

Linear Discriminant Analysis, Redundancy Analysis

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```
if (!require(MASS))
{install.packages("MASS")}
library(MASS)

if (!require(ggplot2))
{install.packages("ggplot2")}
library(ggplot2)

if (!require(vegan))
{install.packages("vegan")}
library(vegan)
```

Section 1: Measures of Association

You were just hired as a new faculty member in the Biology Department at College of William & Mary and must involve undergraduate students in your research. But there is a problem – you study 4 species of plants that are hard to tell apart and you are too busy writing lectures for your new class to really teach the new research students how to identify the plant species. You decide to let statistics teach your research students for you. You will use a Linear Discriminant Analysis to decide which traits are best used to identify the 4 plant species.

Question 1

Question: Load the data set “taxon.txt” (using read.table) and assign that to a variable called taxa. This data set has measurements of seven variables on 120 individual plants. As always, for each step, please have your R script show the content of variables and calculations as they are created. E.g. here, please show the content of taxa (you can use head(taxa) for this).

```
#Here you could just change the "" to your working directory and everything should run smoothly
dir <- "~/Documents/GitHub/code_examples/R/RMarkdown Examples"
taxa <- read.table(paste(dir,"/taxon.txt",sep=""), header = T)
head(taxa) #look at data
```

	Petals	Internode	Sepal	Bract	Petiole	Leaf	Fruit
## 1	5.621498	29.48060	2.462107	18.20341	11.27910	1.128033	7.876151
## 2	4.994617	28.36025	2.429321	17.65205	11.04084	1.197617	7.025416
## 3	4.767505	27.25432	2.570497	19.40838	10.49072	1.003808	7.817479
## 4	6.299446	25.92424	2.066051	18.37915	11.80182	1.614052	7.672492
## 5	6.489375	25.21131	2.901583	17.31305	10.12159	1.813333	7.758443
## 6	5.785868	25.52433	2.655643	17.07216	10.55816	1.955524	7.880880

Question 2

Question: You would like to know which of the variables (fruit size, bract length, internode length, petal width, sepal length, petiole length, or leaf width) are the most useful to distinguish among the 4 plant species. The plants in rows 1-30 are Species I, the plants in rows 31-60 are Species II, the plants in rows 61-90 are species III, and the plants in rows 91-120 are species IV. Create a vector called name, which should be of length 120, that contains these taxonomic labels (“I”, “II”, “III”, “IV”) for each of the rows of the variable taxa. The command rep might be useful here. Like above, make sure that your R script includes a command to show the content of name. Please do this for the remainder of the script (like I asked you to do in HW #1 and HW #2).

```
taxa$name<- rep(c("I", "II", "III", "IV"), each=30) #create a vector called name
table(taxa$name) #ensure names are correct
```

```
##
##  I  II III  IV
## 30 30 30 30
```

```
head(taxa)
```

	Petals	Internode	Sepal	Bract	Petiole	Leaf	Fruit	name
## 1	5.621498	29.48060	2.462107	18.20341	11.27910	1.128033	7.876151	I
## 2	4.994617	28.36025	2.429321	17.65205	11.04084	1.197617	7.025416	I
## 3	4.767505	27.25432	2.570497	19.40838	10.49072	1.003808	7.817479	I
## 4	6.299446	25.92424	2.066051	18.37915	11.80182	1.614052	7.672492	I
## 5	6.489375	25.21131	2.901583	17.31305	10.12159	1.813333	7.758443	I
## 6	5.785868	25.52433	2.655643	17.07216	10.55816	1.955524	7.880880	I

Question 3

We'll conduct a PCA to see if any obvious trait candidates appear.

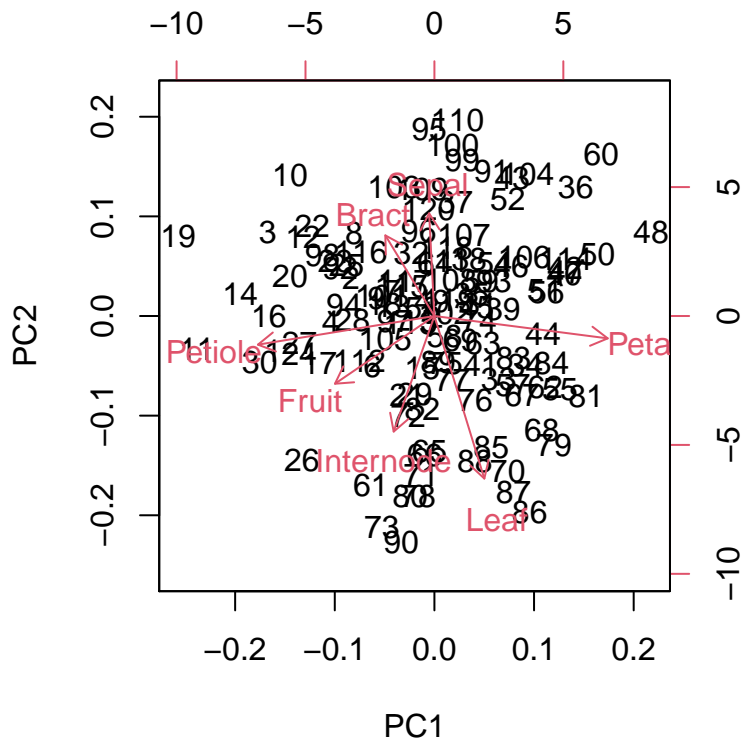
- Part A: Conduct a PCA (on standardized data, using `prcomp`) and save the result to a variable called `pc_taxa`. Recall that you can either standardize your data (which means set all variables to have mean 0, standard deviation 1) yourself using `scale` or you can set options in `prcomp` to do that for you. Use `summary(pc_taxa)` to show the contents of the PCA.
- Part B: Create a PCA biplot (using `biplot`) to visualize the loadings of the trait variables with the PC axes.
- Part C: Draw a scatterplot of the species scores (the rows of `pc_taxa$x`) for the first two PC axes. In this scatterplot, label the species scores with their value in name and color the label using this color scheme: Species I red, Species II blue, Species III black, and Species IV gray. To do this you have three options.
 - i: Draw the scatterplot by hand yourself. Some hints: you can make use of `plot` with the option `type="n"` to initialize a blank plot then add point labels using `text`. Please make the text labels large (using the option `cex=2`) and use a Serif font (using the option `family="serif"`).
- Part D: Can you name a trait that seems like a good candidate to distinguish Species I from the other species? Can you name a trait that seems like a good candidate to distinguish Species III from the other species?

```
pc_taxa<- prcomp(taxa[,1:7], scale. = T) #perform pca with standardization
summary(pc_taxa) #summary of PCA
```

Part A

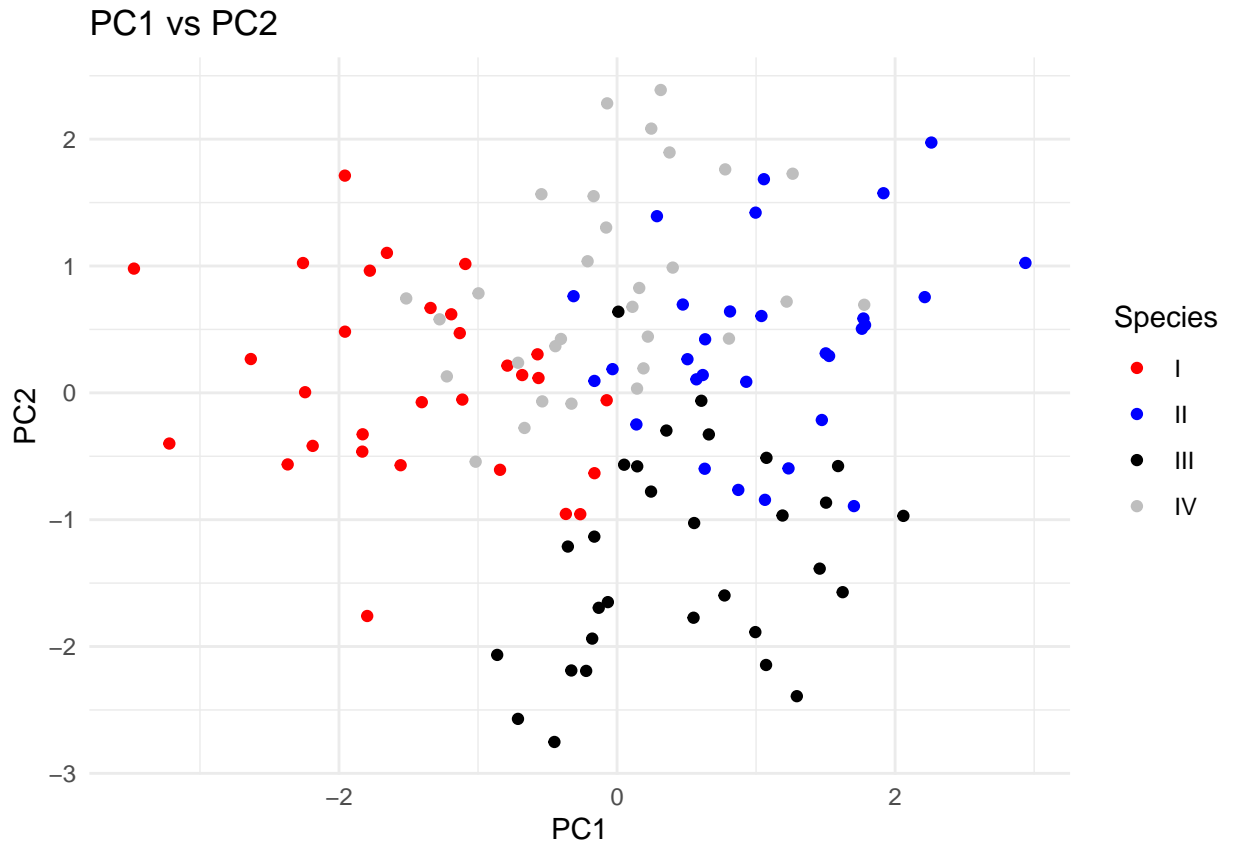
```
## Importance of components:
##              PC1      PC2      PC3      PC4      PC5      PC6      PC7
## Standard deviation    1.2333  1.1085  1.0398  0.9924  0.9740  0.9289  0.61052
## Proportion of Variance 0.2173  0.1755  0.1544  0.1407  0.1355  0.1233  0.05325
## Cumulative Proportion 0.2173  0.3928  0.5473  0.6880  0.8235  0.9467  1.00000
```

