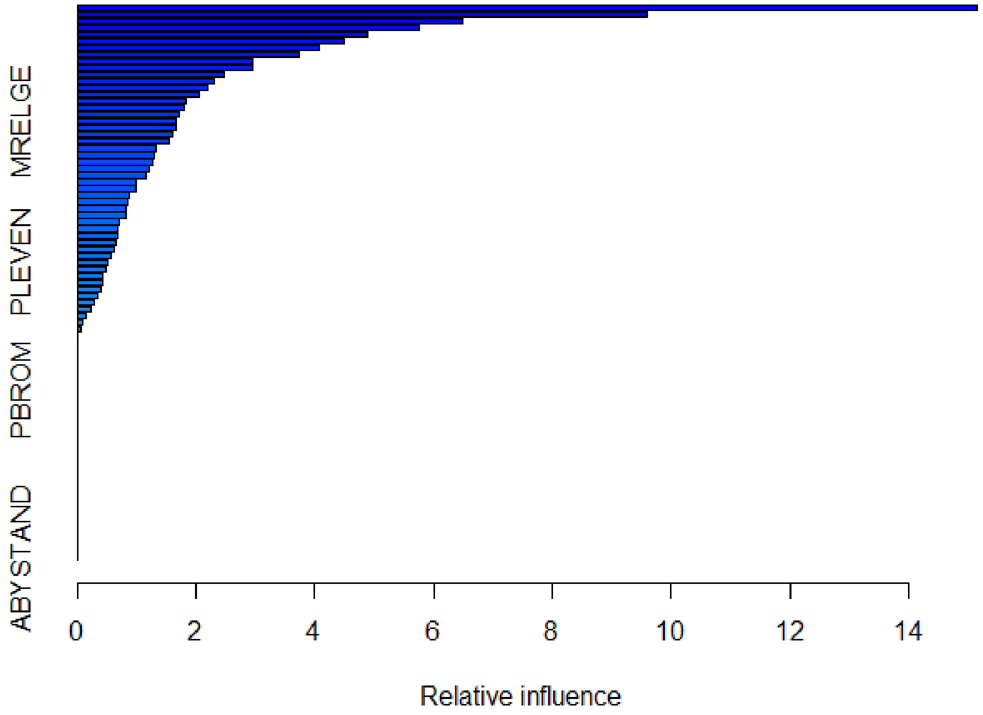
# question 1

```
# question 1
library(ISLR)

sapply(Caravan,table)
table(Caravan$PVRAAUT)
table(Caravan$AVRAAUT)
Caravan
nrow(Caravan)

colnames(Caravan)
d0 = subset(Caravan,select = c(-PVRAAUT,-AVRAAUT))
ncol(Caravan)
ncol(d0)

#a)
str(d0)
levels(d0$Purchase) = c("0","1")
d0$Purchase=as.numeric(d0$Purchase)-1
d0$Purchase
dtrain = d0[1:1000,]
nrow(d0)
dtest = d0[1001:5822,]
head(d0$Purchase)
d0$Purchase
#b)
library(gbm)
set.seed(1)
boost1 = gbm(Purchase~.,data = dtrain,distribution="bernoulli",n.trees = 1000,shrinkage = 0.01)
summary(boost1)
# PPERSAUT seems to be the most important
```

