```
title: "MAT 471 671 Chapter 7 8 10 Exam 3"
author: "kaddour boukaabar"
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output: html document
#Chapter 7 Discriminant Analysis
install.packages("MASS")
library (MASS)
#Q1: Run the below code chunk. What does it do? Briefly describe the data set
"iris."
```{r}
iris
#Q2: Run the below code chunk do. What does it do? Briefly describe the
function "lda."
```{r}
ldaout <- lda(Species~., iris)</pre>
ldaout
#Q3: Run the below code chunk do. What does it do? Briefly describe the
function "predict."
```{r}
ldapred <- predict(ldaout, iris)</pre>
ldapred
#Q4: Run the below code chunk do. What does it do? Explain
"ldapredict$class."
```{r}
ldaclass <- ldapred$class</pre>
ldaclass
#Q5: Run the below code chunk do. What does it do? Describe the "table"
function and Explain "table(ldaclass, iris$Species)." Also, explain and
discuss the output.
ldatable <- table(ldaclass, iris$Species)</pre>
ldatable
```

```
#Q6: Run the below code chunk do. What does it do? Describe and explain
"sum(diag(ldatable))/sum(ldatable)*100." Also, explain and discuss the output.
```{r}
accur <- sum(diag(ldatable))/sum(ldatable)*100</pre>
accur
Chapter 8 Canonical Correlation Analysis
attach(iris)
#Q7: Run the below code chunk. What does it do? Explain the statement
"apply(iris[,-5],2,var)." Explain "sweep(iris[,-5], 2, standarddev, FUN="/")."
Also, explain and discuss the output.
```{r}
iris
variancescolums <- apply(iris[,-5],2,var)</pre>
variancescolums
standarddev <- sqrt(variancescolums)</pre>
standarddev
iris1.std <- sweep(iris[,-5], 2, standarddev, FUN="/")</pre>
iris1.std
#Q8: Run the below code chunk. What does it do? Explain and discuss the
output.
```{r}
sepal.meas <- iris1.std[,1:2]</pre>
petal.meas <- iris1.std[,3:4]</pre>
sepal.meas
petal.meas
#Q9: Run the code chunk. What does it do? Explain and discuss the output.
```{r}
cancor(sepal.meas, petal.meas)
```

#Iris Dataset and PCA

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#Q10: Run the below code chunk. What does it do? Describe the function
"prcomp" Also, explain and discuss the output.
```{r}
myPr1 <- prcomp(iris[, -5])</pre>
myPr <- prcomp(iris[, -5], scale = TRUE)</pre>
myPr
#Q11: Run the below code chunk. What does it do? Describe the function "plot"
```{r}
plot(iris$Sepal.Length, iris$Sepal.Width)
```{r}
plot(scale(iris$Sepal.Length), scale(iris$Sepal.Width))
```{r}
plot((iris$Sepal.Length - mean(iris$Sepal.Length)) / sd(iris$Sepal.Length))
#Q12: Run the code chunk. What does it do? Explain and discuss the output.
```{r}
summary(myPr)
#Q13: Run the code chunk. What does it do? Explain and discuss the output.
```{r}
plot(myPr, type = "1")
#Q14: Run the code chunk. What does it do? Explain and discuss the output.
```{r}
biplot(myPr)
#Q15: Run the code chunk. Compare to Question 14 above.
```{r}
biplot(myPr, scale = 0)
#Q16: Run the code chunk. What does it do?
```{r}
myPr$x
```

```
#Q17: Run the code chunk. What does it do? Explain and discuss the output.
```{r}
iris2 <- cbind(iris, myPr$x)
iris2

```
library(ggplot2)

#Q18: Run the code chunk. What does it do? Explain and discuss the output.

```{r}
ggplot(iris2, aes(PC1, PC2, col = Species, fill = Species)) +
    stat_ellipse(geom = "polygon", col = "black", alpha = 0.5) +
    geom_point(shape = 21, col = "black")

#Q19: Run the code chunk. What does it do? Explain and discuss the output.

```{r}
cor(iris[, -5], iris2[, 6:9])</pre>
```

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