```
biplot(pc_taxa)
```



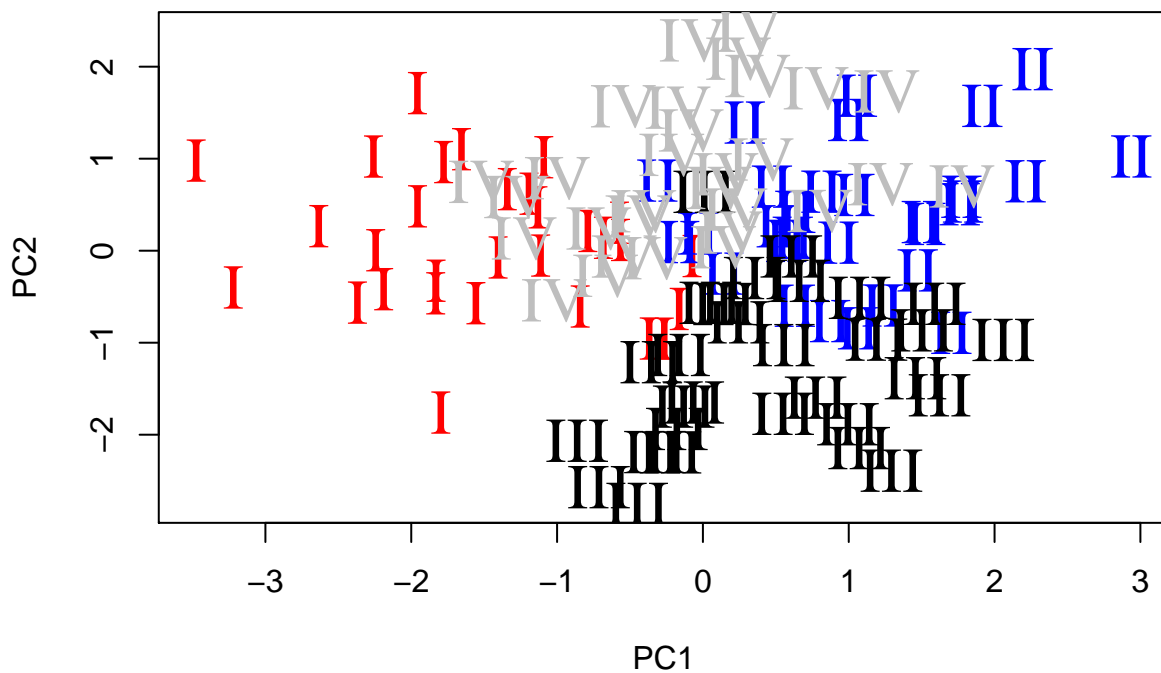
Part B

```
df<- as.data.frame(pc_taxa$x)
df$Species<- factor(taxa$name)
ggplot(df, aes(PC1, PC2, color=Species))+ ggtitle("PC1 vs PC2")+
  geom_point(size=1.5)+scale_color_manual(values = c("red","blue", "black", "gray")) +theme_minimal()
```



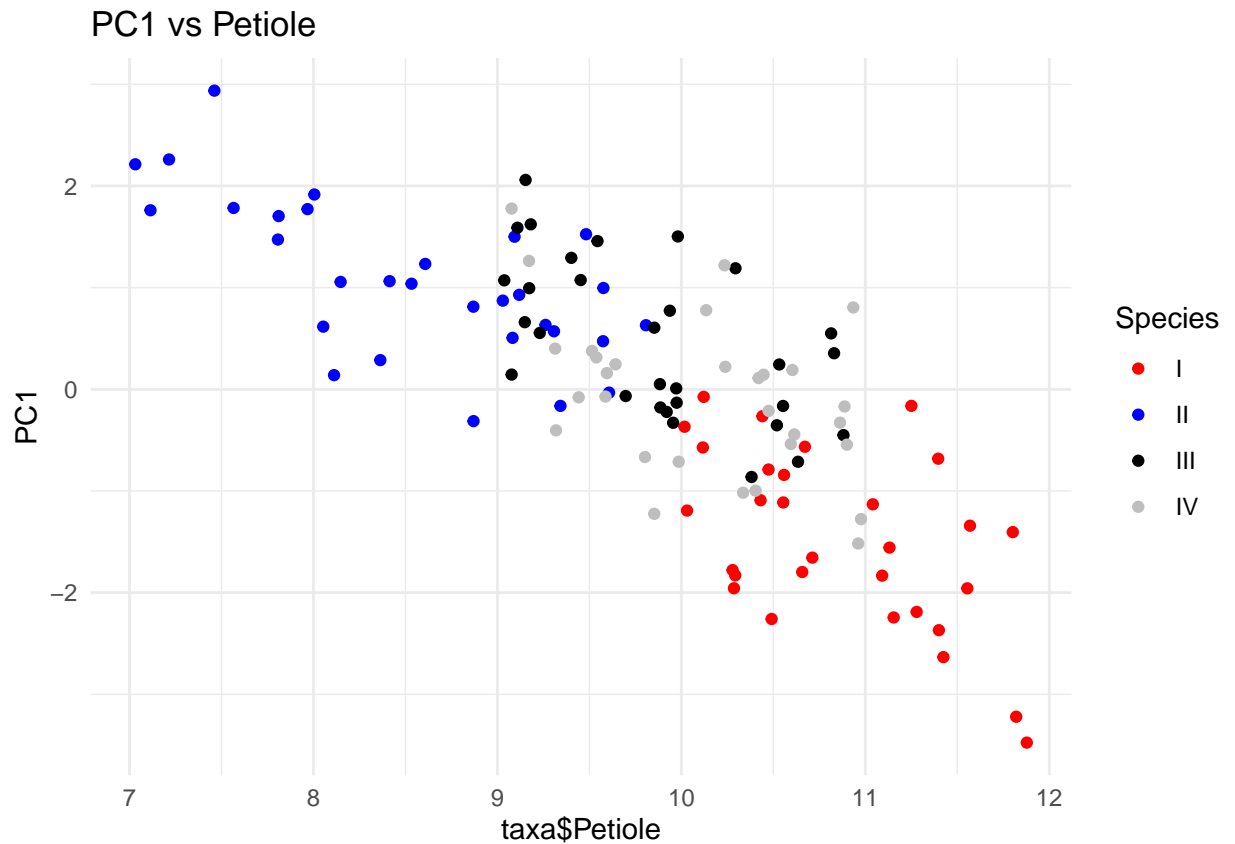
Part C

```
plot(df$PC1, df$PC2, type = "n", xlab = "PC1", ylab = "PC2") #Empty plot
text(df$PC1[1:30], df$PC2[1:30], cex=2, "I", family="serif", col="red") #add labels
text(df$PC1[31:60], df$PC2[31:60], cex=2, "II", family="serif", col="blue") #add labels
text(df$PC1[61:90], df$PC2[61:90], cex=2, "III", family="serif", col="black") #add labels
text(df$PC1[91:120], df$PC2[91:120], cex=2, "IV", family="serif", col="gray") #add labels
```



#Petiole can be used to distinguish species I from others

```
ggplot(df, aes(taxa$Petiole, PC1, color=Species))+ ggtitle("PC1 vs Petiole")+
  geom_point(size=1.5)+scale_color_manual(values = c("red", "blue", "black", "gray")) +theme_minimal()
```

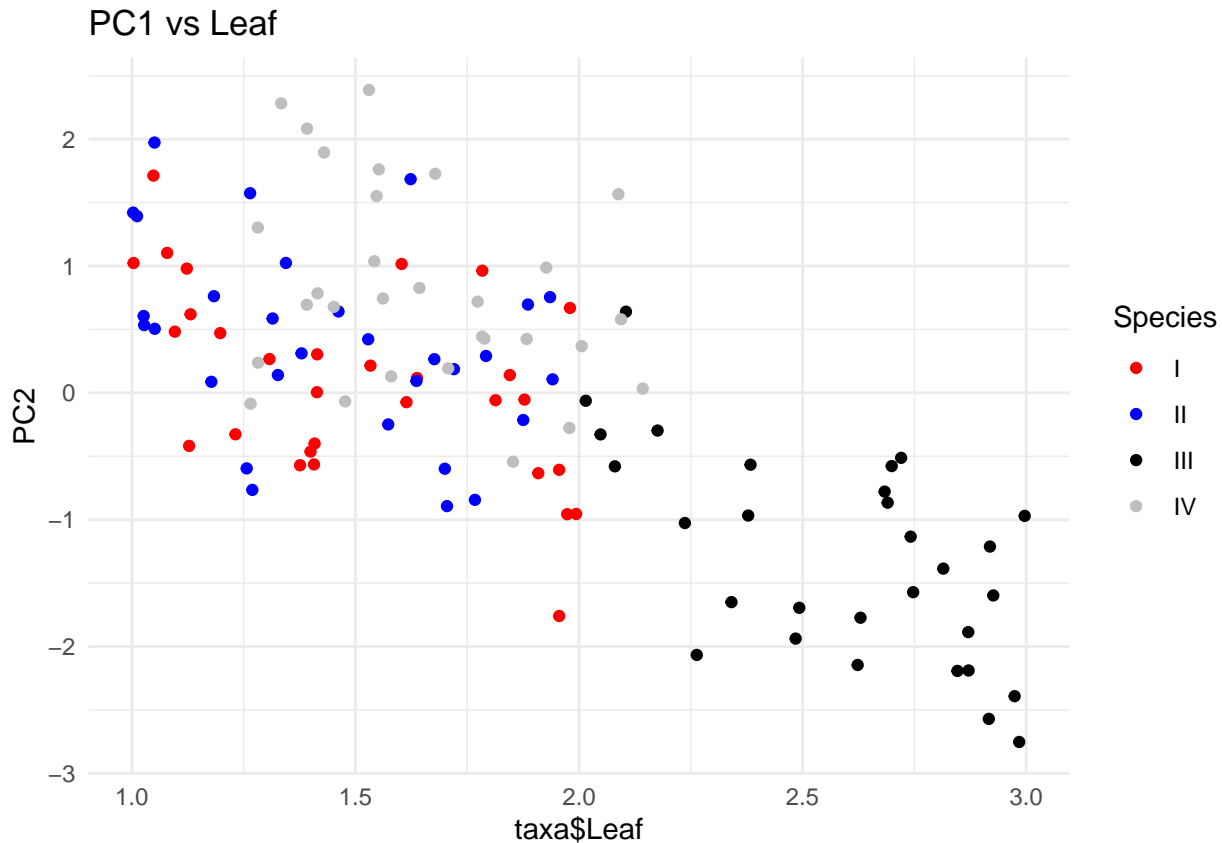


Part D

Species I: Petiole is the best trait which can be used to differentiate Species I from the others. This is due to Petiole having a high PC 1 value, which we can observe on the biplot. We see the Species 1 also has high PC1 values in the plots made during Part C.

#Leaf can be used to distinguish species III from others