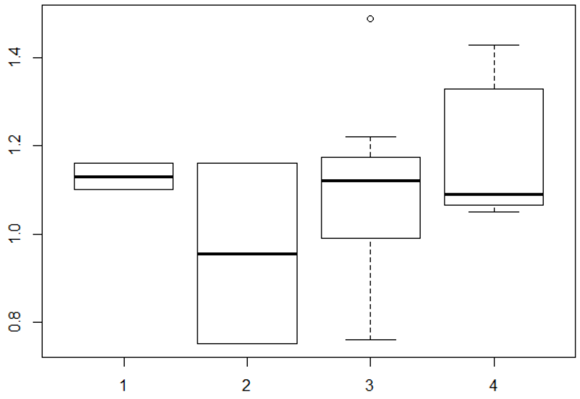


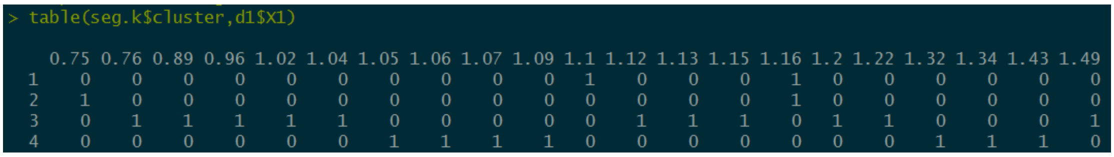
```
#c)
yhat.boost = predict(boost1,newdata = dtest,n.trees=1000,type = "response")
yhat.boost
yhat = ifelse(yhat.boost>0.2,"1","0")
tb = table(yhat,dtest$Purchase)
tb
# yhat       0      1
#       0 4410    256
#       1   123     33

aux = prop.table(tb)
aux
# yhat                  0                  1
#       0 0.914558275 0.053090004
#       1 0.025508088 0.006843633
# 0.025508088 of people predicted to make a purchase do in fact make one
1-sum(diag(aux))
# test error rateis 0.07859809
```

# question 2

```
#a)
library(cluster)
d0 = utilities
d0$X6 = as.numeric(d0$X6)
d1=d0[,-1]
set.seed(1)
seg.k = kmeans(d1,centers = 4)
seg.k$cluster
summary(seg.k)
table(seg.k$cluster)
# [1] 4 3 4 3 3 4 3 1 4 3 2 3 3 4 3 2 3 4 1 3 3 4
# 1    2    3    4
# 2    2 11    7
```

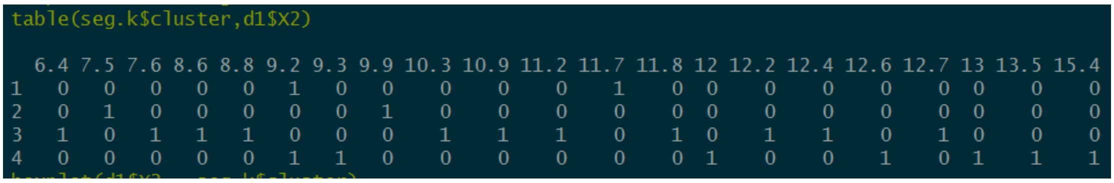
```
#b)
table(seg.k$cluster,d1$X1)
boxplot(d1$X1 ~ seg.k$cluster)
```



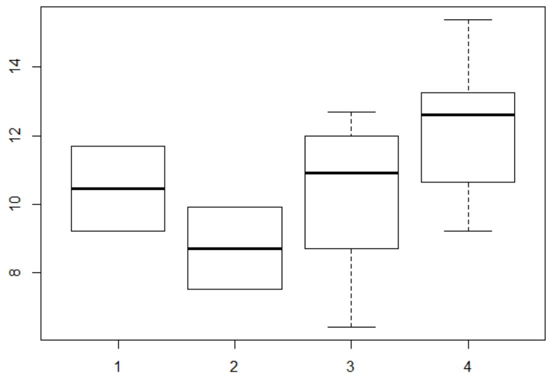


```
> table(seg.k$cluster,d1$X1)

   0.75 0.76 0.89 0.96 1.02 1.04 1.05 1.06 1.07 1.09 1.1 1.12 1.13 1.15 1.16 1.2 1.22 1.32 1.34 1.43 1.49
  1    0    0    0    0    0    0    0    0    0    0   1    0    0    0    1   0    0    0    0    0    0
  2    1    0    0    0    0    0    0    0    0    0   0    0    0    0    1   0    0    0    0    0    0
  3    0    1    1    1    1    1    0    0    0    0   0    1    1    1    0   1    1    0    0    0    1
  4    0    0    0    0    0    0    1    1    1    1   0    0    0    0    0   0    0    1    1    1    0
```

```
# group 2 is smaller than others in X1

table(seg.k$cluster,d1$X2)
boxplot(d1$X2 ~ seg.k$cluster)
```



