

Exercise 5 Trashaj Alberto 1075402

alberto.trashaj

October 2023

1 Point 1

Let's import the libraries

```
“ “{ r}
library(fpc)
library(poLCA)
library(mclust)
library(cluster)
library(smacof)
library(mixsmsn)
library(nomclust)
#install.packages("fda")
library(fda)
“ “
```

```
“ “{ r}
data("election")
election12 <- election[,1:12]
electionwithna <- election12
for (i in 1:12){
  levels(electionwithna[,i]) <- c(levels(election12[,i]),"NA")
  electionwithna[is.na(election12[,i]),i] <- "NA"
}

d_samplematch <- sm(electionwithna)
mds_sm_elect <- mds(d_samplematch)
plot(mds_sm_elect, cex = 0.05)
“ “
```

In the point a

```
“ “{ r}
set.seed(9999)
f3 <- cbind(MORALG, CARESG, KNOWG, LEADG, DISHONG, INTELG, MORALB, CARESB, KNOWE
```

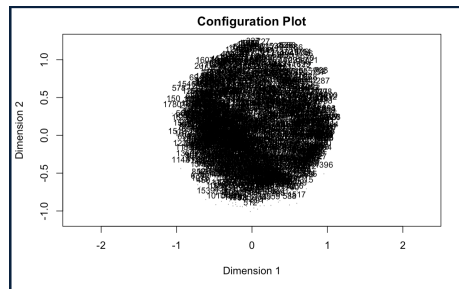


Figure 1: Enter Caption

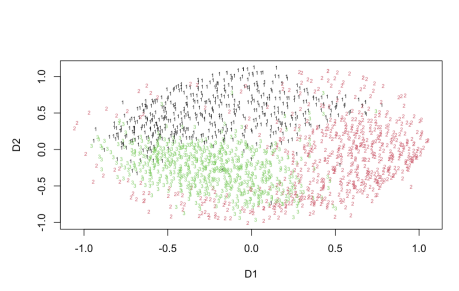


Figure 2: Enter Caption

```
M3 <- poLCA(f3, electionwithna, nclass = 3, graphs = TRUE, maxiter = 5000)
plot(mds_sm_elect$conf, col=M3$predclass, pch=clusym[M3$predclass], cex=0.5)
'''
```

In the point b

```
set.seed(77777)
flexmix_model <- flexmixedruns(electionwithna, continuous = 0, discrete=12, n.cl
str(flexmix_model$flexout[[3]], max.level=2)
flexmix_model$flexout[[3]]@components
table(flexmix_model$flexout[[3]]@cluster)

plot(mds_sm_elect$conf, col= flexmix_model[["flexout"]][[3]]@cluster, pch=clusym
```

Both models doesn't seems too good by looking the mds plot.

Point c

```
'''{r}
complete_clust <- hclust(d_samplematch, method = "complete")
plot(complete_clust, cex=0.2)
'''
```

```
'''{r}
```

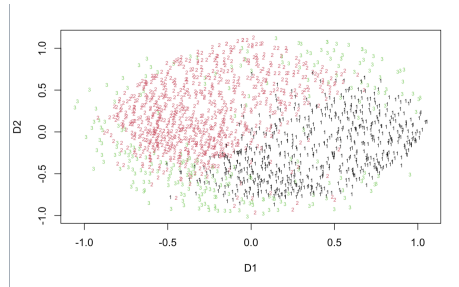


Figure 3: Enter Caption

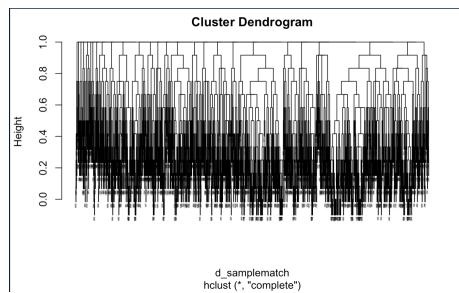


Figure 4: Enter Caption

```

pasw <- NA
pclusk <- list()
psil <- list()

for (k in 2:30){
  pclusk[[k]] <- cutree(complete_clust, k)
  # Computation of silhouettes:
  psil[[k]] <- silhouette(pclusk[[k]], dist= d_samplematch)
  # ASW needs to be extracted:
  pasw[k] <- summary(psil[[k]])$avg.width
}
plot(1:30, pasw, type="l", xlab="Number of clusters", ylab="ASW", main = "Average Silhouette")

class <- cutree(complete_clust, which.max(pasw))
plot(mds_sm_elect$conf, col=class, pch=clusym[class], cex=0.5)
'''

```

Point d

```

flexmix_two <- flexmixedruns(electionwithna, diagonal = F, xvarsorted = F, continue = F)
plot(mds_sm_elect$conf, col= flexmix_two[["flexout"]][[2]]@cluster, pch=clusym[["flexout"]][[2]]@cluster)