```
ggplot(df, aes(taxa$Leaf, PC2, color=Species))+ ggtitle("PC1 vs Leaf")+
  geom_point(size=1.5)+scale_color_manual(values = c("red", "blue", "black", "gray")) +theme_minimal()
```



Species III: Leaf is the best trait which can be used to differentiate Species III from the others. This is due to Petiole having a low PC 2 value, which we can observe on the biplot. We see the Species III also has low PC2 values in the plots made during Part C.

Question 4

We'll conduct a Linear Discriminant Analysis (LDA) to ordinate the data in a reduced dimensional space that maximizes the among-group variance in plant species and carefully identify the traits that are the best candidates to discriminate among all 4 species.

- Part A: Install package MASS (using `install.packages`) and then load the MASS library (using `library`). Use Linear Discriminant Analysis (using command `lda`) on the original data in `taxa` (e.g. don't standardize) and save the result to a variable called `lda_taxa`.
- Part B: Use `plot` on `lda_taxa` (the `plot` command sees that `lda_taxa` is an `lda` object and automatically calls `plot.lda`) to produce scatterplots of the species scores for LD1, LD2, and LD3 (these scatterplots are the default when there are >2 LD axes produced in the analysis).
- Part C: Use the following commands to create a histogram and density plot of all how all groups (Species) align along the first LDA: `dev.new()`, `plot(lda_taxa, dimen=1, type="both")`

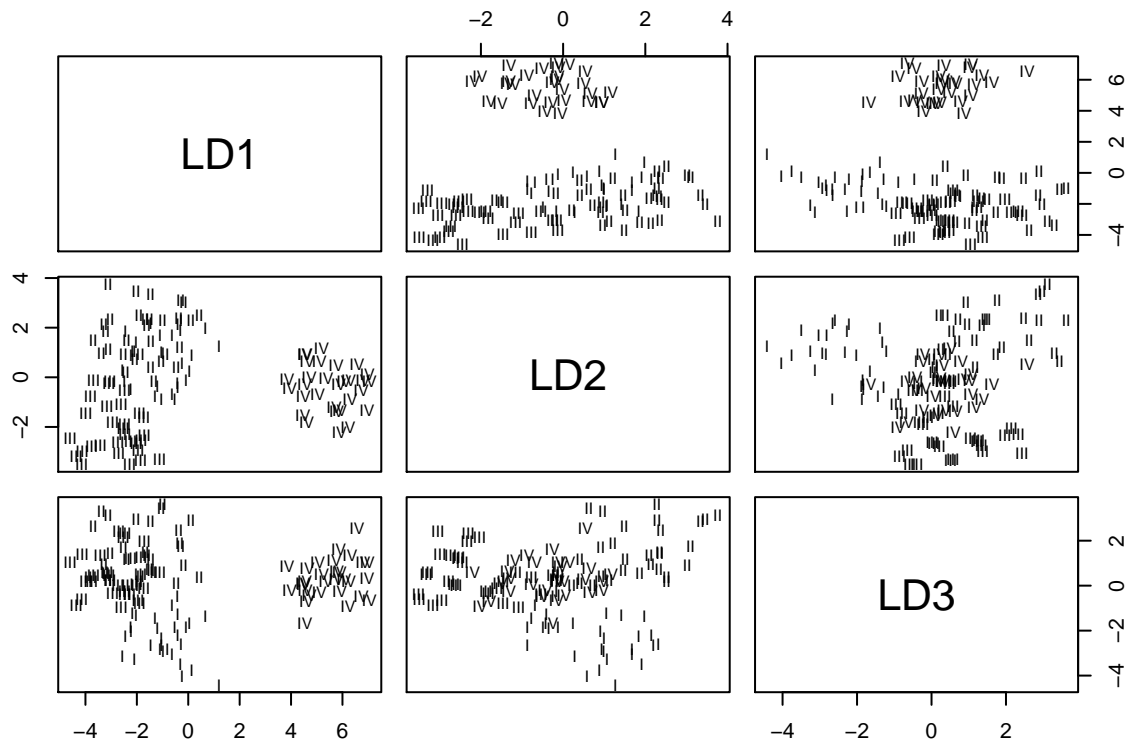
```
#Mass installed at beginning of script
lda_taxa<- lda(name~., data=taxa) #LDA model
summary(lda_taxa)
```

Part A

```
##          Length Class  Mode
```

```
## prior      4      -none- numeric
## counts     4      -none- numeric
## means     28      -none- numeric
## scaling    21      -none- numeric
## lev        4      -none- character
## svd         3      -none- numeric
## N           1      -none- numeric
## call        3      -none- call
## terms       3      terms  call
## xlevels     0      -none- list
```

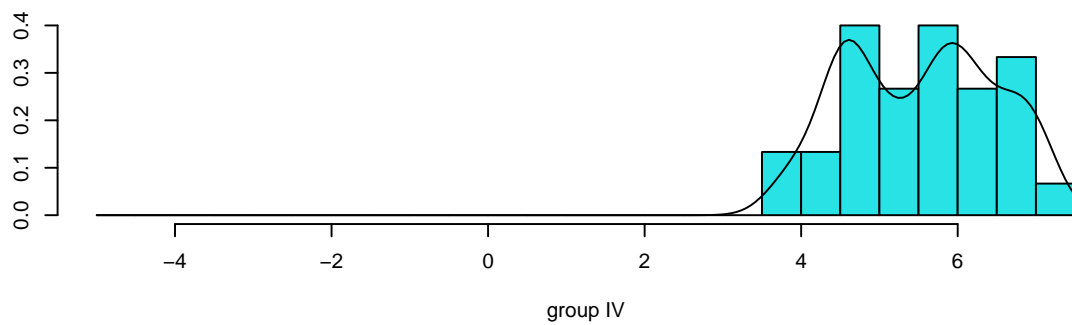
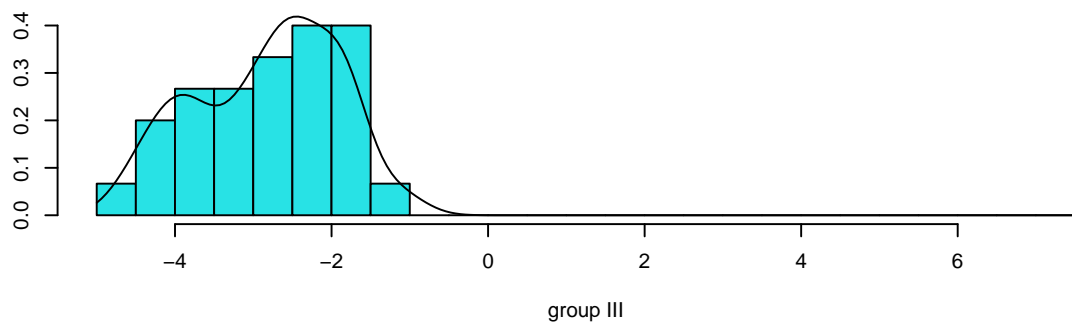
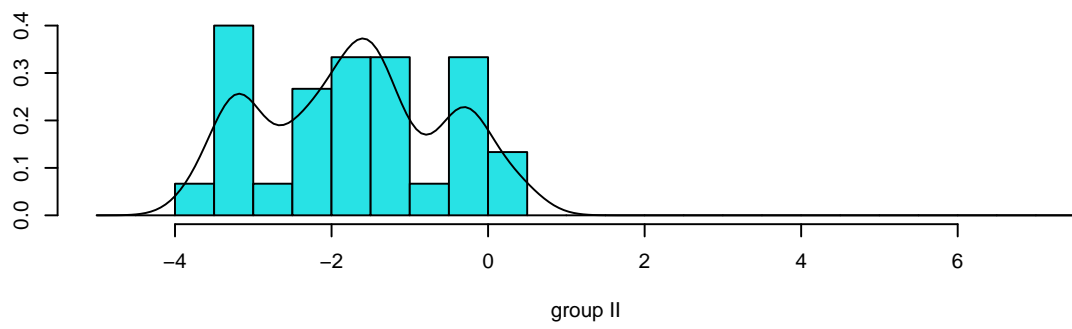
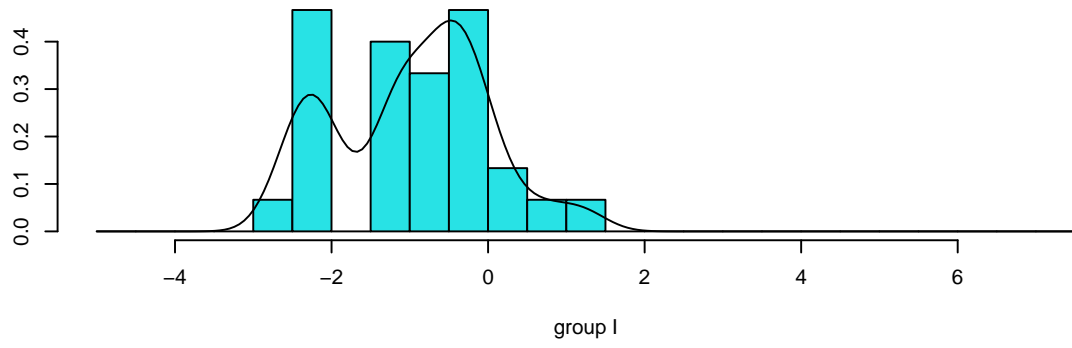
```
plot(lda_taxa) #plot linear discriminant analysis
```



Part B

The above LDA plots show that LD1 is a good indicator for the separation between Species 4.

```
plot(lda_taxa, dimen=1, type="both")
```

Part C

Question 5

These default plots are helpful, but they don't give me the freedom to see the information I want. For plot 4c, I can see easily that LD1 is a great candidate to distinguish Species IV, but I can't coerce the `plot.lda` command to give me this plot for any of the other LDAs. We're going to draw our own histogram + density plots for each LDA. For this you can use an external package like `ggplot` or `lattice`, but it must produce a plot with the elements I ask for here. Here is an example of what the final plot should look like (using the Egyptian skulls data set).

Part A-I

- Part A: Extract the site scores from `lda_taxa` using `predict` and assign those to a new variable called `pred`.
- Part B: Extract the site scores for LDA1 from `pred` (these are in `pred$x`) and assign them to a new variable called `x1`.
- Part C: Use kernel density estimation to construct density estimates for `x1` using the command `density` and assign these values to a new variable called `d1`. Use all the default options for `density`.
- Part D: Make a histogram of the FREQUENCY of `x1` (using the base R function `hist`) with 20 bins (assigned using `breaks`).
- Part E: Use `lines` to add `d1` to the histogram. You can see that `d1` is a list and has elements `d1$x` and `d1$y`. So simply typing `lines(d1)` should be enough to add the density lines.
- Part F: Use `polygon` to add `d1` to the histogram and modify the color of the polygon to be red with alpha transparency level of 75 (out of max RGB values of 255). For example, simply typing `polygon(d1,col="red")` works, but we need to modify the transparency of the polygon. You can use `rgb` to help with modifying color values precisely.
- Part G: Use `segments` to add small lines indicating where individual plants lie along LDA1. Segments will require you to enter the starting x-position of the line segment (which will be `x1`), the starting y-position of the segment (make this 0), the ending x-position (which will again be `x1`), and the ending y-position (make this 0.01).
- Part H: Identify where in the object `lda_taxa` you can find the loadings of the original traits with each LDA. Extract the values for LD1 and assign them to a new variable called `load_ld1`.
- Part I: Now just run this command to add a text label showing where each of the original traits scales with LD1:
- Part J: You can see the command in g sets all the lines to black. Now I want you to use `segments` to color all the lines for Species 1 as red, all the lines for Species 2 as blue, all the lines for Species 3 as black, and all the lines for Species 4 as grey.
- Part K: Repeat to make the figure for LDA2.
- Part L: Repeat to make the figure for LDA3.

