Assignment 7

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Exercise 1

Load data

```
library(fpc)
library(poLCA)

data(election)
election12 <- election[,1:12]
head(election12)</pre>
```

```
##
                MORALG
                                   CARESG
                                                      KNOWG
                                                                        LEADG
## 1
        3 Not too well 1 Extremely well
                                               2 Quite well
                                                                 2 Quite well
                          3 Not too well 4 Not well at all
## 2 4 Not well at all
                                                               3 Not too well
## 3 1 Extremely well
                            2 Quite well
                                               2 Quite well 1 Extremely well
          2 Quite well
                                               2 Quite well
## 4
                            2 Quite well
                                                                 2 Quite well
## 5
          2 Quite well 4 Not well at all
                                               2 Quite well
                                                               3 Not too well
          2 Quite well
                          3 Not too well
                                             3 Not too well
## 6
                                                                 2 Quite well
            DISHONG
                          INTELG
                                            MORALB
                                                             CARESB
                                                                              KNOWB
##
## 1 3 Not too well 2 Quite well 1 Extremely well 1 Extremely well
                                                                       2 Quite well
       2 Quite well 2 Quite well
                                              <NA>
                                                                <NA>
                                                                       2 Quite well
## 2
## 3 3 Not too well 2 Quite well
                                      2 Quite well
                                                       2 Quite well
                                                                       2 Quite well
## 4
       2 Quite well 2 Quite well
                                      2 Quite well
                                                     3 Not too well
                                                                       2 Quite well
## 5
       2 Quite well 2 Quite well 1 Extremely well 1 Extremely well
                                                                       2 Quite well
## 6
       2 Quite well 2 Quite well
                                      2 Ouite well
                                                                <NA> 3 Not too well
                              DISHONB
              LEADB
##
                                                 INTELB
## 1
       2 Quite well 4 Not well at all
                                           2 Quite well
## 2 3 Not too well
                                  <NA> 1 Extremely well
## 3 3 Not too well
                       3 Not too well
                                           2 Quite well
## 4
       2 Quite well
                       3 Not too well 1 Extremely well
## 5
       2 Quite well
                       3 Not too well
                                           2 Quite well
## 6
       2 Ouite well
                         2 Ouite well
                                           2 Quite well
```

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

election14 <- election[14:15]
election14[3:14] <- electionwithna
for (i in 1:2) {
    election14[is.na(election14[,i]),i] <- mean(election14[,i], na.rm=T)
}</pre>
```

Prepare MDS plot

```
library(cluster)
library(smacof)

dist_election <- daisy(electionwithna, metric="gower")

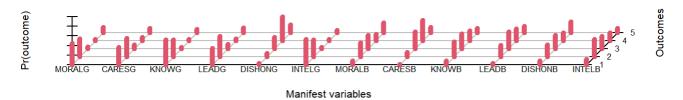
mds_election <- mds(dist_election, ndim=2)
mds_election$stress</pre>
```

```
## [1] 0.3096474
```

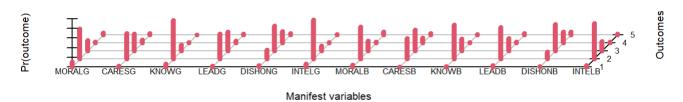
```
show_mds <- function(clustering, title) {
   plot(mds_election$conf, col=clustering$cluster, main=title)
}</pre>
```

a)

Class 1: population share = 0.339



Class 2: population share = 0.389



Class 3: population share = 0.273



