

Final Exam

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PRE-PROCESSING

We start by setting the random seed and loading useful libraries.

```
set.seed(02022018)
library(RCurl)
library(gdata)
library(dplyr)
library(magrittr)
library(ggplot2)
library(MASS)
library(caret)
library(lars)
library(pls)
library(glmnet)
library(ade4)
library(CCA)
library(yacca)
library(cluster)
```

Now we load our data frames for the exercises.

```
urls <- c("https://www.mimuw.edu.pl/~noble/courses/SDA/data/ushighways.txt",
         "https://www.mimuw.edu.pl/~noble/courses/SDA/data/PET.txt",
         "https://www.mimuw.edu.pl/~noble/courses/SDA/data/ozone.csv",
         "https://www.mimuw.edu.pl/~noble/courses/SDA/data/pendigits.txt",
         "https://www.mimuw.edu.pl/~noble/courses/SDA/data/carmarks.txt",
         "https://www.mimuw.edu.pl/~noble/courses/SDA/data/primate.scapulae.txt")
ushighways <- read.table(urls[1], header=T)
bodyfat <- read.xls("bodyfat2.xlsx")
yarn <- read.table(urls[2], header=T)    #data(yarn, package="pls")
ozone <- read.csv(urls[3])
pendigits <- read.table(urls[4])
carmarks <- read.table(urls[5], sep=";", header=T)
scapular <- read.table(urls[6], sep=" ", header=T)
```

EXERCISE 1

Let us take a look at data.

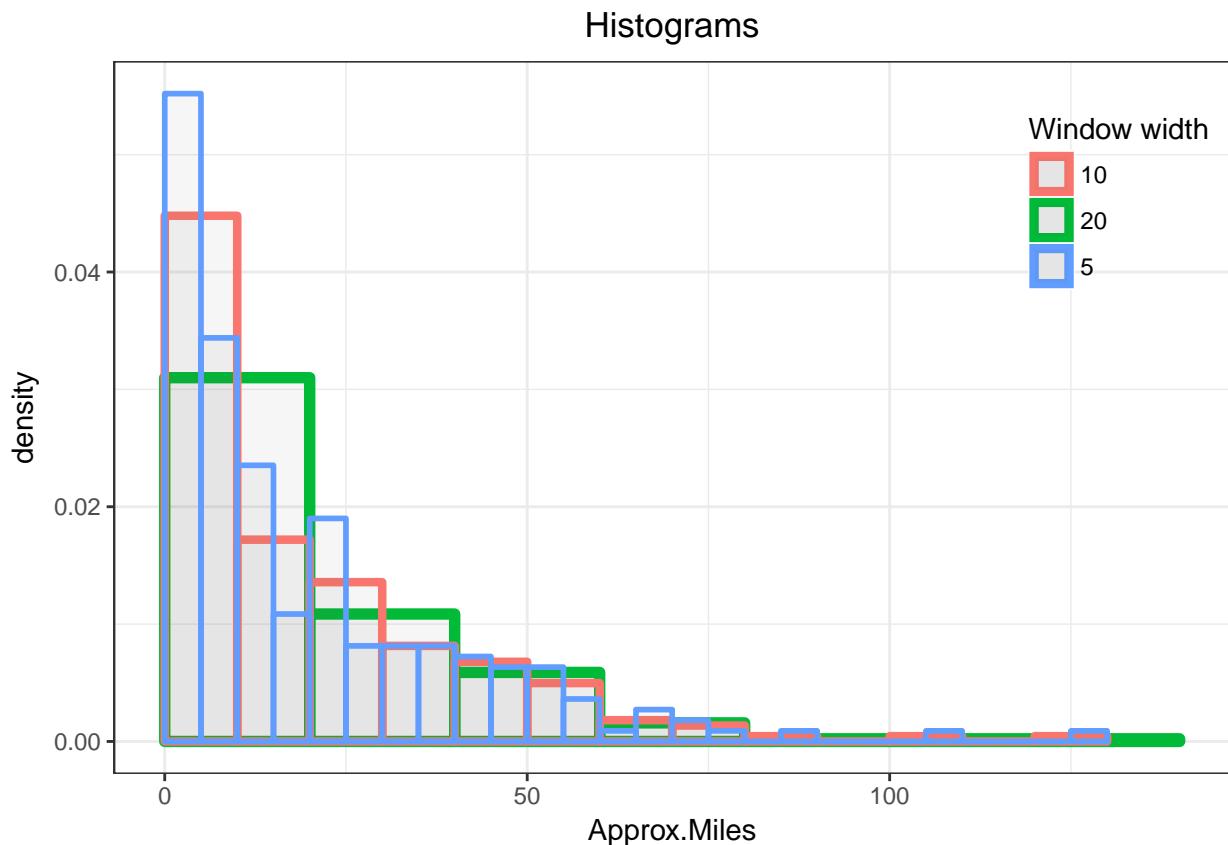
```
head(ushighways)
```

```
##   Interstate.. State Approx.Miles      Location
## 1          165    AL           4       MOBILE
## 2          359    AL           4  TUSCALOOSA
## 3          459    AL          32  BIRMINGHAM
## 4          759    AL           4     GADSDEN
## 5          565    AL          21 HUNTSVILLE
```

```
## 6          430      AR          13 LITTLE ROCK
```

We first draw some histograms with different window widths.

```
ggplot(ushighways, aes(x=Approx.Miles)) +
  geom_histogram(size=2, alpha=0.05, binwidth=20, boundary=0,
                 aes(color="20", y=..density..)) +
  geom_histogram(size=1.5, alpha=0.05, binwidth=10, boundary=0,
                 aes(color="10", y=..density..)) +
  geom_histogram(size=1, alpha=0.05, binwidth=5, boundary=0,
                 aes(color="5", y=..density..)) +
  theme_bw() + theme(plot.title = element_text(hjust = 0.5)) + ggtitle("Histograms") +
  guides(color=guide_legend(title="Window width")) +
  theme(legend.position=c(0.9,0.8), legend.background=element_rect(fill=alpha('blue',0)))
```



The second picture with the window width of 10 miles looks quite good. It is well-divided and shows the monotonicity of the distribution.

Now we will use UCV, BCV and SJPI estimators for window width to plot densities with the gaussian kernel.

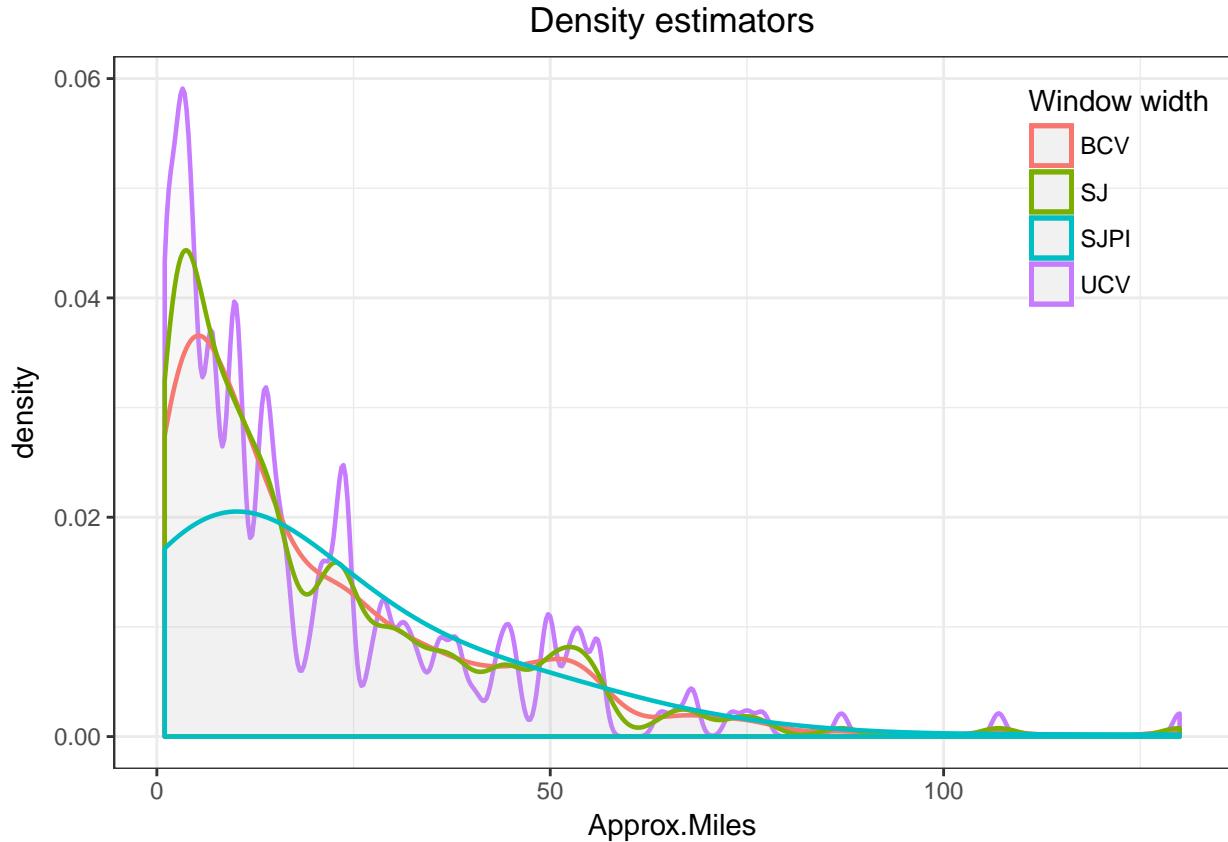
```
sjpi <- width.SJ(ushighways$Approx.Miles, method="dpi")
ggplot(ushighways, aes(x=Approx.Miles)) +
  geom_density(fill="grey", size=0.8, alpha=0.05, bw="ucv", aes(color="UCV")) +
  geom_density(fill="grey", size=0.8, alpha=0.05, bw="bcv", aes(color="BCV")) +
  geom_density(fill="grey", size=0.8, alpha=0.05, bw="sj", aes(color="SJ")) +
  geom_density(fill="grey", size=0.8, alpha=0.05, bw=sjpi, aes(color="SJPI")) +
  theme_bw() + theme(plot.title = element_text(hjust = 0.5)) +
  ggtitle("Density estimators") + guides(color=guide_legend(title="Window width")) +
```

```

theme(legend.position=c(0.9,0.8), legend.background=element_rect(fill=alpha('blue',0)))

## Warning in bw.ucv(x): minimum occurred at one end of the range

```



The BCV estimator (the red one) looks quite well-fitted and monotonic. The other kernel choices (triangular, cosine etc.) gave very similar results.