```
#Part A
pred<- predict(lda_taxa) #scores saved to this variable

#Part B
x1<- pred$x[,1]

#Part C
d1<- density(x1)

#Part D
hist(x1, breaks = 20, freq = F, main = "Histogram of LDA 1", xlab = "LDA 1") #make frequency histogram
```

```

#Part E
lines(d1) #add density

#Part F
mycol <- rgb(255, 0, 0, max = 255, alpha = 75) #Set transparency and save this to a new color
polygon(d1,col=mycol) #add the density color

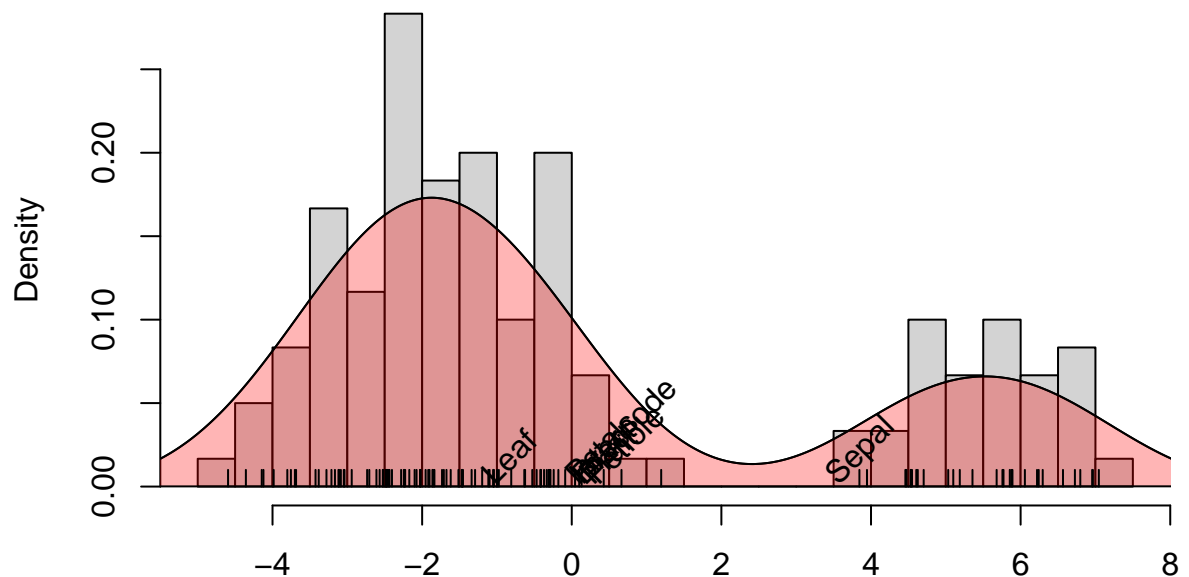
#Part G
segments(x0=x1,y0=0, x1=x1, y1=0.01)

#Part H
load_ld1<- lda_taxa$scaling[,1] #it is saved as (scaling) data frame

#Part I
text(load_ld1,rep(.005,length(load_ld1)),labels=names(load_ld1),srt=45,adj=c(0,.5)) #sepal provide best

```

Histogram of LDA 1



Part A-I Code

LDA 1

Question: Please explain to me what the srt does and what the adj does.

- srt: Provides the string rotation in degrees which is 45 here
- adj: Provides the justification for the text with 0.5 as centered text

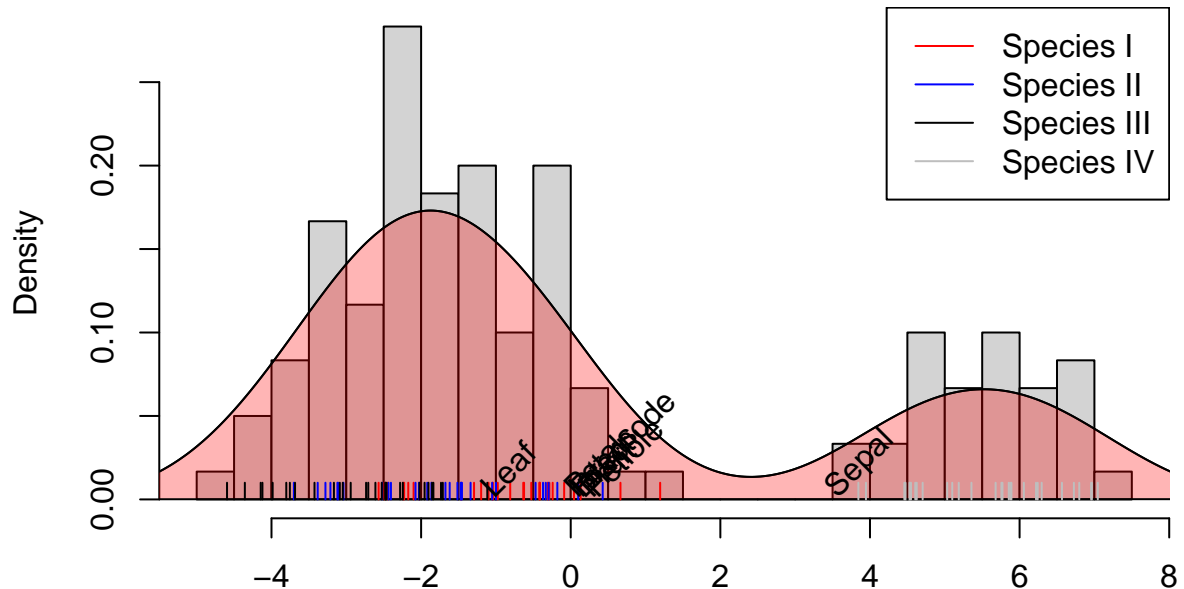
```

{hist(x1, breaks = 20, freq = F, main = "Histogram of LDA 1", xlab = "LDA 1") #make frequency histogram
lines(d1) #add density
mycol <- rgb(255, 0, 0, max = 255, alpha = 75) #Set transparency and save this to a new color
polygon(d1,col=mycol) #add the density color
segments(x0=x1[1:30],y0=0, x1=x1[1:30], y1=0.01, col="red")
segments(x0=x1[31:60],y0=0, x1=x1[31:60], y1=0.01, col="blue")
segments(x0=x1[61:90],y0=0, x1=x1[61:90], y1=0.01, col="black")

```

```
segments(x0=x1[91:120],y0=0, x1=x1[91:120], y1=0.01, col="grey")
load_ld1<- lda_taxa$scaling[,1]
text(load_ld1,rep(.005,length(load_ld1)),labels=names(load_ld1),srt=45,adj=c(0,.5))
legend("topright", legend =c("Species I", "Species II", "Species III", "Species IV"), col = c("red", "blue", "black", "grey"))
```

Histogram of LDA 1



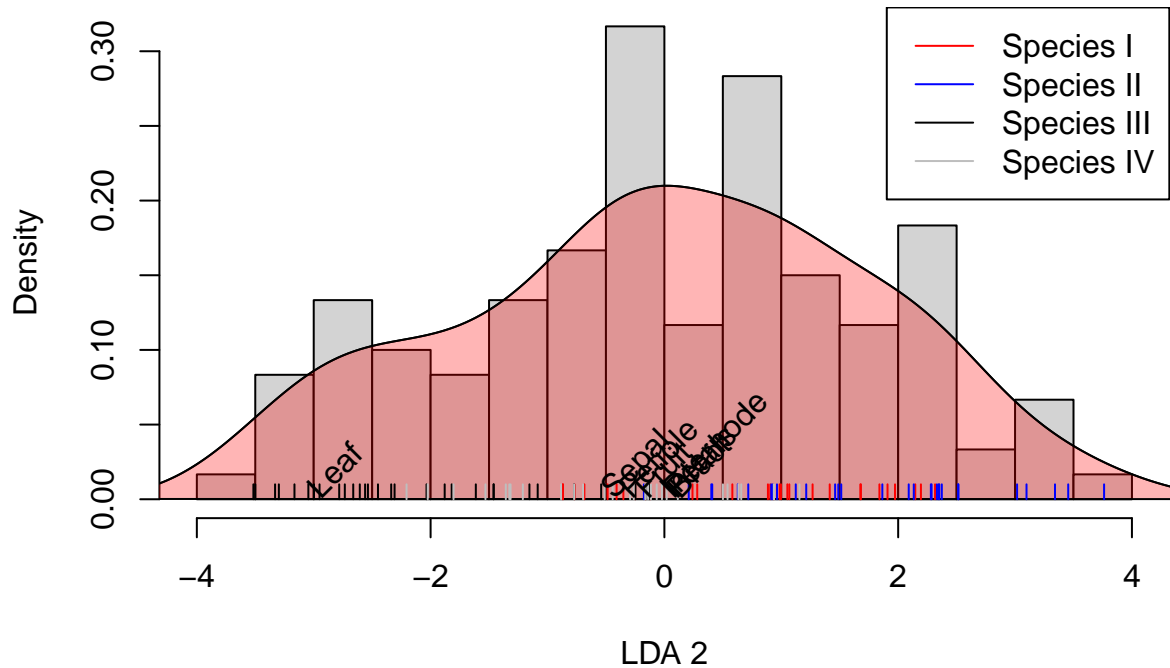
Part J

LDA 1

Using the segments command, it was possible to create different colors for the different species and plot that on the histogram.