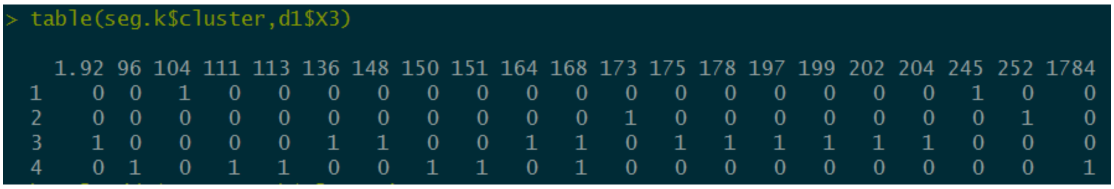
```
table(seg.k$cluster,d1$X2)

  6.4 7.5 7.6 8.6 8.8 9.2 9.3 9.9 10.3 10.9 11.2 11.7 11.8 12 12.2 12.4 12.6 12.7 13 13.5 15.4
1   0   0   0   0   0   1   0   0    0    0    0    1    0  0    0    0    0    0  0    0    0
2   0   1   0   0   0   0   0   1    0    0    0    0    0  0    0    0    0    0  0    0    0
3   1   0   1   1   1   0   0   0    1    1    1    0    1  0    1    1    0    1  0    0    0
4   0   0   0   0   0   1   1   0    0    0    0    0    0  1    0    0    1    0  1    1    1
```



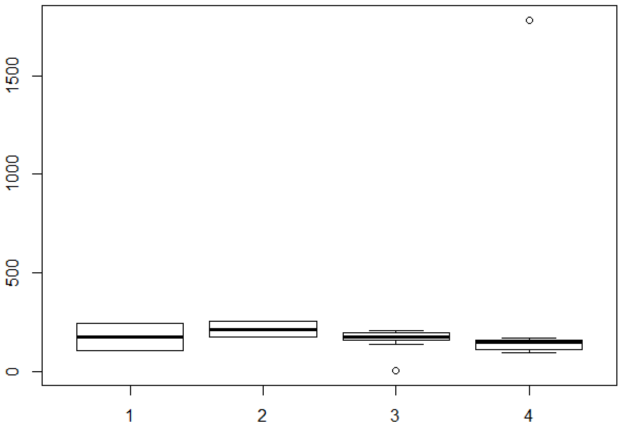
# no big diff

table(seg.k$cluster,d1$X3)

boxplot(d1$X3 ~ seg.k$cluster)



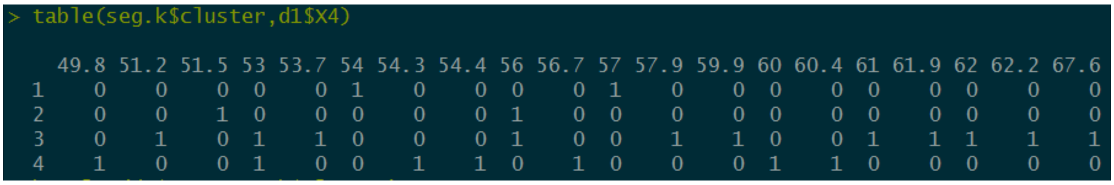
```
> table(seg.k$cluster,d1$X3)

    1.92 96 104 111 113 136 148 150 151 164 168 173 175 178 197 199 202 204 245 252 1784
  1    0  0   1   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   1   0    0
  2    0  0   0   0   0   0   0   0   0   0   0   1   0   0   0   0   0   0   0   1    0
  3    1  0   0   0   0   1   1   0   0   1   1   0   1   1   1   1   1   1   0   0    0
  4    0  1   0   1   1   0   0   1   1   0   1   0   0   0   0   0   0   0   0   0    1
```



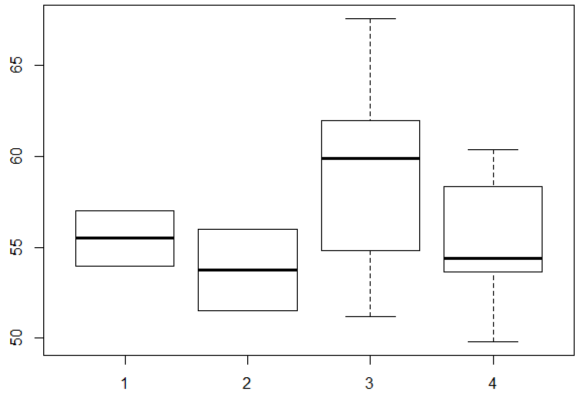
# no big diff

table(seg.k$cluster,d1$X4)

boxplot(d1$X4 ~ seg.k$cluster)

