Lab 1 Topic 1 Block 2 Machine Learning

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11/12/2020

State of contribution

Assignment1: Niklas Larsson

Assignment2: Hugo Knape

Assignment3: Zahra Jalilpour

Assigment 1: Ensembled methods

Task A

Generate test data:

```
library(randomForest)
```

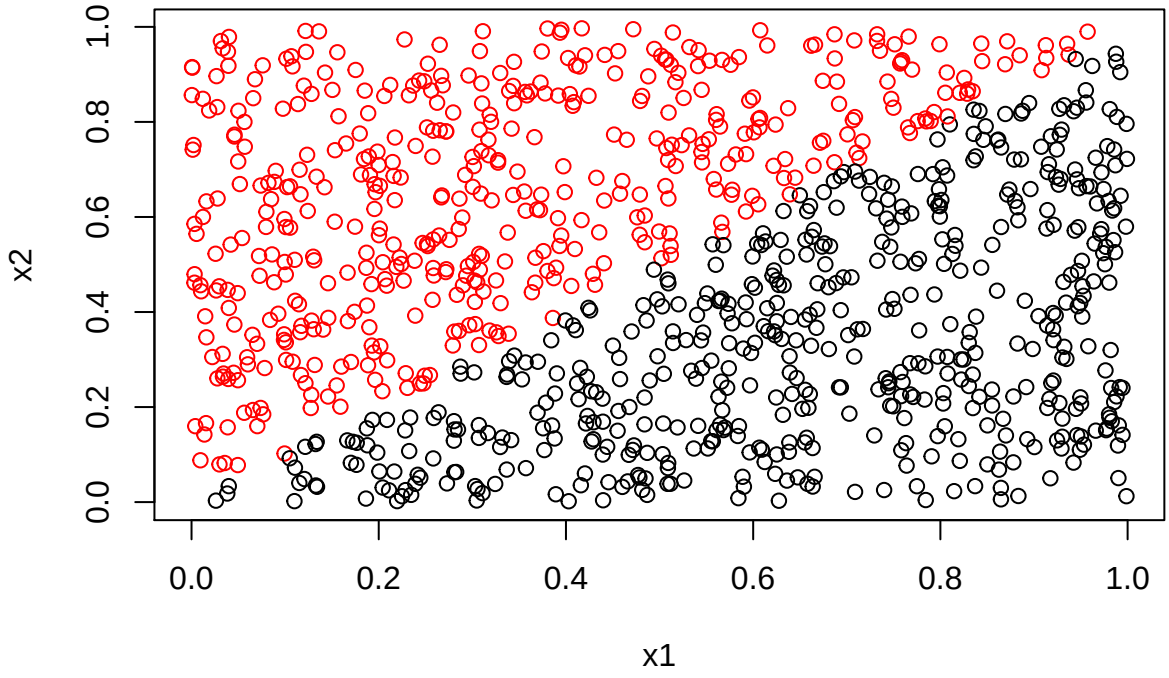
```
## randomForest 4.6-14
```

```
## Type rfNews() to see new features/changes/bug fixes.
```

```
##
## Attaching package: 'randomForest'
```

```
## The following object is masked from 'package:ggplot2':
##
##     margin
```

```
set.seed(1234)

x1<-runif(1000)
x2<-runif(1000)
tedataA<-cbind(x1,x2)
y<-as.numeric(x1<x2)
telabelsA<-as.factor(y)
plot(x1,x2,col=(y+1))
```