```
## Conditional item response (column) probabilities,
## by outcome variable, for each class (row)
##
## $MORALG
##
             1 Extremely well 2 Quite well 3 Not too well 4 Not well at all
## class 1:
                       0.4440
                                    0.3695
                                                   0.0437
                                                                     0.0291 0.1137
                                                   0.2141
## class 2:
                       0.1044
                                    0.6185
                                                                     0.0207 0.0423
## class 3:
                       0.1687
                                    0.3443
                                                   0.2303
                                                                     0.2076 0.0491
##
## $CARESG
             1 Extremely well 2 Quite well 3 Not too well 4 Not well at all
##
                       0.3678
                                    0.3883
                                                   0.0799
                                                                     0.0726 0.0913
## class 1:
## class 2:
                       0.0253
                                    0.5275
                                                   0.3527
                                                                     0.0649 0.0296
## class 3:
                       0.0762
                                    0.2308
                                                   0.3514
                                                                     0.2939 0.0477
##
## $KNOWG
##
             1 Extremely well 2 Quite well 3 Not too well 4 Not well at all
                  0.5214
                                   0.3544
                                                 0.0284
                                                             0.0278 0.0681
## class 1:
                       0.0618
                                    0.8047
                                                   0.1258
                                                                     0.0046 0.0031
## class 2:
## class 3:
                       0.2114
                                    0.4615
                                                   0.2209
                                                                     0.0802 0.0260
##
## $LEADG
             1 Extremely well 2 Quite well 3 Not too well 4 Not well at all
                       0.3472
                                    0.4215
                                                   0.0906
                                                                    0.0419 0.0988
## class 1:
                       0.0213
                                    0.5210
                                                   0.3969
                                                                     0.0374 0.0233
## class 2:
## class 3:
                       0.0684
                                    0.2297
                                                   0.3942
                                                                     0.2746 0.0330
##
## $DISHONG
##
             1 Extremely well 2 Quite well 3 Not too well 4 Not well at all
## class 1:
                       0.0321
                                    0.0714
                                                   0.2353
                                                                    0.4993 0.1619
## class 2:
                       0.0299
                                                   0.5145
                                                                     0.2365 0.0340
                                    0.1852
## class 3:
                       0.1907
                                    0.2884
                                                   0.2669
                                                                     0.1872 0.0668
##
## $INTELG
##
             1 Extremely well 2 Quite well 3 Not too well 4 Not well at all
## class 1:
                       0.5317
                                    0.3556
                                                   0.0302
                                                                     0.0340 0.0486
## class 2:
                       0.0650
                                    0.8058
                                                   0.1072
                                                                     0.0080 0.0140
## class 3:
                                    0.4544
                       0.2618
                                                   0.1836
                                                                     0.0798 0.0204
##
## $MORALB
##
             1 Extremely well 2 Quite well 3 Not too well 4 Not well at all
                                                   0.2809
                                                                     0.1362 0.2074
## class 1:
                      0.0842
                                    0.2912
## class 2:
                       0.0453
                                    0.6663
                                                   0.2103
                                                                     0.0150 0.0630
## class 3:
                       0.5293
                                    0.4165
                                                   0.0294
                                                                     0.0107 0.0141
##
## $CARESB
             1 Extremely well 2 Quite well 3 Not too well 4 Not well at all
                                                                     0.4289 0.1170
## class 1:
                       0.0113
                                    0.0928
                                                   0.3500
                                    0.4230
                       0.0037
                                                   0.4364
## class 2:
                                                                     0.1036 0.0334
                                                   0.0981
## class 3:
                       0.2992
                                    0.5659
                                                                     0.0223 0.0145
##
## $KNOWB
             1 Extremely well 2 Quite well 3 Not too well 4 Not well at all
## class 1:
                       0.0854
                                    0.3073
                                                   0.3072
                                                                      0.204 0.0962
## class 2:
                       0.0122
                                    0.7105
                                                   0.2537
                                                                      0.014 0.0097
```

```
## class 3:
                   0.4394
                                0.5227
                                              0.0356
                                                                0.000 0.0023
##
## $LEADB
           1 Extremely well 2 Quite well 3 Not too well 4 Not well at all
##
## class 1:
                     0.0278
                                0.2357
                                              0.3568
                                                              0.2484 0.1313
## class 2:
                     0.0320
                                 0.6581
                                              0.2590
                                                               0.0192 0.0316
## class 3:
                    0.4663
                                0.4992
                                              0.0239
                                                               0.0051 0.0055
##
## $DISHONB
##
           1 Extremely well 2 Quite well 3 Not too well 4 Not well at all
## class 1:
                    0.0785
                                0.2482
                                              0.2750
                                                              0.1662 0.2322
## class 2:
                     0.0130
                                0.1469
                                              0.5488
                                                              0.2318 0.0595
## class 3:
                                                               0.6425 0.0377
                     0.0277
                                0.0741
                                              0.2180
##
## $INTELB
##
           1 Extremely well 2 Quite well 3 Not too well 4 Not well at all
                    0.1190
                                0.3630
                                              0.2609
                                                              0.1615 0.0956
## class 1:
                    0.0334
                                              0.1989
## class 2:
                                0.7333
                                                              0.0168 0.0175
## class 3:
                     0.4803
                                0.4908
                                              0.0212
                                                              0.0014 0.0063
##
## Estimated class population shares
## 0.3387 0.3885 0.2727
##
## Predicted class memberships (by modal posterior prob.)
  0.3333 0.395 0.2717
##
##
## Fit for 3 latent classes:
## number of observations: 1785
## number of estimated parameters: 146
## residual degrees of freedom: 1639
## maximum log-likelihood: -25972.59
##
## AIC(3): 52237.18
## BIC(3): 53038.31
## G^2(3): 25636.59 (Likelihood ratio/deviance statistic)
## X^2(3): 42945467129 (Chi-square goodness of fit)
##
```

```
clus_a$cluster <- clus_a$predclass
```

b)

```
flex_clus <- flexmixedruns(electionwithna, continuous = 0, discrete=12, n.cluster=3)</pre>
```