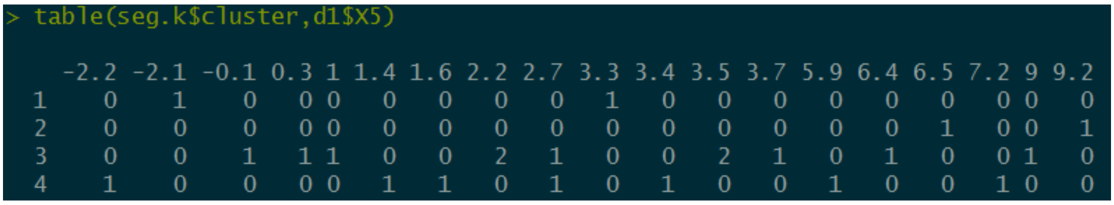


```
> table(seg.k$cluster,d1$X4)

    49.8 51.2 51.5 53 53.7 54 54.3 54.4 56 56.7 57 57.9 59.9 60 60.4 61 61.9 62 62.2 67.6
  1    0    0    0  0    0  1    0    0  0    0  1    0    0  0    0  0    0  0    0    0
  2    0    0    1  0    0  0    0    0  1    0  0    0    0  0    0  0    0  0    0    0
  3    0    1    0  1    1  0    0    0  1    0  0    1    1  0    0  1    1  1    1    1
  4    1    0    0  1    0  0    1    1  0    1  0    0    0  1    1  0    0  0    0    0
```

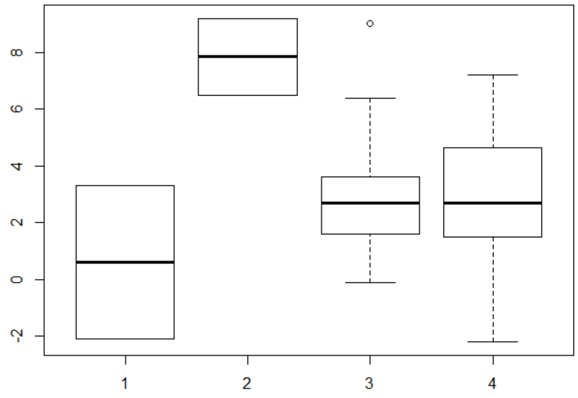


# group 3 is slightly higher than 1,2,4 in X4

table(seg.k$cluster,d1$X5)
boxplot(d1$X5 ~ seg.k$cluster)

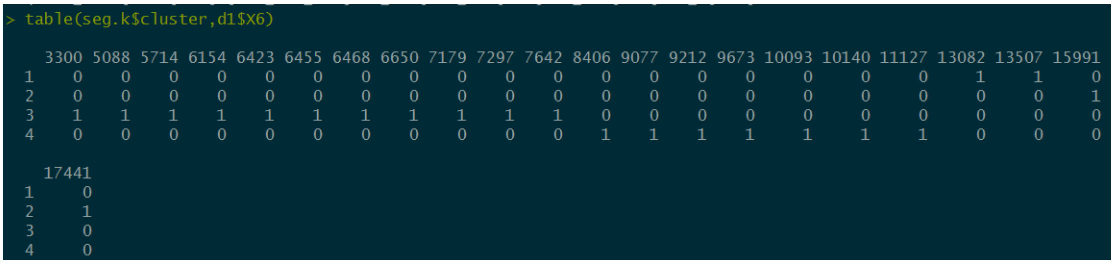


```
> table(seg.k$cluster,d1$X5)

    -2.2 -2.1 -0.1 0.3 1 1.4 1.6 2.2 2.7 3.3 3.4 3.5 3.7 5.9 6.4 6.5 7.2 9 9.2
  1    0    1    0   0 0   0   0   0   0   1   0   0   0   0   0   0   0 0   0
  2    0    0    0   0 0   0   0   0   0   0   0   0   0   0   0   1   0 0   1
  3    0    0    1   1 1   0   0   2   1   0   0   2   1   0   1   0   0 1   0
  4    1    0    0   0 0   1   1   0   1   0   1   0   0   1   0   0   1 0   0
```