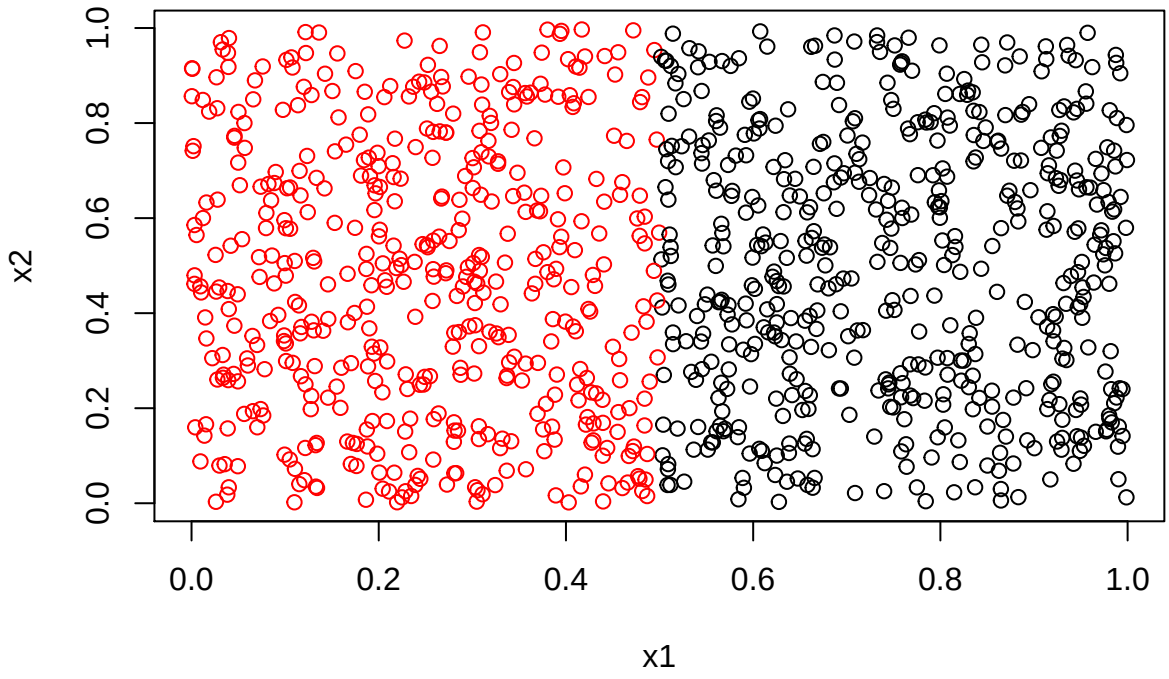



```
forestsize = c(1,10,100)
results = matrix(0,100,3)

for (i in 1:3){
  ntree = forestsize[i]

  for(j in 1:100){
    x1<-runif(100)
    x2<-runif(100)
    trdata<-cbind(x1,x2)
    y<-as.numeric(x1<x2)
    trlabels<-as.factor(y)

    fitA = randomForest(trdata, trlabels, ntree=ntree, nodesize = 25, keep.forest = TRUE)
    predA = predict(fitA, tedataA)
    results[j,i] = sum(as.numeric(predA != telabelsA))/length(telabelsA)
  }
}

resdataA = matrix(0,3,2)
dimnames(resdataA) = list(c("[1]","[10]","[100]"),c("Mean","Variance"))
for(i in 1:3){
  resdataA[i,1] = mean(results[,i])
  resdataA[i,2] = var(results[,i])
}
```

Task B

New data generation

```
set.seed(1234)

x1<-runif(1000)
x2<-runif(1000)
tedataB<-cbind(x1,x2)
y<-as.numeric(x1<0.5)
telabelsB<-as.factor(y)
plot(x1,x2,col=(y+1))
```



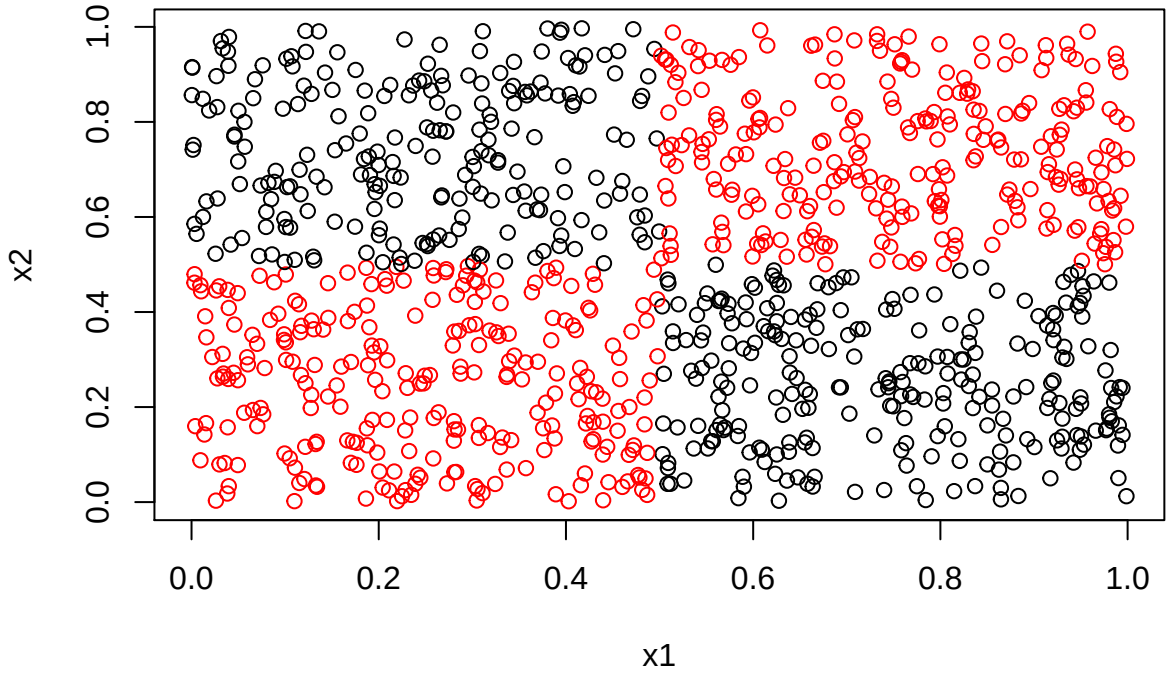

```
forestsize = c(1,10,100)
results = matrix(0,100,3)

for (i in 1:3){
  ntree = forestsize[i]

  for(j in 1:100){
    x1<-runif(100)
    x2<-runif(100)
    trdata<-cbind(x1,x2)
    y<-as.numeric(x1<0.5)
```

```
    trlabels<-as.factor(y)

    fitB = randomForest(trdata, trlabels, ntree=ntree, nodesize = 25, keep.forest = TRUE)
    predB = predict(fitB, tedataB)
    results[j,i] = sum(as.numeric(predB != telabelsB))/length(telabelsB)
  }
}

resdataB = matrix(0,3,2)
dimnames(resdataB) = list(c("[1]","[10]","[100]"),c("Mean","Variance"))
for(i in 1:3){
  resdataB[i,1] = mean(results[,i])
  resdataB[i,2] = var(results[,i])
}
```