```
{x1<- pred$x[,2]
d1<- density(x1)
hist(x1, breaks = 20, freq = F, main = "Histogram of LDA 2", xlab = "LDA 2") #make frequency histogram
lines(d1) #add density
mycol <- rgb(255, 0, 0, max = 255, alpha = 75) #Set transparency and save this to a new color
polygon(d1,col=mycol) #add the density color
segments(x0=x1[1:30],y0=0, x1=x1[1:30], y1=0.01, col="red")
segments(x0=x1[31:60],y0=0, x1=x1[31:60], y1=0.01, col="blue")
segments(x0=x1[61:90],y0=0, x1=x1[61:90], y1=0.01, col="black")
segments(x0=x1[91:120],y0=0, x1=x1[91:120], y1=0.01, col="grey")
load_ld1<- lda_taxa$scaling[,2]
text(load_ld1,rep(.005,length(load_ld1)),labels=names(load_ld1),srt=45,adj=c(0,.5))
legend("topright", legend =c("Species I", "Species II", "Species III", "Species IV"), col = c("red", "blue", "black", "grey"))
```

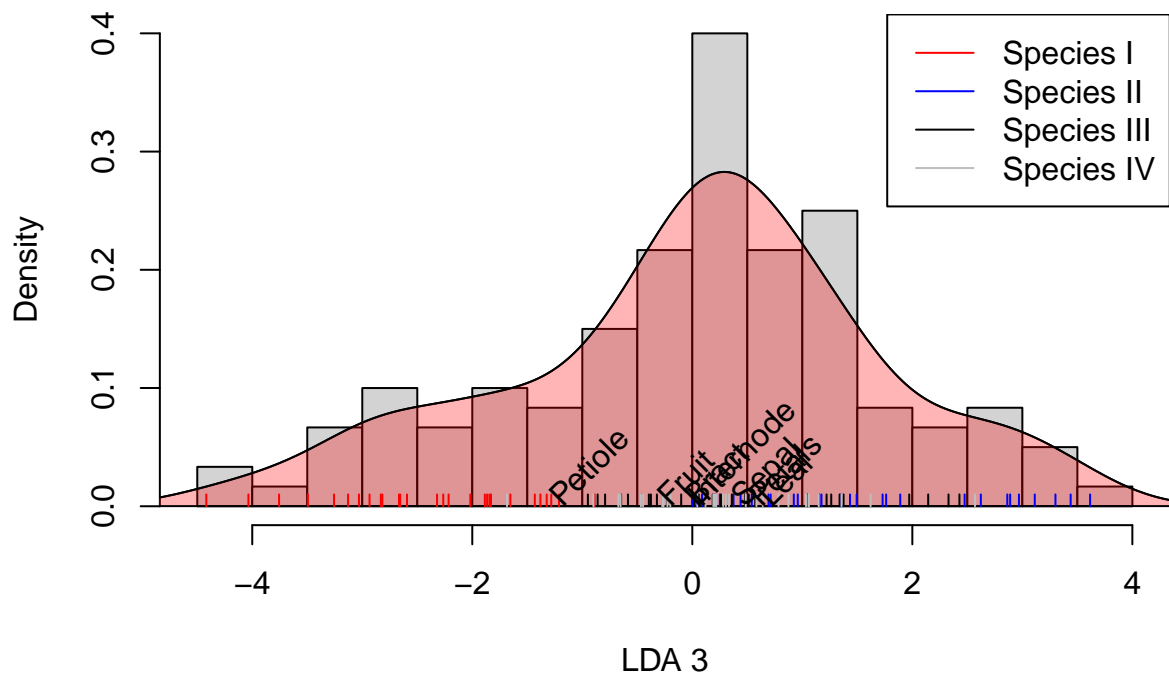
Histogram of LDA 2



Part K

```
{x1<- pred$x[,3]
d1<- density(x1)
hist(x1, breaks = 20, freq = F, main = "Histogram of LDA 3", xlab = "LDA 3") #make frequency histogram
lines(d1) #add density
mycol <- rgb(255, 0, 0, max = 255, alpha = 75) #Set transparency and save this to a new color
polygon(d1,col=mycol) #add the density color
segments(x0=x1[1:30],y0=0, x1=x1[1:30], y1=0.01, col="red")
segments(x0=x1[31:60],y0=0, x1=x1[31:60], y1=0.01, col="blue")
segments(x0=x1[61:90],y0=0, x1=x1[61:90], y1=0.01, col="black")
segments(x0=x1[91:120],y0=0, x1=x1[91:120], y1=0.01, col="grey")
load_ld1<- lda_taxa$scaling[,3]
text(load_ld1,rep(.005,length(load_ld1)),labels=names(load_ld1),srt=45,adj=c(0,.5))
legend("topright", legend =c("Species I", "Species II", "Species III", "Species IV"), col = c("red", "b
```

Histogram of LDA 3



Part L

Question 5.2

Question: Using the histogram + density plots you made in 4 (e.g. just inspect them visually), please tell your research students: which plant trait is best to distinguish Species IV? Confirm by calculating the mean of that trait value for Species IV and for all the other species combined.

#from LDA1 Histogram: Species IV can best be identified by sepal

```
data.frame(mean=tapply(taxa$Sepal, taxa$name, mean), sd=tapply(taxa$Sepal, taxa$name, sd)) #Sepal is mu
```

```
##          mean          sd
## I    2.537955 0.2753774
## II   2.490336 0.3071815
## III  2.446003 0.2774468
## IV   4.532560 0.2971764
```

Species IV can best be identified by sepal

Question 6

Question: Using the histogram + density plots you made in 4 (e.g. just inspect them visually), please tell your research students: which plant trait is best to distinguish Species III? Confirm by calculating the mean of that trait value for Species III and for all the other species combined.

#from LDA2 Histogram: Species III can best be identified by Leaf

```
data.frame(mean=tapply(taxa$Leaf, taxa$name, mean), sd=tapply(taxa$Leaf, taxa$name, sd)) #Leaf is higher
```

```
##          mean          sd
## I    1.508029 0.3336094
## II   1.450260 0.3090852
```

```
## III 2.588555 0.3140849
## IV 1.645945 0.2611370
```

Species III can best be identified by Leaf

Question 7

Question: Using the histogram + density plots you made in 4 (e.g. just inspect them visually), please tell your research students: which plant trait is best to distinguish Species I? Confirm by calculating the mean of that trait value for Species I and for all the other species combined.

```
#from LDA3 Histogram: Species I can best be identified by Petiole
```

```
data.frame(mean=tapply(taxa$Petiole, taxa$name, mean), sd=tapply(taxa$Petiole, taxa$name, sd)) #Petiole
```

```
##          mean          sd
## I    10.864184 0.5788199
## II    8.541085 0.8180661
## III   9.866983 0.5892790
## IV   10.128838 0.6003981
```

Species I can best be identified by Petiole

Section 2: Redundancy Analysis

Question 8

We will evaluate a data set that consists of the relative abundance of 15 different multi-locus genotypes (clones) of the species *Daphnia pulex* at each of 19 ponds in southwest Michigan. We would like to determine how much of the among-site variation in *D. pulex* clonal composition is associated with environmental properties at each site. The clonal data was obtained by extracting DNA from 20 individuals at each site, determining their genotype at 8 microsatellite loci, identifying the total number of unique genotypes at these 8 loci, and counting the relative frequency of each clone in each site. The environmental data consists of an array of abiotic water variables (pH, TN = total Nitrogen concentration, TP = total phosphorus concentration) and biotic variables such as the density of invertebrate predators at each site.

- Part A: Read the data in clone.txt into a variable called clone, and read the data in environment.txt into a variable called env. You can see there are 15 clones, each assigned a letter as a label.
- Part B: Load the external R package “vegan”. Hellinger-transform the clone data and assign it to a new variable called hel_clone.
- Part C: Run an RDA analysis using the RDA command and assign the results to a new variable called model. The response matrix is clone and the predictor matrix is env. Don’t worry for now about any additional variable transformations, you can use the raw environmental values and the Hellinger-transformed clone values.
- Part D: What proportion of the variation in clonal composition is explained by environmental properties? Give the adjusted R² value (using RsquareAdj).
- Part E: Use the summary(model) output to get the “Accumulated constrained eigenvalues” and tell me how much variation in the clone matrix is explained by the first two RDA axes.
- Part F: Use biplot(model) to visually inspect and tell me: what are the environmental preferences of clone h? How about clone b?
- Part G: What is the average value of Notonectid for all sites where clone h appears? How about for clone b?
- Part H: What is the average value of TN for all sites where clone b appears? How about for clone c?

```
clone <- read.table(paste(dir,"/clone.txt",sep=""), header = T)
head(clone)
```

Part A

```
##           a b           c d e f g h i j k l m       n o
## CP      1.0000000 0 0.0000000 0 0 0 0 0 0 0 0 0 0 0.0 0
## HSP      0.0000000 1 0.0000000 0 0 0 0 0 0 0 0 0 0 0.0 0
## KBSF      0.0000000 1 0.0000000 0 0 0 0 0 0 0 0 0 0 0.0 0
## PL10      0.0000000 0 0.9000000 0 0 0 0 0 0 0 0 0 0 0.1 0
## PL11      0.0000000 0 1.0000000 0 0 0 0 0 0 0 0 0 0 0.0 0
## PL15      0.1666667 0 0.8333333 0 0 0 0 0 0 0 0 0 0 0.0 0
```

```
env <- read.table(paste(dir,"/environment.txt", sep=""), header = T)
head(env)
```

```
##           pH           Volume macrophyte shade           DOC Coleoptera Odonata Notonectid
## CP      9.28 2644.048591           5 4.30 0.135877           4           0           8
## HSP      6.53  56.664342           30 5.16 0.356965           12          2           1
## KBSF      7.20   0.983554           70 63.26 0.713930           0           0           0
## PL10      8.27 711.720440           20 1.57 0.096726           74         27           6
## PL11      7.25 703.423627           30 1.75 0.000000           36         44           7
## PL15      7.48 738.804200           20 0.83 0.052969           48          4           0
##           Chaoborus           TN           TP
## CP           0 1346.5354  57.39766
## HSP           3 1937.8542  80.23914
## KBSF           0 5888.5822 1354.49934
## PL10           3 1775.3148  41.75540
## PL11          88  574.7157  14.84317
## PL15           2  389.0772  24.90699
```

```
#Vegan package installed in the beginning of code
hel_clone <- decostand(clone, method = "hellinger")
head(hel_clone)
```

Part B

```
##           a b           c d e f g h i j k l m       n o
## CP      1.0000000 0 0.0000000 0 0 0 0 0 0 0 0 0 0 0.0000000 0
## HSP      0.0000000 1 0.0000000 0 0 0 0 0 0 0 0 0 0 0.0000000 0
## KBSF      0.0000000 1 0.0000000 0 0 0 0 0 0 0 0 0 0 0.0000000 0
## PL10      0.0000000 0 0.9486833 0 0 0 0 0 0 0 0 0 0 0.3162278 0
## PL11      0.0000000 0 1.0000000 0 0 0 0 0 0 0 0 0 0 0.0000000 0
## PL15      0.4082483 0 0.9128709 0 0 0 0 0 0 0 0 0 0 0.0000000 0
```