```
## k= 3 new best fit found in run 1
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run 6
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run 9
## k= 3 new best fit found in run 10
## Nonoptimal or repeated fit found in run 11
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run 15
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run 17
## Nonoptimal or repeated fit found in run 18
## Nonoptimal or repeated fit found in run 19
## Nonoptimal or repeated fit found in run 20
## k= 3 BIC= 52863.7
```

```
clus_b <- list()
clus_b$cluster <- flex_clus$flexout[[3]]@cluster</pre>
```

c)

Hierarchical clustering with average linkage

```
clus_c = list()
clus_c$cluster <- cutree(hclust(dist_election, method="average"), k=3)</pre>
```

d)

```
set.seed(12345)
optimal_k <- flexmixedruns(electionwithna, continuous = 0, discrete=12, n.cluster=1:10)$optim
alk</pre>
```

```
## k=
       1
          new best fit found in run
       1
          BIC=
               57445.61
       2
          new best fit found in run 1
## Nonoptimal or repeated fit found in run 2
      2
         new best fit found in run 3
## Nonoptimal or repeated fit found in run
## k= 2 new best fit found in run 9
## Nonoptimal or repeated fit found in run
                                            10
## Nonoptimal or repeated fit found in run
                                            19
## Nonoptimal or repeated fit found in run
       2
          BIC=
               54295.51
##
          new best fit found in run
      3
          new best fit found in run
## k=
## Nonoptimal or repeated fit found in run
      3
         new best fit found in run
## Nonoptimal or repeated fit found in run
  Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
      3 new best fit found in run 13
## Nonoptimal or repeated fit found in run
                                            17
## Nonoptimal or repeated fit found in run
                                            18
                                            19
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
                                            20
       3
          BIC= 52863.71
  k=
##
          new best fit found in run
##
  k=
      4
## k=
       4
          new best fit found in run
##
      4
          new best fit found in run
##
  Nonoptimal or repeated fit found in run
## k= 4 new best fit found in run
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
                                            7
         new best fit found in run
## k=
      4
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
```

```
## k=
      4
         new best fit found in run
## k=
      4
         new best fit found in run
         new best fit found in run
## Nonoptimal or repeated fit found in run
##
      4
         BIC= 51682.54
       5
## k=
          new best fit found in run
       5
          new best fit found in run
##
      5
         new best fit found in run
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
## k= 5 new best fit found in run 7
## Nonoptimal or repeated fit found in run
## k= 5 new best fit found in run 9
## Nonoptimal or repeated fit found in run
                                            10
## Nonoptimal or repeated fit found in run
      5 BIC= 51158.82
      6 new best fit found in run 1
## Nonoptimal or repeated fit found in run
  Nonoptimal or repeated fit found in run
      6
         new best fit found in run
      6 new best fit found in run 8
## Nonoptimal or repeated fit found in run
                                            15
## Nonoptimal or repeated fit found in run
## k= 6 new best fit found in run 17
## Nonoptimal or repeated fit found in run
                                            18
## Nonoptimal or repeated fit found in run
                                            19
## Nonoptimal or repeated fit found in run
## k=
      6 BIC= 50858.43
## k=
      7
         new best fit found in run 1
## Nonoptimal or repeated fit found in run
                                            2
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
```

Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run ## k= 7 new best fit found in run 7 ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run ## k= 7 new best fit found in run 11 ## Nonoptimal or repeated fit found in run ## k= 7 new best fit found in run ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run new best fit found in run ## k= 7 new best fit found in run 7 BIC= 50761.99 ## k= new best fit found in run 1 8 ## ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run 8 new best fit found in run 4 ## k= 8 new best fit found in run 5 ## k= ## Nonoptimal or repeated fit found in run 17 ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run Nonoptimal or repeated fit found in run ## k= 8 BIC= 50745.88 9 new best fit found in run 1 ## Nonoptimal or repeated fit found in run 2 9 new best fit found in run 3 ## Nonoptimal or repeated fit found in run 11 ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run 13 ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run 15 ## Nonoptimal or repeated fit found in run 16 ## Nonoptimal or repeated fit found in run 17 ## Nonoptimal or repeated fit found in run

```
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
      9 BIC= 50813.49
## k=
      10
          new best fit found in run 1
      10
          new best fit found in run
## k=
          new best fit found in run 3
      10
## Nonoptimal or repeated fit found in run 4
      10 new best fit found in run 5
## Nonoptimal or repeated fit found in run
## k= 10 BIC= 50912.88
```

```
clus_d <- list()
flex_clus <- flexmixedruns(electionwithna, continuous = 0, discrete = 12, n.cluster=optimal_
k)</pre>
```

```
## k= 8 new best fit found in run 1
## Nonoptimal or repeated fit found in run
## k= 8 new best fit found in run 6
## Nonoptimal or repeated fit found in run
                                           15
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
                                           17
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
## k= 8 BIC= 50743.89
```