EXERCISE 2

Let us take a look at data.

```
head(bodyfat[,1:6])
```

```

##   density bodyfat age weight height neck
## 1  1.0708    12.3  23 154.25  67.75 36.2
## 2  1.0853      6.1  22 173.25  72.25 38.5
## 3  1.0414     25.3  22 154.00  66.25 34.0
## 4  1.0751     10.4  26 184.75  72.25 37.4
## 5  1.0340     28.7  24 184.25  71.25 34.4
## 6  1.0502     20.9  24 210.25  74.75 39.0

```

We now calculate the correlation matrix for 13 explanatory variables.

```

cor_matrix <- round(cor(bodyfat[,-(1:2)]), 2)
row.names(cor_matrix) %>% sapply(function(x) substr(x, 1, 1))
colnames(cor_matrix) %>% sapply(function(x) substr(x, 1, 4))
cor_matrix

```

```

##      age  weig  heig neck ches abdo    hip   thig knee  ankl  bice  fore wris
## a  1.00 -0.01 -0.25 0.11 0.18 0.23 -0.05 -0.20 0.02 -0.11 -0.04 -0.09 0.21
## w -0.01  1.00  0.49 0.83 0.89 0.89  0.94  0.87 0.85  0.61  0.80  0.63 0.73
## h -0.25  0.49  1.00 0.32 0.23 0.19  0.37  0.34 0.50  0.39  0.32  0.32 0.40
## n  0.11  0.83  0.32 1.00 0.78 0.75  0.73  0.70 0.67  0.48  0.73  0.62 0.74
## c  0.18  0.89  0.23 0.78 1.00 0.92  0.83  0.73 0.72  0.48  0.73  0.58 0.66
## a  0.23  0.89  0.19 0.75 0.92 1.00  0.87  0.77 0.74  0.45  0.68  0.50 0.62
## h -0.05  0.94  0.37 0.73 0.83 0.87  1.00  0.90 0.82  0.56  0.74  0.55 0.63
## t -0.20  0.87  0.34 0.70 0.73 0.77  0.90  1.00 0.80  0.54  0.76  0.57 0.56
## k  0.02  0.85  0.50 0.67 0.72 0.74  0.82  0.80 1.00  0.61  0.68  0.56 0.66
## a -0.11  0.61  0.39 0.48 0.48 0.45  0.56  0.54 0.61  1.00  0.48  0.42 0.57
## b -0.04  0.80  0.32 0.73 0.73 0.68  0.74  0.76 0.68  0.48  1.00  0.68 0.63
## f -0.09  0.63  0.32 0.62 0.58 0.50  0.55  0.57 0.56  0.42  0.68  1.00 0.59
## w  0.21  0.73  0.40 0.74 0.66 0.62  0.63  0.56 0.66  0.57  0.63  0.59 1.00

```

Some of the variables are highly correlated (around 80-90%), which may lead to ill-conditioning for regression. Let us fit a regression model.

```

bodyfat_fit <- lm(bodyfat~., bodyfat[,-1])
summary(bodyfat_fit)

##
## Call:
## lm(formula = bodyfat ~ ., data = bodyfat[, -1])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11.1966  -2.8824  -0.1111   3.1901   9.9979
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) -21.35323  22.18616 -0.962  0.33680  
## age          0.06457  0.03219  2.006  0.04601 *  
## weight       -0.09638  0.06185 -1.558  0.12047  
## height       -0.04394  0.17870 -0.246  0.80599  
## neck          -0.47547  0.23557 -2.018  0.04467 *  
## chest         -0.01718  0.10322 -0.166  0.86792  
## abdomen       0.95500  0.09016 10.592 < 2e-16 ***
## hip           -0.18859  0.14479 -1.302  0.19401  
## thigh          0.24835  0.14617  1.699  0.09061 .  
## knee          0.01395  0.24775  0.056  0.95516  
## ankle          0.17788  0.22262  0.799  0.42505  
## biceps         0.18230  0.17250  1.057  0.29166  
## forearm        0.45574  0.19930  2.287  0.02309 *  
## wrist          -1.65450  0.53316 -3.103  0.00215 ** 
## ---            
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.309 on 238 degrees of freedom
## Multiple R-squared:  0.7486, Adjusted R-squared:  0.7348 
## F-statistic: 54.5 on 13 and 238 DF,  p-value: < 2.2e-16

```

The significant variables are age, neck, abdomen, forearm, and wrist. Let us now fit regression by stepwise elimination.

```

bodyfat_fit_forward <- step(lm(bodyfat~1, bodyfat[,-1]), direction="forward",
                             scope=formula(bodyfat_fit), trace=0)
summary(bodyfat_fit_forward)$call

## lm(formula = bodyfat ~ abdomen + weight + wrist + forearm + neck +
##      age + thigh + hip, data = bodyfat[, -1])

bodyfat_fit_backward <- step(lm(bodyfat~., bodyfat[,-1]), direction="backward", trace=0)
summary(bodyfat_fit_backward)$call

## lm(formula = bodyfat ~ age + weight + neck + abdomen + hip +
##      thigh + forearm + wrist, data = bodyfat[, -1])

```

Both on the forward and backward stepwise elimination yield the same model based on 8 variables. Now we want to find the best model using leave-one-out cross-validation. It is computationally hard to check all possible models of 13 predictors (approx time 4h). We will then implement and use backward stepwise elimination heuristics instead.

```

stepwise_loocv <- function(variables, trace=F){
  bodyfat_ctrl <- trainControl(method="LOOCV")
  len <- length(variables)
  errors <- data.frame(var=1:len, err=rep(NA,len))
  init_form <- as.formula(paste("bodyfat~", paste(variables, collapse="+")))
  init_fit <- train(init_form, bodyfat[,-1], method="lm", trControl=bodyfat_ctrl)
  init_err <- init_fit$results$RMSE
  for (i in 1:len){
    form <- as.formula(paste("bodyfat~", paste(variables[-i], collapse="+")))
    fit <- train(form, bodyfat[,-1], method="lm", trControl=bodyfat_ctrl)
    errors$err[i] <- fit$results$RMSE
  }
  worst_var <- which.min(errors$err)
  if (trace) print(paste0("bodyfat~", paste(substr(variables, 1, 4), collapse="+"),
                          ":", round(init_err,2)))
  if (errors$err[worst_var]<init_err) stepwise_loocv(variables[-worst_var], trace=T)
  else return(init_fit$finalModel)
}

bodyfat_fit_loocv <- stepwise_loocv(colnames(bodyfat[,-(1:2)]), trace=T)

## [1] "bodyfat~age+weig+heig+neck+ches+abdo+hip+thig+knee+ankl+bice+fore+wris: 4.5"
## [1] "bodyfat~age+weig+neck+ches+abdo+hip+thig+knee+ankl+bice+fore+wris: 4.45"
## [1] "bodyfat~age+weig+neck+ches+abdo+hip+thig+knee+bice+fore+wris: 4.43"
## [1] "bodyfat~age+weig+neck+abdo+hip+thig+knee+bice+fore+wris: 4.4"
## [1] "bodyfat~age+weig+neck+abdo+hip+thig+bice+fore+wris: 4.38"
## [1] "bodyfat~age+weig+neck+abdo+hip+thig+fore+wris: 4.38"

formula(bodyfat_fit_loocv)

## .outcome ~ age + weight + neck + abdomen + hip + thigh + forearm +
##           wrist
## <environment: 0x0000000040bccfa8>

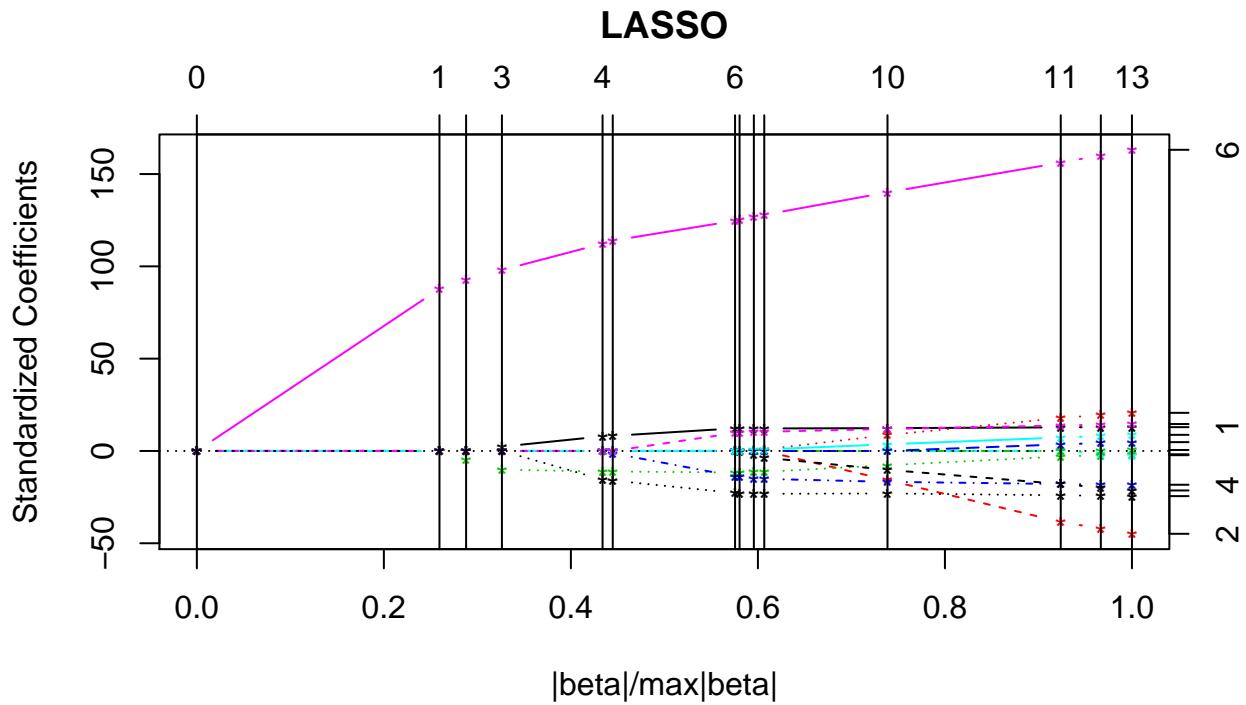
```

