## Tutorial 3

Q1) refer to data uploaded in table2_7 that measured from types of insects :
(a) Ch . Concinna "A" and
(b) Ch . Heikertlingeri . "B"

It shows two variables :

- $X_{1}$ : first the width of the first joint
- $X_{2}$ : the width for the second joint.
(الجنول النالي ييين عطية تشريح حشرات الثاتوكتيميا لعشرين من ذكور الخنافس الصغيرة حيث أن المتغيرات هي
عرض المفصل (الكاحل) الأول والثاني )
Find
1- Find the estimated Fisher's linear discriminant function.
2- Classify the new insect with observation $(194,124)$
Solution:
1-

```
sètwd("C:/Users/Rad16/OneDrive/بi<_|l chw/stat339")
Setwd"c:/Users/Rad16/OneDrive/uic
data
    Type 
l
data1 <- data[1:10,2:3] #data of A insect
m1 <- nrow(datal)
n1
n2 <- nrow(data2)
[1] n2 10
```


## Tutorial 3



```
    > xbarl <- colmeans(datal)
    > xbar1
    \(\begin{array}{rrr}\times 1 & \times 2 \\ 179.1 & 128.4\end{array}\)
    xbar2 <- colmeans (data2)
    \(>\times\) xar2
\(\begin{array}{rr}\times 1 & \times 2 \\ 208.2 & 122.8\end{array}\)
s sl<- cov(datal)\#var each joint and cov jint with other for insect \(A\)
> s2 <- \(\operatorname{cov}(d a t a 2)\)
\(>\) spooled \(<-(((n 1-1) * s 1)+((n 2-1) * s 2)) /(n 1+n 2-2)\) \#since equal variance assumption
\(>\) spooled
\(\begin{array}{rrr}\times 1 & 231.25000 & 87.33333\end{array}\)
\(\times 1\)
\(\times 27.3333381 .88889\)
> inv.spooled <- solve(spooled)
\#nv.spooled <- solve(spooled)
7ibrary (MASS)
\(>\) inv.spooled <- ginv(spooled)
> inv.spooled
\(\begin{array}{rrr}{[1,]} & 0.007240593 & -0.007721989\end{array}\)
0.020447060
\#The cutoff point to determine group membership of the observation vector is then
\(>\) mhat <- ((xbar1-xbar2)\%*\%inv.spooled\%*\%(xbar1+xbar2)) / (2)
\([1]-\),
```

2-

```
[1,] -6.571125
> y <- (xbar1-xbar2)%*%inv.spooled
[r, [,1] 
[1,] -0.2539444 0. 
> yo <- (xbari-xbar2)%*%inv.spooled%*%x0
[1,] -7.202747
>
if (yo >= mhat){
+ } else { print ("A")
+ } else { print ("B")
[1] }
```

we classify it to insect B since $\mathrm{Y}<\mathrm{m}$

Q2) upload "iris" data frame with 150 cases (rows) and 5 variables (columns) where It shows two variables :

- $X_{1}$ : iris where its Species :setosa
- $X_{2}$ : iris where its Species : versicolor

Find
1- the estimated Fisher's linear discriminant function.
2- Classify the new observation of row \#40
Sepal.Length Sepal.Width Petal.Length Petal.Width

| 40 | 5.1 | 3.4 | 1.5 | 0.2 |
| :--- | :--- | :--- | :--- | :--- |

Solution:

we classify it to "setosa" species since $\mathrm{y}>\mathrm{m}$ as it is actual be.

Q3)According to slide 87 about "Longely" dataset in R that describes 7 economic variables observed from 1947 to 1962 used to predict the number of people employed yearly $(\mathrm{n}=16)$.
a. Fit classical multiple linear regression and ridge regression
b. Obtain the estimated regression coefficient. Which technique provide the smallest coefficients?
c. Perform LOOCV to get best lambda?

## Solution:

First we call the data and split it into independent and dependent variable:

a. Fit classical multiple linear regression to find its Coefficients.



Fit ridge regression to find its Coefficients.
Console J
Error in plot(ev.riage) : object ev.rnage not rouna
> \# Loaging the library
> 1ibrary(glmnet)
> 1 ibrary (g1mnet)
Loading required package: Matrix
> \#The glmnet package provides the functionality for ridge regression via g1mnet(
s \#You must specify alpha $=0$ for ridge regression

- \# Find the best lambda using cross-validation
$>$ cv.ridge <-cv.glmnet (x, y, alpha $=0$, family = "gaussian") \#"gaussian" is the default family option if we didn't write the family. Use $\quad$ bino
option grouped=FALSE enforced in cv.glmnet, since $<3$ observations per fold
$>\mathrm{cv}$.ridge
Call: cv.g1mnet( $x=x, y=y, a l p h a=0$, family $=$ "gaussian")
Measure: Mean-Squared Error

$>$ >\#lambda. 1se: the largest lambda at which the MSE is within one standard error of the minimal MSE which gives the most regularized model (few
est coefficients),
$>$ \#\#lambda.min: the lambda at which the minimal MSE is achieved.
> \#\#ロlambda.1se0: second vertical dotted line
> \#\#\#lambda.mind: first vertical dotted line
$>$ best. 1 ambda <- cv.ridgeslambda.min \#lambda.min is the value of lambda that gives minimum mean cross-validated error
$\gg$ best. 1 ambda
\# Fit the final model
> fit <- g! mnet (x, y y, alpha $=0$, family="gaussian", lambda $=$ best.lambda)

b.
- Increasing lambda increases the shrinking of the coefficients.
- If the sample size is very small compared to the number of covariates, estimation is not efficient and therefore we might not get the desirable shrinking.

