitreg, newdata = data.frame(DIAP = newDIAP))
lines(newDIAP, regline)
# Since the data is lined along the regression line for Normal Q-Q plots, it suggests that the data of
conf95 <- predict(fitreg, newdata =data.frame (DIAP = newDIAP), interval = c("confidence"), level = 0.95)
matlines(newDIAP, conf95[, c("lwr", "upr")], type = "l", lty = 2, lwd = 1, col = "black")
```



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

sem <- function(x) {sd(na.omit(x)) / sqrt(length(na.omit(x)))}
#since tapply is used only when calculating means after grouping, this case without the use of NUTS or
species_data <- zoops[, c("CAL", "DIAP", "CYCL", "BOSM", "SIMO", "CERI", "NAUP", "DLUM", "CHYD")]
species_means <- apply(species_data, 2, mean, na.rm = TRUE)
species_means
```

```
##          CAL          DIAP          CYCL          BOSM          SIMO          CERI
## 32.2291667 37.8250000 99.7666667 1.1166667 442.3000000 124.8583333
##          NAUP          DLUM          CHYD
## 0.6208333 0.2750000 2906.6375000
```

```
sem <- function(x) {sd(na.omit(x)) / sqrt(length(na.omit(x)))}
species_sem <- apply(species_data, 2, sem)
species_sem
```

```
##          CAL          DIAP          CYCL          BOSM          SIMO          CERI
## 12.3503557 16.8858006 18.4860941 0.5625597 113.9905815 22.8856965
##          NAUP          DLUM          CHYD
```

```
## 0.1706742 0.2750000 513.1769982
```

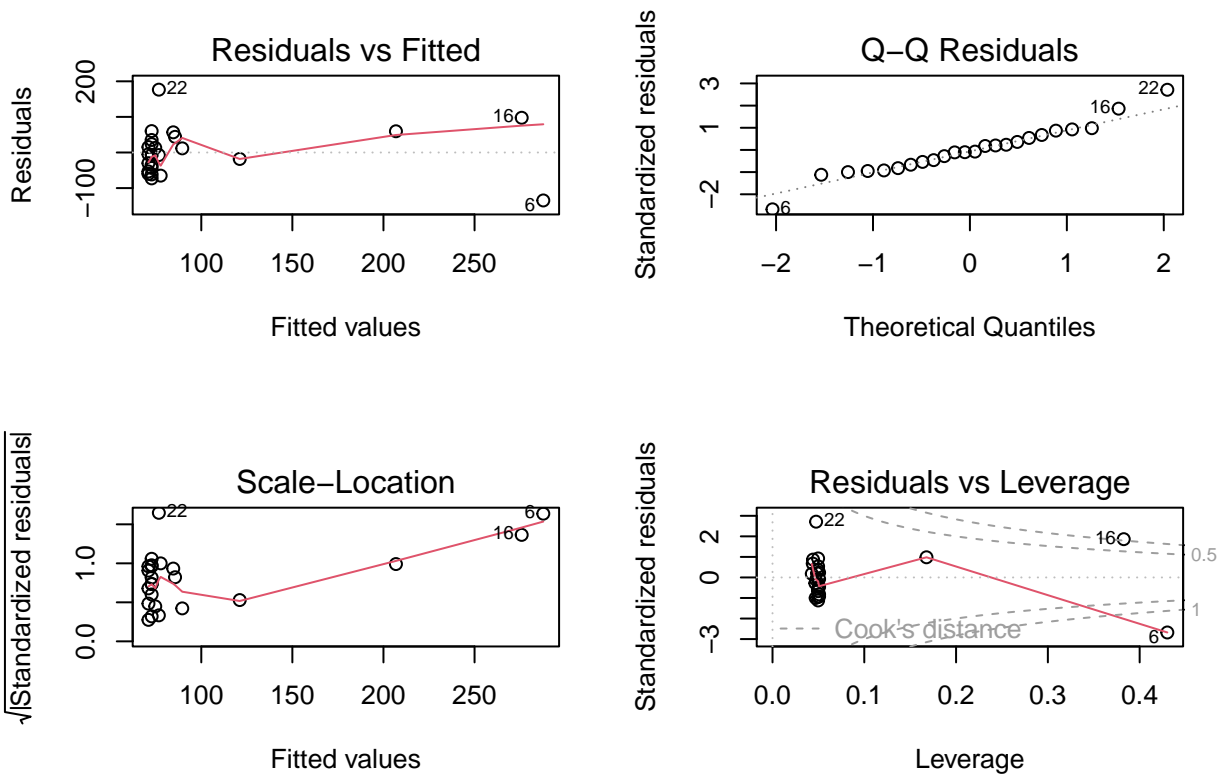
```
site_species_matrix <- zoops[, c("CAL", "DIAP", "CYCL", "BOSM", "SIMO", "CERI", "NAUP", "DLUM", "CHYD")]
site_species_matrix
```

```
##      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
```

```
species_sd <- apply(site_species_matrix, 2, sd, na.rm = TRUE)
species_sd
```

```
##      CAL      DIAP      CYCL      BOSM      SIMO      CERI
## 60.5041391 82.7231908 90.5629959 2.7559685 558.4375205 112.1165578
##      NAUP      DLUM      CHYD
## 0.8361294 1.3472194 2514.0435868
```

```
arrows(x0 = bp, y0 = species_means, y1 = species_means - species_sem, angle = 90, length = 0.1, lwd = 1)
arrows(x0 = bp, y0 = species_means, y1 = species_means + species_sem, angle = 90, length = 0.1, lwd = 1)
```

```
results <- list()
for (i in 1:ncol(site_species_matrix)){
  for (j in 1:ncol(site_species_matrix)){
    if (i != j){
      species_x <- colnames(site_species_matrix)[i]
      species_y <- colnames(site_species_matrix)[j]
      fit <- lm(site_species_matrix[, i] ~ site_species_matrix[, j])
      results[[paste(species_x, "vs", species_y, sep = "_")]] <- summary(fit)}}
results
```

```
## $CAL_vs_DIAP
```

```
##
```

```
## Call:
```

```
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
```

```
##
```

```
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -125.749  -15.532   -9.438    3.057  150.883
```

```
##
```

```
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      14.4514    10.6789   1.353 0.189715
## site_species_matrix[, j]  0.4700     0.1195   3.934 0.000709 ***
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Residual standard error: 47.4 on 22 degrees of freedom
```

```
## Multiple R-squared:  0.4129, Adjusted R-squared:  0.3862
```

```
## F-statistic: 15.47 on 1 and 22 DF, p-value: 0.0007087
```

```
##
##
## $CAL_vs_CYCL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -105.204  -22.236    3.677   14.666  129.627
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -15.2211    13.3508  -1.140   0.267
## site_species_matrix[, j]    0.4756     0.1000   4.755 9.56e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 43.45 on 22 degrees of freedom
## Multiple R-squared:  0.5068, Adjusted R-squared:  0.4844
## F-statistic: 22.61 on 1 and 22 DF,  p-value: 9.559e-05
##
##
## $CAL_vs_BOSM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -147.052  -10.405   -0.563   11.035  106.585
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)     14.380     9.368   1.535   0.139
## site_species_matrix[, j]    15.985     3.208   4.982 5.5e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 42.41 on 22 degrees of freedom
## Multiple R-squared:  0.5301, Adjusted R-squared:  0.5088
## F-statistic: 24.82 on 1 and 22 DF,  p-value: 5.502e-05
##
##
## $CAL_vs_SIMO
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
```