Task C

New data generation

```
set.seed(1234)

x1<-runif(1000)
x2<-runif(1000)
tedataC<-cbind(x1,x2)
y<-as.numeric((x1<0.5 & x2<0.5) | (x1>0.5 & x2>0.5))
telabelsC<-as.factor(y)
plot(x1,x2,col=(y+1))
```




```
forestsize = c(1,10,100)
results = matrix(0,100,3)

for (i in 1:3){
  ntree = forestsize[i]

  for(j in 1:100){
    x1<-runif(100)
    x2<-runif(100)
    trdata<-cbind(x1,x2)
    y<-as.numeric( (x1<0.5 & x2<0.5) | (x1>0.5 & x2>0.5) )
    trlabels<-as.factor(y)

    fitC = randomForest(trdata, trlabels, ntree=ntree, nodesize = 12, keep.forest = TRUE)
    predC = predict(fitC, tedataC)
    results[j,i] = sum(as.numeric(predC != telabelsC))/length(telabelsC)
  }
}

resdataC = matrix(0,3,2)
dimnames(resdataC) = list(c("[1]","[10]","[100]"),c("Mean","Variance"))
for(i in 1:3){
  resdataC[i,1] = mean(results[,i])
  resdataC[i,2] = var(results[,i])
}
```

Task D

Question A

Question: What happens with the mean and variance of the error rate when the number of trees in the random forest grows ?

As seen in all three cases the mean error rate decreases with an increasing number of trees in the forest. The same applies for the variance of the error except for case 1 where the variance increased just slightly between the 10- and 100-trees models.

```
print("Task A results:", quote = FALSE)
```

```
## [1] Task A results:
```

```
print(resdataA)
```

```
##          Mean     Variance
## [1]   0.20471 0.0034907130
## [10]  0.13291 0.0008548302
## [100] 0.11047 0.0009660900
```

```
print("Task B results:", quote = FALSE)
```

```
## [1] Task B results:
```

```
print(resdataB)
```

```
##          Mean     Variance
## [1]   0.09324 0.0195394570
## [10]  0.01463 0.0003040334
## [100] 0.00692 0.0001089228
```

```
print("Task B results:", quote = FALSE)
```

```
## [1] Task B results:
```

```
print(resdataC)
```

```
##          Mean    Variance
## [1]   0.23886 0.011984303
## [10]  0.11890 0.003328333
## [100] 0.07728 0.001224567
```

Question B

Due to the node size parameter. Using a smaller minimum node size allows the tree to grow more, in other words the model can divide the data into more specific sections where it can label data. Using smaller node size will need more computation power and could potentially overfit to the data while too large size does the opposite.

Question C

The variance is a measure which tells how much the resulting misclassification are deviating from the mean error. Having a lower variance gives a higher certainty regarding the mean error rate.