```

Point e

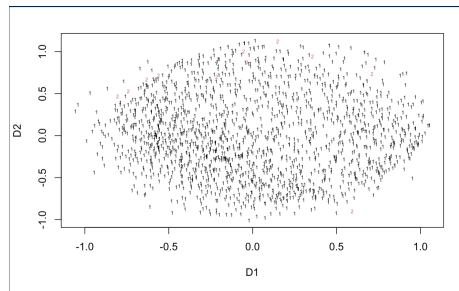


Figure 5: Enter Caption

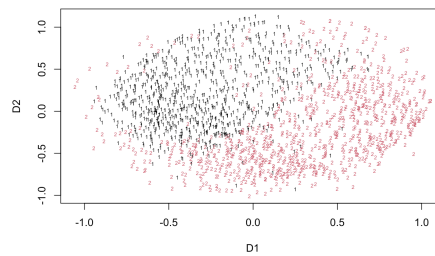


Figure 6: Enter Caption

```
election14 <- cbind(election[,14:15],election12)

for(i in 1:1885) {
  if (is.na(election14[i,1])) election14[i,1] <- mean(election14[,1], na.rm = T)
  if (is.na(election14[i,2])) election14[i,2] <- mean(election14[,2], na.rm = T)
}

# Assuming 'election14' is your data frame
transformation <- as.data.frame(lapply(election14, function(col) {
  ifelse(is.na(col), NA,
    ifelse(col == "1-Extremely well", 1,
      ifelse(col == "2-Quite well", 2,
        ifelse(col == "3-Not too well", 3,
          ifelse(col == "4-Not well at all", 4, NA))))))
}))

colnames(transformation) <- colnames(election14)

flexmixed_three <- flexmixedruns(transformation, diagonal = T, xvarsorted = T, c
```

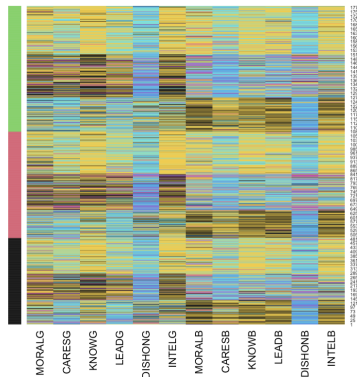


Figure 7: Enter Caption

Unfortunately, I receive an error which I couldn't solve for this point.

2 Point 2

```

{r}
electionwithna_m = data.matrix(electionwithna)

cluster_ord = order(M3$predclass)
electionwithna_m_ord = electionwithna_m[cluster_ord, ]
col_vector = c(9,7,5,12,14)

heatmap(
  electionwithna_m_ord[order(M3$predclass),],
  Rowv = NA,
  Colv = NA,
  RowSideColors = palette() [M3$predclass][order(M3$predclass)] ,
  col = col_vector ,
  scale = "none" ,
)

```

3 Point 3

Point 3

3.a

Parameters for binary variables = $1 * 5$

Parameters for the variables with 3 categories = $2 * 3$

Parameters for the variables with 5 categories = $4 * 2$

Total number of parameters = $5 + 6 + 8 = 19$

3.b

Parameters for mixing components = $4 * (4 - 1) = 12$

Parameters for binary variables = $4 * 5 = 20$

Parameters for variables with three categories = $3 * 2 * 3 = 18$

Parameters for variables with five categories = $2 * 4 * 5 = 40$

Total number of parameters = $12 + 20 + 18 + 40$

4 Point 4

```
““{ r}
““{ r}
covid <- read.csv("/Users/albertotrashaj/Desktop/Universita /Unsupervised/covid
head(covid)

continent <- covid[,2]
covid <- as.matrix(covid[,5:555])
Ita <- covid[79,]
Hai <- covid[69,]
USA <- covid[164,]
plot(1:555, covid[1,], type="l", ylim=c(0,10), ylab="New cases over one week per 100
points(1:555, Ita, type="l", col = "green")
points(1:555, USA, type="l", col = "red")
points(1:555, Hai, type="l", col = "blue")
““

““{ r}
bbasis <- create.bspline.basis(c(1,555), nbasis=100)
fdcovid <- Data2fd(1:555, y=t(as.matrix(covid)), basisobj=bbasis)
plotfit.fd(t(covid), 1:555, fdcovid, index=79, cex.pch=0.5)
```