This method yields the same model as the ones from the elimination based on AIC. Now we fit a LASSO model and look for the best fit by a leave-one-out cross-validation.

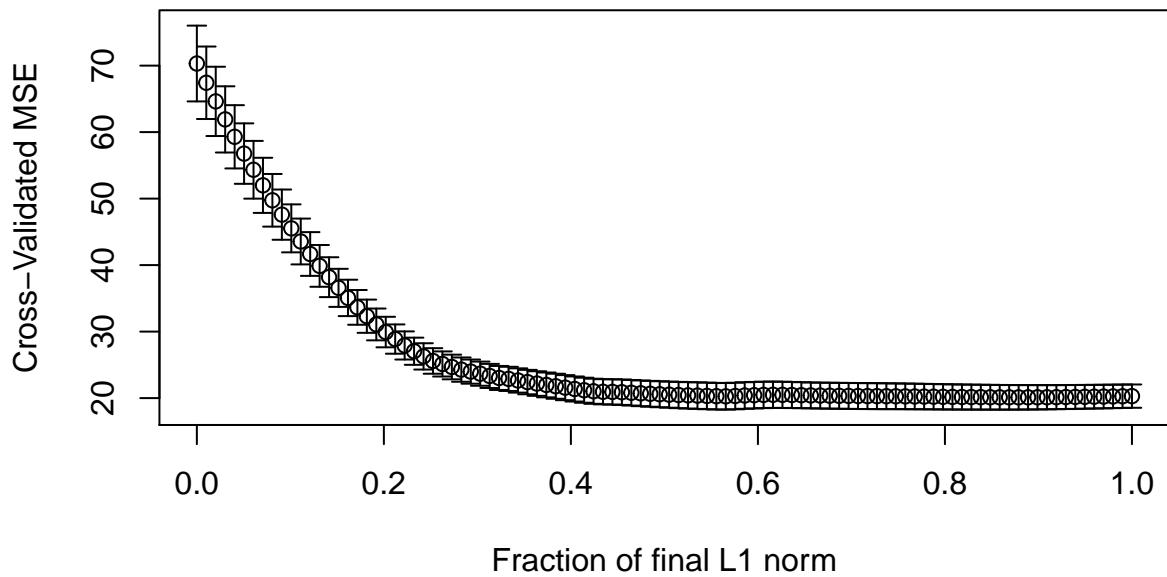
```

bodyfat_fit_lasso <- lars(as.matrix(bodyfat[,-(1:2)]), bodyfat[,2], type="lasso")
plot(bodyfat_fit_lasso)

```

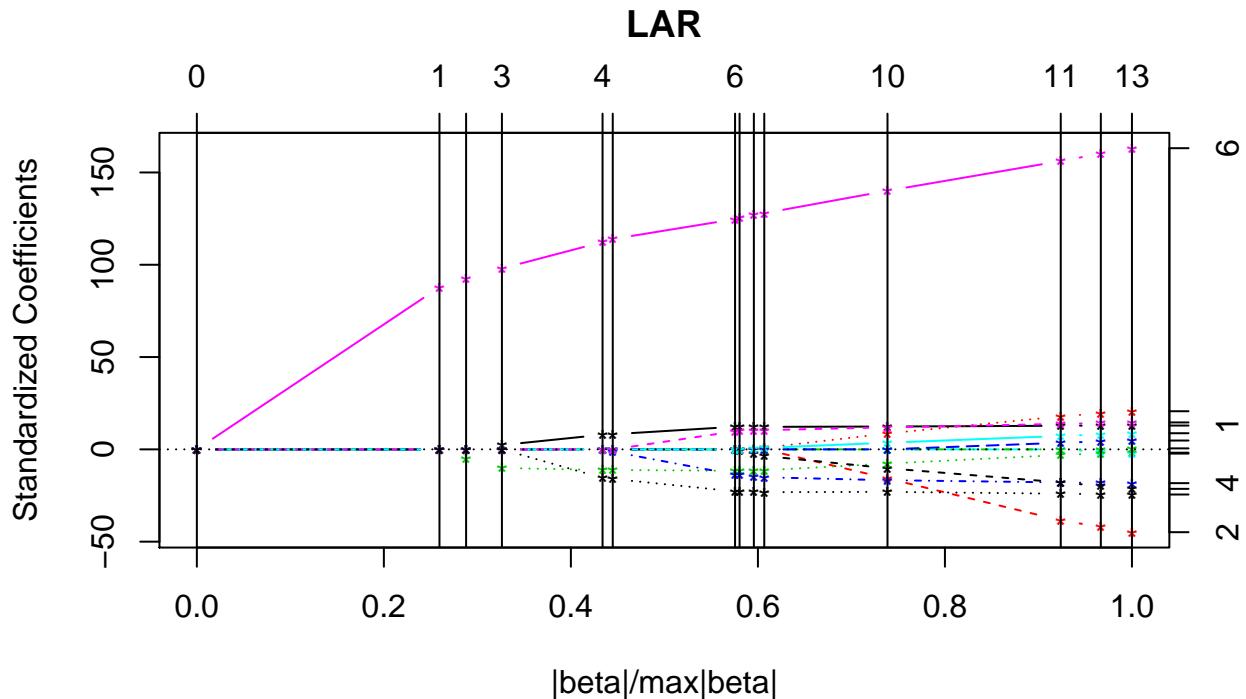


```
bodyfat_lasso <- cv.lars(as.matrix(bodyfat[,-(1:2)]), bodyfat[,2], K=252, type="lasso")
```

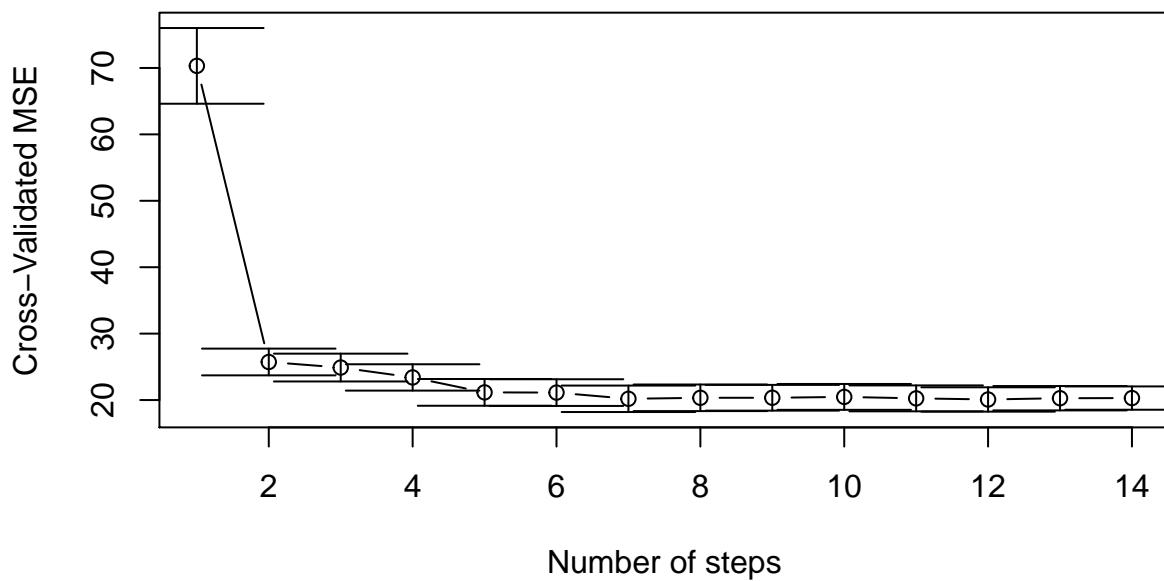


From this we estimate that the lowest MSE of 88 is obtained for LASSO model with parameter 0.8787879. Now we do the same analysis for LARS model.

```
bodyfat_fit_lars <- lars(as.matrix(bodyfat[,-(1:2)]), bodyfat[,2], type="lar")
plot(bodyfat_fit_lars)
```



```
bodyfat_lars <- cv.lars(as.matrix(bodyfat[,-(1:2)]), bodyfat[,2], K=252, type="lar")
```



From this we estimate that the lowest MSE of 88 is obtained for LARS model with parameter 0.8787879. This is a much better result comparing to LASSO model.