Min	1Q	Median	3Q	Max

```

## -45.238 -28.680 -14.509 4.263 246.762
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      45.23755    15.63349   2.894  0.00843 **
## site_species_matrix[, j] -0.02941     0.02223  -1.323  0.19945
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 59.54 on 22 degrees of freedom
## Multiple R-squared:  0.07369,    Adjusted R-squared:  0.03158
## F-statistic: 1.75 on 1 and 22 DF,  p-value: 0.1995
##
##
## $CAL_vs_CERI
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -43.08 -29.52 -22.00  15.32 247.76
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      45.1124    18.7739   2.403   0.0251 *
## site_species_matrix[, j] -0.1032     0.1129  -0.914   0.3708
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 60.72 on 22 degrees of freedom
## Multiple R-squared:  0.03656,    Adjusted R-squared: -0.007234
## F-statistic: 0.8348 on 1 and 22 DF,  p-value: 0.3708
##
##
## $CAL_vs_NAUP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -36.316 -29.638 -18.092  -1.463 257.353
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      29.638     15.823   1.873   0.0744 .
## site_species_matrix[, j]  4.174     15.402   0.271   0.7889
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 61.76 on 22 degrees of freedom

```

```

## Multiple R-squared:  0.003327,  Adjusted R-squared:  -0.04198
## F-statistic: 0.07344 on 1 and 22 DF,  p-value: 0.7889
##
##
## $CAL_vs_DLUM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -32.643 -28.668 -18.643   0.764 259.357
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      32.643     12.892   2.532   0.019 *
## site_species_matrix[, j]  -1.507      9.570  -0.157   0.876
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 61.83 on 22 degrees of freedom
## Multiple R-squared:  0.001125,  Adjusted R-squared:  -0.04428
## F-statistic: 0.02479 on 1 and 22 DF,  p-value: 0.8763
##
##
## $CAL_vs_CHYD
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -45.85 -26.47 -16.41  11.35 248.55
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    54.732962   18.503166   2.958  0.00727 **
## site_species_matrix[, j] -0.007742    0.004858  -1.594  0.12529
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 58.58 on 22 degrees of freedom
## Multiple R-squared:  0.1035, Adjusted R-squared:  0.06274
## F-statistic:  2.54 on 1 and 22 DF,  p-value: 0.1253
##
##
## $DIAP_vs_CAL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##