```
model <- rda(hel_clone, env)
summary(model)
```

Part C

```
##
## Call:
## rda(X = hel_clone, Y = env)
##
```



```

## Partitioning of variance:
##           Inertia Proportion
## Total           0.7334      1.0000
## Constrained     0.5349      0.7294
## Unconstrained   0.1985      0.2706
##
## Eigenvalues, and their contribution to the variance
##
## Importance of components:
##           RDA1   RDA2   RDA3   RDA4   RDA5   RDA6   RDA7
## Eigenvalue      0.2049 0.1059 0.07487 0.06773 0.04851 0.02201 0.005616
## Proportion Explained 0.2794 0.1444 0.10209 0.09235 0.06615 0.03002 0.007657
## Cumulative Proportion 0.2794 0.4238 0.52585 0.61820 0.68435 0.71437 0.722025
##           RDA8   RDA9   RDA10   RDA11   PC1   PC2
## Eigenvalue      0.003068 0.001159 0.0009343 0.0002452 0.09517 0.04854
## Proportion Explained 0.004184 0.001580 0.0012739 0.0003344 0.12977 0.06618
## Cumulative Proportion 0.726209 0.727789 0.7290628 0.7293972 0.85916 0.92535
##           PC3   PC4   PC5   PC6   PC7
## Eigenvalue      0.02946 0.01333 0.005560 0.004152 0.002253
## Proportion Explained 0.04017 0.01817 0.007581 0.005661 0.003072
## Cumulative Proportion 0.96552 0.98369 0.991267 0.996928 1.000000
##
## Accumulated constrained eigenvalues
## Importance of components:
##           RDA1   RDA2   RDA3   RDA4   RDA5   RDA6   RDA7
## Eigenvalue      0.2049 0.1059 0.07487 0.06773 0.04851 0.02201 0.005616
## Proportion Explained 0.3831 0.1979 0.13996 0.12661 0.09069 0.04115 0.010498
## Cumulative Proportion 0.3831 0.5810 0.72094 0.84755 0.93824 0.97939 0.989892
##           RDA8   RDA9   RDA10   RDA11
## Eigenvalue      0.003068 0.001159 0.0009343 0.0002452
## Proportion Explained 0.005736 0.002166 0.0017465 0.0004584
## Cumulative Proportion 0.995629 0.997795 0.9995416 1.0000000
##
## Scaling 2 for species and site scores
## * Species are scaled proportional to eigenvalues
## * Sites are unscaled: weighted dispersion equal on all dimensions
## * General scaling constant of scores: 1.906129
##
##
## Species scores
##
##           RDA1   RDA2   RDA3   RDA4   RDA5   RDA6
## a -0.057022 -0.2469832 -0.50430 -0.0871548 0.03439 -0.0327484
## b -0.165318 0.5318456 -0.06631 0.1716989 0.04882 -0.1013865
## c 0.878426 -0.1071679 0.05390 0.1629621 -0.04321 -0.0290905
## d 0.032398 -0.0001824 0.07412 -0.0926103 -0.05624 0.0025715
## e -0.042524 0.0079839 0.14723 -0.3355344 -0.15552 -0.0404920
## f -0.013447 0.0025247 0.04656 -0.1061053 -0.04918 -0.0128047
## g 0.072039 0.1893443 -0.06774 -0.0331495 -0.01341 0.2968186
## h -0.398014 -0.2556011 0.07466 0.3143536 -0.26332 0.0251259
## i -0.198859 -0.2502563 0.23356 0.0250360 0.34730 0.0232599
## j -0.007324 -0.0194434 0.02410 -0.1187258 -0.05184 -0.0220865
## k -0.013447 0.0025247 0.04656 -0.1061053 -0.04918 -0.0128047
## l -0.013487 -0.0635092 -0.09783 0.0006367 0.02661 0.0001011

```

```

## m -0.013447  0.0025247  0.04656 -0.1061053 -0.04918 -0.0128047
## n  0.031802  0.0173092  0.01130 -0.0079198  0.02515 -0.0704295
## o -0.071701 -0.0242483  0.02493  0.0475428 -0.07835  0.0010246
##
##
## Site scores (weighted sums of species scores)
##
##          RDA1      RDA2      RDA3      RDA4      RDA5      RDA6
## CP   -0.34271 -0.38789 -1.270082 -0.58029  0.23849 -0.30052
## HSP   -0.44939  1.09690 -0.089231  0.19118  0.29852 -0.92989
## KBSF  -0.44939  1.09690 -0.089231  0.19118  0.29852 -0.92989
## PL10  0.54428 -0.10042  0.237042  0.13276 -0.04206 -0.45751
## PL11  0.57877 -0.12134  0.234868  0.16515 -0.08438 -0.26698
## PL15  0.48045 -0.29577 -0.332863  0.01678 -0.01030 -0.36633
## PL16  0.48522  0.15447  0.230269  0.19247 -0.07993 -0.48251
## PL17  0.57877 -0.12134  0.234868  0.16515 -0.08438 -0.26698
## PL18  0.51661 -0.25975 -0.202545  0.05808 -0.02991 -0.34825
## PL2   -0.06397  0.15924 -0.402663  0.53175 -0.27999 -0.71951
## PL4   -0.21558  0.44394 -0.093082 -0.41934  0.03960  2.72140
## PL6    0.18396  0.30500 -0.003016 -0.17872 -0.03856  2.27428
## PL8    0.50719  0.14791  0.183671  0.28099 -0.02571 -0.49839
## PM2   -0.68032 -0.39296  0.301768  0.61164 -1.04669  0.22073
## PM3   -0.72320 -0.58175  0.590064  0.51740 -0.08428  0.30762
## QP    -0.48243 -0.39413  0.719241 -0.24592  1.54045  0.21304
## R      0.38532 -0.28433  0.074741 -0.05083  0.39403  0.36715
## SP    -0.52894 -0.55416 -0.903080 -0.03482 -0.29587 -0.09691
## PM1   -0.32463  0.08946  0.579262 -1.54462 -0.70754 -0.44054
##
##
## Site constraints (linear combinations of constraining variables)
##
##          RDA1      RDA2      RDA3      RDA4      RDA5      RDA6
## CP   -0.46837 -0.40038 -1.15268 -0.548799  0.12042 -0.0681995
## HSP   -0.39605  0.85730 -0.07609  0.171279  0.10093  0.1674427
## KBSF  -0.45334  1.09265 -0.07883  0.171980  0.30300 -0.8167490
## PL10  0.36539  0.19888  0.12980 -0.090996  0.28898 -0.8092064
## PL11  0.57651 -0.11595  0.22722  0.167007 -0.08296 -0.3181670
## PL15  0.25523 -0.06739  0.02685  0.013961  0.29498 -0.0040942
## PL16  0.64513 -0.03809  0.38787  0.189899 -0.09930  0.2163714
## PL17  0.27796  0.19758  0.03649 -0.048854 -0.01705  0.8393053
## PL18  0.68472 -0.30641 -0.02625  0.363211 -0.33374 -0.5682947
## PL2   -0.03057  0.08221 -0.24013  0.377620 -0.33662  0.4012267
## PL4    0.10465  0.44137 -0.27406  0.069544 -0.15576  0.3698224
## PL6    0.15290  0.37009  0.12418 -0.163431  0.13230  0.8417352
## PL8    0.38582 -0.21341 -0.18372  0.052300 -0.02544 -0.0254340
## PM2   -0.80296 -0.27155  0.27916  0.532416 -0.87739  0.0114746
## PM3   -0.73301 -0.55656  0.54021  0.565264 -0.10091 -0.0981827
## QP    -0.37118 -0.50573  0.68185 -0.139388  1.32822  0.1834777
## R      0.09439 -0.33864 -0.34613 -0.194544 -0.04097 -0.1430775
## SP    -0.09800 -0.46150 -0.71088  0.004627  0.19334  0.0007344
## PM1   -0.18923  0.03553  0.65515 -1.493095 -0.69206 -0.1801854
##
##
## Biplot scores for constraining variables

```

```
##
##           RDA1      RDA2      RDA3      RDA4      RDA5      RDA6
## pH          0.55586 -0.25046 -0.26328 -0.22710  0.080878  0.23975
## Volume      -0.17885 -0.16369  0.13233 -0.80259 -0.494092 -0.09475
## macrophyte  -0.47434  0.19094  0.24727  0.47977  0.063857 -0.26450
## shade       -0.57073  0.24899  0.27173  0.09833  0.104208 -0.27685
## DOC         -0.61728  0.03205  0.19539  0.32512 -0.024059 -0.24177
## Coleoptera  -0.03265 -0.26959  0.43217 -0.07487  0.751158 -0.06879
## Odonata      0.62649 -0.13314  0.20674  0.16520  0.059843 -0.46533
## Notonectid  -0.04028 -0.56650 -0.20646  0.16761  0.099067 -0.44650
## Chaoborus    0.31177 -0.06402  0.15634  0.09510  0.004333 -0.17573
## TN          -0.61439  0.33257  0.26251  0.08281  0.230290 -0.42395
## TP          -0.41806  0.46629  0.06042  0.19507  0.153947 -0.43757
```

```
R_Adj <- RsquareAdj(model)
cat("The Adjusted R2 is:", round(R_Adj$adj.r.squared,4))
```

Part D

```
## The Adjusted R2 is: 0.3042
```

```
summary(model)
```

Part E

```
##
## Call:
## rda(X = hel_clone, Y = env)
##
## Partitioning of variance:
##           Inertia Proportion
## Total          0.7334      1.0000
## Constrained    0.5349      0.7294
## Unconstrained  0.1985      0.2706
##
## Eigenvalues, and their contribution to the variance
##
## Importance of components:
##           RDA1      RDA2      RDA3      RDA4      RDA5      RDA6      RDA7
## Eigenvalue      0.2049  0.1059  0.07487  0.06773  0.04851  0.02201  0.005616
## Proportion Explained 0.2794  0.1444  0.10209  0.09235  0.06615  0.03002  0.007657
## Cumulative Proportion 0.2794  0.4238  0.52585  0.61820  0.68435  0.71437  0.722025
##           RDA8      RDA9      RDA10      RDA11      PC1      PC2
## Eigenvalue      0.003068  0.001159  0.0009343  0.0002452  0.09517  0.04854
## Proportion Explained 0.004184  0.001580  0.0012739  0.0003344  0.12977  0.06618
## Cumulative Proportion 0.726209  0.727789  0.7290628  0.7293972  0.85916  0.92535
##           PC3      PC4      PC5      PC6      PC7
## Eigenvalue      0.02946  0.01333  0.005560  0.004152  0.002253
## Proportion Explained 0.04017  0.01817  0.007581  0.005661  0.003072
## Cumulative Proportion 0.96552  0.98369  0.991267  0.996928  1.000000
##
## Accumulated constrained eigenvalues
## Importance of components:
```