```
clus_d$cluster <- flex_clus$flexout[[optimal_k]]@cluster
clus_d$n.class <- optimal_k
optimal_k</pre>
```

```
## [1] 8
```

The best number of clusters here is 8 clusters.

e)

```
set.seed(12345)
election14_numeric <- sapply(election14, unclass)
clus_e <- flexmixedruns(election14_numeric, continuous=2, discrete=12, n.cluster=1:10)</pre>
```

```
## k=
       1
         new best fit found in run
       1
          BIC=
               79391.33
       2
         new best fit found in run 1
## Nonoptimal or repeated fit found in run 2
      2
         new best fit found in run 3
## Nonoptimal or repeated fit found in run
## k= 2 new best fit found in run 9
## Nonoptimal or repeated fit found in run
                                            10
## Nonoptimal or repeated fit found in run
                                            19
## Nonoptimal or repeated fit found in run
## k=
      2 BIC= 76256.63
      3 new best fit found in run 1
## Nonoptimal or repeated fit found in run 2
         new best fit found in run
      3
## Nonoptimal or repeated fit found in run
## k=
      3
         new best fit found in run
       3 new best fit found in run
## Nonoptimal or repeated fit found in run
## k= 3 new best fit found in run 18
## Nonoptimal or repeated fit found in run
                                            19
## Nonoptimal or repeated fit found in run
                                            20
## k=
      3
         BIC= 74828.7
## k= 4 new best fit found in run 1
## Nonoptimal or repeated fit found in run
                                            7
## Nonoptimal or repeated fit found in run
```

```
## Nonoptimal or repeated fit found in run
##
      4
         BIC= 73635.65
       5
## k=
          new best fit found in run
          new best fit found in run
##
      5
         new best fit found in run
## Nonoptimal or repeated fit found in run
## k= 5 new best fit found in run 5
## Nonoptimal or repeated fit found in run
      5 BIC= 73114.55
      6 new best fit found in run 1
## Nonoptimal or repeated fit found in run
## k= 6 new best fit found in run 7
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
## k= 6 new best fit found in run 11
## Nonoptimal or repeated fit found in run
                                            15
## Nonoptimal or repeated fit found in run
                                            16
## Nonoptimal or repeated fit found in run
                                            17
## Nonoptimal or repeated fit found in run
                                            18
## Nonoptimal or repeated fit found in run
                                            19
## Nonoptimal or repeated fit found in run
## k=
      6
         BIC= 72831.04
## k=
      7
         new best fit found in run 1
## Nonoptimal or repeated fit found in run
                                            2
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
```

Nonoptimal or repeated fit found in run ## k= 7 new best fit found in run 6 ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run new best fit found in run 7 ## k= new best fit found in run 7 new best fit found in run ## Nonoptimal or repeated fit found in run 7 new best fit found in run 20 7 BIC= 72765.21 ## k= ## new best fit found in run 8 new best fit found in run ## k= ## Nonoptimal or repeated fit found in run ## k= 8 new best fit found in run 4 ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run ## k= 8 new best fit found in run 8 ## Nonoptimal or repeated fit found in run 17 ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run Nonoptimal or repeated fit found in run ## k= 8 BIC= 72764.94 9 new best fit found in run 1 ## Nonoptimal or repeated fit found in run 2 9 new best fit found in run ## k= 9 new best fit found in run 4 ## Nonoptimal or repeated fit found in run 13 ## Nonoptimal or repeated fit found in run ## k= 9 new best fit found in run 15 ## Nonoptimal or repeated fit found in run ## Nonoptimal or repeated fit found in run 9 new best fit found in run 18

```
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
## k= 9 BIC= 72818.13
## k= 10 new best fit found in run 1
## Nonoptimal or repeated fit found in run
## Nonoptimal or repeated fit found in run
## k= 10 new best fit found in run 4
## Nonoptimal or repeated fit found in run
          new best fit found in run
## Nonoptimal or repeated fit found in run
## k= 10 BIC= 72927.52
```