```

```

## Residuals:
##      Min       1Q   Median       3Q      Max
## -71.449 -19.509 -10.687  -4.526 255.647
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      9.5090     15.0603   0.631 0.534288
## site_species_matrix[, j]  0.8786      0.2233   3.934 0.000709 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 64.81 on 22 degrees of freedom
## Multiple R-squared:  0.4129, Adjusted R-squared:  0.3862
## F-statistic: 15.47 on 1 and 22 DF,  p-value: 0.0007087
##
##
## $DIAP_vs_CYCL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -127.640 -30.231  -5.872   22.103  213.512
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -25.4521     18.7045  -1.361 0.187371
## site_species_matrix[, j]  0.6343      0.1401   4.526 0.000167 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 60.87 on 22 degrees of freedom
## Multiple R-squared:  0.4821, Adjusted R-squared:  0.4586
## F-statistic: 20.48 on 1 and 22 DF,  p-value: 0.000167
##
##
## $DIAP_vs_BOSM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -112.49  -25.05  -22.75  -13.65   260.05
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)     25.053     17.276   1.450  0.1611
## site_species_matrix[, j]  11.438      5.917   1.933  0.0662 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

##
## Residual standard error: 78.2 on 22 degrees of freedom
## Multiple R-squared:  0.1452, Adjusted R-squared:  0.1064
## F-statistic: 3.737 on 1 and 22 DF,  p-value: 0.06619
##
##
## $DIAP_vs_SIMO
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -53.917 -40.323 -30.009  -4.076  238.752
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      56.59869     21.27728   2.660   0.0143 *
## site_species_matrix[, j] -0.04245     0.03026  -1.403   0.1746
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 81.04 on 22 degrees of freedom
## Multiple R-squared:  0.0821, Adjusted R-squared:  0.04038
## F-statistic: 1.968 on 1 and 22 DF,  p-value: 0.1746
##
##
## $DIAP_vs_CERI
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -52.506 -40.621 -32.290  -9.585  248.628
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      53.7008     25.7595   2.085   0.0489 *
## site_species_matrix[, j] -0.1272     0.1550  -0.821   0.4207
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 83.32 on 22 degrees of freedom
## Multiple R-squared:  0.0297, Adjusted R-squared: -0.01441
## F-statistic: 0.6733 on 1 and 22 DF,  p-value: 0.4207
##
##
## $DIAP_vs_NAUP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,

```

```

##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -56.52 -43.07 -23.36 -14.41  234.85
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)       24.51      21.15   1.159   0.259
## site_species_matrix[, j]    21.45      20.59   1.041   0.309
##
## Residual standard error: 82.57 on 22 degrees of freedom
## Multiple R-squared:  0.04699,    Adjusted R-squared:  0.003668
## F-statistic: 1.085 on 1 and 22 DF,  p-value: 0.309
##
##
## $DIAP_vs_DLUM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -27.074 -24.774 -24.774  -8.849  242.426
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)       27.07      13.60   1.991 0.059074 .
## site_species_matrix[, j]    39.09      10.09   3.873 0.000822 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 65.22 on 22 degrees of freedom
## Multiple R-squared:  0.4054, Adjusted R-squared:  0.3784
## F-statistic: 15 on 1 and 22 DF,  p-value: 0.0008221
##
##
## $DIAP_vs_CHYD
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -65.06 -45.33 -29.51  12.92  219.99
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    67.814297  25.370983   2.673   0.0139 *
## site_species_matrix[, j] -0.010318   0.006661  -1.549   0.1357
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

##
## Residual standard error: 80.32 on 22 degrees of freedom
## Multiple R-squared:  0.09832,    Adjusted R-squared:  0.05733
## F-statistic: 2.399 on 1 and 22 DF,  p-value: 0.1357
##
##
## $CYCL_vs_CAL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -87.883 -49.399  -5.845   27.671  187.776
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      65.4240     15.1121   4.329  0.00027 ***
## site_species_matrix[, j]   1.0656      0.2241   4.755 9.56e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 65.03 on 22 degrees of freedom
## Multiple R-squared:  0.5068, Adjusted R-squared:  0.4844
## F-statistic: 22.61 on 1 and 22 DF,  p-value: 9.559e-05
##
##
## $CYCL_vs_DIAP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -134.737  -45.850   -5.788   37.352  176.485
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      71.0134     15.0127   4.730 0.000101 ***
## site_species_matrix[, j]   0.7602      0.1680   4.526 0.000167 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 66.64 on 22 degrees of freedom
## Multiple R-squared:  0.4821, Adjusted R-squared:  0.4586
## F-statistic: 20.48 on 1 and 22 DF,  p-value: 0.000167
##
##
## $CYCL_vs_BOSM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,