EXERCISE 3

Let us take a look at data. We will separate the test set to use it for performance test later.

```
head(yarn[,1:6])

##      X.1     X.2     X.3     X.4     X.5     X.6
## 1 3.0663 3.0861 3.1079 3.0972 2.9979 2.8273
## 2 3.0675 3.0857 3.0958 3.0692 2.9818 2.8408
## 3 3.0750 3.0966 3.0916 3.0288 2.8849 2.6885
## 4 3.0828 3.0973 3.1010 3.0735 2.9913 2.8709
## 5 3.1029 3.1034 3.0848 3.0228 2.8927 2.7159
## 6 3.0815 3.0849 3.0487 2.9305 2.7323 2.5089

yarn_train <- (yarn %>% filter(train==1)) [,-270]
yarn_test <- (yarn %>% filter(train==0)) [,-270]
```

Now we perform PCR and PSLR. We will estimate the error for a different number of components by the leave-one-out cross-validation.

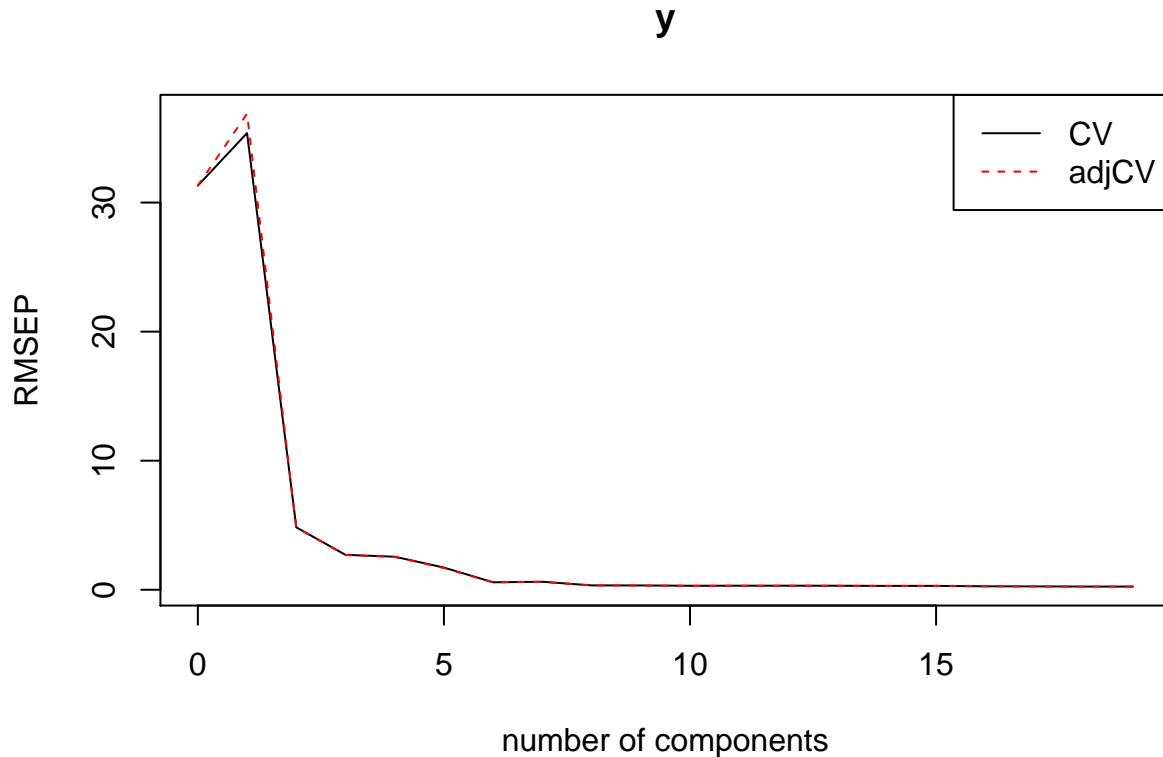
```
yarn_fit_pcr <- pcr(y~., ncomp=20, data=yarn_train, validation="LOO")

## Warning in pls::mvr(y ~ ., ncomp = 20, data = yarn_train, validation =
## "LOO", : `ncomp' reduced to 19 due to cross-validation

summary(yarn_fit_pcr)

## Data:      X dimension: 21 268
##   Y dimension: 21 1
## Fit method: svdpc
## Number of components considered: 19
##
## VALIDATION: RMSEP
## Cross-validated using 21 leave-one-out segments.
##                (Intercept) 1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV            31.31    35.38    4.836   2.703   2.562   1.719   0.5782
## adjCV        31.31    36.88    4.816   2.687   2.543   1.680   0.5712
##               7 comps  8 comps  9 comps  10 comps 11 comps 12 comps 13 comps
## CV           0.6199   0.3394   0.3345   0.3099   0.3143   0.3159   0.3111
## adjCV       0.6140   0.3326   0.3288   0.3042   0.3096   0.3103   0.3043
##               14 comps 15 comps 16 comps 17 comps 18 comps 19 comps
## CV           0.3001   0.3009   0.2677   0.2608   0.2479   0.2474
## adjCV       0.2934   0.2959   0.2616   0.2550   0.2422   0.2421
##
## TRAINING: % variance explained
##      1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps  8 comps
## X    52.053   98.78   99.51   99.74   99.89   99.98   99.99   99.99
## y     5.173   98.21   99.47   99.77   99.95   99.99   99.99   100.00
##      9 comps  10 comps 11 comps 12 comps 13 comps 14 comps 15 comps
## X    99.99     100     100     100     100     100     100
## y    100.00    100     100     100     100     100     100
##      16 comps 17 comps 18 comps 19 comps
## X     100     100     100     100
```

```
## y      100      100      100      100
plot(RMSEP(yarn_fit_pcr), legendpos="topright")
```



We get the lowest cross-validated error for 19 components, so we choose this number. By the look of the graph we could take fewer components for simplicity (not much difference after 6-th component).

```
yarn_fit_plsr <- plsr(y ~ ., ncomp=20, data=yarn_train, validation="LOO")
```

```
## Warning in pls::mvr(y ~ ., ncomp = 20, data = yarn_train, validation =
## "LOO", : `ncomp` reduced to 19 due to cross-validation
```

```
summary(yarn_fit_plsr)
```

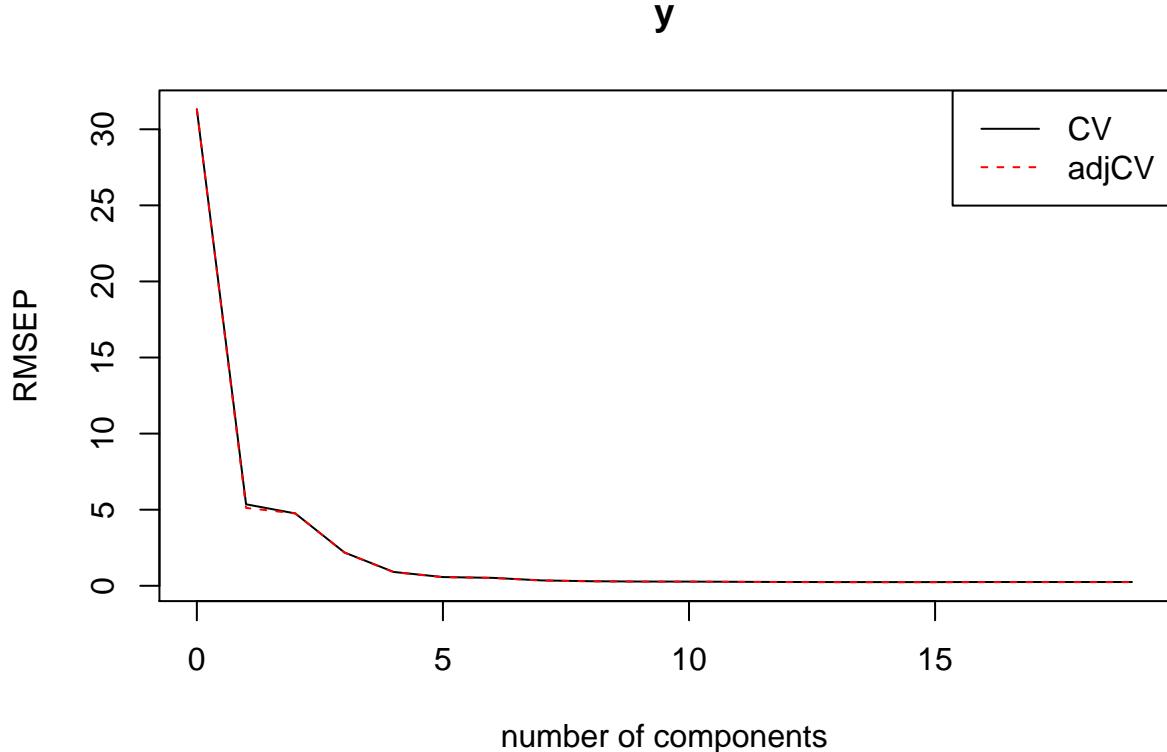
```
## Data: X dimension: 21 268
## Y dimension: 21 1
## Fit method: kernelpls
## Number of components considered: 19
##
## VALIDATION: RMSEP
## Cross-validated using 21 leave-one-out segments.
##          (Intercept) 1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV          31.31    5.356   4.754   2.187   0.9078   0.5737   0.5228
## adjCV       31.31    5.117   4.755   2.177   0.8933   0.5675   0.5191
##          7 comps  8 comps  9 comps 10 comps 11 comps 12 comps 13 comps
## CV          0.3544   0.2988   0.2777   0.2745   0.2611   0.2488   0.2431
## adjCV       0.3474   0.2933   0.2718   0.2682   0.2549   0.2430   0.2374
##          14 comps 15 comps 16 comps 17 comps 18 comps 19 comps
```

```

## CV      0.2410    0.2425    0.2466    0.2477    0.2472    0.2474
## adjCV   0.2353    0.2367    0.2407    0.2417    0.2412    0.2414
##
## TRAINING: % variance explained
##   1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps  8 comps
## X     47.07    98.58    99.50    99.72    99.87    99.98    99.98    99.99
## y     98.19    98.29    99.71    99.97    99.99    99.99    100.00   100.00
##   9 comps  10 comps 11 comps 12 comps 13 comps 14 comps 15 comps
## X     99.99    99.99    100      100      100      100      100
## y     100.00   100.00   100      100      100      100      100
##   16 comps 17 comps 18 comps 19 comps
## X     100      100      100      100
## y     100      100      100      100

plot(RMSEP(yarn_fit_plsr), legendpos="topright")

