Morphometrics

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The following analyses are done to determine the spawning group for samples of unknown origin. I begin by creating a Linear Discriminate Analysis model for a dataset of individuals with known spawning origin. Using that model I then apply it to my dataset of unknown spawning origin to get posterior probabilities of assignment to each group.

```
####################################
###### Data & Package Loading ######
####################################

  # Set working directory and load packages
  #setwd("./data/Morphometrics/")
  #install.packages("MASS")
  library(MASS)
```

```
## Warning: package 'MASS' was built under R version 3.4.3
```

```
  # Load unknown data
  unknown.morph <- read.csv("/Users/saraschaal/Documents/Northeastern/LotterhosLab/Research/Data/CodEco

  # Load known data
  known.morph <- read.csv("/Users/saraschaal/Documents/Northeastern/LotterhosLab/Research/Data/CodEcoty


############################
#### Data Manipulation ####
############################

  # convert unknown data to mm
  unknown.morph[,4:26] <- 25.4*unknown.morph[,4:26]

  # add column with red or olive for unknown samples
  unknown.morph$ColorType <- NA
  for(i in 1:nrow(unknown.morph)){
    if(unknown.morph$RedGreenRatio[i] >= 1.3){
      unknown.morph$ColorType[i] <- "Red"
    } else {
      unknown.morph$ColorType[i] <- "Olive"
    }
  }

  # convert to cm and take out only the natural log transformed morph data
  unknown.morphlog <- log(unknown.morph[,4:26])
  known.morphlog <- log(known.morph[,c(16:38)]) # already in mm
  #colnames(known.morphlog)[23] <- "TotalLength"

  # remove data from landmark 11 - excludes gut fullness from affecting results
  unknown.morphlog <- unknown.morphlog[,c("TotalLength", "D1", "D2", "D3", "D4", "D5",
                                          "D6", "D7", "D8", "D10", "D13", "D14", "D16",
```

```
                                          "D17", "D18", "D19", "D21", "D22")]
  known.morphlog <- known.morphlog[,c( "D1", "D2", "D3", "D4", "D5", "D6", "D7", "D8",
                                       "D10", "D13", "D14", "D16", "D17", "D18", "D19",
                                       "D21", "D22")]
```

Perform Statistical Analysis on Known Data

```
##################
#### Run PCA ####
##################
  # Principle Components Analysis to Account for Total Length of Individuals
  pca.known <- prcomp(known.morphlog, scale. = TRUE)
  pca.known.noScale <- prcomp(known.morphlog)
  summary(pca.known)
```

```
## Importance of components%s:
##                           PC1     PC2     PC3     PC4     PC5     PC6
## Standard deviation     3.8588 0.90691 0.70229 0.41778 0.40647 0.31715
## Proportion of Variance 0.8759 0.04838 0.02901 0.01027 0.00972 0.00592
## Cumulative Proportion  0.8759 0.92428 0.95329 0.96356 0.97328 0.97920
##                           PC7     PC8     PC9    PC10    PC11    PC12
## Standard deviation     0.30079 0.27433 0.23872 0.19824 0.18315 0.15678
## Proportion of Variance 0.00532 0.00443 0.00335 0.00231 0.00197 0.00145
## Cumulative Proportion  0.98452 0.98894 0.99230 0.99461 0.99658 0.99803
##                           PC13    PC14    PC15    PC16    PC17
## Standard deviation     0.10246 0.10043 0.07596 0.06592 0.05322
## Proportion of Variance 0.00062 0.00059 0.00034 0.00026 0.00017
## Cumulative Proportion  0.99865 0.99924 0.99958 0.99983 1.00000
```

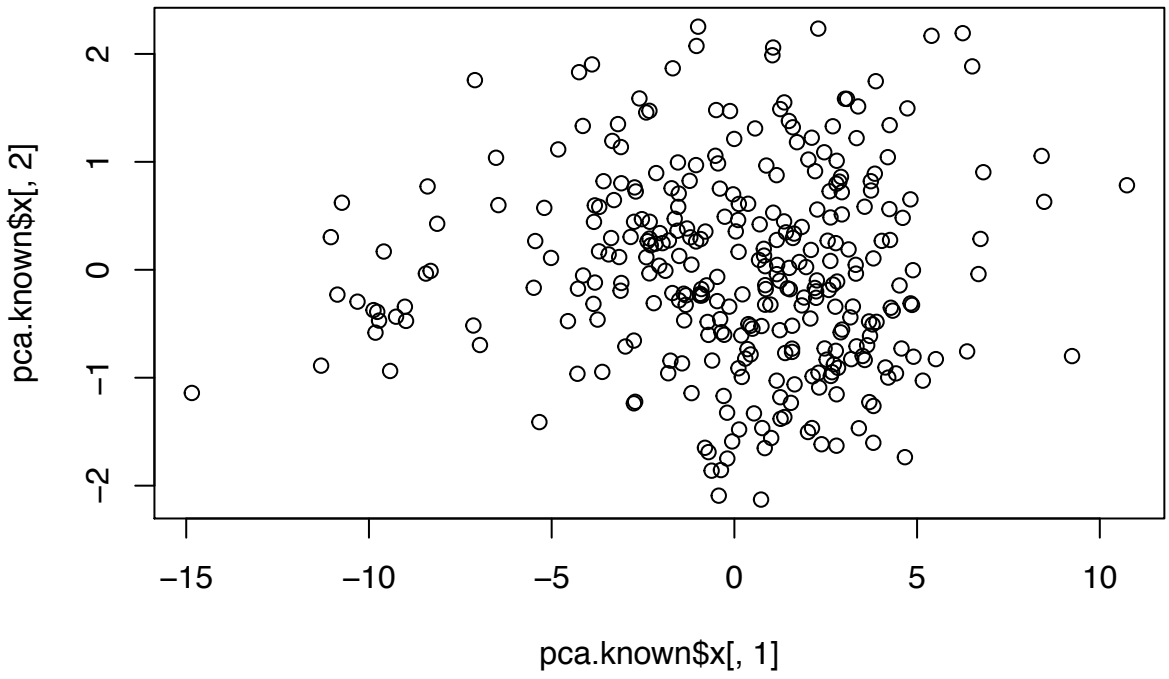
```
  max(pca.known$x[,1])
```

```
## [1] 10.74289
```

