Compulsory exercise 2: Group 5 TMA4268 Statistical Learning V2022

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Problem 1

```
set.seed(1)
boston <- scale(Boston, center = T, scale = T)

train.ind = sample(1:nrow(boston), 0.8 * nrow(boston))
boston.train = data.frame(boston[train.ind, ])
boston.test = data.frame(boston[-train.ind, ])</pre>
```

```
a)
set.seed(1)
forward_stepwise = regsubsets(medv ~ ., data = boston.train, nvmax = 13, method = 'forward')
backward_stepwise = regsubsets(medv ~ ., data = boston.train, nvmax = 13, method = 'backward')
forward_stepwise_summary = summary(forward_stepwise)
```

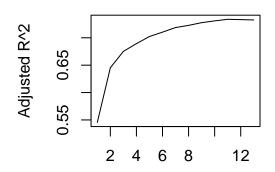
```
backward_stepwise_summary = summary(forward_stepwise)
backward_stepwise_summary = summary(backward_stepwise)
#forward_stepwise_summary
#backward_stepwise_summary
```

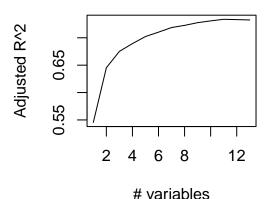
Forwards

variables

```
par(mfrow=c(1,2))
```

```
plot(forward_stepwise_summary$adjr2, xlab = '# variables', ylab = 'Adjusted R^2', type='l', main='Forward_stepwise_summary$adjr2, xlab = '# variables', ylab = 'Adjusted R^2', type='l', main='Backw
```





Backwards

b)

```
forward_stepwise_summary$outmat
```

```
indus chas nox rm age dis rad tax ptratio black lstat
                                                                          "*"
## 1
      (1)
                                                                          "*"
## 2
      (1
                                                                          "*"
      ( 1
## 5
      (1
                                                                    "*"
                                                                          "*"
      (1
                                                                          "*"
      ( 1
                                                                          "*"
## 8
                                                                          "*"
## 10
                                                                          "*"
## 12
       (1
## 13
       (1)
                                                                          "*"
```

We choose the predictors 'rm, 'dis', 'ptratio' and 'lstat'.

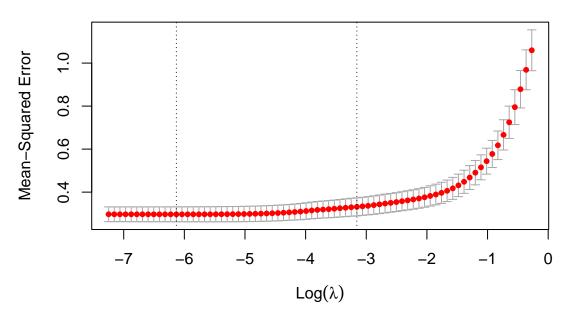
c)

i)

```
set.seed(1)
y = boston.train$medv
x = data.matrix(boston.train[, -14])

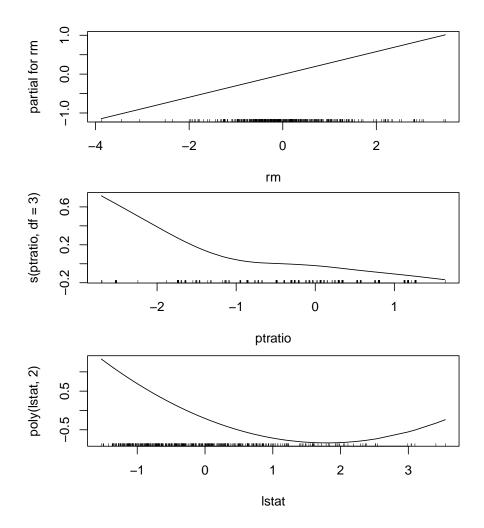
cv_lasso = cv.glmnet(x, y, alpha=1, nfolds=5)
plot(cv_lasso)
```

13 13 13 12 12 11 11 9 6 6 5 4 3 3 2 2



```
ii)
lasso_best_lambda = cv_lasso$lambda.min
lasso_best_lambda
## [1] 0.002172032
iii)
coef(glmnet(x, y, alpha=1, lambda=lasso_best_lambda))
## 14 x 1 sparse Matrix of class "dgCMatrix"
##
## (Intercept) 0.023622904
## crim
              -0.081992849
## zn
              0.094717791
## indus
              0.002619428
## chas
              0.087341100
              -0.175365927
## nox
## rm
              0.312648954
## age
              -0.011212120
              -0.317143728
## dis
              0.270168177
## rad
## tax
              -0.207314714
## ptratio
              -0.204052488
## black
              0.102877803
## lstat
              -0.428298373
d)
TRUE, FALSE, FALSE, TRUE
Problem 2
a)
b)
Problem 3
a)
TRUE, FALSE, FALSE, TRUE
b)
additive_model = gam(medv ~ rm + s(ptratio, df=3) + poly(lstat, 2), data=boston.train)
```

plot(additive_model)



Problem 4

a)

 ${\rm FALSE,\ TRUE,\ TRUE,\ TRUE}$

b)