```
clus_e$cluster <- flex_clus$flexout[[flex_clus$optimalk]]@cluster
flex_clus$optimalk</pre>
```

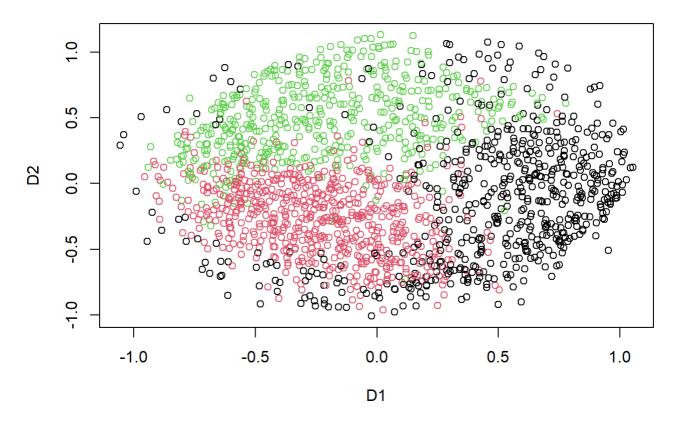
```
## [1] 8
```

The best number of clusters is in this case 8 clusters.

Compare clusterings

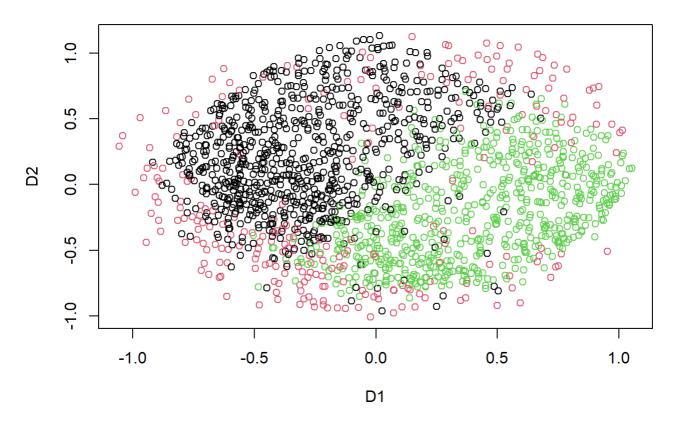
```
show_mds(clus_a, "poLCA (3 clusters)")
```

poLCA (3 clusters)



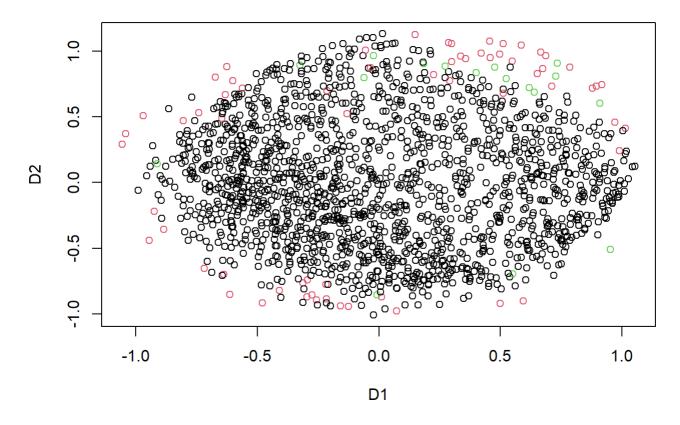
show_mds(clus_b, "flexmixedruns (3 clusters)")

flexmixedruns (3 clusters)



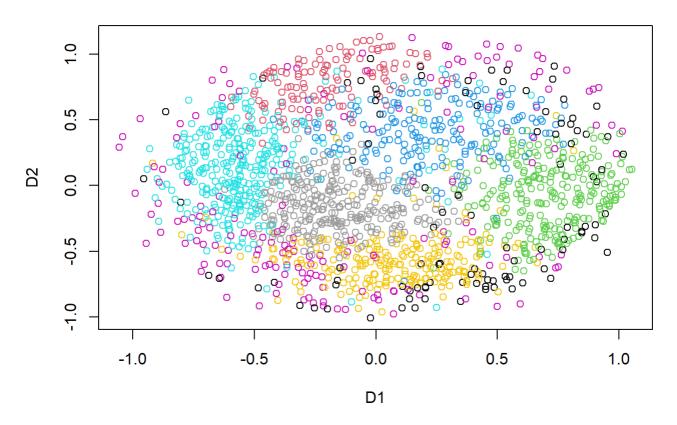
show_mds(clus_c, "Hierarchical clustering - average (3 clusters)")

Hierarchical clustering - average (3 clusters)



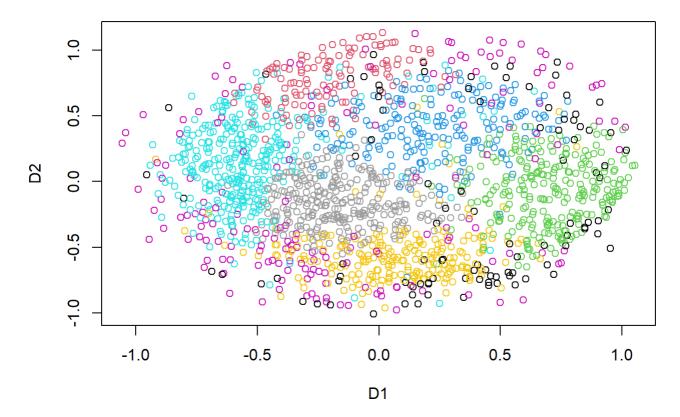
show_mds(clus_d, "flexmixedruns (optimal k -> 8 clusters)")

flexmixedruns (optimal k -> 8 clusters)



show_mds(clus_e, "flexmixedruns - continuous + discrete (optimal k -> 8 clusters)")

flexmixedruns - continuous + discrete (optimal k -> 8 clusters)



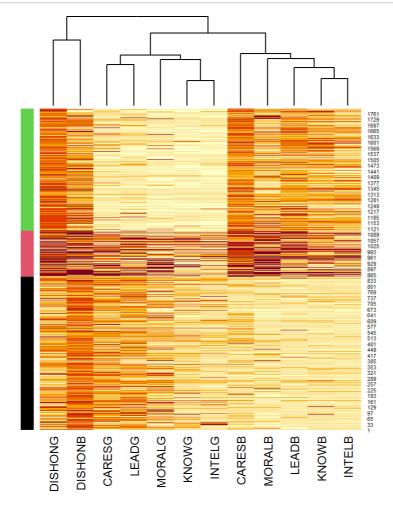
From the mds plot it is hard to tell which clustering seems more convincing. No clear distinctive clusters regarding both separation or density are visible. However, the clearest distinction and close clusters are generated by the poLCA clustering method, although the green cluster is not a clear cluster, since it spans into the realm of other clusters, according to the mds.

In addition, both flexmixedruns clusterings with flexible clusters behave very similarly and show a fairly good separation for some of the clusters. But overall, the clusters are noisier than for the poLCA.

Hierarchical clustering rarely catches any significant cluster, rather it detects some outliers and assigns them to different groups. All other observations are assigned to the same main cluster.

Exercise 2

Create clustering for clus b (flexmixedruns -> 3 clusters)



We think the clustering clearly differentiates between inherently different observations. Each group shows a distinctive pattern. While the black cluster is constantly higher than the other two clusters, the other two clusters show different columns in which they have high or low values, respectively. Thus, the clustering seems

like a good clustering to me.

Local independence is hard to spot. But from the given plot, no clear violation of local independence is visible. A violation of this assumption would be characterized by two columns showing similar patterns of the observations within each cluster. This is not the case.

Exercise 3