Assignment 2: Mixture models

```
EM_algo <- function(k_num){
set.seed(1234567890)
max_it <- 100 # max number of EM iterations
min_change <- 0.1 # min change in log likelihood between two consecutive EM iterations
N=1000 # number of training points
D=10 # number of dimensions
x <- matrix(nrow=N, ncol=D) # training data

true_pi <- vector(length = 3) # true mixing coefficients
true_mu <- matrix(nrow=3, ncol=D) # true conditional distributions
true_pi=c(1/3, 1/3, 1/3)
true_mu[1,]=c(0.5,0.6,0.4,0.7,0.3,0.8,0.2,0.9,0.1,1)
true_mu[2,]=c(0.5,0.4,0.6,0.3,0.7,0.2,0.8,0.1,0.9,0)
true_mu[3,]=c(0.5,0.5,0.5,0.5,0.5,0.5,0.5,0.5,0.5,0.5)

# Producing the training data
for(n in 1:N) {
  k <- sample(1:3,1,prob=true_pi)
  for(d in 1:D) {
    x[n,d] <- rbinom(1,1,true_mu[k,d])
  }
}

K <- k_num# number of guessed components
z <- matrix(nrow=N, ncol=K) # fractional component assignments
pi <- vector(length = K) # mixing coefficients
mu <- matrix(nrow=K, ncol=D) # conditional distributions
llik <- vector(length = max_it) # log likelihood of the EM iterations

# Random initialization of the paramters
pi <- runif(K,0.49,0.51)
pi <- pi / sum(pi)
for(k in 1:K) {
  mu[k,] <- runif(D,0.49,0.51)
}

#pi
#mu

for(it in 1:max_it) {
  #plot(mu[1,], type="o", col="blue", ylim=c(0,1))
  #points(mu[2,], type="o", col="red")
  #points(mu[3,], type="o", col="green")
  #points(mu[4,], type="o", col="yellow")
```

```
  Sys.sleep(0.5)

  # E-step: Computation of the fractional component assignments
  for (j in 1:k) {
    for (i in 1:n) {
      z[i,j] <- pi[j]*prod((mu[j,]^x[i,])*((1-mu[j,])^(1-x[i,])))
    }
  }
  for(j in 1:nrow(z)) {
    z[j,] <- z[j,]/sum(z[j,])
  }

  #Log likelihood computation.
  for(i in 1:n ){
    for(j in 1:k){
      llik[it] <- llik[it] + z[i,j] * (log(pi[j]) + sum(x[i,] * log(mu[j,]) + (1- x[i,])*log(1- mu[j,]))
    }
  }

  cat("iteration: ", it, "log likelihood: ", llik[it], "\n")
  flush.console()
  # Stop if the lok likelihood has not changed significantly
  if(it > 1 ){
    if(( abs(llik[it]- llik[it-1])  < min_change)){
      break
    }
  }
  #M-step: ML parameter estimation from the data and fractional component assignments
  row_sum_z <- c(rep(NA, ncol(z)))
  for (i in 1:ncol(z)) {
    row_sum_z[i] <- sum(z[,i])
  }
  pi <- row_sum_z/N
  mu <- t(z) %*% x /row_sum_z

}
return(list(pi = pi))
}
```

For the E-step for mixtures of multivariate Bernoulli distributions we compute:

$$p\left(z_{nk} \mid \boldsymbol{x}_n, \boldsymbol{\mu}, \boldsymbol{\pi}\right) = \frac{p\left(\boldsymbol{z}_{nk}, \boldsymbol{x}_n \mid \boldsymbol{\mu}, \boldsymbol{\pi}\right)}{\sum_k p\left(z_{nk}, \boldsymbol{x}_n \mid \boldsymbol{\mu}, \boldsymbol{\pi}\right)} = \frac{\pi_k p\left(\boldsymbol{x}_n \mid \boldsymbol{\mu}_k\right)}{\sum_k \pi_k p\left(\boldsymbol{x}_n \mid \boldsymbol{\mu}_k\right)}$$

for all n and k

where

$$p(\boldsymbol{x}_n \mid \boldsymbol{\mu}_k) = \prod_i \mu_{ki}^{x_i} \left(1 - \mu_{ki}\right)^{(1-x_i)}$$

The code is:

```
  # E-step: Computation of the fractional component assignments
  for (j in 1:k) {
    for (i in 1:n) {
      z[i,j] <- pi[j]*prod((mu[j,]^x[i,])*((1-mu[j,])^(1-x[i,])))
    }
  }
  for(j in 1:nrow(z)) {
    z[j,] <- z[j,]/sum(z[j,])
  }
```

For computing the Log likelihood we use:

$$\sum_n \sum_k p\left(z_{nk} \mid \boldsymbol{x}_n, \boldsymbol{\mu}, \boldsymbol{\pi}\right) \left[\log \pi_k + \sum_i \left[x_{ni} \log \mu_{ki} + \left(1 - x_{ni}\right) \log\left(1 - \mu_{ki}\right)\right]\right]$$

The code is:

```
  #Log likelihood computation.
  for(i in 1:n ){
    for(j in 1:k){
      llik[it] <- llik[it] + z[i,j] * (log(pi[j]) + sum(x[i,] * log(mu[j,]) + (1- x[i,])*log(1- mu[j,]))
    }
  }
```

ML parameter estimation from the data and fractional component assignments we use:

$$\pi_k^{ML} = \frac{\sum_n p\left(z_{nk} \mid \boldsymbol{x}_n, \boldsymbol{\mu}, \boldsymbol{\pi}\right)}{N}$$
$$\mu_{ki}^{ML} = \frac{\sum_n x_{ni} p\left(z_{nk} \mid \boldsymbol{x}_n, \boldsymbol{\mu}, \boldsymbol{\pi}\right)}{\sum_n p\left(z_{nk} \mid \boldsymbol{x}_n, \boldsymbol{\mu}, \boldsymbol{\pi}\right)}$$

