Question ? A) Laplace (x/µ, x) = 2 e-x/x-x1 megative log: log(= -2/x-M/)

(-log(x) = log(\frac{1}{x}))

Differentiate de de logt 1 de logt 2 e - 2/x-pel = 2 d [2 e x | X - MI] = 2 e x | X - MI] = 2 d [e x | X - MI] 2 e - 2 | X - MI] $= e^{\frac{1}{2}|x-\mu|} \frac{d}{dx} \left[\frac{1}{2} |x-\mu| \right] \cdot e^{-\frac{1}{2}|x-\mu|}$ = L d [IX-M] = L . x - M . d [x - M] - 2 - (d (x) + d [- m] (x - m) $[x - \mu]$

 $= \frac{2 \cdot (1+0)(x-\mu)}{|x-\mu|} = \frac{2 \cdot (x-\mu)}{|x-\mu|}$

Con [P/ y 1 x . 12) + Con [bly] x int] 1 1818 1 kg Cog [PIYIX; wi leg ply 1x; w) plus 1 + Roy (p(m) + Coy [Tin 2 0-21 + lag II plum 1x 2-2/X/

10) mai [p(y/x, w)p(w)) = max [log /p(y/x; in)] + log /p(in)) This corresponds to L7 regularisation because $g(m) = \frac{1}{2}e^{-2|x|}$ has an absolute value.

Assignment 5

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Question 2

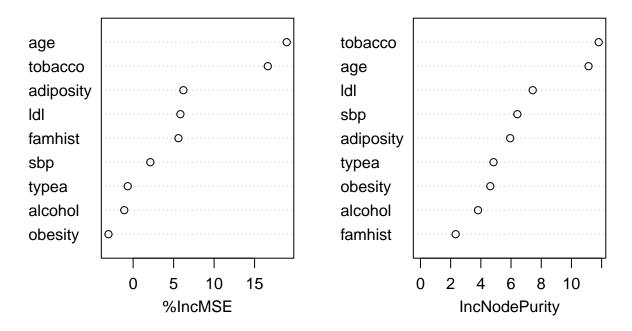
A)

```
coris = read.csv("coris.dat")
coris[["id"]] = NULL # remove "row.names" column
# Normalize the numeric columns:
normalise = function(x) {
return ((x - mean(x)) / sd(x)) }
normcoris <- as.data.frame(lapply(coris, normalise))</pre>
# use the unnormalized versions of the binary variables:
normcoris$famhist <- coris$famhist</pre>
normcoris$chd <- coris$chd # this is the response variable</pre>
library(caret)
## Warning: package 'caret' was built under R version 4.1.3
## Loading required package: ggplot2
## Warning: package 'ggplot2' was built under R version 4.1.3
## Loading required package: lattice
set.seed(1)
ind <- createDataPartition(normcoris$chd, p = .6, list=FALSE)</pre>
train = normcoris[ind,]
test = normcoris[-ind,]
model <- glm(chd ~ ., data=train, family=binomial)</pre>
summary(model)
##
## Call:
## glm(formula = chd ~ ., family = binomial, data = train)
## Deviance Residuals:
##
            1Q Median
                                3Q
       Min
                                            Max
```

```
## -1.8537 -0.7747 -0.4293
                               0.8638
                                        2.5509
##
## Coefficients:
##
               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.15474
                           0.21026 -5.492 3.97e-08 ***
                           0.15495
                                    0.195 0.84572
               0.03015
## sbp
               0.37981
                                    2.390 0.01683 *
## tobacco
                           0.15889
                                     2.672 0.00754 **
## ldl
                0.44514
                           0.16659
## adiposity
               0.15991
                           0.30610
                                     0.522 0.60139
## famhist
               0.75893
                           0.29746
                                     2.551 0.01073 *
## typea
               0.30349
                           0.15524
                                     1.955 0.05058
               -0.30672
                                    -1.212 0.22535
## obesity
                           0.25298
## alcohol
               0.13022
                           0.13808
                                     0.943 0.34561
                                     3.174 0.00150 **
## age
                0.72812
                           0.22941
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##
       Null deviance: 359.61 on 277 degrees of freedom
## Residual deviance: 281.52 on 268 degrees of freedom
## AIC: 301.52
##
## Number of Fisher Scoring iterations: 5
yprobs = predict(model, newdata=test, type='response')
ypred = round(yprobs)
table(ypred, test$chd)
##
## ypred 0 1
##
       0 96 29
##
       1 25 34
error_rate = mean(ypred != test$chd)
error rate
## [1] 0.2934783
The variable with the most effect is the famhist because it has the highest estimated value (0.75893) meaning
it has the most effect on the variable chd.
The miscalculation rate is: 0.2934783
library (randomForest)
## Warning: package 'randomForest' was built under R version 4.1.3
## randomForest 4.7-1.1
## Type rfNews() to see new features/changes/bug fixes.
```

```
##
## Attaching package: 'randomForest'
## The following object is masked from 'package:ggplot2':
##
##
      margin
set.seed (1)
rf.coris <- randomForest (chd ~ ., data = train,mtry=6, importance = TRUE)</pre>
## Warning in randomForest.default(m, y, \dots): The response has five or fewer
## unique values. Are you sure you want to do regression?
importance(rf.coris)
##
               %IncMSE IncNodePurity
## sbp
            2.1265043
                           6.418943
## tobacco 16.6329001
                          11.804149
## ldl
                           7.435982
           5.8404232
## adiposity 6.2063156
                          5.943725
## famhist 5.5952444
                            2.331843
## typea
            -0.6661421
                           4.838857
## obesity -3.0476706
                            4.626176
## alcohol -1.0952868
                            3.812399
## age
            18.9628772
                           11.132201
yprobs = predict(rf.coris, newdata=test, type='response')
ypred = round(yprobs)
miscalulation_rate = mean(ypred != test$chd)
print(paste("The miscalculation rate is: ",miscalulation_rate))
## [1] "The miscalculation rate is: 0.33695652173913"
varImpPlot(rf.coris)
```