```
# a )
(2**5)*(3**3)*(5**2) - 1
```

```
## [1] 21599
```

```
# b)
4 * ((2 - 1) * 5 + (3 - 1) * 3 + (5 - 1) * 2 + 1) - 1
```

```
## [1] 79
```

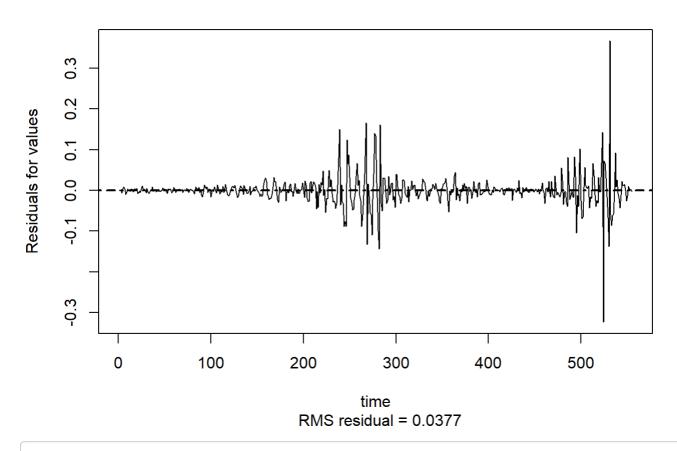
Exercise 4

```
library(fda)
# Load data
covid21 <- read.table("data/covid2021.dat")
covid21v <- as.matrix(covid21[,5:559])

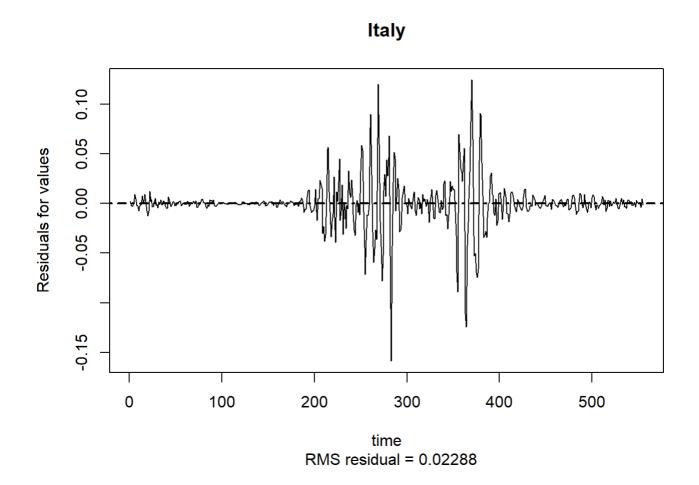
# B-spline basis
bbasis100 <- create.bspline.basis(c(1,555), nbasis=100)
fdcovid100 <- Data2fd(1:555, y=t(as.matrix(covid21v)), basisobj=bbasis100)