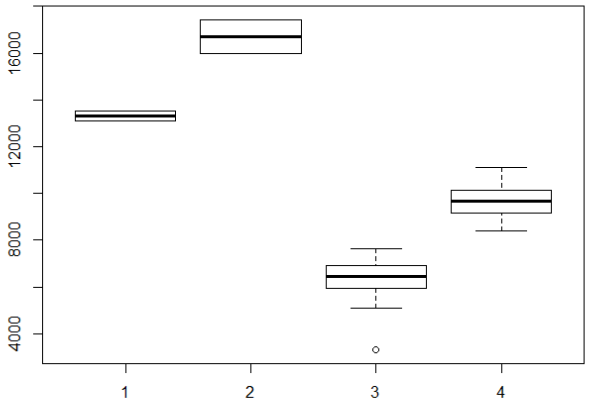


# group 2 is higher than group 1,3,4 in X5

table(seg.k$cluster,d1$X6)
boxplot(d1$X6 ~ seg.k$cluster)



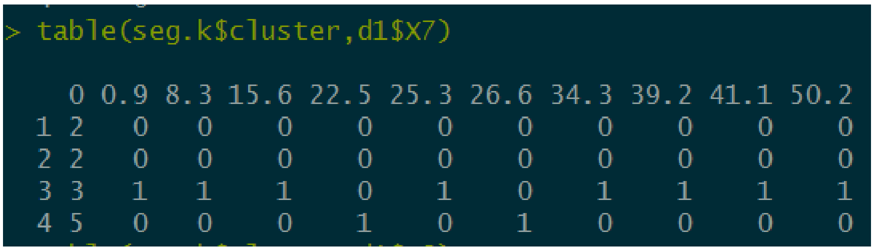
```
> table(seg.k$cluster,d1$X6)

  3300 5088 5714 6154 6423 6455 6468 6650 7179 7297 7642 8406 9077 9212 9673 10093 10140 11127 13082 13507 15991
1    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0     0     0     0     1     1     0
2    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0     0     0     0     0     0     1
3    1    1    1    1    1    1    1    1    1    1    1    0    0    0    0     0     0     0     0     0     0
4    0    0    0    0    0    0    0    0    0    0    0    1    1    1    1     1     1     1     0     0     0

  17441
1     0
2     1
3     0
4     0
```



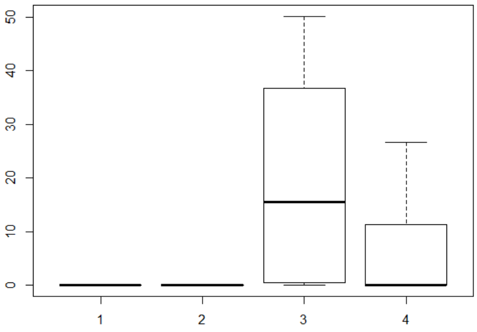
# group 1,2,3 and 4 are all different in X6, group 2 is highest, followed by group 1,4,and 3.

table(seg.k$cluster,d1$X7)

boxplot(d1$X7 ~ seg.k$cluster)



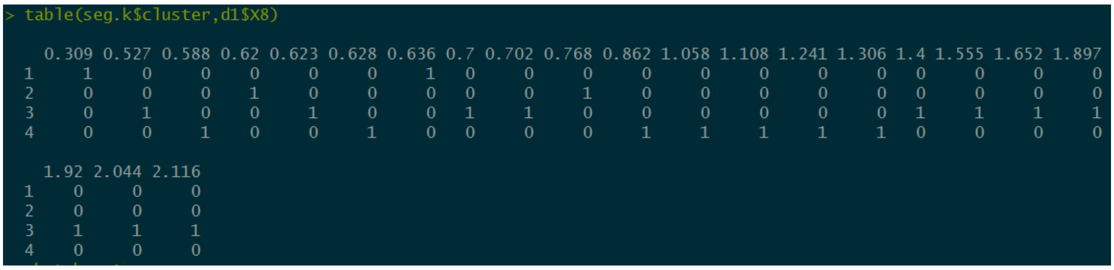
```
> table(seg.k$cluster,d1$X7)

    0 0.9 8.3 15.6 22.5 25.3 26.6 34.3 39.2 41.1 50.2
  1 2   0   0    0    0    0    0    0    0    0    0
  2 2   0   0    0    0    0    0    0    0    0    0
  3 3   1   1    1    0    1    0    1    1    1    1
  4 5   0   0    0    1    0    1    0    0    0    0
```