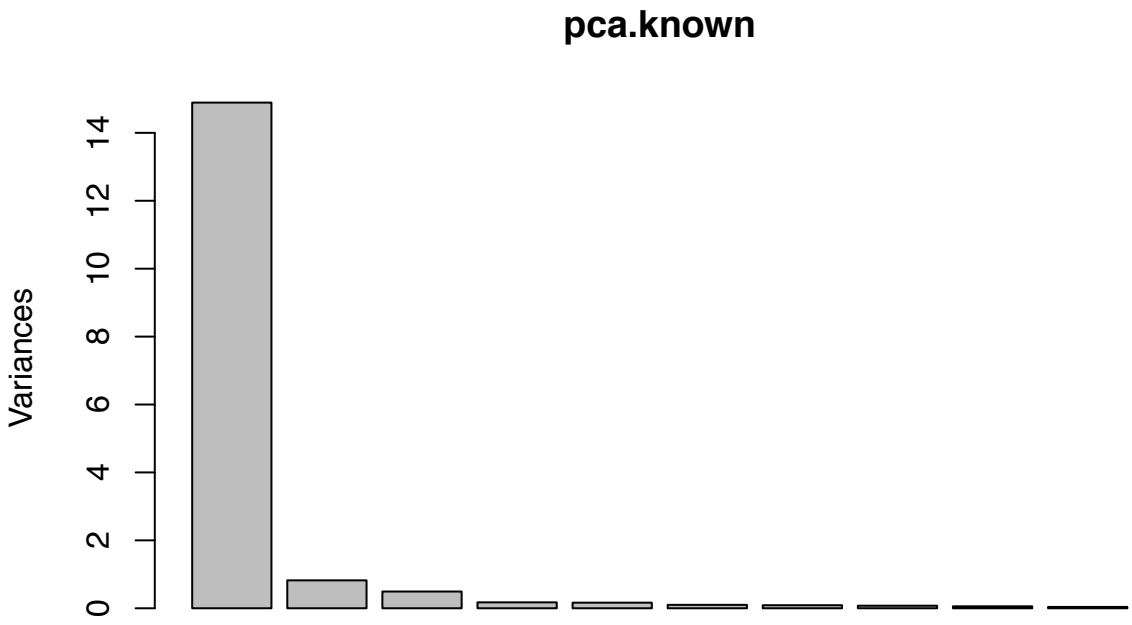
```
  min(pca.known$x[,1])
```

```
## [1] -14.84626
```

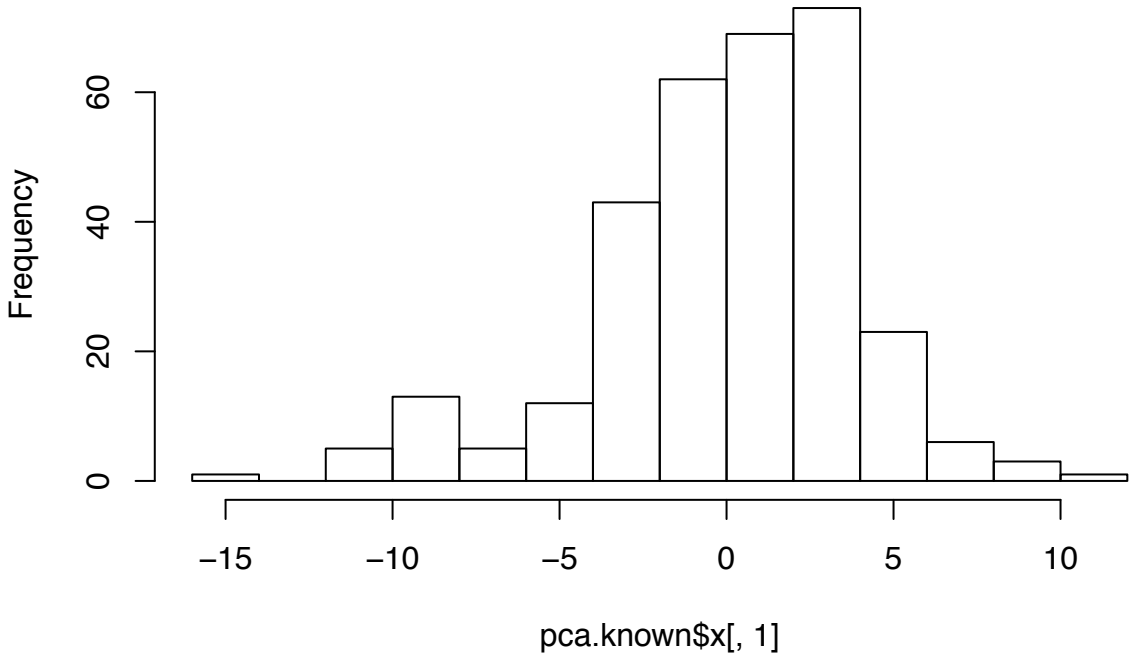
```
  # Plot PCA
  plot(pca.known$x[,1], pca.known$x[,2])
```




```
screeplot(pca.known)
```




```
hist(pca.known$x[,1])
```

