STAT 501 Homework 6

Multinomial

April 5, 2018

1. (a) We perform PCA crab dataset and calculate the proportion of variance for the first several PCs.

```r
library(MASS)
crabs.data <- crabs[,-c(1,2,3)]

#1(a)
crabs.pc <- prcomp(crabs.data)



#   compute proportion of total variance explained by
#   each component

    s <- crabs.pc$sdev^2

    pvar<-s/sum(s)
    cat("proportion of variance: ", pvar, fill=T)

#   cumulative proportion of total variance explained
#   by each component

    cpvar <- cumsum(s)/sum(s)
    cat("cumulative proportion of variance: ", cpvar, fill=T)
```

And we get

```
proportion of variance:  0.9824718 0.009055108 0.006984337
 ↪  0.0009447218 0.0005440328

cumulative proportion of variance:  0.9824718 0.9915269 0.9985112
 ↪  0.999456 1
```

We can see with first 2 PCs, 99% of variance is explained. Then we plot the first PC scores for each observation in a scatter plot.

```r
    crabs.type <-as.factor(paste(crabs[,1], crabs[,2], sep = ""))
     plot(crabs.pc$x[,1],crabs.pc$x[,2],
            xlab="PC1",
            ylab="PC2",type="n")
     text(crabs.pc$x[,1],crabs.pc$x[,2],labels=crabs.type, col =
       ↪  rainbow(4)[as.numeric(crabs.type)])
```

The plot is shown in Figure 1. From the plot we can see we can kind of distiguish these 4

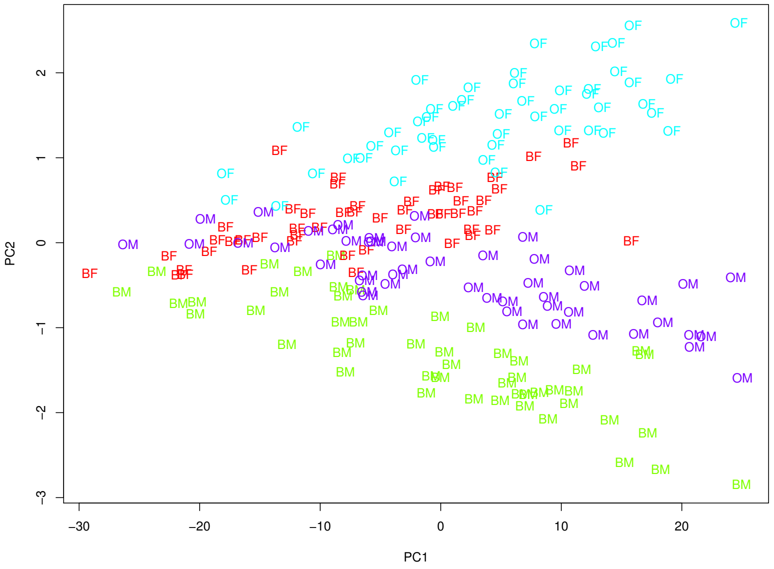


Figure 1: scatter plot of first two PC scores

classes with PC1 and PC2, especially when PC1 score is large.
We also did MANOVA with PC1 and PC2 as explanatory variables in the linear model.

```
fit.lm <- lm(crabs.pc$x[,1:2]~as.factor(crabs.type))
library(car)
fit.manova <- Manova(fit.lm)
summary(fit.manova)
```

The result is

```
Type II MANOVA Tests:

Sum of squares and products for error:
           PC1         PC2
PC1 24686.6698 -245.89146
PC2  -245.8915   50.83784

------------------------------------------

Term: as.factor(crabs.type)

Sum of squares and products for the hypothesis:
          PC1      PC2
PC1 3313.7682 245.8915
PC2  245.8915 207.2327

Multivariate Tests: as.factor(crabs.type)
                 Df test stat  approx F num Df den Df     Pr(>F)
```

```
Pillai            3  0.921355  55.80630      6    392 < 2.22e-16
 ↪  ***
Wilks             3  0.165311  94.86817      6    390 < 2.22e-16
 ↪  ***
Hotelling-Lawley  3  4.524930 146.30607      6    388 < 2.22e-16
 ↪  ***
Roy               3  4.405940 287.85476      3    196 < 2.22e-16
 ↪  ***
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1
```

The p-value is small, so with PC1 and PC2 as explanatory variable, we can tell that these 4 classes are different.