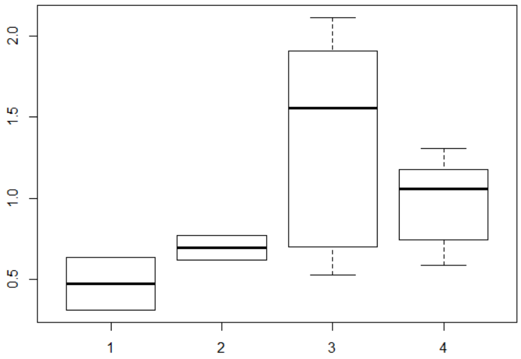
# group 3 is higher than others in X7

table(seg.k$cluster,d1$X8)

boxplot(d1$X8 ~ seg.k$cluster)



```
> table(seg.k$cluster,d1$X8)

    0.309 0.527 0.588 0.62 0.623 0.628 0.636 0.7 0.702 0.768 0.862 1.058 1.108 1.241 1.306 1.4 1.555 1.652 1.897
  1     1     0     0    0     0     0     1   0     0     0     0     0     0     0     0   0     0     0     0
  2     0     0     0    1     0     0     0   0     0     1     0     0     0     0     0   0     0     0     0
  3     0     1     0    0     1     0     0   1     1     0     0     0     0     0     0   1     1     1     1
  4     0     0     1    0     0     1     0   0     0     0     1     1     1     1     1   0     0     0     0

    1.92 2.044 2.116
  1    0     0     0
  2    0     0     0
  3    1     1     1
  4    0     0     0
```



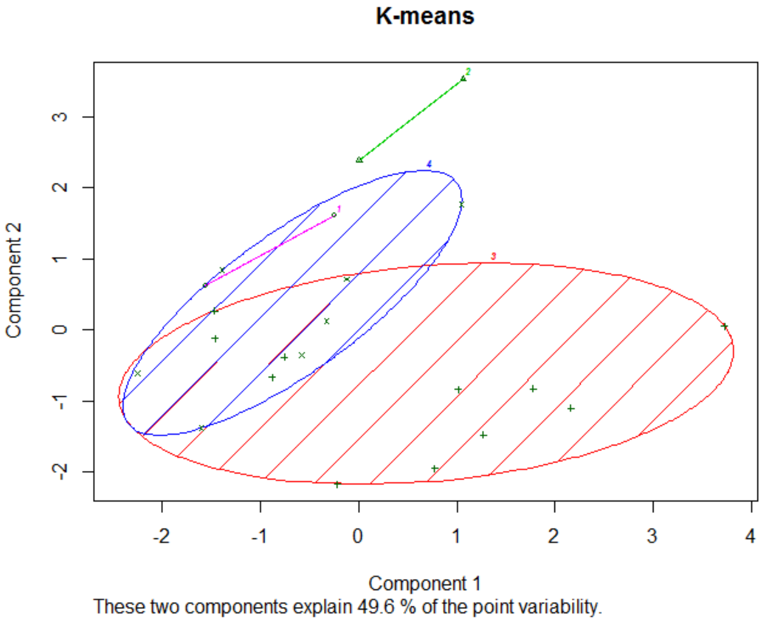
# group 3 is higher than and group 1 is lower than others in X8

#c)

pic=clusplot(d1,seg.k$cluster,color=T,shade=T,labels = 1,lines=0,main="K-means",cex=0.5)