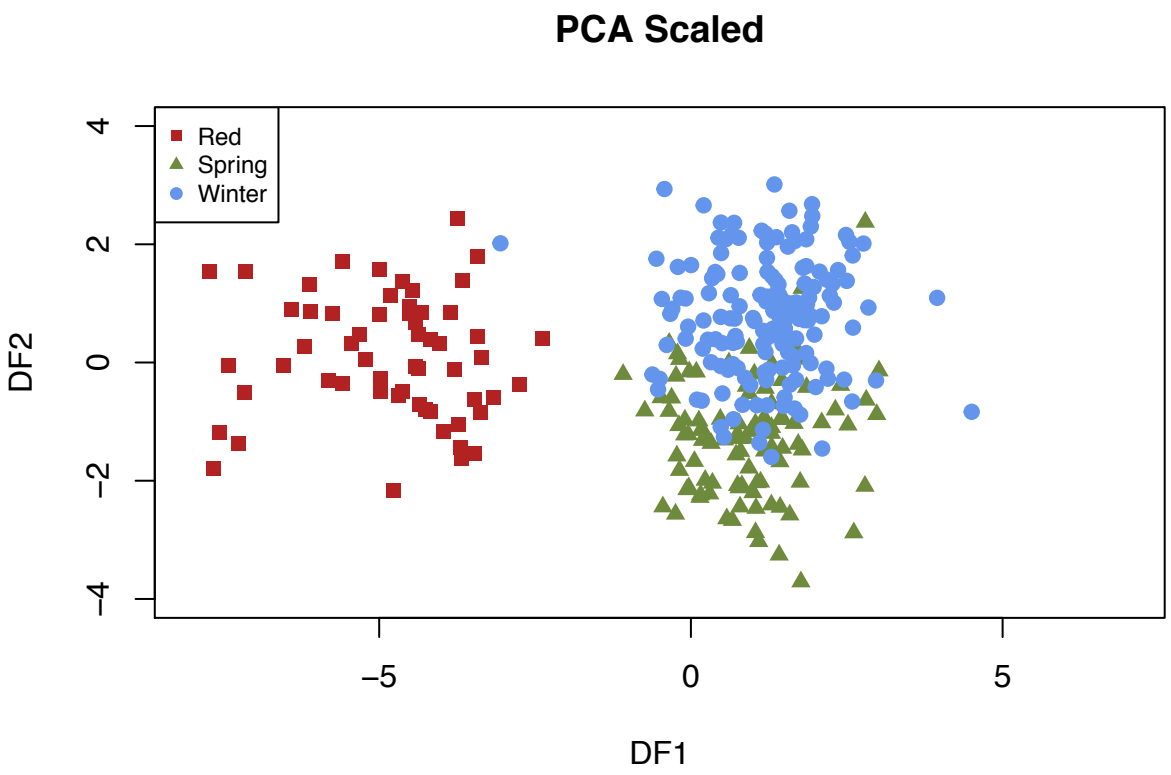



```
##############################################
#### Regress PC1 on Log Transformed Data ####
##############################################
  # Because PC1 corresponds to variance in morphology due to total length of the
  # fish we can regressing PC1 on our data to account for that variance in downstream
  # analyses

  # for loop to regress PC1 onto log transformed data and pull out residuals
  regress.known <- matrix(nrow = nrow(pca.known$x), ncol = ncol(pca.known$x))
  for(i in 1:ncol(pca.known$x)){
    regress.known[,i] <- lm(pca.known$x[,1]~known.morphlog[,i])$residuals
  }

  # Create dataframe with Spawning Season and Residuals of Regressed Data for DFA
  df.knowndata <- data.frame(known.morph$Season, regress.known)

##############################################
#### Perform Linear Discriminate Analysis ####
##############################################
  # Run DFA
  LDAknown.results <- lda(known.morph.Season ~ ., data = df.knowndata)
  LDAknown.predict <- predict(LDAknown.results)
  str(LDAknown.predict)
```

```
## List of 3
##  $ class    : Factor w/ 3 levels "Red","Spring",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ posterior: num [1:316, 1:3] 0.999 1 1 1 1 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:316] "1" "2" "3" "4" ...
##   .. ..$ : chr [1:3] "Red" "Spring" "Winter"
```

```
##  $ x        : num [1:316, 1:2] 47 -3.43 -4.97 -4.41 -4.37 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:316] "1" "2" "3" "4" ...
##   .. ..$ : chr [1:2] "LD1" "LD2"
```

```r
# Plot DFA
plot.data <- data.frame(LDAknown.predict$x, df.knowndata$known.morph.Season)
colnames(plot.data)[3] <- "Season"
plot(plot.data$LD1[plot.data$Season == "Red"],
     plot.data$LD2[plot.data$Season == "Red"], col = "firebrick",
     ylim = c(-4,4), xlim = c(-8, 7), pch = 15,
     ylab = "DF2", xlab = "DF1", main = "PCA Scaled")
points(plot.data$LD1[plot.data$Season == "Spring"],
       plot.data$LD2[plot.data$Season == "Spring"], col = "darkolivegreen4",
       pch = 17)
points(plot.data$LD1[plot.data$Season == "Winter"],
       plot.data$LD2[plot.data$Season == "Winter"], col = "cornflowerblue",
       pch = 19)
legend("topleft", legend = c("Red", "Spring", "Winter"),
       pch = c(15, 17, 19), cex = 0.75,
       col = c("firebrick", "darkolivegreen4", "cornflowerblue"))
```



Results from SPSS

Essentially the same as R just has an inverted sign for DF2 for some reason... haven't figured that out yet

```
SPSS.data <- read.csv("/Users/saraschaal/Desktop/GrahamMorph/GrahamSPSSData.csv")
SPSS.LDA <- read.csv("~/Desktop/GrahamMorph/GrahamDataLDA.csv")
SPSS.Log <- SPSS.data[,grep("Ln", names(SPSS.data))] # Same as R
regress.known.SPSS <- SPSS.data[,grep("RES", names(SPSS.data))] # Same as R when PCA is NOT scaled

head(SPSS.LDA$LDA1)
```

```
## [1] -3.40 -3.42 -5.02 -4.32 -4.29 -7.00
```

```
head(SPSS.LDA$LDA2)
```

```
## [1]  1.35 -1.69  0.29 -0.73 -0.49  0.64
```

```
head(LDAknown.predict$x[,1])
```