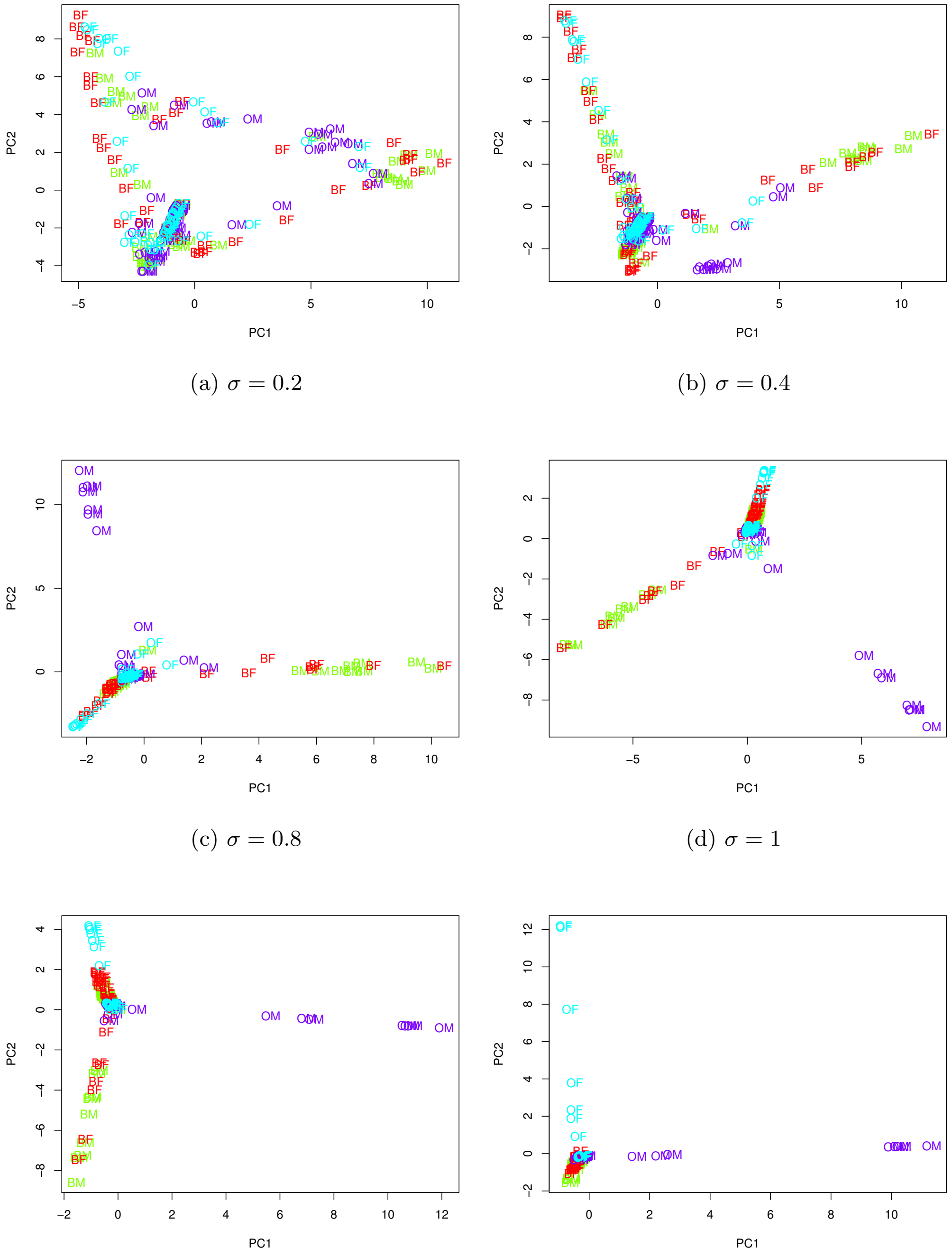
(b) Now we perform kernel PCA with different $\sigma = 0.2, 0.4, 0.8, 1.0, 1.5, 3.0$. We plot scatter plots for each σ like we what did in (a).

```
library(kernlab)
for(sigma in c(0.2, 0.4, 0.8, 1, 1.5, 3)){
  crabs.kpc <- kpca(x = as.matrix(crabs.data),kernel = "rbfdot",
   ↪  kpar = list(sigma = sigma), features = 2)
  plot(crabs.kpc@rotated[,1],crabs.kpc@rotated[,2],
       xlab="PC1",
       ylab="PC2",type="n")

   ↪  text(crabs.kpc@rotated[,1],crabs.kpc@rotated[,2],labels=crabs.type,
   ↪  col = rainbow(4)[as.numeric(crabs.type)])
}
```

The plots are shown in Figure 2. From the plots, we can see with kernel PCA with these given σs, we cannot distinct these 4 classes.

