

Lab 9

1.

```
df <- read.table("lung_cancer.txt",header=T, sep="\t",row.names=1)
```

2.

```
dat = as.data.frame(t(df))
clas <- names(df)
clas[grepl("Adeno",clas)] <- rep("A",length(clas[grepl("Adeno",clas)]))
clas[grepl("SCLC",clas)] <- rep("T",length(clas[grepl("SCLC",clas)]))
clas[grepl("Norm",clas)] <- rep("N",length(clas[grepl("Norm",clas)]))
datx <- data.frame(clas,dat)
```

3.

```
train = rbind(datx[1:6,], datx[11:16,], datx[20:22,])
test<- rbind(datx[7:10,], datx[17:19,], datx[23:24,])
test_class = test$clas
class <- test[,1]
test_ = test[,-1]
```

4.

```
datx2 = train[, 2:3]
dat.lda <- lda(train$clas~,datx2)
dat.pred <- predict(dat.lda,test_[1:2])
```

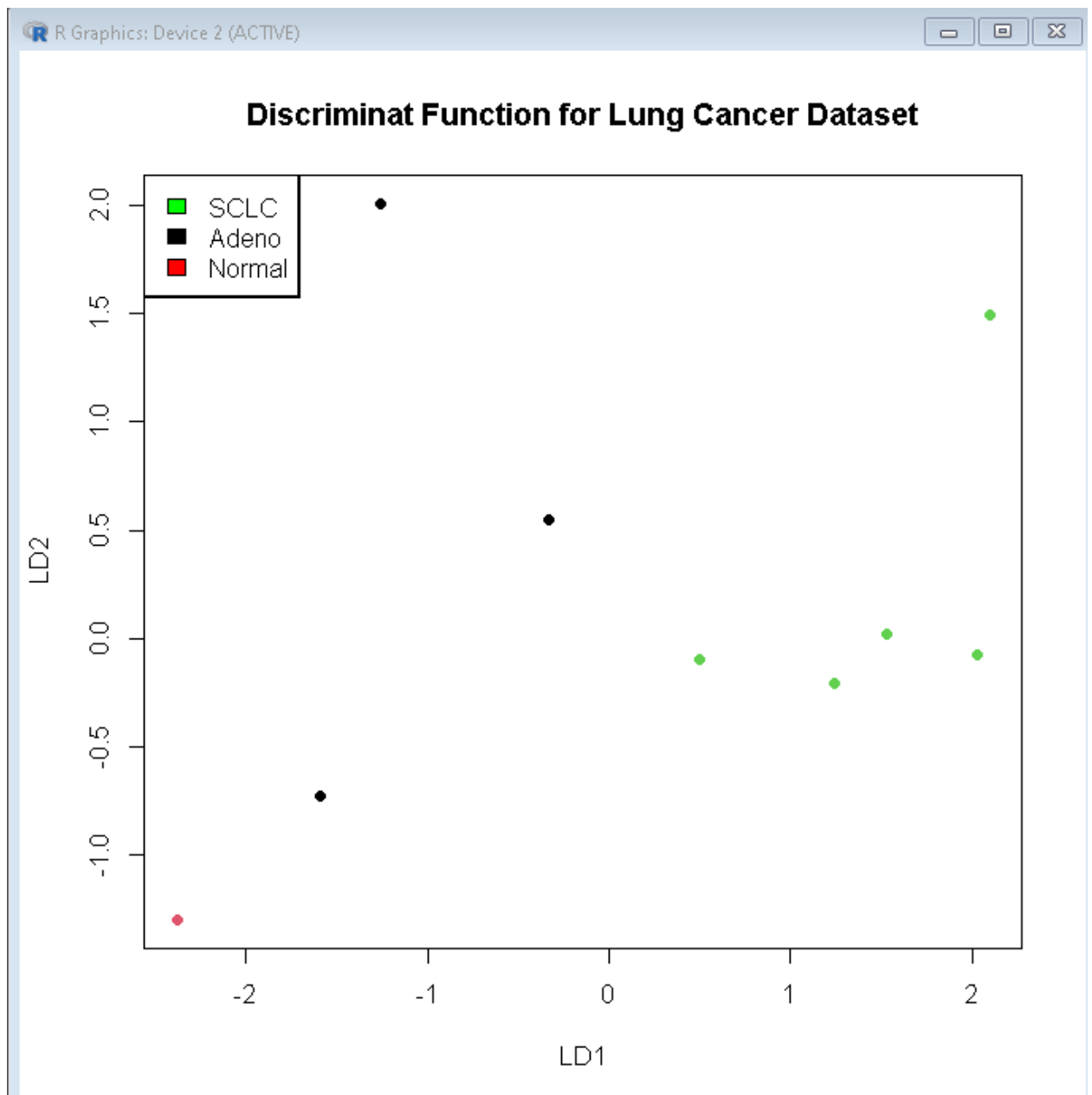
```
table(dat.pred$clas, class)
```

```
class
  A N T
A 1 1 1
N 0 1 0
T 3 0 2
```

5 samples were misclassified.

5.

```
plot(dat.pred$x, col = dat.pred$class , bg=as.numeric(factor(dat.pred$class)), pch=21, main='Discriminat
Function for Lung Cancer Dataset')
legend(x = "topleft", box.col = "black",
, box.lwd = 2 ,legend=c("SCLC", "Adeno", "Normal"),
fill = c("green", "black", "red"))
```



6.

```
dat.lda2 <- lda(clas ~ ., train)
dat.pred2 <- predict(dat.lda, test_)
```

```
table(dat.pred2$class, class)
```

```

class
  A N T
A 4 0 0
N 0 2 0
T 0 0 3

```

0 misclassified samples

```

plot(dat.pred2$x, col = dat.pred2$class, bg= as.numeric(factor(dat.pred2$class)), pch=21,main='Comparing
LD Variables')

```

```

legend(x = "topright", box.col = "black",
      box.lwd = 2 , legend=c("SCLC", "Adeno", "Normal"),
      fill = c("green", "black", "red"))

```