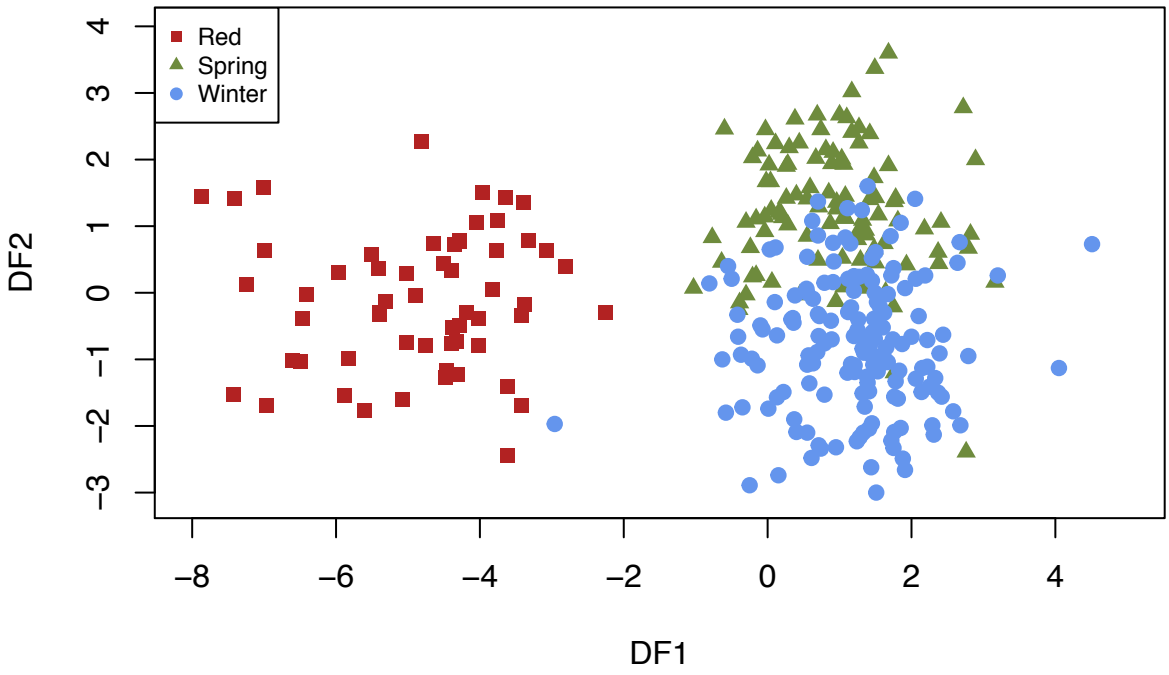
```
##         1         2         3         4         5         6
## -3.473184 -3.430827 -4.974498 -4.413652 -4.365435 -7.166811
```

```
head(LDAknown.predict$x[,2])
```

```
##          1          2          3          4          5          6
## -1.5317829  1.8005379 -0.2702528  0.6791140  0.4759889 -0.5073993
```

```
# sign is flipped and numbers are SLIGHTLY different from SPSS
# R and SPSS may calculate the LDA slightly differently,
# but doesn't have large impacts on the results

plot(SPSS.LDA$LDA1[SPSS.LDA$Season == "Spring"],
     SPSS.LDA$LDA2[SPSS.LDA$Season == "Spring"], col = "darkolivegreen4",
     pch = 17, xlim = c(-8, 5), ylim = c(-3.1, 4),
     xlab = "DF1", ylab = "DF2", main = "SPSS")
points(SPSS.LDA$LDA1[SPSS.LDA$Season == "Winter"],
     SPSS.LDA$LDA2[SPSS.LDA$Season == "Winter"], col = "cornflowerblue",
     pch = 19)
points(SPSS.LDA$LDA1[SPSS.LDA$Season == "Red"],
     SPSS.LDA$LDA2[SPSS.LDA$Season == "Red"], col = "firebrick",
     pch = 15)
legend("topleft", legend = c("Red", "Spring", "Winter"),
         pch = c(15, 17, 19), cex = 0.75,
         col = c("firebrick", "darkolivegreen4", "cornflowerblue"))
```

SPSS



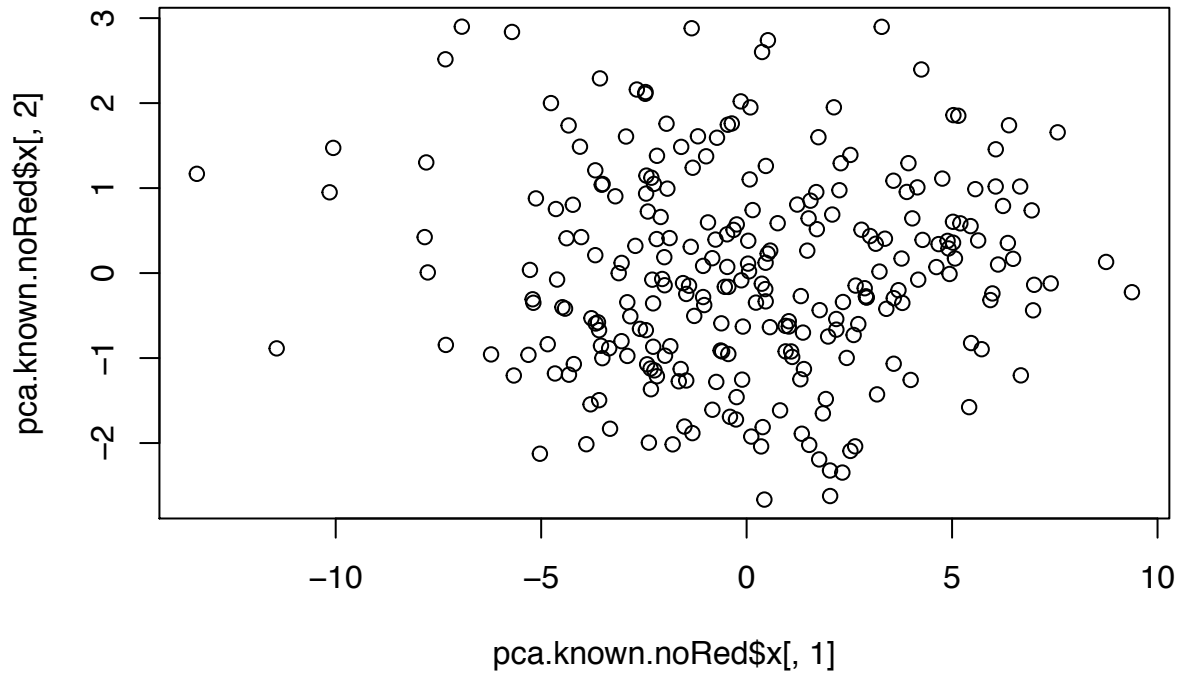
Remove Red cod and reanalyze

The red cod in the known dataset did not have any length measurements so I had to exclude total length from that analysis. Here I removed red cod from both the known dataset and the unknown dataset to specifiy just spring or winter spawners in my data. This results in a single LD axis.