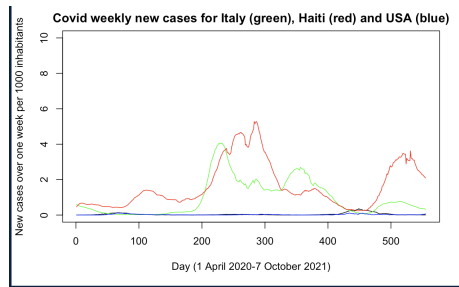


Figure 8: Enter Caption

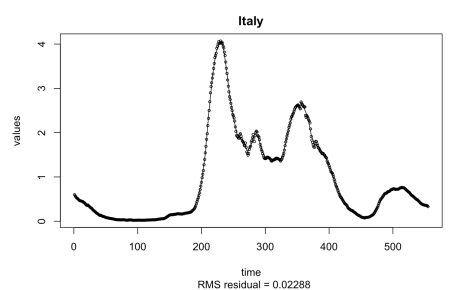


Figure 9: Enter Caption

“ “ “

```

“ “ { r }
plotfit.fd(t(covid),1:555,fdcovid ,index=69,cex.pch=0.5)

plotfit.fd(t(covid),1:555,fdcovid ,index=164,cex.pch=0.5)
“ “

covidpca <- pca.fd(fdcovid , nharm = 5)
plot(covidpca$harmonics)

mcovid <- mean.fd(fdcovid)
covidpcaapprox <- covidpca$harmonics
i <- 1
pcacoefi <- covidpca$harmonics$coefs %*% covidpca$scores[i,]+mcovid$coefs
covidpcaapprox$coefs <- pcacoefi
for (i in 2:179){
pcacoefi <- covidpca$harmonics$coefs %*% covidpca$scores[i,]+mcovid$coefs
covidpcaapprox$coefs <- cbind(covidpcaapprox$coefs , pcacoefi)
}
dimnames(covidpcaapprox$coefs )[[2]] <- rownames(covid)
plotfit.fd(t(covid),1:555,covidpcaapprox , index = 79 ,cex.pch=0.5)

```

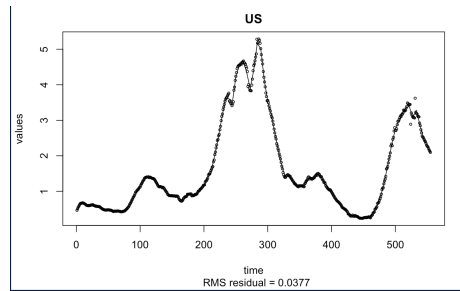


Figure 10: Enter Caption

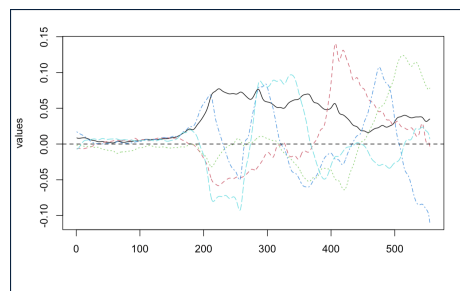


Figure 11: Enter Caption

```
plotfit.fd(t(covid),1:555,covidpcaapprox, index = 69 ,cex.pch=0.5)
```

5 Point 5

```
““{ r}
covidpca_2 <- pca.fd(fdcovid, nharm = 1)
summary(covidpca_2$scores)

mean_analysis_df <- data.frame(scores = covidpca_2$scores, continent = factor(con
barplot(mean_analysis_df$scores, col=mean_analysis_df$continent)
““
```

```
““{ r}
ANOVA <- aov(scores ~ continent, data = mean_analysis_df)
summary(ANOVA)
““
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
continent	6	25062	4177	27.62	<2e-16 ***

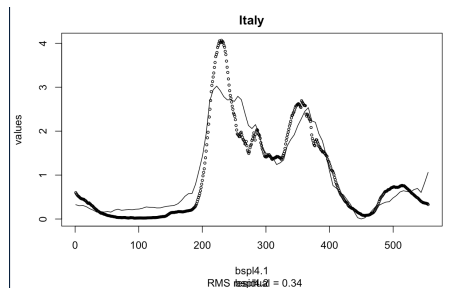


Figure 12: Enter Caption

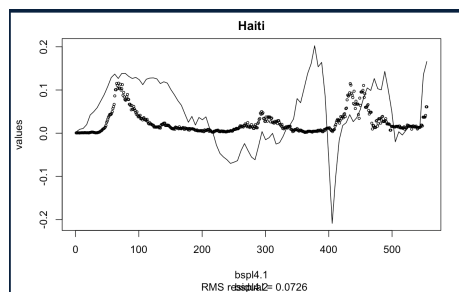


Figure 13: Enter Caption

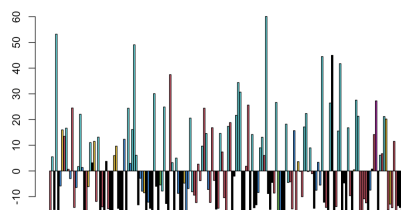


Figure 14: Enter Caption

Residuals	172	26008	151						
Signif. codes:	0	***	0.001	**	0.01	*	0.05	.	0.1