```



We get the lowest cross-validated error for 14 components, so we choose this number. By the look of the graph we could take fewer components for simplicity (not much difference after 5-th component).

Now we perform a ridge regression with cross-validation.

```
yarn_fit_ridge <- cv.glmnet(as.matrix(yarn_train[,-269]), yarn_train[,269], nfolds=21)
```

```
## Warning: Option grouped=FALSE enforced in cv.glmnet, since < 3 observations
## per fold
```

We choose the model with lambda.1se estimator, which equals to 0.8926168.

Now we compare all models.

```

predict(yarn_fit_pcr, newdata=yarn_test)[,,19] -> a
RMSEP(yarn_fit_pcr, newdata=yarn_test)$val[19]

## [1] 0.08475492
RMSEP(yarn_fit_plsr, newdata=yarn_test)$val[14]

## [1] 0.09504633
sqrt(mean((predict(yarn_fit_ridge, newx=as.matrix(yarn_test[,-269]),
s=yarn_fit_ridge$lambda.1se)-yarn_test[,269])^2))

## [1] 0.4837982

```

We can see that the PCR and PLSR models perform very well. The ridge model gives slightly worse results for this example. More precise lambda search might be helpful.

EXERCISE 4

Let us take a look at data.

```

head(ozone)

##   Station Av8top      Lat      Lon
## 1       60 7.225806 34.13583 -117.9236
## 2       69 5.899194 34.17611 -118.3153
## 3       72 4.052885 33.82361 -118.1875
## 4       74 7.181452 34.19944 -118.5347
## 5       75 6.076613 34.06694 -117.7514
## 6       84 3.157258 33.92917 -118.2097

```

To perform Mantel test, we need to calculate two matrices - one with measurement differences and one with geographic distances.

```

ozone_m1 <- dist(ozone$Av8top)
ozone_m2 <- dist(cbind(ozone$Lon, ozone$Lat))
set.seed(06022018)
mantel.rtest(ozone_m1, ozone_m2)

## Warning in is.euclid(m1): Zero distance(s)
## Warning in is.euclid(distmat): Zero distance(s)
## Monte-Carlo test
## Call: mantel.rtest(m1 = ozone_m1, m2 = ozone_m2)
##
## Observation: 0.1636308
##
## Based on 99 replicates
## Simulated p-value: 0.03
## Alternative hypothesis: greater
##
##      Std.Obs  Expectation      Variance
## 2.311312808 -0.013827128  0.005894858

```

The simulated p-value is lower than 0.05, which suggest that the alternative hypothesis of related distances is true. We can say that stations, which are closer, have similar ozone measurements.

EXERCISE 5

Let us take a look at data.

```
head(pendigits[,1:6])
```

```
##      V1     V2     V3     V4     V5     V6
## 1  47 100 27  81  57  37
## 2   0  89 27 100  42  75
## 3   0  57 31  68  72  90
## 4   0 100  7  92   5  68
## 5   0  67 49  83 100 100
## 6 100 100 88  99  49  74
```

Some of the columns are redundant. We will throw them away.

```
pendigits <- pendigits[,1:17]
```

We start by computing the variances.

```
sapply(pendigits[,-17], var)
```

```
##          V1          V2          V3          V4          V5          V6          V7
## 1173.5957 263.0420 693.9528 367.2453 1162.8451 728.8211 934.9457
##          V8          V9          V10         V11         V12         V13         V14
## 894.3750 1165.2344 742.6469 1390.4013 735.4934 498.8763 1099.2847
##          V15         V16
## 1743.9310 1280.0720
```

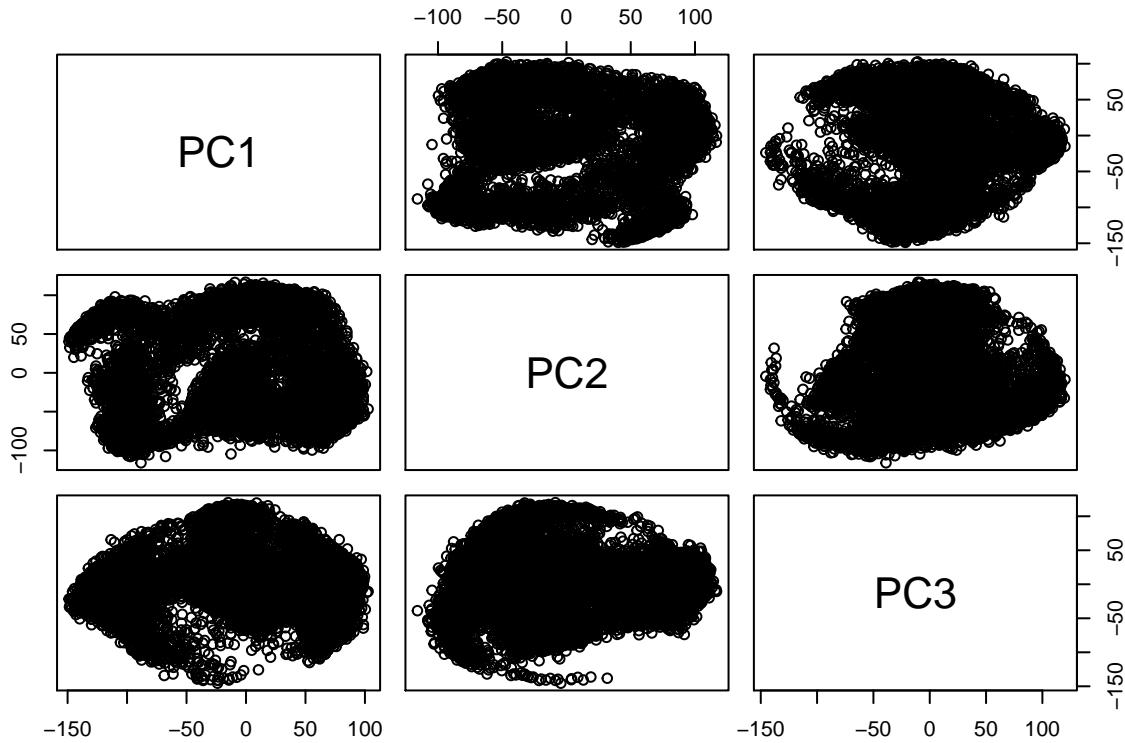
We see that variables differ. Now we perform a PCA on the covariance matrix.

```
pendigits_pcacov <- prcomp(pendigits[,-17], scale=F)
summary(pendigits_pcacov)
```

```
## Importance of components%>%s:
##                               PC1       PC2       PC3       PC4       PC5       PC6
## Standard deviation    64.9131 60.8446 47.8075 36.62327 29.35851 26.80043
## Proportion of Variance 0.2833 0.2489 0.1537 0.09017 0.05795 0.04829
## Cumulative Proportion  0.2833 0.5322 0.6858 0.77599 0.83393 0.88222
##                               PC7       PC8       PC9       PC10      PC11
## Standard deviation    21.38547 19.93971 16.93488 14.29245 11.36052
## Proportion of Variance 0.03075 0.02673 0.01928 0.01373 0.00868
## Cumulative Proportion  0.91296 0.93969 0.95897 0.97271 0.98138
##                               PC12      PC13      PC14      PC15      PC16
## Standard deviation    10.01589 8.13346 7.66022 5.23502 4.93634
## Proportion of Variance 0.00674 0.00445 0.00394 0.00184 0.00164
## Cumulative Proportion  0.98813 0.99257 0.99652 0.99836 1.00000
```

As we can see, taking just 5 components retain more than 80% of data variance; taking 7 retain more than 90%. Now we visualize three first components on the scatterplots.