The code is:

```
  #M-step: ML parameter estimation from the data and fractional component assignments
  row_sum_z <- c(rep(NA, ncol(z)))
  for (i in 1:ncol(z)) {
    row_sum_z[i] <- sum(z[,i])
  }
```

```
EM_algo(2)
```

```
## iteration:  1 log likelihood:  -7623.873
## iteration:  2 log likelihood:  -7621.944
## iteration:  3 log likelihood:  -7620.533
## iteration:  4 log likelihood:  -7609.638
## iteration:  5 log likelihood:  -7532.2
## iteration:  6 log likelihood:  -7173.56
## iteration:  7 log likelihood:  -6661.821
## iteration:  8 log likelihood:  -6520.028
## iteration:  9 log likelihood:  -6503.563
## iteration:  10 log likelihood:  -6499.807
## iteration:  11 log likelihood:  -6498.296
```

```
## iteration:  12 log likelihood:  -6497.535
## iteration:  13 log likelihood:  -6497.12
## iteration:  14 log likelihood:  -6496.883
## iteration:  15 log likelihood:  -6496.745
## iteration:  16 log likelihood:  -6496.662
```

```
## $pi
## [1] 0.4981919 0.5018081
```

When K is equal to 2 the EM-algorithm stops after 16 iterations and the pi values are very close to each other. In this case we miss one true pi.

```
EM_algo(3)
```

```
## iteration:  1 log likelihood:  -8029.723
## iteration:  2 log likelihood:  -8027.183
## iteration:  3 log likelihood:  -8024.696
## iteration:  4 log likelihood:  -8005.631
## iteration:  5 log likelihood:  -7877.606
## iteration:  6 log likelihood:  -7403.513
## iteration:  7 log likelihood:  -6936.919
## iteration:  8 log likelihood:  -6818.582
## iteration:  9 log likelihood:  -6791.377
## iteration:  10 log likelihood:  -6780.713
## iteration:  11 log likelihood:  -6774.958
## iteration:  12 log likelihood:  -6771.261
## iteration:  13 log likelihood:  -6768.606
## iteration:  14 log likelihood:  -6766.535
## iteration:  15 log likelihood:  -6764.815
## iteration:  16 log likelihood:  -6763.316
## iteration:  17 log likelihood:  -6761.967
## iteration:  18 log likelihood:  -6760.727
## iteration:  19 log likelihood:  -6759.572
## iteration:  20 log likelihood:  -6758.491
## iteration:  21 log likelihood:  -6757.475
## iteration:  22 log likelihood:  -6756.521
## iteration:  23 log likelihood:  -6755.625
## iteration:  24 log likelihood:  -6754.784
## iteration:  25 log likelihood:  -6753.996
## iteration:  26 log likelihood:  -6753.26
## iteration:  27 log likelihood:  -6752.571
## iteration:  28 log likelihood:  -6751.928
## iteration:  29 log likelihood:  -6751.328
## iteration:  30 log likelihood:  -6750.768
## iteration:  31 log likelihood:  -6750.246
## iteration:  32 log likelihood:  -6749.758
## iteration:  33 log likelihood:  -6749.304
## iteration:  34 log likelihood:  -6748.88
## iteration:  35 log likelihood:  -6748.484
## iteration:  36 log likelihood:  -6748.114
## iteration:  37 log likelihood:  -6747.767
## iteration:  38 log likelihood:  -6747.444
## iteration:  39 log likelihood:  -6747.14
```

```
## iteration:  40 log likelihood:  -6746.856
## iteration:  41 log likelihood:  -6746.589
## iteration:  42 log likelihood:  -6746.338
## iteration:  43 log likelihood:  -6746.102
## iteration:  44 log likelihood:  -6745.88
## iteration:  45 log likelihood:  -6745.67
## iteration:  46 log likelihood:  -6745.472
## iteration:  47 log likelihood:  -6745.285
## iteration:  48 log likelihood:  -6745.108
## iteration:  49 log likelihood:  -6744.939
## iteration:  50 log likelihood:  -6744.78
## iteration:  51 log likelihood:  -6744.627
## iteration:  52 log likelihood:  -6744.483
## iteration:  53 log likelihood:  -6744.344
## iteration:  54 log likelihood:  -6744.212
## iteration:  55 log likelihood:  -6744.086
## iteration:  56 log likelihood:  -6743.964
## iteration:  57 log likelihood:  -6743.848
## iteration:  58 log likelihood:  -6743.736
## iteration:  59 log likelihood:  -6743.628
## iteration:  60 log likelihood:  -6743.524
## iteration:  61 log likelihood:  -6743.423
## iteration:  62 log likelihood:  -6743.326

## $pi
## [1] 0.3259592 0.3044579 0.3695828
```