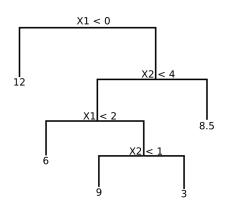
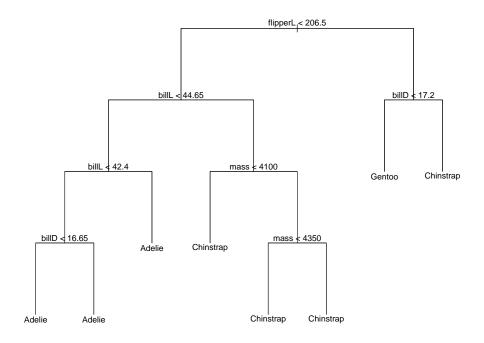


Figure 1: Tree

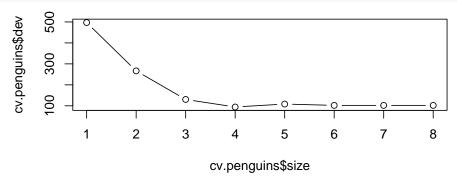
c)

```
library(tidyverse)
library(palmerpenguins) # Contains the data set "penguins".
data(penguins)
names(penguins) <- c("species", "island", "billL", "billD", "flipperL", "mass", "sex", "year")
Penguins_reduced <- penguins %% dplyr::mutate(mass = as.numeric(mass), flipperL = as.numeric(flipperL)
# We do not want "year" in the data (this will not help for future predictions)
Penguins_reduced <- Penguins_reduced[,-c(8)]</pre>
set.seed(4268)
# 70% of the sample size for training set
training_set_size <- floor(0.7 * nrow(Penguins_reduced))</pre>
train_ind <- sample(seq_len(nrow(Penguins_reduced)), size = training_set_size)</pre>
train <- Penguins_reduced[train_ind, ]</pre>
test <- Penguins_reduced[-train_ind, ]</pre>
i)
penguin.tree = tree(formula=species ~ ., data=train, split='gini' )
summary(penguin.tree)
## Classification tree:
## tree(formula = species ~ ., data = train, split = "gini")
## Variables actually used in tree construction:
## [1] "flipperL" "billL"
                              "billD"
                                         "mass"
## Number of terminal nodes: 8
## Residual mean deviance: 0.1869 = 42.06 / 225
## Misclassification error rate: 0.04292 = 10 / 233
plot(penguin.tree, type='uniform')
text(penguin.tree, pretty=0)
```



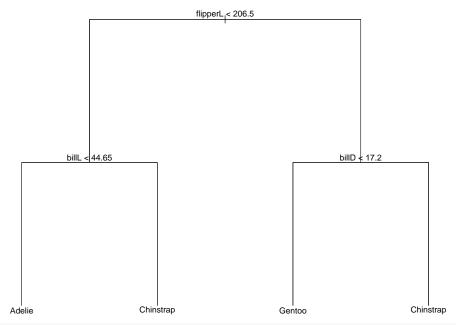
ii)

```
set.seed(123)
cv.penguins = cv.tree(penguin.tree, K=10)
#cv.penguins$dev
plot(cv.penguins$dev ~ cv.penguins$size, type='b')
```



iii)

```
prune.penguins = prune.tree(penguin.tree, best=4)
plot(prune.penguins, type='uniform')
text(prune.penguins, pretty=0)
```



```
tree.predict = predict(prune.penguins, test, type='class')
misclass = table(tree.predict, test$species)
misclass
```

```
## tree.predict Adelie Chinstrap Gentoo
## Adelie 42 5 1
## Chinstrap 0 15 0
## Gentoo 0 0 37
```

1-sum(diag(misclass))/sum(misclass)

[1] 0.06

d)

Using random forest. Trying different choices for variable mtry, and plotting the misclassification errors.

```
set.seed(1001)

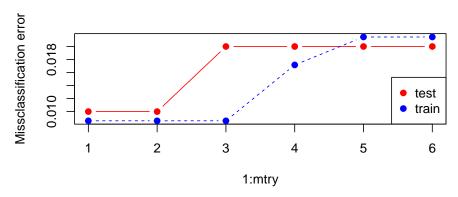
train.err = double(6)

test.err = double(6)

for(mtry in 1:6) {
    rf.penguins = randomForest(species ~ ., data=train, mtry=mtry, ntree=500)
    train.err[mtry] = rf.penguins$err.rate[500]

    rf.predict = predict(rf.penguins, newdata=test, type='class')
    misclass = table(rf.predict, test$species)
    misclass
    test.err[mtry] = 1-sum(diag(misclass))/sum(misclass)
}

matplot(1:mtry, cbind(test.err, train.err), pch=19, type='b', ylab='Missclassification error', col=c('relegend('bottomright', legend=c('test', 'train'), pch=19, col=c('red', 'blue'))
```



We find that a good choice for mtry is 2, which also approximately corresponds to the square root of the number of covariates.

```
rf.penguins = randomForest(species ~ ., data=train, mtry=2, ntree=500)
rf.predict = predict(rf.penguins, newdata=test, type='class')
misclass = table(rf.predict, test$species)
misclass
##
## rf.predict Adelie Chinstrap Gentoo
##
     Adelie
                   42
                    0
                             18
                                     0
##
     Chinstrap
     Gentoo
                    0
                                    38
1-sum(diag(misclass))/sum(misclass)
## [1] 0.02
importance(rf.penguins)
```

##		MeanDecreaseGini
##	island	17.3964364
##	billL	52.2639236
##	billD	25.0545916
##	flipperL	37.1186075
##	mass	14.5237520
##	sex	0.9137075

We see that the two most influential variables are 'billL' and 'flipperL'.

Problem 5