```



```

##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -72.37 -45.89 -10.38  29.26 194.13
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)       72.37      13.61   5.318 2.45e-05 ***
## site_species_matrix[, j]    24.54       4.66   5.265 2.78e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 61.59 on 22 degrees of freedom
## Multiple R-squared:  0.5575, Adjusted R-squared:  0.5374
## F-statistic: 27.72 on 1 and 22 DF,  p-value: 2.778e-05
##
##
## $CYCL_vs_SIMO
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -111.19 -44.45 -12.87  27.64 250.34
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    123.06250   22.99523   5.352 2.26e-05 ***
## site_species_matrix[, j] -0.05267    0.03270  -1.611   0.122
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 87.58 on 22 degrees of freedom
## Multiple R-squared:  0.1055, Adjusted R-squared:  0.06482
## F-statistic: 2.594 on 1 and 22 DF,  p-value: 0.1215
##
##
## $CYCL_vs_CERI
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -110.501 -68.702  -9.726  29.647 261.212
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    113.0955    28.3779   3.985 0.000625 ***
## site_species_matrix[, j]  -0.1068     0.1707  -0.625 0.538168

```

```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 91.79 on 22 degrees of freedom
## Multiple R-squared:  0.01747,    Adjusted R-squared:  -0.02719
## F-statistic: 0.3911 on 1 and 22 DF,  p-value: 0.5382
##
##
## $CYCL_vs_NAUP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -108.45  -54.59  -21.19   26.52  261.99
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         87.29      23.31   3.744  0.00112 **
## site_species_matrix[, j]    20.10      22.69   0.886  0.38526
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 90.99 on 22 degrees of freedom
## Multiple R-squared:  0.03444,    Adjusted R-squared:  -0.009445
## F-statistic: 0.7848 on 1 and 22 DF,  p-value: 0.3853
##
##
## $CYCL_vs_DLUM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
##  -97.45  -61.83  -10.45   15.87  275.95
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)       97.452      19.156   5.087 4.27e-05 ***
## site_species_matrix[, j]    8.416      14.219   0.592    0.56
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 91.87 on 22 degrees of freedom
## Multiple R-squared:  0.01568,    Adjusted R-squared:  -0.02907
## F-statistic: 0.3504 on 1 and 22 DF,  p-value: 0.5599
##
##
## $CYCL_vs_CHYD
##

```

```

## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -119.65  -49.47  -10.95   10.24  254.39
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    138.35377    27.19180     5.088 4.26e-05 ***
## site_species_matrix[, j]  -0.01328     0.00714    -1.859  0.0764 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 86.08 on 22 degrees of freedom
## Multiple R-squared:  0.1358, Adjusted R-squared:  0.09653
## F-statistic: 3.458 on 1 and 22 DF,  p-value: 0.07639
##
##
## $BOSM_vs_CAL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
##  -2.5285  -0.5486  -0.2236  -0.0478   8.2522
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)     0.047788    0.448877     0.106   0.916
## site_species_matrix[, j] 0.033165    0.006657     4.982 5.5e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.932 on 22 degrees of freedom
## Multiple R-squared:  0.5301, Adjusted R-squared:  0.5088
## F-statistic: 24.82 on 1 and 22 DF,  p-value: 5.502e-05
##
##
## $BOSM_vs_DIAP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
##  -4.2559  -0.7358  -0.6657  -0.6365   7.5683
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)

```

```

## (Intercept)          0.636474    0.586956    1.084    0.2899
## site_species_matrix[, j] 0.012695    0.006567    1.933    0.0662 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.605 on 22 degrees of freedom
## Multiple R-squared:  0.1452, Adjusted R-squared:  0.1064
## F-statistic: 3.737 on 1 and 22 DF,  p-value: 0.06619
##
##
## $BOSM_vs_CYCL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.9053 -1.0640  0.2550  0.9004  3.6969
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -1.150326    0.575993  -1.997   0.0583 .
## site_species_matrix[, j]  0.022723    0.004316   5.265 2.78e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.874 on 22 degrees of freedom
## Multiple R-squared:  0.5575, Adjusted R-squared:  0.5374
## F-statistic: 27.72 on 1 and 22 DF,  p-value: 2.778e-05
##
##
## $BOSM_vs_SIMO
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7897 -1.4771 -0.9709  0.1920  8.9103
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)     1.789722    0.703837   2.543   0.0185 *
## site_species_matrix[, j] -0.001522    0.001001  -1.520   0.1427
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.681 on 22 degrees of freedom
## Multiple R-squared:  0.09508, Adjusted R-squared:  0.05394
## F-statistic: 2.311 on 1 and 22 DF,  p-value: 0.1427
##
##

```

```

## $BOSM_vs_CERI
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.544 -1.279 -1.128 -0.262  9.179
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.550574   0.862475   1.798  0.0859 .
## site_species_matrix[, j] -0.003475   0.005188  -0.670  0.5099
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.79 on 22 degrees of freedom
## Multiple R-squared:  0.01999,    Adjusted R-squared:  -0.02456
## F-statistic: 0.4487 on 1 and 22 DF,  p-value: 0.5099
##
##
## $BOSM_vs_NAUP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.5786 -1.4582 -0.7506 -0.7506  9.2418
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.7506   0.7103   1.057  0.302
## site_species_matrix[, j]  0.5897   0.6914   0.853  0.403
##
## Residual standard error: 2.772 on 22 degrees of freedom
## Multiple R-squared:  0.03201,    Adjusted R-squared:  -0.01199
## F-statistic: 0.7274 on 1 and 22 DF,  p-value: 0.4029
##
##
## $BOSM_vs_DLUM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.1652 -1.1652 -1.1652 -0.8739  9.5348
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)