When K is equal to 3 the EM-algorithm stops after 62 iterations and the pi values are pretty close to each other.

```
EM_algo(4)
```

```
## iteration:  1 log likelihood:  -8317.187
## iteration:  2 log likelihood:  -8314.81
## iteration:  3 log likelihood:  -8312.256
## iteration:  4 log likelihood:  -8292.606
## iteration:  5 log likelihood:  -8159.059
## iteration:  6 log likelihood:  -7666.637
## iteration:  7 log likelihood:  -7196.701
## iteration:  8 log likelihood:  -7061.15
## iteration:  9 log likelihood:  -7018.948
## iteration:  10 log likelihood:  -6999.971
## iteration:  11 log likelihood:  -6989.735
## iteration:  12 log likelihood:  -6983.5
## iteration:  13 log likelihood:  -6979.315
## iteration:  14 log likelihood:  -6976.279
## iteration:  15 log likelihood:  -6973.932
## iteration:  16 log likelihood:  -6972.026
## iteration:  17 log likelihood:  -6970.415
## iteration:  18 log likelihood:  -6969.009
## iteration:  19 log likelihood:  -6967.751
## iteration:  20 log likelihood:  -6966.598
## iteration:  21 log likelihood:  -6965.517
```

```
## iteration:  22 log likelihood:  -6964.48
## iteration:  23 log likelihood:  -6963.457
## iteration:  24 log likelihood:  -6962.415
## iteration:  25 log likelihood:  -6961.313
## iteration:  26 log likelihood:  -6960.098
## iteration:  27 log likelihood:  -6958.703
## iteration:  28 log likelihood:  -6957.042
## iteration:  29 log likelihood:  -6955.01
## iteration:  30 log likelihood:  -6952.485
## iteration:  31 log likelihood:  -6949.342
## iteration:  32 log likelihood:  -6945.475
## iteration:  33 log likelihood:  -6940.834
## iteration:  34 log likelihood:  -6935.458
## iteration:  35 log likelihood:  -6929.501
## iteration:  36 log likelihood:  -6923.217
## iteration:  37 log likelihood:  -6916.917
## iteration:  38 log likelihood:  -6910.896
## iteration:  39 log likelihood:  -6905.381
## iteration:  40 log likelihood:  -6900.502
## iteration:  41 log likelihood:  -6896.299
## iteration:  42 log likelihood:  -6892.745
## iteration:  43 log likelihood:  -6889.776
## iteration:  44 log likelihood:  -6887.313
## iteration:  45 log likelihood:  -6885.273
## iteration:  46 log likelihood:  -6883.583
## iteration:  47 log likelihood:  -6882.178
## iteration:  48 log likelihood:  -6881.007
## iteration:  49 log likelihood:  -6880.024
## iteration:  50 log likelihood:  -6879.196
## iteration:  51 log likelihood:  -6878.494
## iteration:  52 log likelihood:  -6877.895
## iteration:  53 log likelihood:  -6877.383
## iteration:  54 log likelihood:  -6876.941
## iteration:  55 log likelihood:  -6876.56
## iteration:  56 log likelihood:  -6876.228
## iteration:  57 log likelihood:  -6875.939
## iteration:  58 log likelihood:  -6875.687
## iteration:  59 log likelihood:  -6875.465
## iteration:  60 log likelihood:  -6875.27
## iteration:  61 log likelihood:  -6875.098
## iteration:  62 log likelihood:  -6874.947
## iteration:  63 log likelihood:  -6874.813
## iteration:  64 log likelihood:  -6874.694
## iteration:  65 log likelihood:  -6874.59
## iteration:  66 log likelihood:  -6874.497

## $pi
## [1] 0.1614155 0.1383613 0.3609912 0.3392319
```

When K is equal to 4 the EM-algorithm stops after 16 iterations and the pi values are pretty far from each other. In this task we have one extra pi.

Assignment3 . High Dimentional Methods

1 Diviving data to train and test(70/30) and performing NSC classification.

Then run to train a nearest shrunken centroid classifier.(NSC) For 30 different values of the threshold the number of nonzero genes and the number of misclassifications on the training set will be listed

```
model
```

```
## Call:
## pamr.train(data = mydata)
##    threshold nonzero errors
## 1   0.000    2058    18
## 2   0.801    1040    21
## 3   1.603     374    23
## 4   2.404     226    25
## 5   3.206     147    21
## 6   4.007     102    20
## 7   4.809      78    19
## 8   5.610      54    20
## 9   6.412      35    20
## 10  7.213      25    19
## 11  8.014      19    18
## 12  8.816      11    19
## 13  9.617      10    27
## 14 10.419       8    40
## 15 11.220       7    73
## 16 12.022       4    72
## 17 12.823       4    72
## 18 13.624       3    72
## 19 14.426       2    73
## 20 15.227       1    73
## 21 16.029       1    73
## 22 16.830       1    72
## 23 17.632       1    72
## 24 18.433       1    72
## 25 19.235       1    72
## 26 20.036       1    70
## 27 20.837       1    70
## 28 21.639       1    70
## 29 22.440       1    69
## 30 23.242       0    137
```

```
cvmodel
```