```

##          RDA1   RDA2   RDA3   RDA4   RDA5   RDA6   RDA7
## Eigenvalue      0.2049 0.1059 0.07487 0.06773 0.04851 0.02201 0.005616
## Proportion Explained 0.3831 0.1979 0.13996 0.12661 0.09069 0.04115 0.010498
## Cumulative Proportion 0.3831 0.5810 0.72094 0.84755 0.93824 0.97939 0.989892
##          RDA8   RDA9   RDA10   RDA11
## Eigenvalue      0.003068 0.001159 0.0009343 0.0002452
## Proportion Explained 0.005736 0.002166 0.0017465 0.0004584
## Cumulative Proportion 0.995629 0.997795 0.9995416 1.0000000
##
## Scaling 2 for species and site scores
## * Species are scaled proportional to eigenvalues
## * Sites are unscaled: weighted dispersion equal on all dimensions
## * General scaling constant of scores: 1.906129
##
##
## Species scores
##
##          RDA1   RDA2   RDA3   RDA4   RDA5   RDA6
## a -0.057022 -0.2469832 -0.50430 -0.0871548 0.03439 -0.0327484
## b -0.165318 0.5318456 -0.06631 0.1716989 0.04882 -0.1013865
## c 0.878426 -0.1071679 0.05390 0.1629621 -0.04321 -0.0290905
## d 0.032398 -0.0001824 0.07412 -0.0926103 -0.05624 0.0025715
## e -0.042524 0.0079839 0.14723 -0.3355344 -0.15552 -0.0404920
## f -0.013447 0.0025247 0.04656 -0.1061053 -0.04918 -0.0128047
## g 0.072039 0.1893443 -0.06774 -0.0331495 -0.01341 0.2968186
## h -0.398014 -0.2556011 0.07466 0.3143536 -0.26332 0.0251259
## i -0.198859 -0.2502563 0.23356 0.0250360 0.34730 0.0232599
## j -0.007324 -0.0194434 0.02410 -0.1187258 -0.05184 -0.0220865
## k -0.013447 0.0025247 0.04656 -0.1061053 -0.04918 -0.0128047
## l -0.013487 -0.0635092 -0.09783 0.0006367 0.02661 0.0001011
## m -0.013447 0.0025247 0.04656 -0.1061053 -0.04918 -0.0128047
## n 0.031802 0.0173092 0.01130 -0.0079198 0.02515 -0.0704295
## o -0.071701 -0.0242483 0.02493 0.0475428 -0.07835 0.0010246
##
##
## Site scores (weighted sums of species scores)
##
##          RDA1   RDA2   RDA3   RDA4   RDA5   RDA6
## CP -0.34271 -0.38789 -1.270082 -0.58029 0.23849 -0.30052
## HSP -0.44939 1.09690 -0.089231 0.19118 0.29852 -0.92989
## KBSF -0.44939 1.09690 -0.089231 0.19118 0.29852 -0.92989
## PL10 0.54428 -0.10042 0.237042 0.13276 -0.04206 -0.45751
## PL11 0.57877 -0.12134 0.234868 0.16515 -0.08438 -0.26698
## PL15 0.48045 -0.29577 -0.332863 0.01678 -0.01030 -0.36633
## PL16 0.48522 0.15447 0.230269 0.19247 -0.07993 -0.48251
## PL17 0.57877 -0.12134 0.234868 0.16515 -0.08438 -0.26698
## PL18 0.51661 -0.25975 -0.202545 0.05808 -0.02991 -0.34825
## PL2 -0.06397 0.15924 -0.402663 0.53175 -0.27999 -0.71951
## PL4 -0.21558 0.44394 -0.093082 -0.41934 0.03960 2.72140
## PL6 0.18396 0.30500 -0.003016 -0.17872 -0.03856 2.27428
## PL8 0.50719 0.14791 0.183671 0.28099 -0.02571 -0.49839
## PM2 -0.68032 -0.39296 0.301768 0.61164 -1.04669 0.22073
## PM3 -0.72320 -0.58175 0.590064 0.51740 -0.08428 0.30762
## QP -0.48243 -0.39413 0.719241 -0.24592 1.54045 0.21304

```

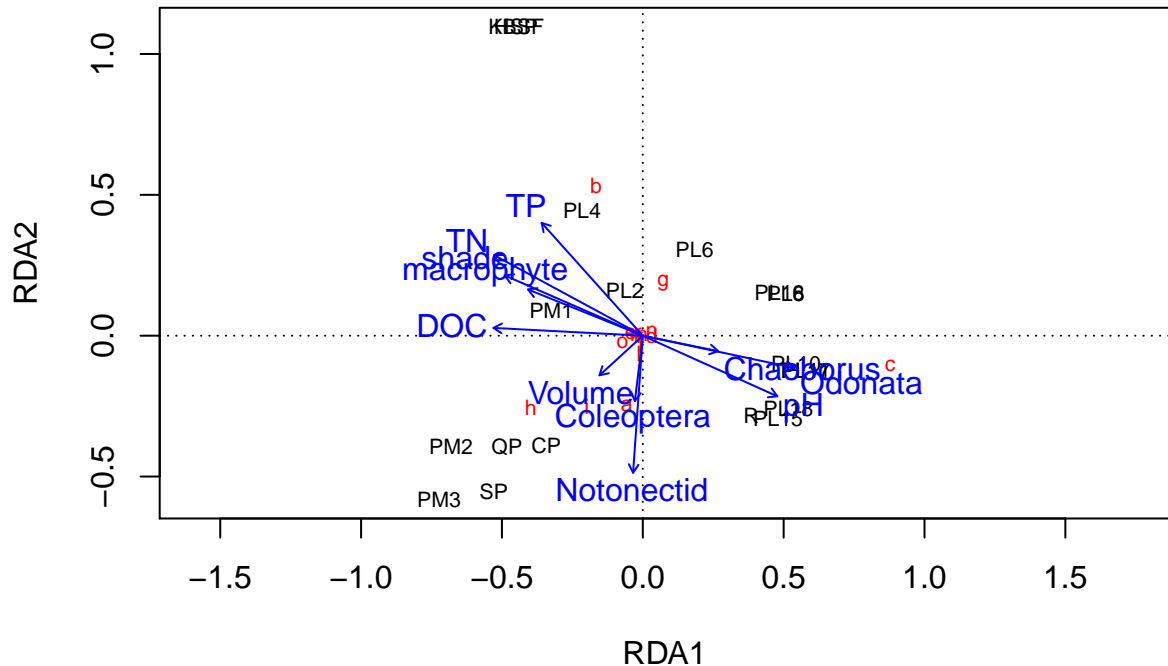
```

## R      0.38532 -0.28433  0.074741 -0.05083  0.39403  0.36715
## SP     -0.52894 -0.55416 -0.903080 -0.03482 -0.29587 -0.09691
## PM1    -0.32463  0.08946  0.579262 -1.54462 -0.70754 -0.44054
##
##
## Site constraints (linear combinations of constraining variables)
##
##          RDA1      RDA2      RDA3      RDA4      RDA5      RDA6
## CP      -0.46837 -0.40038 -1.15268 -0.548799  0.12042 -0.0681995
## HSP     -0.39605  0.85730 -0.07609  0.171279  0.10093  0.1674427
## KBSF    -0.45334  1.09265 -0.07883  0.171980  0.30300 -0.8167490
## PL10     0.36539  0.19888  0.12980 -0.090996  0.28898 -0.8092064
## PL11     0.57651 -0.11595  0.22722  0.167007 -0.08296 -0.3181670
## PL15     0.25523 -0.06739  0.02685  0.013961  0.29498 -0.0040942
## PL16     0.64513 -0.03809  0.38787  0.189899 -0.09930  0.2163714
## PL17     0.27796  0.19758  0.03649 -0.048854 -0.01705  0.8393053
## PL18     0.68472 -0.30641 -0.02625  0.363211 -0.33374 -0.5682947
## PL2      -0.03057  0.08221 -0.24013  0.377620 -0.33662  0.4012267
## PL4       0.10465  0.44137 -0.27406  0.069544 -0.15576  0.3698224
## PL6       0.15290  0.37009  0.12418 -0.163431  0.13230  0.8417352
## PL8       0.38582 -0.21341 -0.18372  0.052300 -0.02544 -0.0254340
## PM2      -0.80296 -0.27155  0.27916  0.532416 -0.87739  0.0114746
## PM3      -0.73301 -0.55656  0.54021  0.565264 -0.10091 -0.0981827
## QP       -0.37118 -0.50573  0.68185 -0.139388  1.32822  0.1834777
## R         0.09439 -0.33864 -0.34613 -0.194544 -0.04097 -0.1430775
## SP       -0.09800 -0.46150 -0.71088  0.004627  0.19334  0.0007344
## PM1      -0.18923  0.03553  0.65515 -1.493095 -0.69206 -0.1801854
##
##
## Biplot scores for constraining variables
##
##          RDA1      RDA2      RDA3      RDA4      RDA5      RDA6
## pH         0.55586 -0.25046 -0.26328 -0.22710  0.080878  0.23975
## Volume     -0.17885 -0.16369  0.13233 -0.80259 -0.494092 -0.09475
## macrophyte -0.47434  0.19094  0.24727  0.47977  0.063857 -0.26450
## shade      -0.57073  0.24899  0.27173  0.09833  0.104208 -0.27685
## DOC        -0.61728  0.03205  0.19539  0.32512 -0.024059 -0.24177
## Coleoptera -0.03265 -0.26959  0.43217 -0.07487  0.751158 -0.06879
## Odonata     0.62649 -0.13314  0.20674  0.16520  0.059843 -0.46533
## Notonectid -0.04028 -0.56650 -0.20646  0.16761  0.099067 -0.44650
## Chaoborus   0.31177 -0.06402  0.15634  0.09510  0.004333 -0.17573
## TN         -0.61439  0.33257  0.26251  0.08281  0.230290 -0.42395
## TP         -0.41806  0.46629  0.06042  0.19507  0.153947 -0.43757

```

The percent variation is .4238 or 42.38% which we get by combining the RDA1 and RDA2.