```

```

## (Intercept)          1.1652      0.5854   1.991   0.0591 .
## site_species_matrix[, j] -0.1765      0.4345  -0.406   0.6884
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.807 on 22 degrees of freedom
## Multiple R-squared:  0.007448,   Adjusted R-squared:  -0.03767
## F-statistic: 0.1651 on 1 and 22 DF,  p-value: 0.6884
##
##
## $BOSM_vs_CHYD
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7379 -1.4927 -0.9419 -0.0098  9.2556
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.7737504   0.8710067    2.036   0.0539 .
## site_species_matrix[, j] -0.0002261   0.0002287   -0.988   0.3337
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.757 on 22 degrees of freedom
## Multiple R-squared:  0.04253,   Adjusted R-squared:  -0.0009953
## F-statistic: 0.9771 on 1 and 22 DF,  p-value: 0.3337
##
##
## $SIMO_vs_CAL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -523.0 -381.3 -146.3  225.6 1899.0
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      523.049   127.708    4.096 0.000478 ***
## site_species_matrix[, j]   -2.505     1.894   -1.323 0.199454
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 549.5 on 22 degrees of freedom
## Multiple R-squared:  0.07369,   Adjusted R-squared:  0.03158
## F-statistic:  1.75 on 1 and 22 DF,  p-value: 0.1995
##
##

```

```

## $SIMO_vs_DIAP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -502.0 -397.3 -107.4  276.1 1882.3
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      515.465     123.246   4.182 0.000386 ***
## site_species_matrix[, j]   -1.934       1.379  -1.403 0.174633
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 547 on 22 degrees of freedom
## Multiple R-squared:  0.0821, Adjusted R-squared:  0.04038
## F-statistic: 1.968 on 1 and 22 DF,  p-value: 0.1746
##
##
## $SIMO_vs_CYCL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -547.0 -391.1 -117.1  158.5 1838.0
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      642.100     165.951   3.869 0.000829 ***
## site_species_matrix[, j]   -2.003       1.243  -1.611 0.121512
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 540 on 22 degrees of freedom
## Multiple R-squared:  0.1055, Adjusted R-squared:  0.06482
## F-statistic: 2.594 on 1 and 22 DF,  p-value: 0.1215
##
##
## $SIMO_vs_BOSM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -512.07 -365.90  -82.22  185.98 1885.73
##

```

```

## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      512.07    120.00   4.267 0.000314 ***
## site_species_matrix[, j]   -62.48     41.10  -1.520 0.142670
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 543.2 on 22 degrees of freedom
## Multiple R-squared:  0.09508,    Adjusted R-squared:  0.05394
## F-statistic: 2.311 on 1 and 22 DF,  p-value: 0.1427
##
##
## $SIMO_vs_CERI
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -554.1  -386.9  -136.4   312.4  1850.5
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      555.8271    173.5687   3.202  0.00411 **
## site_species_matrix[, j]   -0.9092     1.0441  -0.871  0.39323
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 561.4 on 22 degrees of freedom
## Multiple R-squared:  0.03332,    Adjusted R-squared:  -0.01062
## F-statistic: 0.7584 on 1 and 22 DF,  p-value: 0.3932
##
##
## $SIMO_vs_NAUP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -540.5  -323.9  -115.9   147.9  1857.3
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      540.5      142.1   3.803 0.000974 ***
## site_species_matrix[, j]   -158.1     138.3  -1.143 0.265264
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 554.7 on 22 degrees of freedom
## Multiple R-squared:  0.05607,    Adjusted R-squared:  0.01316
## F-statistic: 1.307 on 1 and 22 DF,  p-value: 0.2653

```



```

##
##
## $SIMO_vs_DLUM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -451.03 -444.28  -97.33  191.27 1946.77
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      451.03     118.71   3.799 0.000982 ***
## site_species_matrix[, j]   -31.75      88.11  -0.360 0.722064
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 569.3 on 22 degrees of freedom
## Multiple R-squared:  0.005866, Adjusted R-squared:  -0.03932
## F-statistic: 0.1298 on 1 and 22 DF, p-value: 0.7221
##
##
## $SIMO_vs_CHYD
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -532.5 -361.5 -222.2  193.2 1792.8
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    272.90684    174.04911   1.568   0.131
## site_species_matrix[, j]   0.05828     0.04570   1.275   0.216
##
## Residual standard error: 551 on 22 degrees of freedom
## Multiple R-squared:  0.06883, Adjusted R-squared:  0.02651
## F-statistic: 1.626 on 1 and 22 DF, p-value: 0.2155
##
##
## $CERI_vs_CAL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -123.44  -53.74  -24.25   23.46  393.30
##