2. (a) We use ANOVA to test the equality of the 10 means for each component. Then we adjust the p-values with Bonfferroni and FDR. The result shows there is only one non-significant component for Bonfferoni and no non-significant component for FDR. Then pick the 100 components with smallest p-values.

```
#2(a)
#i
ziptrain <- read.table("ziptrain.dat")
zipdigit <- as.factor(read.table("zipdigit.dat")[,1])
pval_equal_mean<- function(x, cl){
  fit <- lm(x~cl)
  return(anova(fit)[[5]][1])
}
pvals <- sapply(ziptrain, FUN = pval_equal_mean, cl = zipdigit)
pval.bonf <- p.adjust(pvals, "bonferroni")
which(pval.bonf > 0.05)
pval.fdr <- p.adjust(pvals, "fdr")
which(pval.fdr > 0.05)

id <- order(pvals, decreasing = F)
id100 <- id[1:100]
```



(a) $\sigma = 0.2$

(b) $\sigma = 0.4$

(c) $\sigma = 0.8$

(d) $\sigma = 1$

(e) $\sigma = 1.5$

(f) $\sigma = 3$

Figure 2: scatter plots for scores of PC1 and PC2 from kernel PCA

```

ziptrain100 <- ziptrain[,id100]
```

i. We did Box's M test to test the equality of variance covariance matrices using the data with 100 components.

```r
source("BoxMTest-2.R")
BoxMTest(X = ziptrain100, cl = zipdigit)
```

The result is

```
[1] 10
--------------------------------------------------
 MBox Chi-sqr. df P
--------------------------------------------------
       Inf         Inf        45450        0.0000
--------------------------------------------------
Covariance matrices are significantly different.
$MBox
  0
Inf

$ChiSq
  0
Inf

$df
[1] 45450

$pValue
0
0
```

The p-value is small and we conclude that these 10 digits' variance-covariance matrices are different.

ii. Now we assume the variance-covariance matrices are not equal and they are known parameters. Let $\boldsymbol{x}_{ij}$ be the jth observation for digit i, $i = 0, 1, \ldots, 9$, $j = 1, 2, \ldots, n_i$, then the likelihood ratio test statistic is

$$\sum_{i=0}^{10}\sum_{j=1}^{n_i}\left[(\boldsymbol{x}_{ij}-\hat{\boldsymbol{\mu}}_i)^T\boldsymbol{\Sigma}_i^{-1}(\boldsymbol{x}_{ij}-\hat{\boldsymbol{\mu}})-(\boldsymbol{x}_{ij}-\hat{\boldsymbol{\mu}})^T\boldsymbol{\Sigma}_i^{-1}(\boldsymbol{x}_{ij}-\hat{\boldsymbol{\mu}}_i)\right]$$

where

$$\hat{\boldsymbol{\mu}}_i = \sum_{j=1}^{n_i}\boldsymbol{x}_{ij}/n_i$$

$$\hat{\boldsymbol{\mu}} = \left(\sum_{i=0}^{\mathbf{10}} n_i\boldsymbol{\Sigma}_i^{-1}\right)^{-1}\left(\sum_{i=0}^{10} n_i\boldsymbol{\Sigma}_i^{-1}\hat{\boldsymbol{\mu}}_i\right)$$