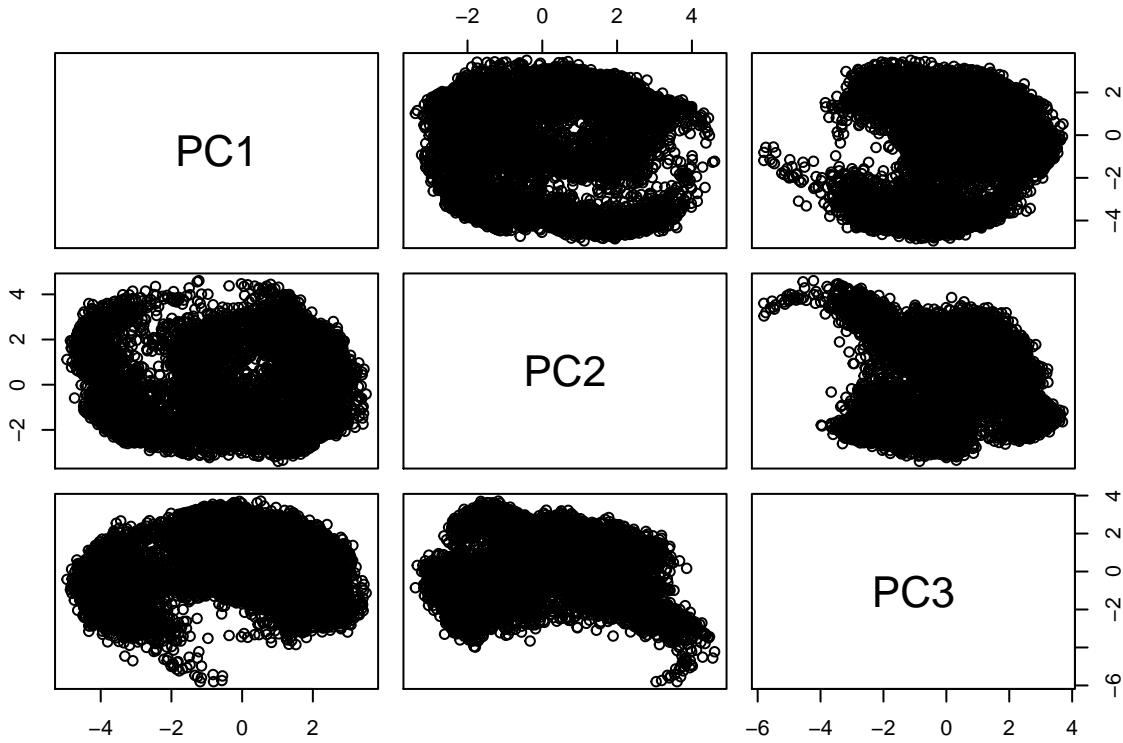
```
plot(data.frame(pendigits_pcacov$x[, 1:3]))
```



We will now carry a PCA with the correlation matrix.

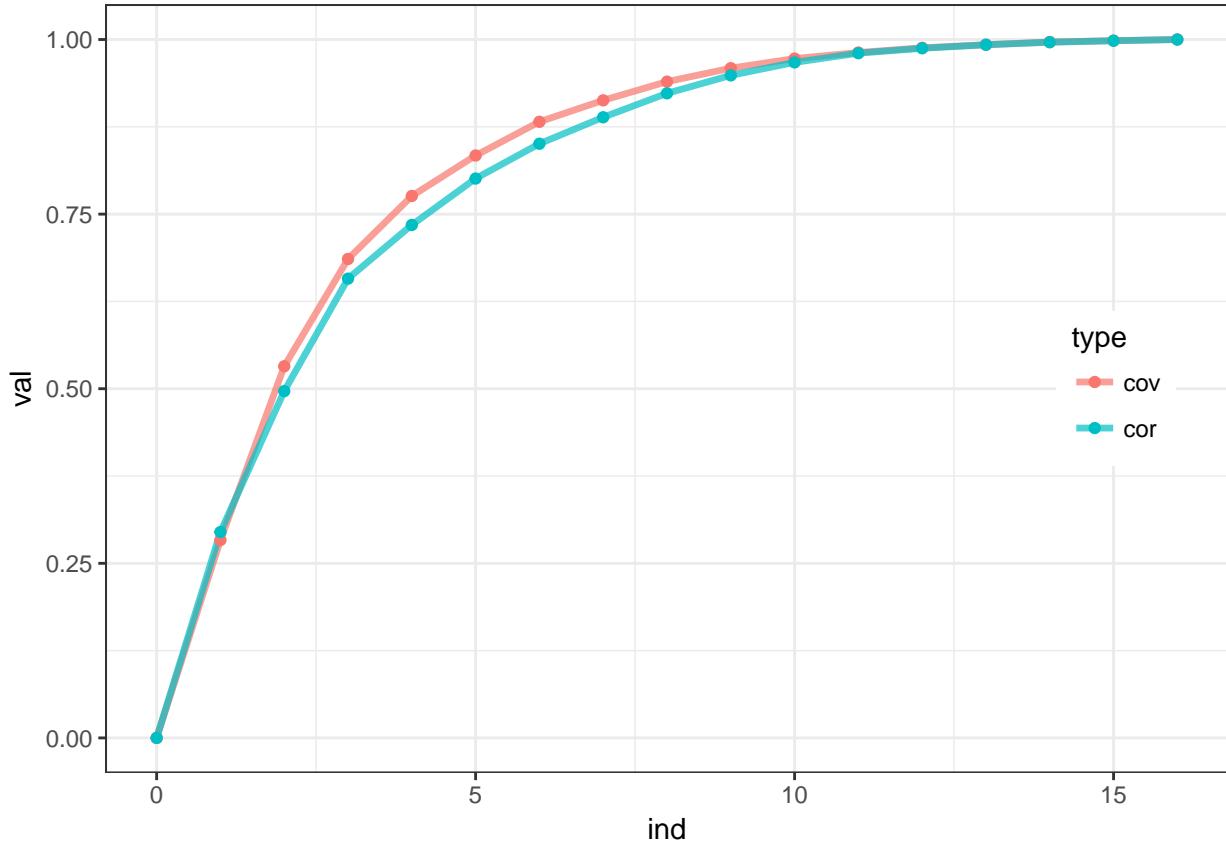
```
pendigits_pcacor <- prcomp(pendigits[,-17], scale=T)
summary(pendigits_pcacor)
```

```
## Importance of components%>%:
##          PC1      PC2      PC3      PC4      PC5      PC6
## Standard deviation   2.1718  1.7970  1.6052  1.10894 1.03107 0.89294
## Proportion of Variance 0.2948  0.2018  0.1610  0.07686 0.06644 0.04983
## Cumulative Proportion 0.2948  0.4966  0.6577  0.73452 0.80096 0.85079
##          PC7      PC8      PC9      PC10     PC11     PC12
## Standard deviation   0.77888 0.74044 0.64096 0.54611 0.45882 0.33511
## Proportion of Variance 0.03792 0.03427 0.02568 0.01864 0.01316 0.00702
## Cumulative Proportion 0.88871 0.92297 0.94865 0.96729 0.98045 0.98747
##          PC13     PC14     PC15     PC16
## Standard deviation   0.28369 0.24084 0.18511 0.16673
## Proportion of Variance 0.00503 0.00363 0.00214 0.00174
## Cumulative Proportion 0.99250 0.99612 0.99826 1.00000
plot(data.frame(pendigits_pcacor$x[, 1:3]))
```



The scaled PCA performs slightly worse on this data (we need one more component to explain 80% or 90% of variance). Some of the components are more informative and some are less. Now we make scree plots for both approaches.

```
cov<-data.frame(ind=1:16, val=summary(pendigits_pcacov)$importance[3,], type=rep("cov",16))
cov<-rbind(list(0,0,"cov"), cov)
cor<-data.frame(ind=1:16, val=summary(pendigits_pcacor)$importance[3,], type=rep("cor",16))
cor<-rbind(list(0,0,"cor"), cor)
ggplot(rbind(cov,cor), aes(x=ind, y=val, color=type)) + geom_line(size=1.2, alpha=0.7) +
  theme_bw() + theme(position=c(0.9,0.5)) + geom_point()
```



We can see that except the first component, the covariance matrix gave better principal components in terms of explained variance. Using elbow method we would take 10 components for further analysis. If we had to reduce dimension even further, we would take 4-5 components.

From the PCA we can see that there is some ill-conditioning of the data matrix - the fractions of variance added from each component are not equal. By taking simply 2 first components, we get more than half information (average of 8 initial variables).