# the green ellipse, which is group 2 is different from others, because 1,3,4 are overlapping each other

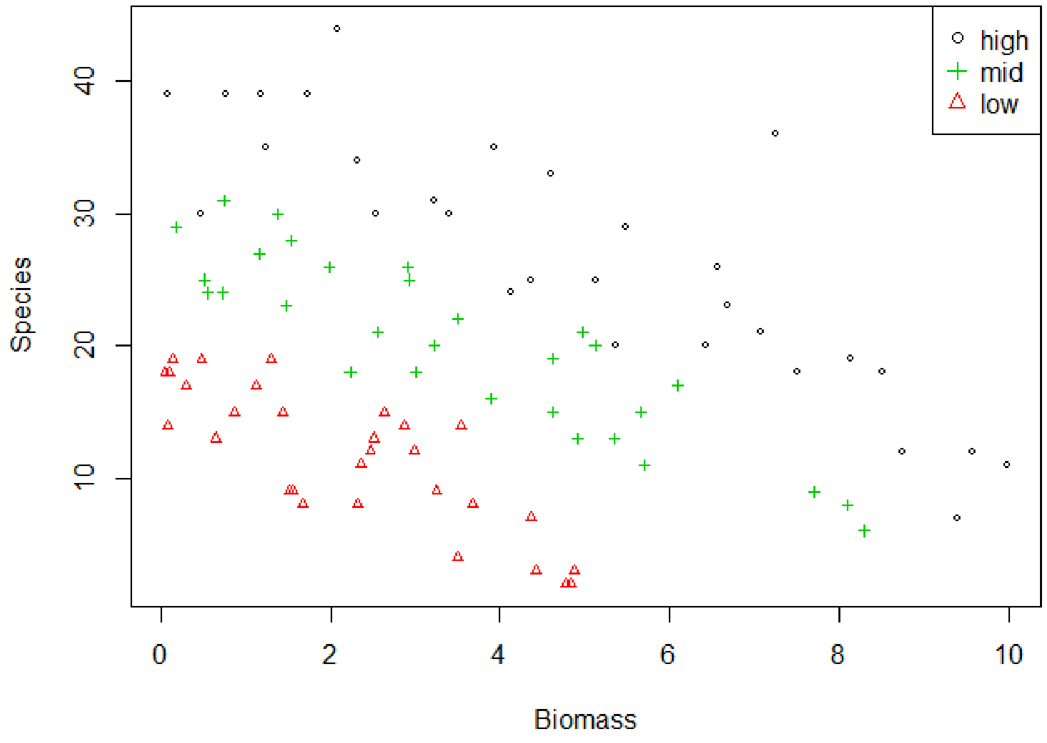
# and group 1 is different from group 3 and 2. Group 3 and 4 is similar



```
#d)
pr = prcomp(d1,scale=T)
rot = pr$rotation
rot
pr$x
as.matrix(scale(d1))%*%rot
PC1.scaled = rot[,1]
PC1.scaled
#         X1          X2          X3          X4          X5          X6          X7
X8
# 0.4451538   0.5647231  -0.1333447  -0.3561666  -0.2684790   0.1404794   0.1970019  -
0.4557031
# is the PC1 eigonvector for scaled X
# the defining equation of scaled data is:
#         PC1         =         0.4451538*C1+0.5647231*C2-0.1333447*C3-0.3561666*C4-
0.2684790*C5+0.1404794*C6+0.1970019*C7-0.4557031*C8
# and C[i] = (X[i]-meanX[i])/std(X[i])
```