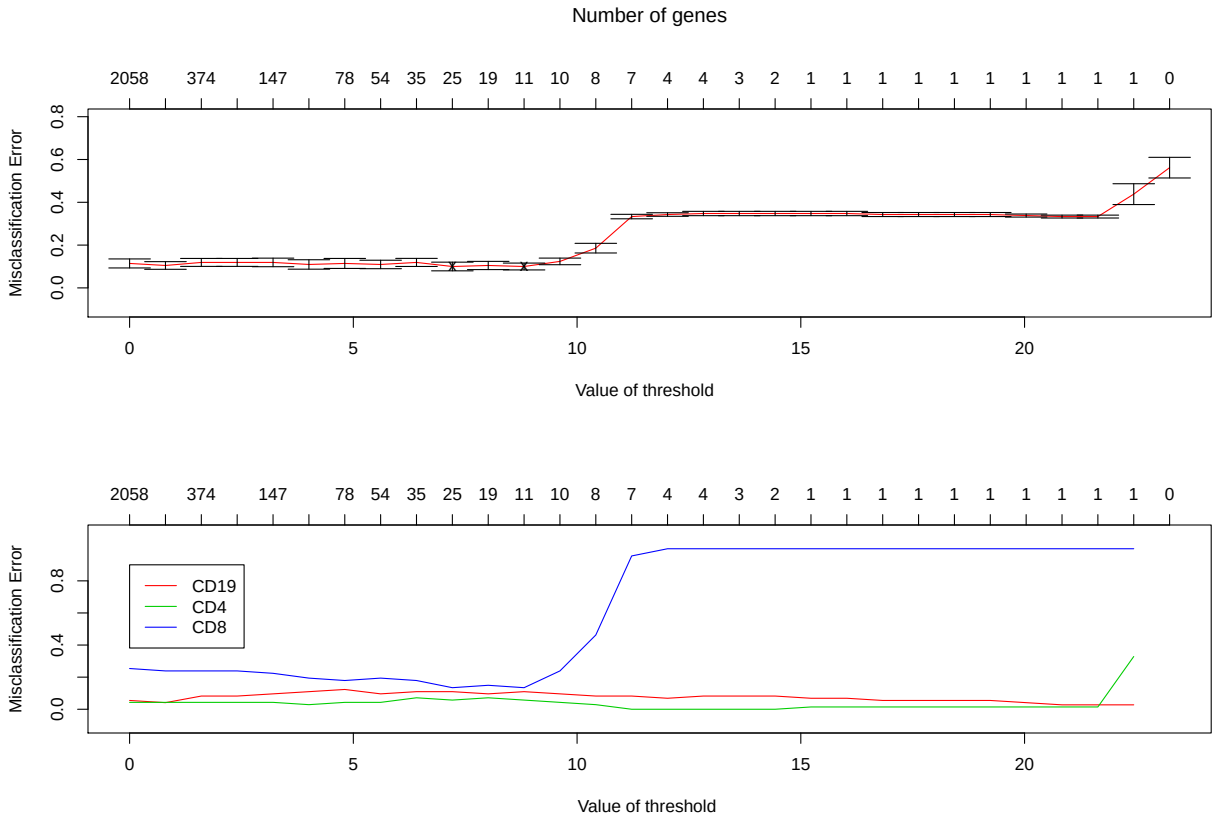
```
## Call:
## pamr.cv(fit = model, data = mydata)
##    threshold nonzero errors
## 1   0.000    2058    24
## 2   0.801    1040    22
## 3   1.603     374    25
## 4   2.404     226    25
## 5   3.206     147    25
```

```
## 6   4.007     102    23
## 7   4.809      78    24
## 8   5.610      54    23
## 9   6.412      35    25
## 10  7.213      25    21
## 11  8.014      19    22
## 12  8.816      11    21
## 13  9.617      10    26
## 14 10.419       8    39
## 15 11.220       7    70
## 16 12.022       4    72
## 17 12.823       4    73
## 18 13.624       3    73
## 19 14.426       2    73
## 20 15.227       1    73
## 21 16.029       1    73
## 22 16.830       1    72
## 23 17.632       1    72
## 24 18.433       1    72
## 25 19.235       1    72
## 26 20.036       1    71
## 27 20.837       1    70
## 28 21.639       1    70
## 29 22.440       1    92
## 30 23.242       0    118
```

The output of this function looks very similar to the model. The numbers in the errors column are now the summed errors of all 10 cross validation steps. The CV error usually is bigger than the training error.

Missclassification Error Plot. In both figures, the x-axis represents different values of threshold (corresponding to different numbers of nonzero genes as shown on top of each figure and the y-axis shows the number of misclassifications. The upper figure describes the whole dataset, the lower one describes each class individually

```
pamr.plotcv(cvmodel)
```