EXERCISE 6

Let us take a look at data.

```
head(carmarks)
```

```
##   CARMARK ECONOMY SERVICE VALUE PRICE DESIGN SPORT SAFETY EASYINESS
## 1    A100     3.9     2.8    2.2    4.2     3.0    3.1    2.4     2.8
## 2    BMW3     4.8     1.6    1.9    5.0     2.0    2.5    1.6     2.8
## 3    CiAX     3.0     3.8    3.8    2.7     4.0    4.4    4.0     2.6
## 4    Ferr     5.3     2.9    2.2    5.9     1.7    1.1    3.3     4.3
## 5    FiUn     2.1     3.9    4.0    2.6     4.5    4.4    4.4     2.2
## 6    FoFi     2.3     3.1    3.4    2.6     3.2    3.3    3.6     2.8
```

We divide the data into X and Y matrices and check the correlations inside these groups. and perform a CCA.

```
carmarks_X <- carmarks[,4:5]
carmarks_Y <- carmarks[,c(2:3,6:9)]
round(cor(carmarks_X),2)
```

```

##      VALUE PRICE
## VALUE  1.00 -0.86
## PRICE -0.86  1.00
round(cor(carmarks_Y),2)

##          ECONOMY SERVICE DESIGN SPORT SAFETY EASYINESS
## ECONOMY      1.00   -0.33  -0.62 -0.48  -0.28     0.58
## SERVICE     -0.33    1.00   0.76   0.69   0.94     0.30
## DESIGN      -0.62    0.76   1.00   0.88   0.71    -0.22
## SPORT       -0.48    0.69   0.88   1.00   0.66    -0.25
## SAFETY      -0.28    0.94   0.71   0.66   1.00     0.35
## EASYINESS    0.58    0.30  -0.22  -0.25   0.35     1.00

```

Some of the variables are highly correlated, which may cause problems in CCA. Nevertheless, we will perform CCA and interpret results.

```

carmarks_cca <- cca(carmarks_X, carmarks_Y,
                      xcenter=T, ycenter=T, xscale=T, yscale=T, standardize.score=T)

```

Before we move into conclusions, we will perform a chi-squared test for the significance of canonical correlations.

```
pchisq(carmarks_cca$chisq, carmarks_cca$df, ncp=0)
```

```

##      CV 1      CV 2
## 1.0000000 0.9999369

```

There is no basis to reject the null hypothesis, so we can assume that canonical correlations are significant. Now let us take a look at the cca object.

```

carmarks_cca

##
## Canonical Correlation Analysis
##
## Canonical Correlations:
##      CV 1      CV 2
## 0.9791972 0.8851224
##
## X Coefficients:
##      CV 1      CV 2
## VALUE -0.6394099 -1.836135
## PRICE  0.3960227 -1.903524
##
## Y Coefficients:
##      CV 1      CV 2
## ECONOMY  0.373639712 -0.49066038
## SERVICE -0.154752889 -0.44050947
## DESIGN   -0.004035987  0.01002372
## SPORT    -0.470514635  0.09819083
## SAFETY   -0.249874034  0.01592503
## EASYINESS -0.212274064 -0.51621224
##
## Structural Correlations (Loadings) - X Vars:
##      CV 1      CV 2
## VALUE -0.9790363 -0.2036857

```

```

## PRICE  0.9443764 -0.3288667
##
## Structural Correlations (Loadings) - Y Vars:
##          CV 1      CV 2
## ECONOMY    0.599208060 -0.7014229
## SERVICE   -0.903830572 -0.3397643
## DESIGN     -0.899920751  0.1897638
## SPORT      -0.869474987  0.1778602
## SAFETY     -0.887267495 -0.3656884
## EASYINESS  -0.008497496 -0.9543117
##
## Aggregate Redundancy Coefficients (Total Variance Explained):
## X | Y: 0.9457047
## Y | X: 0.7884929

```

As the smaller group has 2 variables, we have two canonical variables CV1 and CV2. We can see that the highest correlation (0.979) is between PRICE-VALUE and ECONOMY-SERVICE-SPORT-SAFETY-EASYINESS (with some large coefficients). So the higher price and lower value stability, the more economy and less service, sporty, safety and easy to use the car is. The second canonical variable with correlation 0.885 is between -VALUE-PRICE and -ECONOMY-SERVICE-EASINESS (with some large coefficients). So the larger is the value stability and price, the more economy, service and easy to use car is.

If we look at the correlations instead of coefficients, the numbers differ. For example, the first variable is VALUE-PRICE but correlated with ECONOMY-SERVICE-DESIGN-SPORT-SAFETY (design instead of easyiness) and with different coefficients.

This is the main result and it should be considered that the input correlation matrices were quite ill-conditioned. It gives some intuition about the main probable dependencies between X and Y groups of variables.

EXERCISE 7

Let us take a look at data.

```
head(scapular)
```

```

##   genus AD.BD AD.CD EA.CD Dx.CD SH.ACR EAD beta gamma      class classdigit
## 1    54 65.56 166.0 50.55 12.80    70.3 115    14    45 Hylobates      1
## 2    54 50.91  93.9 61.82 13.09    75.0 121    20    54 Hylobates      1
## 3    54 46.15  80.8 64.10 11.80    70.0 120    25    61 Hylobates      1
## 4    54 70.29 220.5 50.00 12.75    61.1 113    12    45 Hylobates      1
## 5    54 63.16 144.0 57.89 12.98    64.9 115    14    46 Hylobates      1
## 6    54 50.72 134.6 56.23 11.88    52.6 136    14    46 Hylobates      1

```

Before we start cluster analysis, we scale the columns, so the euclidean distance will have a better interpretation.

```
scapular <- scapular[,-9]
scapular[,2:8] %>% scale
```

Now we cluster our data using kmeans, pam (divisive) and single, average, complete and ward linkage (hierarchical). For divisive methods we use k=5. For hierarchical we plot dendograms and cut them to get 5 clusters as well.

```
scapular_kmeans <- kmeans(scapular[,2:8], centers=5)
table(scapular_kmeans$cluster)
```

```
##
## 1 2 3 4 5
```

```

## 16 11 36 19 23
scapular_pam <- pam(scapular[,2:8], k=5)
table(scapular_pam$cluster)

##
## 1 2 3 4 5
## 16 16 34 20 19
scapular_dist <- dist(scapular[,2:8], method="euclidean")

scapular_single <- hclust(scapular_dist, method="single")
scapular_average <- hclust(scapular_dist, method="average")
scapular_complete <- hclust(scapular_dist, method="complete")
scapular_ward <- hclust(scapular_dist, method="ward")

## The "ward" method has been renamed to "ward.D"; note new "ward.D2"
plot(scapular_single)
rect.hclust(scapular_single, k=5, border="red")

```

Cluster Dendrogram



scapular_dist
hclust (*, "single")

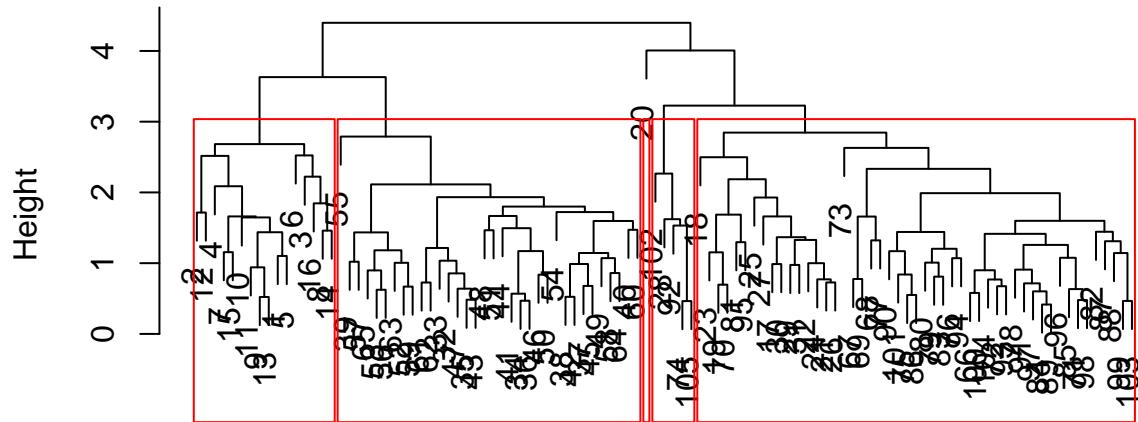
```

scapular_single %>% cutree(k=5)

plot(scapular_average)
rect.hclust(scapular_average, k=5, border="red")

```

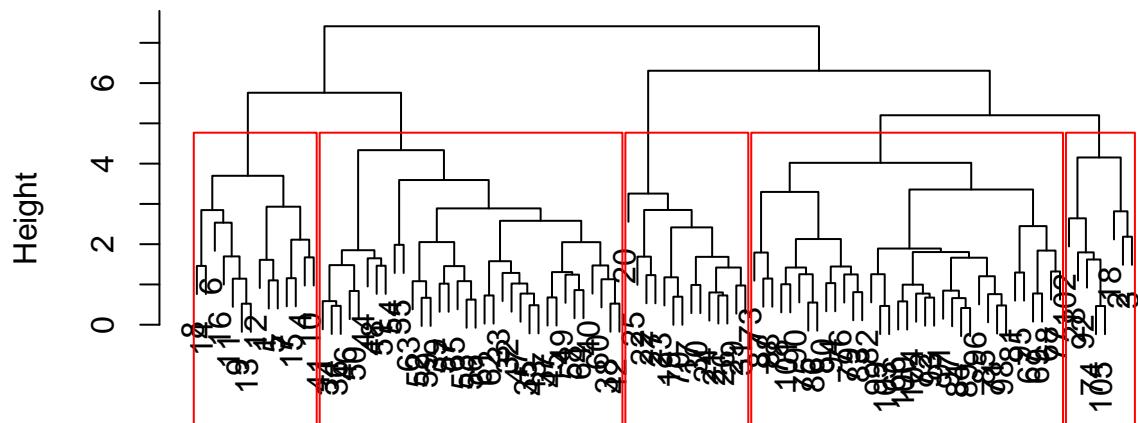
Cluster Dendrogram



```
scapular_dist  
hclust (*, "average")
```

```
scapular_average %<-%>% cutree(k=5)  
  
plot(scapular_complete)  
rect.hclust(scapular_complete, k=5, border="red")
```