```

```

## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      136.2773     26.1484   5.212 3.16e-05 ***
## site_species_matrix[, j]  -0.3543     0.3878  -0.914   0.371
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 112.5 on 22 degrees of freedom
## Multiple R-squared:  0.03656, Adjusted R-squared:  -0.007234
## F-statistic: 0.8348 on 1 and 22 DF, p-value: 0.3708
##
##
## $CERI_vs_DIAP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -124.29  -57.01  -27.97   31.73   394.01
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      133.6928     25.4404   5.255 2.85e-05 ***
## site_species_matrix[, j]  -0.2336     0.2846  -0.821   0.421
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 112.9 on 22 degrees of freedom
## Multiple R-squared:  0.0297, Adjusted R-squared:  -0.01441
## F-statistic: 0.6733 on 1 and 22 DF, p-value: 0.4207
##
##
## $CERI_vs_CYCL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -125.06  -53.54  -26.47   21.87   400.62
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      141.1812     34.9184   4.043 0.000543 ***
## site_species_matrix[, j]  -0.1636     0.2616  -0.625 0.538168
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 113.6 on 22 degrees of freedom
## Multiple R-squared:  0.01747, Adjusted R-squared:  -0.02719
## F-statistic: 0.3911 on 1 and 22 DF, p-value: 0.5382

```

```

##
##
## $CERI_vs_BOSM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -129.38  -55.13  -26.58   31.71  396.42
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      131.281     25.071   5.236 2.98e-05 ***
## site_species_matrix[, j]   -5.751     8.586  -0.670    0.51
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 113.5 on 22 degrees of freedom
## Multiple R-squared:  0.01999,    Adjusted R-squared:  -0.02456
## F-statistic: 0.4487 on 1 and 22 DF,  p-value: 0.5099
##
##
## $CERI_vs_SIMO
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -139.17  -41.54  -20.95   34.44  403.71
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      141.06857     29.59390   4.767 9.28e-05 ***
## site_species_matrix[, j]   -0.03665     0.04208  -0.871    0.393
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 112.7 on 22 degrees of freedom
## Multiple R-squared:  0.03332,    Adjusted R-squared:  -0.01062
## F-statistic: 0.7584 on 1 and 22 DF,  p-value: 0.3932
##
##
## $CERI_vs_NAUP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max

```

```

## -153.21 -61.69 -9.65 21.38 365.99
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      85.35      25.85   3.302  0.00325 **
## site_species_matrix[, j]    63.63      25.16   2.529  0.01913 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 100.9 on 22 degrees of freedom
## Multiple R-squared:  0.2252, Adjusted R-squared:  0.19
## F-statistic: 6.394 on 1 and 22 DF, p-value: 0.01913
##
##
## $CERI_vs_DLUM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -122.50  -48.25  -19.70   26.25  403.30
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      124.396      23.898   5.205 3.21e-05 ***
## site_species_matrix[, j]    1.682      17.739   0.095   0.925
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 114.6 on 22 degrees of freedom
## Multiple R-squared:  0.0004087, Adjusted R-squared: -0.04503
## F-statistic: 0.008996 on 1 and 22 DF, p-value: 0.9253
##
##
## $CERI_vs_CHYD
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -133.32  -62.30  -16.84   22.88  404.29
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    142.412928    35.878480   3.969  0.00065 ***
## site_species_matrix[, j]  -0.006039    0.009420  -0.641  0.52807
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 113.6 on 22 degrees of freedom

```

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## Multiple R-squared:  0.01834,    Adjusted R-squared:  -0.02628
## F-statistic: 0.411 on 1 and 22 DF,  p-value: 0.5281
##
##
## $NAUP_vs_CAL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.6583 -0.6089 -0.5951  0.5954  2.4764
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.5951428   0.1983412     3.001  0.00659 **
## site_species_matrix[, j] 0.0007971   0.0029414     0.271  0.78892
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8535 on 22 degrees of freedom
## Multiple R-squared:  0.003327,    Adjusted R-squared:  -0.04198
## F-statistic: 0.07344 on 1 and 22 DF,  p-value: 0.7889
##
##
## $NAUP_vs_DIAP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.9295 -0.5430 -0.5380  0.6570  2.4177
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.537961   0.188028     2.861  0.00908 **
## site_species_matrix[, j] 0.002191   0.002104     1.041  0.30897
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8346 on 22 degrees of freedom
## Multiple R-squared:  0.04699,    Adjusted R-squared:  0.003668
## F-statistic: 1.085 on 1 and 22 DF,  p-value: 0.309
##
##
## $NAUP_vs_CYCL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
##

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## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.9065 -0.5804 -0.4745  0.6267  2.4738
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.449886   0.258150   1.743   0.0953 .
## site_species_matrix[, j] 0.001713   0.001934   0.886   0.3853
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8401 on 22 degrees of freedom
## Multiple R-squared:  0.03444,    Adjusted R-squared:  -0.009445
## F-statistic: 0.7848 on 1 and 22 DF,  p-value: 0.3853
##
##
## $NAUP_vs_BOSM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.7448 -0.5602 -0.5602  0.6398  2.5398
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.56023   0.18582   3.015  0.00637 **
## site_species_matrix[, j] 0.05428   0.06364   0.853  0.40292
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8411 on 22 degrees of freedom
## Multiple R-squared:  0.03201,    Adjusted R-squared:  -0.01199
## F-statistic: 0.7274 on 1 and 22 DF,  p-value: 0.4029
##
##
## $NAUP_vs_SIMO
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.7776 -0.6743 -0.4093  0.5684  2.3224
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.7776448  0.2180899   3.566  0.00173 **
## site_species_matrix[, j] -0.0003545  0.0003101  -1.143  0.26526
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