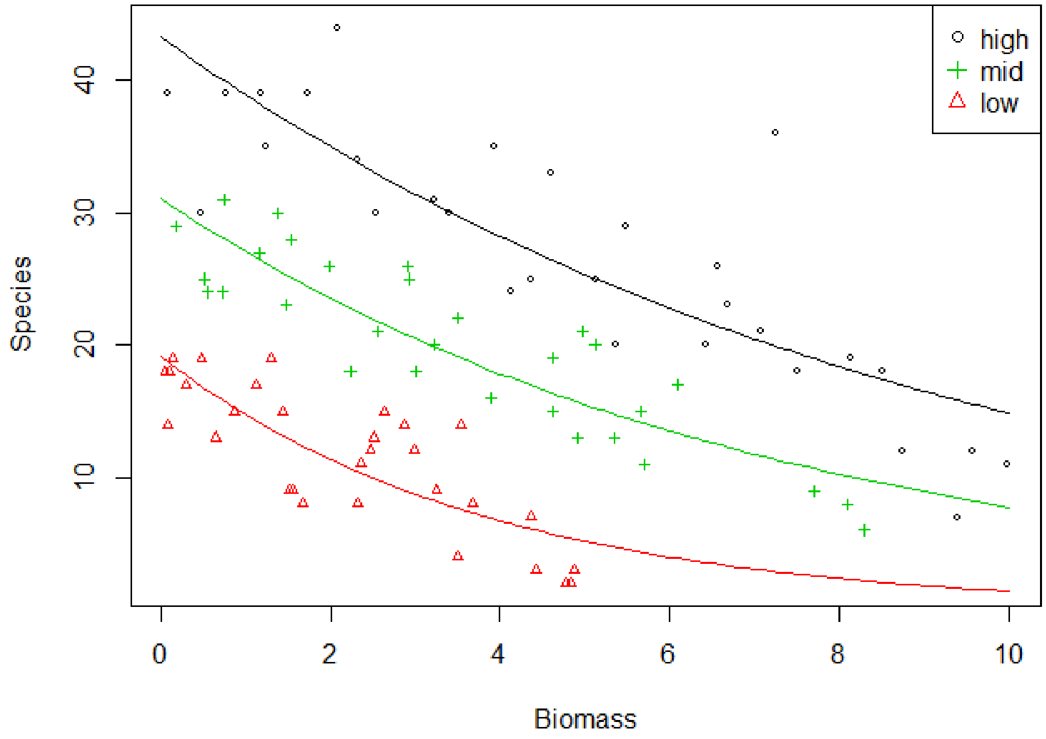
# question 3

```
#a)
getwd()
d0 = read.table("species.txt")
d1 = d0
colnames(d1) = c("pH","Biomass","Species")
d1$Biomass = as.numeric(d1$Biomass)
d1$Species = as.numeric(d1$Species)
aux = as.numeric(d1$pH)
aux
d1$pH
levels(d1$pH)
plot(Species~Biomass,d1,col = aux,pch = aux,cex = 0.6)
legend("topright",c("high","mid","low"),pch = c(1,3,2),col = c(1,3,2) )
# according to the plot, we can not find evidence saying that the slope for each PH level is
different
```



```
#b)
m1 = glm(Species~Biomass*pH,d1,family = poisson)

#c)
m2 = glm(Species~.,d1,family = poisson)
anova(m2,m1, test = "Chisq")

# Analysis of Deviance Table

# Model 1: Species ~ pH + Biomass
# Model 2: Species ~ Biomass * pH
# Resid. Df Resid. Dev Df Deviance    Pr(>Chi)
# 1             86         99.242
# 2             84         83.201    2       16.04 0.0003288 ***
#    ---
#    Signif. codes:   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# P-value is small, we can not reject m1(Model 2: Species ~ Biomass * pH) is better than
m2(Model 1: Species ~ pH + Biomass)
```

```
#d)
llow = rep("low",101)
lmid = rep("mid",101)
lhigh = rep("high",101)
lbio = seq(0,10,0.1)
dlow = data.frame(pH = llow,Biomass = lbio)
dmid = data.frame(pH = lmid,Biomass = lbio)
dhigh = data.frame(pH = lhigh,Biomass = lbio)
ylow = predict(m1,dlow,type = "response")
ymid = predict(m1,dmid,type = "response")
yhigh = predict(m1,dhigh,type = "response")
lines(ylow~lbio,col= 2,pch=".",cex = 0.6,xlim = c(0,10),ylim = c(0,40))
lines(ymid~lbio,col= 3,pch=".",cex = 0.6,xlim = c(0,10),ylim = c(0,40))
lines(yhigh~lbio,col= 1,pch=".",cex = 0.6,xlim = c(0,10),ylim = c(0,40))
```



```
#e)
newval = data.frame(pH = "low",Biomass = 2.0)
alpha = 0.05
yhat = predict(m1, newval, se.fit=T, type="link")
lower95 = exp(yhat$fit - qnorm(1-alpha/2)*yhat$se.fit)
lower95 = round(lower95,3)
```

```
upper95 = exp(yhat$fit + qnorm(1-alpha/2)*yhat$se.fit)
upper95 = round(upper95,3)
cat("(",lower95,",",upper95,")\n")
# ( 10.173 , 12.639 )

#f)
yhat = predict(m1,d1,type = "response")
res = yhat-d1$Species
which.max(abs(res))
d1[18,]
#           pH    Biomass Species
# 18 high 7.242062           36
# the number of species is 36, which associated with largest residual
```