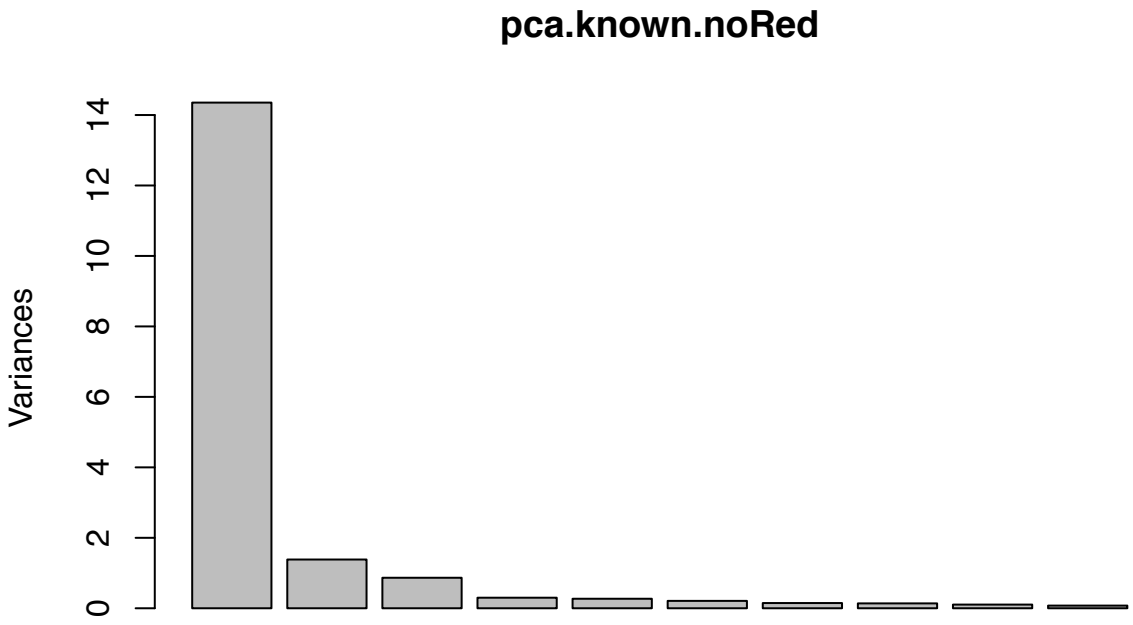
```
################################################
#### Run LDA for only Spring and Winter cod ####
################################################

  # remove Red cod data
  known.noRed <- known.morph[known.morph$Season != "Red", ]
  unknown.noRed <- unknown.morph[unknown.morph$ColorType != "Red", ]
  unknown.lognoRed <- log(unknown.noRed[,c("TotalLength", "D1", "D2", "D3", "D4", "D5",
                                           "D6", "D7", "D8", "D10", "D13", "D14", "D16",
                                           "D17", "D18", "D19", "D21", "D22")])
  colnames(unknown.lognoRed)[1] <- "D23"
  unknown.lognoRed <- unknown.lognoRed[,c(2:18, 1)]
  known.noRed$Season <- factor(known.noRed$Season)
  known.lognoRed <- log(known.noRed[,c(16:23, 25, 28:29, 31:34, 36:38)])

# Run a Principle Components Analysis on both datasets
  pca.known.noRed <- prcomp(known.lognoRed, scale. = TRUE)
  summary(pca.known.noRed)
```

```
## Importance of components%s:
##                            PC1     PC2    PC3     PC4     PC5     PC6
## Standard deviation     3.7885 1.17616 0.9305 0.54720 0.51997 0.45794
## Proportion of Variance 0.7974 0.07685 0.0481 0.01664 0.01502 0.01165
## Cumulative Proportion  0.7974 0.87421 0.9223 0.93895 0.95397 0.96562
##                            PC7    PC8     PC9    PC10    PC11    PC12
## Standard deviation     0.38550 0.3722 0.32288 0.27569 0.23523 0.20398
## Proportion of Variance 0.00826 0.0077 0.00579 0.00422 0.00307 0.00231
## Cumulative Proportion  0.97387 0.9816 0.98736 0.99158 0.99466 0.99697
##                           PC13    PC14    PC15    PC16    PC17    PC18
## Standard deviation     0.13744 0.10235 0.09400 0.08306 0.07746 0.05865
## Proportion of Variance 0.00105 0.00058 0.00049 0.00038 0.00033 0.00019
## Cumulative Proportion  0.99802 0.99860 0.99909 0.99948 0.99981 1.00000
```