rf.coris



The variable with the greatest importance is to bacco with an importance of 16.6329001. The miscalculation rate is: 0.33695652173913.

Question3)

```
load('mnist23small.Rdata') # 1000 training digits, 1000 test
# When first loaded, the y column in each data frame is of type integer
# and takes values 1 or 2 (the digit shown in the image).
# Convert these integer variables into nominal variables, i.e. factors.
# This is needed by some classification algorithms
test$y = as.factor(test$y)
train$y = as.factor(train$y)
# "Normalise" the intensity of each pixel
normalise <- function(x) {</pre>
return(x / 255)
}
train[,-1] = lapply(train[, -1], normalise)
test[,-1] = lapply(test[,-1], normalise)
# Note that "normalise" often means: centre (i.e. subtract the mean), and
# scale to variance 1, which is not what we've done here, but it's similar.
showdigit = function(imrow, label) {
im = matrix(imrow, nrow=28)[,28:1] #reverse
image(im, col=gray((0:255)/255),
xaxt='n', yaxt='n', main=label, asp = 1
```

```
par(mfrow=c(2,4))
for(i in 1:8){
    showdigit(as.matrix(train[i, 2:785]), paste(train$y[i]))
}
```

A)KNN with K=30

library(class)

Warning: package 'class' was built under R version 4.1.3

```
library(caret)

Xtrain = train[,2:785]

Xtrain_matrix = data.matrix(Xtrain)

Xtest = test[,2:785]

Xtest_matrix = data.matrix(Xtest)

Ntest = 1000
ypred = knn(Xtrain_matrix , Xtest_matrix ,train$y, k = 30, prob = TRUE)

error.rate = function(ypred, ytrue){
```

```
err.rate = mean(ypred != ytrue)
return(err.rate)
print(paste('Error rate = ', error.rate(ypred,test$y)))
## [1] "Error rate = 0.026"
 B)
library(randomForest)
set.seed(1)
bag.mnist <- randomForest(train$y ~ ., data = train, mtry = ncol(train)-1, importance = TRUE)</pre>
ypred <- predict (bag.mnist , newdata = test)</pre>
print(paste('Error rate = ', error.rate(ypred,test$y)))
## [1] "Error rate = 0.053"
 C)
set.seed(1)
rf.mnist <- randomForest(train$y ~ ., data = train, mtry = sqrt(ncol(train)-1), importance = TRUE)
ypred <- predict (rf.mnist , newdata = test)</pre>
print(paste('Error rate = ', error.rate(ypred,test$y)))
## [1] "Error rate = 0.021"
 D)
library(nnet)
mnist.nn2 <- nnet(train$y ~ ., data = train, size = 10,rang = 0.01,</pre>
decay = 0.01, maxit = 50, MaxNWts = 7862)
## # weights: 7861
## initial value 693.167695
## iter 10 value 50.936814
## iter 20 value 4.752770
## iter 30 value 2.954903
## iter 40 value 2.449441
## iter 50 value 2.335438
## final value 2.335438
## stopped after 50 iterations
ypred <- predict (mnist.nn2 , newdata = test, type="class")</pre>
print(paste('Error rate = ', error.rate(ypred,test$y)))
```

```
## [1] "Error rate = 0.036" 
E)
```

```
for (i in 1:10){
w=mnist.nn2$wts
recep = w[(785*(i-1)+1):(785*(i-1)+784)]
showdigit(as.matrix(recep), paste(i))}
```