##
## Residual standard error: 0.8306 on 22 degrees of freedom
## Multiple R-squared:  0.05607,    Adjusted R-squared:  0.01316
## F-statistic: 1.307 on 1 and 22 DF,  p-value: 0.2653
##
##
## $NAUP_vs_CERI
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.8832 -0.4950 -0.2568  0.6489  1.7939
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.178964   0.232663   0.769   0.4500
## site_species_matrix[, j] 0.003539   0.001400   2.529   0.0191 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7525 on 22 degrees of freedom
## Multiple R-squared:  0.2252, Adjusted R-squared:  0.19
## F-statistic: 6.394 on 1 and 22 DF,  p-value: 0.01913
##
##
## $NAUP_vs_DLUM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.5957 -0.5957 -0.5957  0.6044  2.5044
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.59565   0.17631   3.378  0.00271 **
## site_species_matrix[, j] 0.09157   0.13087   0.700  0.49146
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8456 on 22 degrees of freedom
## Multiple R-squared:  0.02177,    Adjusted R-squared:  -0.0227
## F-statistic: 0.4895 on 1 and 22 DF,  p-value: 0.4915
##
##
## $NAUP_vs_CHYD
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,

```

```

##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.8380 -0.6655 -0.2488  0.5984  2.3491
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      8.506e-01  2.623e-01   3.243  0.00374 **
## site_species_matrix[, j] -7.905e-05  6.888e-05  -1.148  0.26342
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8304 on 22 degrees of freedom
## Multiple R-squared:  0.05649,    Adjusted R-squared:  0.01361
## F-statistic: 1.317 on 1 and 22 DF,  p-value: 0.2634
##
##
## $DLUM_vs_CAL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.2991 -0.2961 -0.2886 -0.2700  6.3179
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.299074  0.319931   0.935   0.360
## site_species_matrix[, j] -0.000747  0.004745  -0.157   0.876
##
## Residual standard error: 1.377 on 22 degrees of freedom
## Multiple R-squared:  0.001125,    Adjusted R-squared:  -0.04428
## F-statistic: 0.02479 on 1 and 22 DF,  p-value: 0.8763
##
##
## $DLUM_vs_DIAP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##      j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.6773  0.0024  0.0934  0.0993  3.7610
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -0.117212  0.239309  -0.490  0.629129
## site_species_matrix[, j]  0.010369  0.002677   3.873  0.000822 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```



```

##
## Residual standard error: 1.062 on 22 degrees of freedom
## Multiple R-squared:  0.4054, Adjusted R-squared:  0.3784
## F-statistic:    15 on 1 and 22 DF,  p-value: 0.0008221
##
##
## $DLUM_vs_CYCL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.7846 -0.3003 -0.2342 -0.1385  6.2259
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.089184   0.419969   0.212   0.834
## site_species_matrix[, j] 0.001863   0.003147   0.592   0.560
##
## Residual standard error: 1.367 on 22 degrees of freedom
## Multiple R-squared:  0.01568, Adjusted R-squared: -0.02907
## F-statistic: 0.3504 on 1 and 22 DF,  p-value: 0.5599
##
##
## $DLUM_vs_BOSM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.3221 -0.3221 -0.3221 -0.2989  6.2779
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.32211   0.30318   1.062   0.300
## site_species_matrix[, j] -0.04219   0.10383  -0.406   0.688
##
## Residual standard error: 1.372 on 22 degrees of freedom
## Multiple R-squared:  0.007448, Adjusted R-squared: -0.03767
## F-statistic: 0.1651 on 1 and 22 DF,  p-value: 0.6884
##
##
## $DLUM_vs_SIMO
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max

```

```

## -0.3567 -0.3555 -0.2914 -0.2099  6.2879
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.3567236  0.3606224   0.989   0.333
## site_species_matrix[, j] -0.0001848  0.0005128  -0.360   0.722
##
## Residual standard error: 1.373 on 22 degrees of freedom
## Multiple R-squared:  0.005866, Adjusted R-squared:  -0.03932
## F-statistic: 0.1298 on 1 and 22 DF, p-value: 0.7221
##
##
## $DLUM_vs_CERI
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.3729 -0.2813 -0.2690 -0.2598  6.3224
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.2446678  0.4258001   0.575   0.571
## site_species_matrix[, j] 0.0002429  0.0025613   0.095   0.925
##
## Residual standard error: 1.377 on 22 degrees of freedom
## Multiple R-squared:  0.0004087, Adjusted R-squared:  -0.04503
## F-statistic: 0.008996 on 1 and 22 DF, p-value: 0.9253
##
##
## $DLUM_vs_NAUP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.8644 -0.4127 -0.1274 -0.1274  6.1873
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.1274     0.3490   0.365   0.719
## site_species_matrix[, j]  0.2377     0.3398   0.700   0.491
##
## Residual standard error: 1.362 on 22 degrees of freedom
## Multiple R-squared:  0.02177, Adjusted R-squared:  -0.0227
## F-statistic: 0.4895 on 1 and 22 DF, p-value: 0.4915
##
##
## $DLUM_vs_CHYD
##