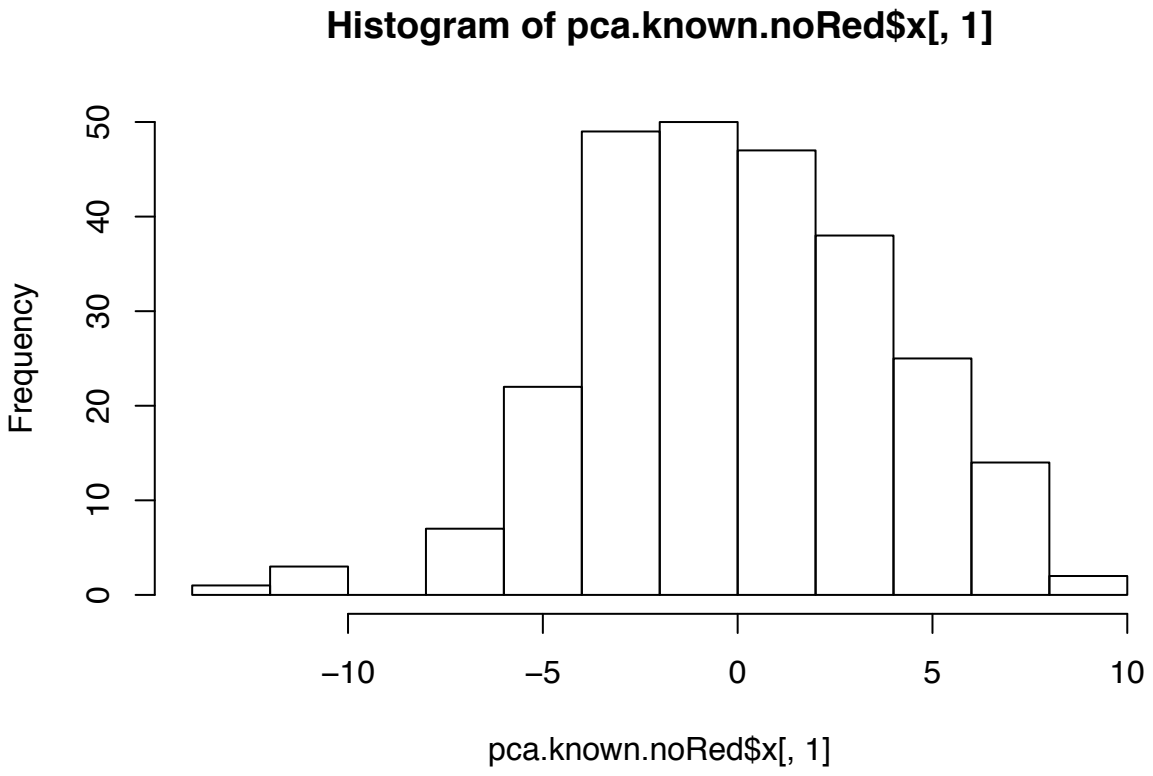
```
  pca.unknown.noRed<- prcomp(unknown.lognoRed, scale. = TRUE)

# Plot PCA
  plot(pca.known.noRed$x[,1], pca.known.noRed$x[,2])
```



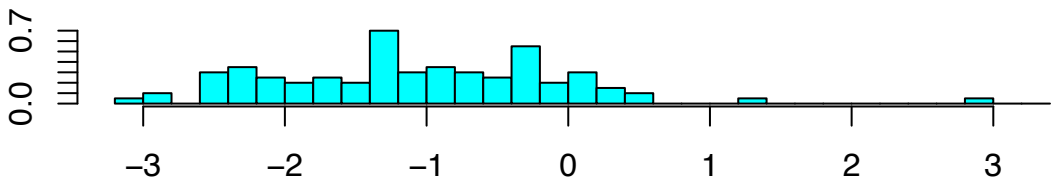

```
screeplot(pca.known.noRed)
```



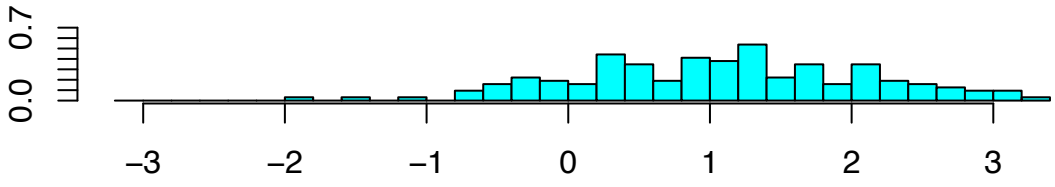

```
hist(pca.known.noRed$x[,1])
```




```
# for loop to regress PC1 onto log transformed data and pull out residuals
  #Grahams Data
  regress.known.noRed <- matrix(nrow = nrow(pca.known.noRed$x),
                                ncol = ncol(pca.known.noRed$x))
  for(i in 1:ncol(pca.known.noRed$x)){
    regress.known.noRed[,i] <- lm(pca.known.noRed$x[,1]~known.lognoRed[,i])$residuals
  }

  #Sara Data
  regress.unknown.noRed <- matrix(nrow = nrow(pca.unknown.noRed$x),
                                  ncol = ncol(pca.unknown.noRed$x))
  for(i in 1:ncol(pca.unknown.noRed$x)){
    regress.unknown.noRed[,i] <- lm(pca.unknown.noRed$x[,1]~unknown.lognoRed[,i])$residuals
  }

# Create dataframe with data for Linear Discriminate Function Analysis
  df.known.noRed <- data.frame(known.noRed$Season, regress.known.noRed)

# Run DFA
  LDA.known.noRed <- lda(known.noRed.Season ~ ., data = df.known.noRed)
  colnames(regress.unknown.noRed) <- c("X1", "X2", "X3", "X4", "X5", "X6",
                                       "X7", "X8", "X9", "X10", "X11", "X12",
                                       "X13", "X14", "X15", "X16", "X17", "X18")
  regress.unknown.noRed <- as.data.frame(regress.unknown.noRed)
  LDApredict.known.noRed <- predict(LDA.known.noRed)
  plot(LDA.known.noRed)
```



group Spring



group Winter

```
  str(LDApredict.known.noRed)
```

```
## List of 3
##  $ class    : Factor w/ 2 levels "Spring","Winter": 2 2 2 2 1 1 2 2 2 2 ...
##  $ posterior: num [1:258, 1:2] 0.208211 0.000604 0.03184 0.035521 0.715746 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:258] "1" "2" "3" "4" ...
##   .. ..$ : chr [1:2] "Spring" "Winter"
##  $ x        : num [1:258, 1] 0.167 2.994 1.134 1.082 -0.884 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:258] "1" "2" "3" "4" ...
##   .. ..$ : chr "LD1"
```

```
  # Evaluate Performance of LDA on Known Data
  df.prediction <- as.data.frame(cbind(as.character(df.known.noRed$known.noRed.Season),
                                       as.character(LDApredict.known.noRed$class),
                                       LDApredict.known.noRed$posterior, LDApredict.known.noRed$x))
  colnames(df.prediction)[1:2] <- c("Known", "Predicted")

  incorrect <- NULL
  for(i in 1:nrow(df.prediction)){
    if(df.prediction[i,1] != df.prediction[i,2]){
      incorrect <- as.data.frame(rbind(incorrect, df.prediction[i,]))
    }
  }
  incorrect
```

```
##      Known Predicted              Spring              Winter
## 5   Winter    Spring   0.715746478295315  0.284253521704685
## 6   Winter    Spring   0.539324272221415  0.460675727778585
## 37  Winter    Spring   0.680815830430658  0.319184169569342
## 46  Winter    Spring   0.557338879673612  0.442661120326388
## 52  Spring    Winter   0.406328758060528  0.593671241939472
```