The R code to calculate the p-value of the likelihood ratio test is

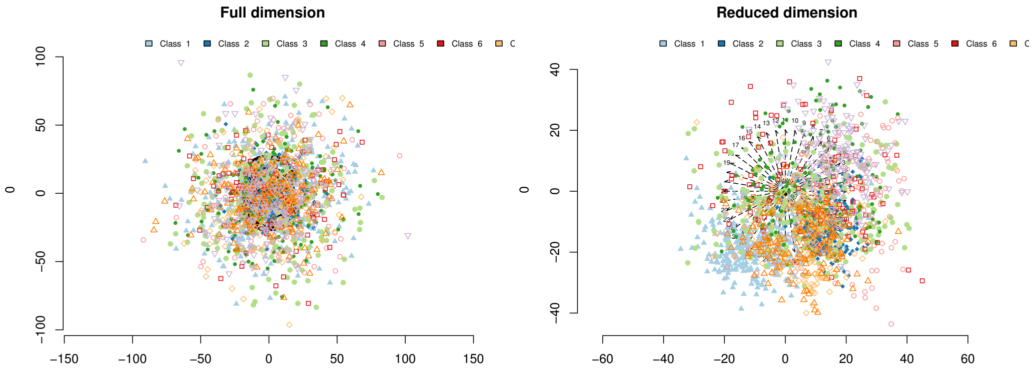
```r
                                    #ii
n <- as.vector(table(zipdigit))
means <- list()
for(i in 1:10){
  means[[i]] <- apply(ziptrain100[zipdigit == i-1,], MARGIN =
   ↪  2, FUN = mean)
}
vars <- list()
for(i in 1:10){
  vars[[i]] <- cov(ziptrain100[zipdigit == i-1,])
}

quard <- function(x, A){
  x <- as.vector(x)
  return(t(x)%*%A%*%x)
}

lambda <- 0


r <- 0
l <- 0
for(i in 1:10){
  r <- r + n[i]*ginv(vars[[i]]) %*% means[[i]]
  l <- l + n[i]*ginv(vars[[i]])
}
muhat <- as.vector(ginv(l)%*%r)

for(i in 1:10){
  Xi <- ziptrain100[zipdigit == i-1,]
  Xicentered <- Xi - matrix(rep(means[[i]], n[i]), ncol = 100, byrow = T)
  Xim <- Xi - matrix(rep(muhat, n[i]), ncol = 100, byrow = T)
  fulli <- sum(apply(Xicentered, MARGIN = 1, FUN = quard, A = ginv(vars[[i]])))
  reducedi <-  sum(apply(Xim, MARGIN = 1, FUN = quard, A = ginv(vars[[i]])))
  lambda <- reducedi - fulli
}

pchisq(lambda, df = 9, lower.tail = F)
```

Then we have the test statistic **12856.64** and p-value very close to **0**. Hence we conclude that the means are different.

(b) i. We displayed the full dimension one and the reduced dimension one in Figure 3. We can see the 40 dimensions one can pretty much show the variance in the full one.

```
#(b)
ziptrain.centered <- NULL
for(i in 1:10){
  mean <- apply(ziptrain[zipdigit == i-1,], MARGIN = 2, FUN = mean)
  ziptrain.centered <- rbind(ziptrain.centered, ziptrain[zipdigit == i-1,] - matrix(rep(mean, n[i]), ncol = 256, byrow = T))
}

ziptrain.pc <- prcomp(ziptrain.centered)
```

```r
source("PCs.proportion.variation.enuff.R")
p <- rep(0, 256)
for(i in 1:256){
  p[i] <- PCs.proportion.variation.enuff(lambda = ziptrain.pc$sdev^2, q = i, propn = 0.8, nobs = nrow(ziptrain.centered))
}
min(which(p > 0.05))

zipmean <- NULL
for(i in 1:10){
  mean <- apply(ziptrain[zipdigit == i-1,], MARGIN = 2, FUN = mean)
  zipmean <- rbind(zipmean,  matrix(rep(mean, n[i]), ncol = 256, byrow = T))
}

zipproj_full <- ziptrain.pc$x + zipmean%*%ziptrain.pc$rotation
zipproj <- ziptrain.pc$x[,1:40] + zipmean%*%ziptrain.pc$rotation[,1:40]

source("radviz2d.R")
class <- NULL
for(i in 0:9){
  class <- c(class, rep(i, n[i+1]))
}

class <- as.factor(class)

source("starcoord.R")
starcoord(data = cbind(zipproj_full,class), class = T, main = "Full dimension")
starcoord(data = cbind(zipproj,class), class = T, main = "Reduced dimension")
```



(a) Full dimension

(b) Reduced dimension

Figure 3: Star coordinate plots