plotfit.fd(t(covid21v), 1:555, fdcovid100, index=164, cex.pch=0.5, residual=T)</pre>
```

US

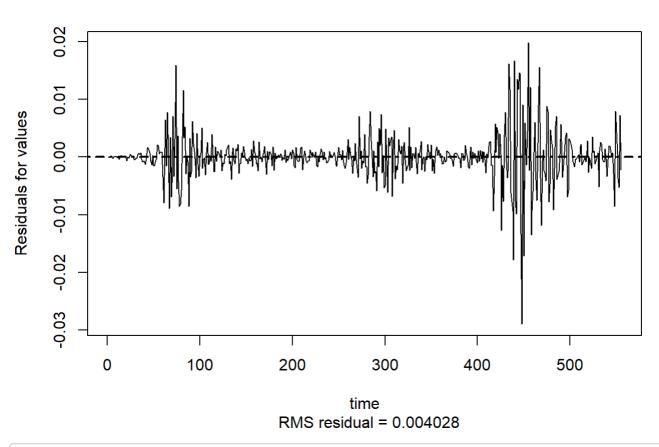


plotfit.fd(t(covid21v), 1:555, fdcovid100, index=79, cex.pch=0.5, residual=T)



plotfit.fd(t(covid21v), 1:555, fdcovid100, index=69, cex.pch=0.5, residual=T)

Haiti



```
# Principal Component basis
covidpca <- pca.fd(fdcovid100, nharm = 5)
covidpca$varprop</pre>
```

[1] 0.40871917 0.18555649 0.11717077 0.05581147 0.04606967

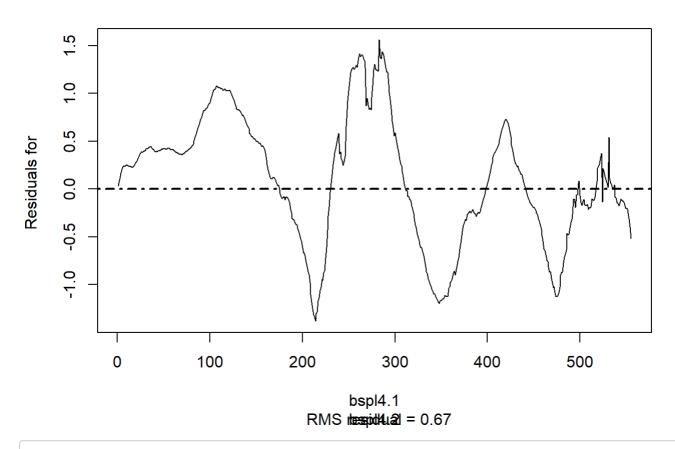
cumsum(covidpca\$varprop)

[1] 0.4087192 0.5942757 0.7114464 0.7672579 0.8133276

```
mcovid <- mean.fd(fdcovid100)