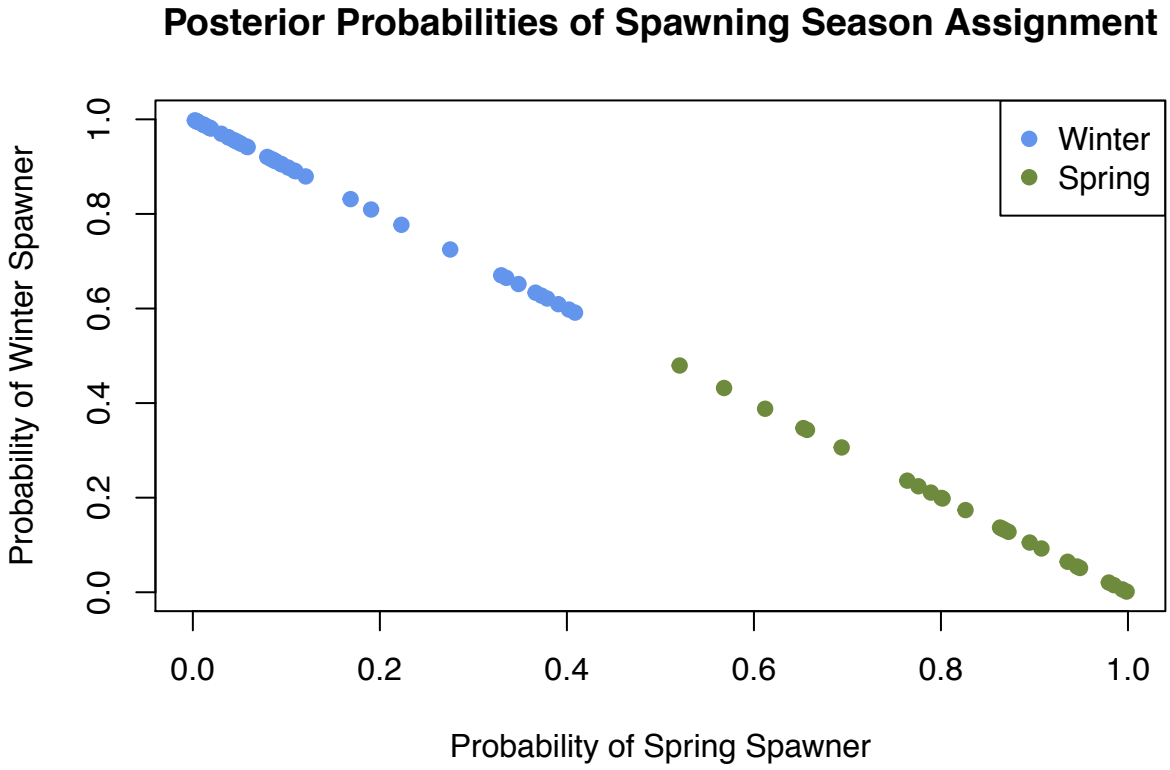
```
## 54  Spring    Winter   0.323005235740977  0.676994764259023
## 60  Spring    Winter   0.382153303347702  0.617846696652298
## 63  Spring    Winter 0.00133651242893634  0.998663487571064
## 67  Spring    Winter   0.222031105243401  0.777968894756599
## 77  Spring    Winter   0.370903918124947  0.629096081875053
## 78  Spring    Winter   0.332252128665705  0.667747871334295
## 84  Spring    Winter   0.185394158899518  0.814605841100483
## 94  Spring    Winter   0.375055238423931  0.624944761576069
## 99  Spring    Winter   0.357380266153132  0.642619733846868
## 102 Spring    Winter   0.031738228220128  0.968261771779872
## 115 Spring    Winter   0.285542029149455  0.714457970850545
## 116 Spring    Winter   0.399638019806927  0.600361980193073
## 117 Spring    Winter    0.23488778633572   0.765112213667428
## 118 Spring    Winter      0.484120287316     0.515879712684
## 122 Spring    Winter   0.154766537483756  0.845233462516244
## 129 Spring    Winter   0.448792063006006  0.551207936993994
## 149 Winter    Spring   0.968255048968999 0.0317449510310011
## 150 Winter    Spring   0.719239632554336  0.280760367445664
## 152 Winter    Spring   0.874407331862631  0.125592668137369
## 159 Winter    Spring   0.592615952117972  0.407384047882028
## 172 Winter    Spring   0.594393267054408  0.405606732945592
## 176 Winter    Spring   0.930951607174555 0.0690483928254448
## 186 Winter    Spring   0.706465602062873  0.293534397937127
## 192 Winter    Spring   0.672942393135026  0.327057606864974
## 193 Winter    Spring   0.694381154962197  0.305618845037803
## 211 Winter    Spring   0.588104486232286  0.411895513767714
## 227 Winter    Spring   0.635504986779821  0.364495013220179
## 238 Winter    Spring   0.605504650636466  0.394495349363534
##                      LD1
## 5    -0.884102565132994
## 6    -0.527753482806401
## 37   -0.806891448242201
## 46   -0.561602838456431
## 52   -0.277983443554045
## 54   -0.110085925177766
## 60   -0.230868622223722
## 63     2.62422382996081
## 67    0.129023148036207
## 77   -0.208569989885309
## 78   -0.129618780447428
## 84    0.234345875487061
## 94   -0.216829651885938
## 99   -0.181390575081886
## 102    1.13599888743628
## 115 -0.0276615144195706
## 116  -0.265043045439139
## 117  0.0950769514647321
## 118   -0.42484491514902
## 122   0.335538411733237
## 129  -0.358765663489633
## 149   -2.04471832463799
## 150   -0.89212145993589
## 152    -1.3573395291277
## 159  -0.628803029003236
```

```
## 172  -0.632230900878384
## 176    -1.6648594913396
## 186  -0.863080089121929
## 192  -0.790140333085543
## 193  -0.836279639196352
## 211  -0.620122597915824
## 227  -0.713077930079367
## 238  -0.653773570370474
```