Cluster Dendrogram



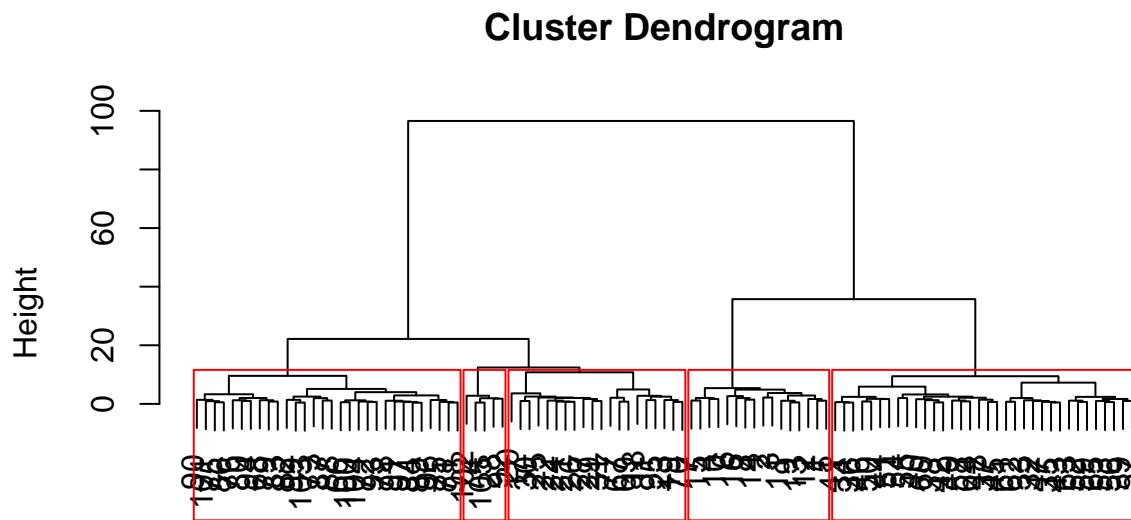
```
scapular_dist  
hclust (*, "complete")
```

```

scapular_complete %<-% cutree(k=5)

plot(scapular_ward)
rect.hclust(scapular_ward, k=5, border="red")

```



scapular_dist
hclust (*, "ward.D")

```

scapular_ward %<-% cutree(k=5)

```

From the summaries and pictures, we can see that divisive algorithms don't give outliers. From the hierarchical methods, single and average linkage produce outliers, while complete and ward linkage does not. Now we compare the results with theoretical groups and write confusion matrices.

```

confusionMatrix(scapular_kmeans$cluster, scapular$classdigit)$table

```

```

##          Reference
## Prediction 1 2 3 4 5
##           1 16 0 0 0 0
##           2 0 0 1 10 0
##           3 0 0 0 0 36
##           4 0 15 0 0 4
##           5 0 0 19 4 0

```

```

confusionMatrix(scapular_kmeans$cluster, scapular$classdigit)$overall[1]

```

```

## Accuracy
## 0.152381

```

```

confusionMatrix(scapular_pam$cluster, scapular$classdigit)$table

```

```

##          Reference
## Prediction 1 2 3 4 5
##           1 16 0 0 0 0

```

```

##          2 0 15 0 0 1
##          3 0 0 20 14 0
##          4 0 0 0 0 20
##          5 0 0 0 0 19
confusionMatrix(scapular_pam$cluster, scapular$classdigit)$overall[1]

## Accuracy
## 0.6666667

confusionMatrix(scapular_single, scapular$classdigit)$table

##          Reference
## Prediction 1 2 3 4 5
##          1 16 0 20 14 0
##          2 0 13 0 0 39
##          3 0 1 0 0 0
##          4 0 1 0 0 0
##          5 0 0 0 0 1
confusionMatrix(scapular_single, scapular$classdigit)$overall[1]

## Accuracy
## 0.2857143

confusionMatrix(scapular_average, scapular$classdigit)$table

##          Reference
## Prediction 1 2 3 4 5
##          1 16 0 0 0 0
##          2 0 13 0 0 36
##          3 0 1 0 0 0
##          4 0 1 0 0 4
##          5 0 0 20 14 0
confusionMatrix(scapular_average, scapular$classdigit)$overall[1]

## Accuracy
## 0.2761905

confusionMatrix(scapular_complete, scapular$classdigit)$table

##          Reference
## Prediction 1 2 3 4 5
##          1 14 0 0 0 0
##          2 2 2 0 0 4
##          3 0 13 0 0 1
##          4 0 0 20 14 0
##          5 0 0 0 0 35
confusionMatrix(scapular_complete, scapular$classdigit)$overall[1]

## Accuracy
## 0.6190476

confusionMatrix(scapular_ward, scapular$classdigit)$table

##          Reference
## Prediction 1 2 3 4 5
##          1 16 0 0 0 0

```

```

##      2   0 14   0   0   6
##      3   0   1   0   0   4
##      4   0   0 20 14   0
##      5   0   0   0   0 30
confusionMatrix(scapular_ward, scapular$classdigit)$overall[1]

```

```

## Accuracy
## 0.7047619

```

The divisive methods gave quite good results: 0.55 acc for kmeans and 0.67 acc for pam. The hierarchical methods with single and average linkage are worse on this dataset (0.29 and 0.28 acc) but complete and ward linkage works well (0.62 and 0.70 acc).

EXERCISE 8

Let us take a look at data.

```

scapular <- read.table(urls[6], sep=" ", header=T)
head(scapular)

```

```

##   genus AD.BD AD.CD EA.CD Dx.CD SH.ACR EAD beta gamma      class classdigit
## 1    54 65.56 166.0 50.55 12.80    70.3 115    14    45 Hylobates        1
## 2    54 50.91  93.9 61.82 13.09    75.0 121    20    54 Hylobates        1
## 3    54 46.15  80.8 64.10 11.80    70.0 120    25    61 Hylobates        1
## 4    54 70.29 220.5 50.00 12.75   61.1 113    12    45 Hylobates        1
## 5    54 63.16 144.0 57.89 12.98   64.9 115    14    46 Hylobates        1
## 6    54 50.72 134.6 56.23 11.88   52.6 136    14    46 Hylobates        1

```

We have checked that the data points inside particular classes are generally multivariate normal, which satisfies the assumptions for lda. We perform a leave-one-out cross-validated lda for each reference primates vs others and check, which individuals were classified to certain regions.

```

ambireg <- 1:105
primates <- c("Gorilla", "Homo", "Hylobates", "Pan", "Pongo")
for (prim in primates) {
  df <- scapular
  df$class %>% sapply(function(x) ifelse(x==prim, prim, "other"))
  df$class %>% factor
  fit <- lda(class~, data=df[,c(2:8,10)], CV=T)
  specreg <- which(fit$class==prim)
  len <- min(length(specreg), 20)
  text <- paste(prim, "region:", paste(specreg[1:len], collapse=" "))
  if (length(specreg)>20) text <- paste(text, "[...]")
  print(text)
  ambireg <- setdiff(ambireg, specreg)
}

## [1] "Gorilla region: 32 33 35 41 49 52 59 63 64 65 102"
## [1] "Homo region: 19 23 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 [...]"
## [1] "Hylobates region: 1 2 4 5 6 7 8 9 10 11 12 13 14 15 16"
## [1] "Pan region: 32 33 34 35 36 37 38 40 41 42 43 44 45 46 47 48 49 50 51 54 [...]"
## [1] "Pongo region: 6 17 18 19 20 21 22 23 24 25 26 27 29 30 31"
print(paste("Ambiguous region:", paste(ambireg, collapse=" ")))

## [1] "Ambiguous region: 3 28 39 53 55 56 57 58"

```

Now we perform 10 lda for each pair of primates and predict the whole data. We then classify the species by the majority vote.

```

pairs <- combn(primates, 2)
preds <- data.frame(matrix(NA, 105, 10))
for (i in 1:10) {
  pair <- pairs[,i]
  df <- scapular %>% filter(class %in% pair)
  df$class %>>% drop.levels()
  fit <- lda(class~., data=df[,c(2:8,10)])
  preds[,i] <- predict(fit, scapular[,c(2:8)])$class
}
vote <- function(x) names(sort(table(t(x)), decreasing=T))[1])
scapular_pred <- apply(preds, 1, vote)
confusionMatrix(scapular_pred, scapular$class)$table

```

```

##             Reference
## Prediction Gorilla Homo Hylobates Pan Pongo
##   Gorilla      14    0      0   1    0
##   Homo         0   40      0   0    0
##   Hylobates    0    0     16   0    0
##   Pan          0    0      0  19    0
##   Pongo        0    0      0   0   15

```

We have obtained the almost perfect fit to the training data with 99% accuracy (only 1 misclassification). Let us now compare it with the straight use of lda with 5 boundaries.

```

scapular_fit <- lda(class~., data=scapular[,c(2:8,10)], CV=T)
confusionMatrix(scapular_fit$class, scapular$class)$table

```

```

##             Reference
## Prediction Gorilla Homo Hylobates Pan Pongo
##   Gorilla      13    0      0   1    0
##   Homo         0   40      0   0    0
##   Hylobates    0    0     15   0    0
##   Pan          1    0      0  19    0
##   Pongo        0    0      1   0   15

```

We can see that this classifier is slightly worse on training data with 97% accuracy (3 misclassifications). It seems like the voting method is better. To be sure, we would need some test data to check how it generalizes to new examples.