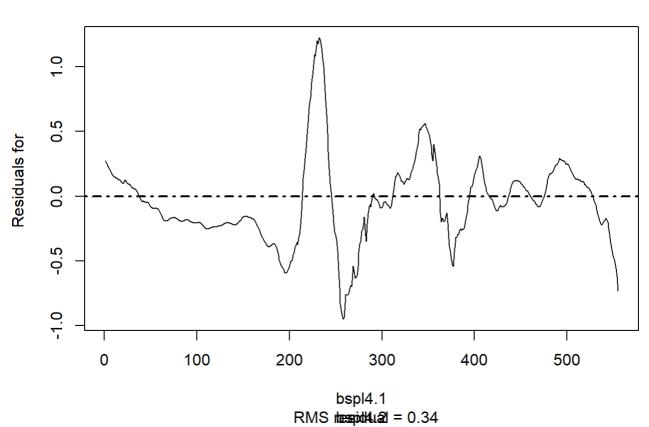
covidpcaapprox <- covidpca$harmonics
i <- 1
pcacoefi <- covidpca$harmonics$coefs %*% covidpca$scores[i,]+mcovid$coefs
covidpcaapprox$coefs <- pcacoefi
for (i in 2:179) {
    pcacoefi <- covidpca$harmonics$coefs %*% covidpca$scores[i,]+mcovid$coefs
    covidpcaapprox$coefs <- cbind(covidpcaapprox$coefs, pcacoefi)
}
dimnames(covidpcaapprox$coefs)[[2]] <- covid21[,1]
plotfit.fd(t(covid21v),1:555,covidpcaapprox,index=164,cex.pch=0.5, residual=T)</pre>
```





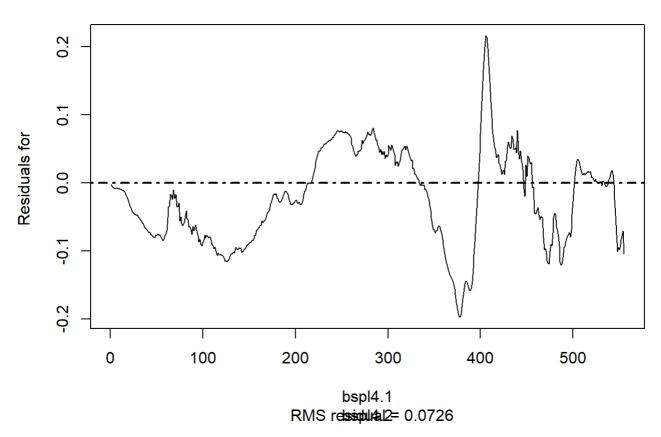
plotfit.fd(t(covid21v),1:555,covidpcaapprox,index=79,cex.pch=0.5, residual=T)





plotfit.fd(t(covid21v),1:555,covidpcaapprox,index=69,cex.pch=0.5, residual=T)





For the B-spline basis, all approximations are fairly close to the original timeseries of the three different countries. The range of absolute maximum deviation from the original data ranges from 0.03 (Haiti) to 0.3 (US). Anyway, for evey country there is some areas where the approximation systematically differs from the original data for consecutive time steps. For example, for Italy, between step 200 to 300: While the approximation is correct on average, the approximation is seems to miss some error noise. This probably happens in areas where a lot of Covid cases are present and thus the numbers fluctuate more.

For the PCA basis with 5 components, on the other hand, relatively much higher deviation can be observed from the residual plot. There the range of absolute maximum deviation from the original data ranges from 0.2 (Haiti) to 1.0 (Italy and US). This indicates a great loss by a 5-dimensional PCA representation. Characteristic patterns of the single countries are not displayed appropriately.

Exercise 5

```
library(dplyr)
covidpca1 <- pca.fd(fdcovid100, nharm = 1)
ncontinent <- as.numeric(as.factor(covid21$continent))
con_names <- levels(as.factor(covid21$continent))

con_scores_all <- data.frame(scores = covidpca1$scores, continent = as.factor(ncontinent))

res.aov <- aov(scores ~ continent, data = con_scores_all)
# Significant difference between continent mean scores
summary(res.aov)</pre>
```

```
## Df Sum Sq Mean Sq F value Pr(>F)

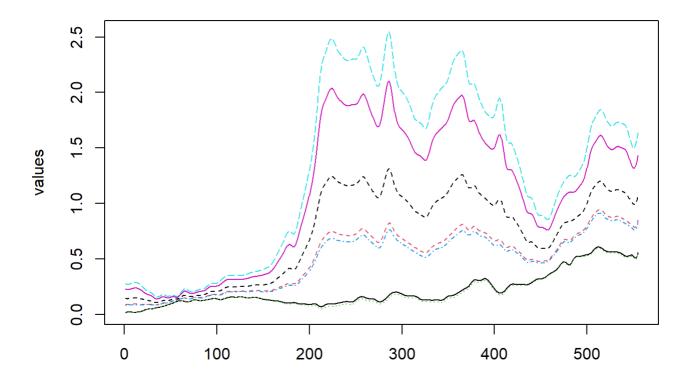
## continent 6 25062 4177 27.62 <2e-16 ***

## Residuals 172 26008 151

## ---

## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
con_scores <- group_by(con_scores_all, continent) %>%
    summarise(
        mean = mean(scores)
    )
covidpca1 <- pca.fd(fdcovid100, nharm = 1)</pre>
covidpca1$scores <- con_scores$mean</pre>
covidpca1approx <- covidpca1$harmonics</pre>
i <- 1
pcacoefi1 <- covidpca1$harmonics$coefs %*% con_scores$mean[i]+mcovid$coefs</pre>
covidpca1approx$coefs <- pcacoefi1</pre>
for (i in 2:length(con_scores$mean)) {
    pcacoefi1 <- covidpca1$harmonics$coefs %*% con_scores$mean[i]+mcovid$coefs</pre>
    covidpca1approx$coefs <- cbind(covidpca1approx$coefs, pcacoefi1)</pre>
}
attributes(covidpca1approx$coefs)$dimnames[[2]] <- con_names</pre>
plot(covidpca1approx)
```



```
## [1] "done"
```

The continents differ significantly from each other, regarding the scores of the first principal component.

The plot indicates that in general, a great amount of the data is explained by the first PC for Europe and, to a lesser amount, in North America. This indicates that in these continents, the greatest variation took place.

On the other hand, for Africa and Australia, very low negative mean scores are reported. This indicates a contrary dynamic in comparison to the dynamics of the first component of the PCs.

Values close to zero (Asia, Central America and South America) indicate a low variation from the general mean function.