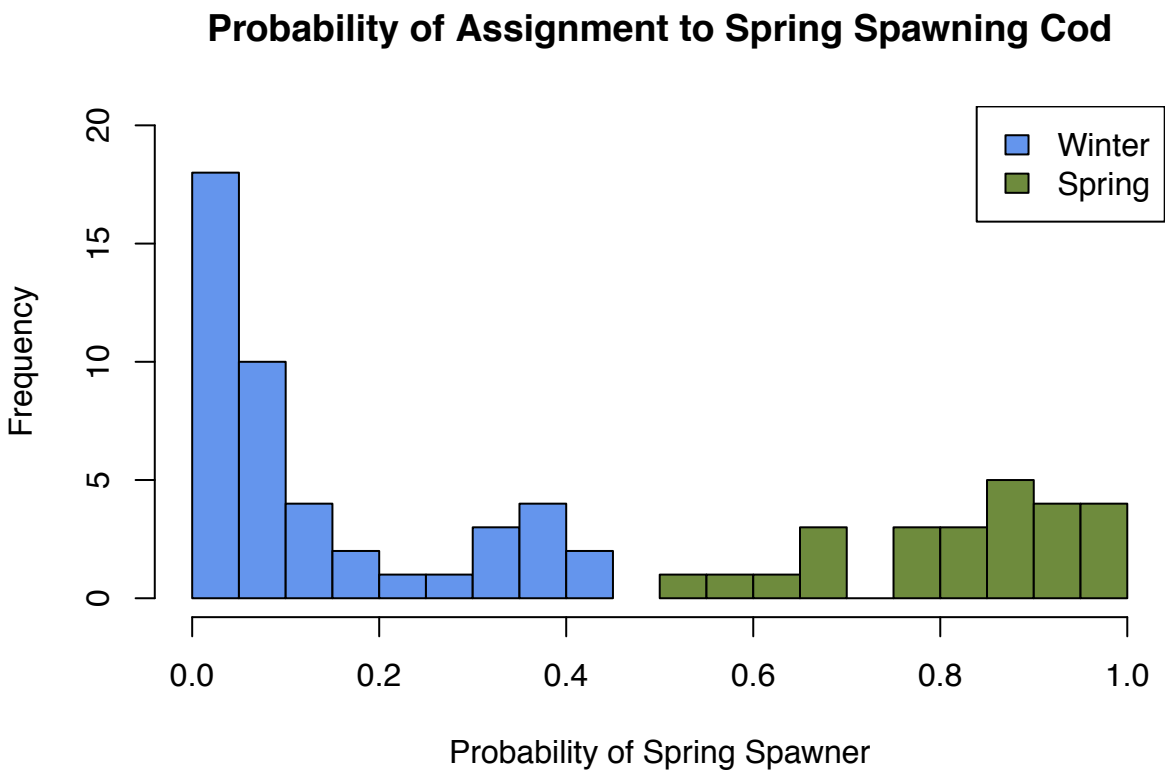
```
  (nrow(regress.known.noRed) - nrow(incorrect))/nrow(regress.known.noRed)*100
```

```
## [1] 87.2093
```

```
  # Run DFA on my samples to determine which spawning groups they belong to
  LDApredictnoRed <- predict(LDA.known.noRed, newdata = regress.unknown.noRed)

  #Create dataframe for plotting
  df.finalunknown <- cbind(regress.unknown.noRed, LDApredictnoRed$posterior)

  # Based on posterior probabilities determine which spawning group samples are from
  df.finalunknown$Spawning <- NA
  for(i in 1:nrow(df.finalunknown)){
    if(df.finalunknown$Spring[i] > 0.5){
     df.finalunknown$Spawning[i] <- "Spring"
    } else {
     df.finalunknown$Spawning[i] <- "Winter"
    }
  }

  df.finalunknown <- data.frame(df.finalunknown, unknown.noRed$Sample)
  colnames(df.finalunknown)[22] <- "SampleID"
  write.csv(df.finalunknown, "SamplingSpawningAssignment.csv")

  ##(nrow(all.data)-nrow(df.unknown))/nrow(all.data)*100

## Plot
  #pdf(file = "/Users/saraschaal/Documents/Northeastern/LotterhosLab/Research/Data/CodEcotypes/Atlantic
  par(mfrow = c(1,1))
  plot(df.finalunknown$Spring[df.finalunknown$Spring > 0.5],
       df.finalunknown$Winter[df.finalunknown$Winter < 0.5],
       col = "darkolivegreen4", pch = 19, ylim = c(0, 1), xlim = c(0,1),
       xlab = "Probability of Spring Spawner", ylab = "Probability of Winter Spawner",
       main = "Posterior Probabilities of Spawning Season Assignment")
  points(df.finalunknown$Spring[df.finalunknown$Spring < 0.5],
         df.finalunknown$Winter[df.finalunknown$Winter > 0.5],
         col = "cornflowerblue", pch = 19)
  legend("topright", legend = c("Winter", "Spring"),
         col = c("cornflowerblue", "darkolivegreen4"), pch = 19)
```




```
  #dev.off()

#pdf(file = "/Users/saraschaal/Documents/Northeastern/LotterhosLab/Research/Data/CodEcotypes/AtlanticCo

  hist(df.finalunknown$Spring[df.finalunknown$Spring > 0.5], breaks = 10,
       col = "darkolivegreen4", xlim = c(0,1), ylim = c(0, 20),
       xlab = "Probability of Spring Spawner",
       main = "Probability of Assignment to Spring Spawning Cod")
  hist(df.finalunknown$Spring[df.finalunknown$Spring < 0.5], breaks = 10,
       col = "cornflowerblue", add = TRUE)
  legend("topright", legend = c("Winter", "Spring"),
         fill = c("cornflowerblue", "darkolivegreen4"))
```


Probability of Assignment to Spring Spawning Cod
Winter
Spring
Frequency
0
5
10
15
20
0.0
0.2
0.4
0.6
0.8
1.0
Probability of Spring Spawner

```
#dev.off()
```