```
plot(model)
```



Part F

```
df <- cbind.data.frame(hel_clone, env)
clone_h <- subset(df, df$h>0)
cat("Average value of Notonectid where clone h appears:",mean(clone_h$Notonectid))
```

Part G

```
## Average value of Notonectid where clone h appears: 3.75
```

```
clone_b <- subset(df, df$b>0)
cat("\nAverage value of Notonectid where clone b appears:",mean(clone_b$Notonectid))
```

```
##
```

```
## Average value of Notonectid where clone b appears: 1.4
```

```
clone_b <- subset(df, df$b>0)
cat("Average value of TN where clone b appears:",mean(clone_b$TN))
```

Part H

```
## Average value of TN where clone b appears: 1814.378
```

```
clone_c <- subset(df, df$c>0)
cat("\nAverage value of TN where clone c appears:",mean(clone_c$TN))
```

```
##
```

```
## Average value of TN where clone c appears: 603.8922
```

Question 9

Sites that are close to one another may have more similar clonal composition than sites that are far away from one another. Sites that are close to one another may also have more similar environmental properties than sites that are far away. We need to remove the potential for spatial proximity of sites to confound

the signal between clone and environment. We will conduct a partial RDA, where we come up with new ordinations of the Y matrix (hel_clone) in reduced dimensional space that are constrained by X (env), but only after that X matrix has the effects of the potentially covarying matrix Z removed.

- Part A: Read the data in space.txt into a variable called space. Use the help documentation for the RDA command (?rda) to add the additional Z matrix into the analysis.
- Part B: What is the proportion of variation explained (adjusted R2 value) of the comparison between clone and environment now?

```
space <- read.table(paste(dir,"/space.txt", sep = ""), header = T)
model_z <- rda(hel_clone, env, space)
summary(model_z)
```

Part A

```
##
## Call:
## rda(X = hel_clone, Y = env, Z = space)
##
## Partitioning of variance:
##              Inertia Proportion
## Total          0.7334      1.0000
## Conditioned    0.1817      0.2477
## Constrained    0.4066      0.5545
## Unconstrained  0.1451      0.1978
##
## Eigenvalues, and their contribution to the variance
## after removing the contribution of conditiniong variables
##
## Importance of components:
##              RDA1      RDA2      RDA3      RDA4      RDA5      RDA6      RDA7
## Eigenvalue          0.1501 0.07948 0.07547 0.06154 0.01814 0.00769 0.006237
## Proportion Explained 0.2721 0.14407 0.13680 0.11155 0.03288 0.01394 0.011305
## Cumulative Proportion 0.2721 0.41614 0.55293 0.66448 0.69737 0.71130 0.722608
##              RDA8      RDA9      RDA10      RDA11      PC1      PC2
## Eigenvalue          0.004631 0.002981 0.0003517 1.197e-05 0.07777 0.04481
## Proportion Explained 0.008393 0.005404 0.0006375 2.170e-05 0.14096 0.08123
## Cumulative Proportion 0.731002 0.736405 0.7370427 7.371e-01 0.87802 0.95925
##              PC3      PC4      PC5
## Eigenvalue          0.01303 0.005789 0.003660
## Proportion Explained 0.02363 0.010493 0.006633
## Cumulative Proportion 0.98287 0.993367 1.000000
##
## Accumulated constrained eigenvalues
## Importance of components:
##              RDA1      RDA2      RDA3      RDA4      RDA5      RDA6      RDA7
## Eigenvalue          0.1501 0.07948 0.07547 0.06154 0.01814 0.00769 0.006237
## Proportion Explained 0.3691 0.19546 0.18560 0.15134 0.04461 0.01891 0.015338
## Cumulative Proportion 0.3691 0.56459 0.75018 0.90153 0.94614 0.96505 0.980387
##              RDA8      RDA9      RDA10      RDA11
## Eigenvalue          0.004631 0.002981 0.0003517 1.197e-05
## Proportion Explained 0.011387 0.007331 0.0008649 2.944e-05
## Cumulative Proportion 0.991774 0.999106 0.9999706 1.000e+00
##
```

```

## Scaling 2 for species and site scores
## * Species are scaled proportional to eigenvalues
## * Sites are unscaled: weighted dispersion equal on all dimensions
## * General scaling constant of scores: 1.906129
##
##
## Species scores
##
##      RDA1      RDA2      RDA3      RDA4      RDA5      RDA6
## a -0.16533  0.161262  0.49339  0.17061  0.02876 -0.013864
## b  0.31937 -0.118558  0.11600 -0.24885  0.17078 -0.076981
## c  0.55306  0.324459 -0.14713  0.08658 -0.01158  0.032840
## d  0.03385 -0.069928 -0.06509  0.08038  0.01915 -0.009064
## e -0.03619 -0.265663 -0.11662  0.21931 -0.04508 -0.053304
## f -0.01145 -0.084010 -0.03688  0.06935 -0.01425 -0.016856
## g  0.02238 -0.255105  0.08362 -0.26575 -0.07778  0.082008
## h -0.42673  0.272910 -0.15493 -0.22723 -0.03305 -0.056943
## i -0.32927  0.004296 -0.18410  0.08042  0.20269  0.069549
## j -0.03079 -0.097778 -0.01499  0.07870  0.02159 -0.021868
## k -0.01145 -0.084010 -0.03688  0.06935 -0.01425 -0.016856
## l -0.09936  0.022959  0.08190 -0.02793 -0.06032  0.064410
## m -0.01145 -0.084010 -0.03688  0.06935 -0.01425 -0.016856
## n  0.02711  0.010186 -0.01411  0.01607 -0.02089 -0.012560
## o -0.05487  0.045114 -0.03773 -0.03772 -0.06303 -0.086798
##
##
## Site scores (weighted sums of species scores)
##
##      RDA1      RDA2      RDA3      RDA4      RDA5      RDA6
## CP  -0.30036  0.21175  1.27509  0.814777 -0.22297  0.522677
## HSP  0.36649 -0.47910  0.26049 -0.539657  1.30628 -1.066775
## KBSF 0.71067  0.03240  0.14514 -0.024305 -0.35873  0.094231
## PL10 0.38837  0.31482 -0.33816  0.209831 -0.32194  0.147390
## PL11 0.43060  0.36904 -0.35189  0.229671 -0.30498  0.367935
## PL15 0.24085  0.41896  0.23300  0.384641 -0.04224 -0.005007
## PL16 0.45211  0.12296 -0.27222 -0.003275  0.42038 -0.496075
## PL17 0.36523  0.28333 -0.32907  0.137061 -0.08426  0.074578
## PL18 0.23597  0.34373  0.11570  0.270192  0.09009 -0.180807
## PL2  0.05778  0.32246  0.35668 -0.410584  0.75609 -1.844645
## PL4  -0.29097 -1.11129  0.26817 -0.936299 -1.03043  1.610997
## PL6  0.02489 -0.68661  0.06720 -0.743384 -0.88914  1.619070
## PL8  0.46961  0.20276 -0.24184 -0.056947  0.34073 -0.400292
## PM2  -0.59263  0.50372 -0.49211 -0.443498 -0.79650 -0.652760
## PM3  -0.72243  0.43674 -0.68654 -0.163292  0.58311  1.303359
## QP   -0.76504 -0.21973 -0.42883  0.305395  0.13617 -0.215023
## R     0.05637  0.05219 -0.08201  0.175767  0.62594  0.887108
## SP   -0.91239  0.08986  0.90750 -0.204348 -0.13227 -1.020197
## PM1  -0.21513 -1.20799 -0.40629  0.998257 -0.07534 -0.745766
##
##
## Site constraints (linear combinations of constraining variables)
##
##      RDA1      RDA2      RDA3      RDA4      RDA5      RDA6
## CP  -0.23669  0.2217836  1.24415  0.81381  0.04169  0.08697

```



```
## HSP    0.27398 -0.5635349  0.23068 -0.63440  0.82190 -0.12405
## KBSF   0.69191 -0.0007513  0.13693 -0.04274 -0.42241  0.21530
## PL10   0.31149  0.1170372 -0.16209  0.18467 -0.23998 -0.14431
## PL11   0.42604  0.3724795 -0.34730  0.23069 -0.30052  0.33344
## PL15   0.33328  0.4538006  0.01934  0.26389  0.16732 -0.25772
## PL16   0.63739  0.1981635 -0.39700  0.15523  0.47009  0.10965
## PL17   0.11392 -0.2531820 -0.03578 -0.38137 -0.47710  0.54323
## PL18   0.32807  0.4039786 -0.14789  0.11893  0.21983 -0.27154
## PL2    -0.05637 -0.0412129  0.21315 -0.56267  0.25641 -0.63444
## PL4     0.11818 -0.4546400  0.29833 -0.58517  0.09722 -0.29252
## PL6     0.03787 -0.4787488 -0.08398 -0.46983 -0.57835  0.69019
## PL8     0.24145  0.4103559  0.12865  0.22330 -0.18708 -0.12740
## PM2    -0.61451  0.5052151 -0.42254 -0.42242 -0.70582 -0.97202
## PM3    -0.68617  0.5242649 -0.64236 -0.11120  0.77631  0.86484
## QP     -0.73860 -0.1874376 -0.44592  0.30224  0.14683 -0.17320
## R      -0.29821 -0.2122299  0.33744  0.14410  0.55258 -0.07726
## SP     -0.72200  0.1668320  0.59513 -0.20297 -0.43835  0.46804
## PM1    -0.16105 -1.1821736 -0.51895  0.97589 -0.20058 -0.23720
##
##
## Biplot scores for constraining variables
##
##          RDA1      RDA2      RDA3      RDA4      RDA5      RDA6
## pH          0.14376  0.030170  0.24065  0.24119 -0.26483  0.177645
## Volume     -0.23149 -0.495601 -0.08785  0.57923 -0.20548 -0.252891
## macrophyte -0.04703  0.267984 -0.27545 -0.25818  0.25446  0.280739
## shade      -0.11163  0.015623 -0.22290 -0.01975 -0.36101 -0.275656
## DOC        -0.24774  0.208133 -0.21975 -0.13313  0.33550  0.382673
## Coleoptera -0.25575  0.021653 -0.32560  0.25155  0.04034 -0.087288
## Odonata     0.42193  0.365335 -0.29743  0.24969 -0.07101  0.008373
## Notonectid -0.26656  0.567228  0.11664  0.33881  0.02743  0.088472
## Chaoborus   0.23120  0.200823 -0.21226  0.13178 -0.13240  0.175030
## TN         -0.03558 -0.005223 -0.20705  0.04451  0.04438  0.277668
## TP          0.20165  0.088411 -0.04188 -0.05177 -0.06895  0.248679
```

```
R2 <- RsquareAdj(model_z)
cat("The Adjusted R2 now is:", round(R2$adj.r.squared,4))
```

Part B

```
## The Adjusted R2 now is: 0.1342
```