```

```

## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.6049 -0.4923 -0.2882 -0.0286  6.0076
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.6239489   0.4240730    1.471   0.155
## site_species_matrix[, j] -0.0001201   0.0001113   -1.078   0.293
##
## Residual standard error: 1.342 on 22 degrees of freedom
## Multiple R-squared:  0.05019, Adjusted R-squared:  0.007016
## F-statistic: 1.163 on 1 and 22 DF, p-value: 0.2926
##
##
## $CHYD_vs_CAL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2816.5 -2017.2  -375.9   1805.7   4985.7
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3337.451    565.605    5.901 6.15e-06 ***
## site_species_matrix[, j]  -13.367     8.388   -1.594   0.125
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2434 on 22 degrees of freedom
## Multiple R-squared:  0.1035, Adjusted R-squared:  0.06274
## F-statistic:  2.54 on 1 and 22 DF, p-value: 0.1253
##
##
## $CHYD_vs_DIAP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3000.2 -1641.5  -330.6   1103.9   5078.0
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3267.088    549.920    5.941 5.59e-06 ***
## site_species_matrix[, j]   -9.529     6.153   -1.549   0.136

```

```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2441 on 22 degrees of freedom
## Multiple R-squared:  0.09832,    Adjusted R-squared:  0.05733
## F-statistic: 2.399 on 1 and 22 DF,  p-value: 0.1357
##
##
## $CHYD_vs_CYCL
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3234.6 -1882.7   -49.7   1280.8  4705.6
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3927.297      734.322   5.348 2.28e-05 ***
## site_species_matrix[, j]   -10.230        5.502  -1.859   0.0764 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2390 on 22 degrees of freedom
## Multiple R-squared:  0.1358, Adjusted R-squared:  0.09653
## F-statistic: 3.458 on 1 and 22 DF,  p-value: 0.07639
##
##
## $CHYD_vs_BOSM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2958.0 -2209.5   -73.5   1248.8  5206.5
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3116.7      555.7   5.609 1.22e-05 ***
## site_species_matrix[, j]   -188.1      190.3  -0.988   0.334
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2515 on 22 degrees of freedom
## Multiple R-squared:  0.04253,    Adjusted R-squared:  -0.0009953
## F-statistic: 0.9771 on 1 and 22 DF,  p-value: 0.3337
##
##
## $CHYD_vs_SIMO
##

```

```

## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2850.3 -2120.7  -604.5   927.2  5672.6
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2384.2192    651.2956   3.661  0.00137 **
## site_species_matrix[, j]    1.1811     0.9262   1.275  0.21552
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2480 on 22 degrees of freedom
## Multiple R-squared:  0.06883,    Adjusted R-squared:  0.02651
## F-statistic: 1.626 on 1 and 22 DF,  p-value: 0.2155
##
##
## $CHYD_vs_CERI
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2886.0 -2225.8  -341.9  1602.6  5111.2
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    3285.798    787.426   4.173 0.000396 ***
## site_species_matrix[, j]   -3.037     4.737  -0.641 0.528073
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2547 on 22 degrees of freedom
## Multiple R-squared:  0.01834,    Adjusted R-squared:  -0.02628
## F-statistic: 0.411 on 1 and 22 DF,  p-value: 0.5281
##
##
## $CHYD_vs_NAUP
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3191.6 -2177.1   -38.3  1116.6  4972.9
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)

```

```
## (Intercept)          3350.3      639.7   5.237 2.97e-05 ***
## site_species_matrix[, j]   -714.6      622.7  -1.148   0.263
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2497 on 22 degrees of freedom
## Multiple R-squared:  0.05649,    Adjusted R-squared:  0.01361
## F-statistic: 1.317 on 1 and 22 DF,  p-value: 0.2634
##
##
## $CHYD_vs_DLUM
##
## Call:
## lm(formula = site_species_matrix[, i] ~ site_species_matrix[,
##     j])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2862.9 -1924.8  -225.1   1343.9   5301.6
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3021.6      522.4   5.784 8.08e-06 ***
## site_species_matrix[, j]   -418.1      387.7  -1.078   0.293
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2505 on 22 degrees of freedom
## Multiple R-squared:  0.05019,    Adjusted R-squared:  0.007016
## F-statistic: 1.163 on 1 and 22 DF,  p-value: 0.2926
```

#suggests there is a significant influence of the variables in NAUP and CERI as there is a significant

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)**.