Minimum threshold:

```
## [1] "Best threshold equals:  7.2129439923563"
```

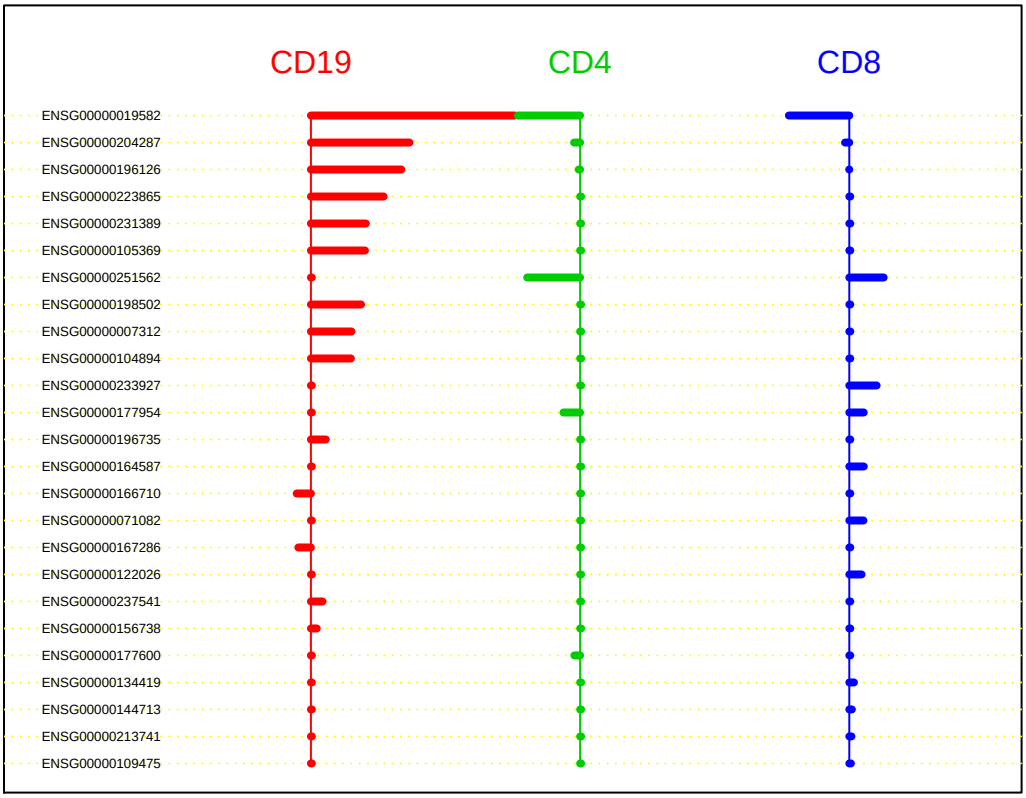
```
## [1] "Number of features:  25"
```

The value of 7.2 of the threshold has the lowest error of cv.model.

Centroid plot(threshold = 7.2):

The function pamr.plotcen() plots the shrunken class centroids for each class.NSC classification shrink each of the class centroid toward the overall centroid for all classes by threshold.This shrinkage consists of moving the centroid toward zero by threshold, setting it equal to zero if it hits zero. Here the threshold is 7.2, hence the class centroid would be shrink be minus by the threshold. It is the reason that we see positive and negative values in the centroid plot.

```
pamr.plotcen(model, mydata, threshold = best_Th)
```



Number of genes selected by this model:

```
##       id  CD19-score CD4-score CD8-score
##  [1,] 2   1.5153     -0.4617   -0.4489
##  [2,] 15  0.7328     -0.0448   -0.032
##  [3,] 31  0.6715     -0.0105   -0.001
##  [4,] 32  0.5403     0         0
##  [5,] 37  0.4089     0         0
##  [6,] 138 0.4019     0         0
##  [7,] 1   0          -0.3933   0.2553
##  [8,] 90  0.3727     0         0
##  [9,] 172 0.3016     0         0
## [10,] 126 0.2974     0         0
## [11,] 79  0          0         0.2028
## [12,] 11  0          -0.1239   0.1074
## [13,] 110 0.1109     0         0
## [14,] 21  0          0         0.1078
## [15,] 3   -0.1057    0         0
## [16,] 50  0          0         0.1051
## [17,] 207 -0.0933    0         0
## [18,] 29  0          0         0.0914
## [19,] 192 0.0862     0         0
## [20,] 309 0.0438     0         0
## [21,] 28  0          -0.0426   0
## [22,] 38  0          0         0.0346
## [23,] 18  0          0         0.0189
## [24,] 127 0          0         0.0156
```

```
## [25,] 36  0          0         0.0119
```

```
## [1] 25
```

```
paste("Number of genes selected by this model : ", nrow(a))
```

```
## [1] "Number of genes selected by this model :  25"
```

task_2 names of the 2 most contributing genes

```
##       id  CD19-score CD4-score CD8-score
##  [1,] 2   1.5153     -0.4617   -0.4489
##  [2,] 15  0.7328     -0.0448   -0.032
##  [3,] 31  0.6715     -0.0105   -0.001
##  [4,] 32  0.5403     0         0
##  [5,] 37  0.4089     0         0
##  [6,] 138 0.4019     0         0
##  [7,] 1   0          -0.3933   0.2553
##  [8,] 90  0.3727     0         0
##  [9,] 172 0.3016     0         0
## [10,] 126 0.2974     0         0
## [11,] 79  0          0         0.2028
## [12,] 11  0          -0.1239   0.1074
## [13,] 110 0.1109     0         0
## [14,] 21  0          0         0.1078
## [15,] 3   -0.1057    0         0
## [16,] 50  0          0         0.1051
## [17,] 207 -0.0933    0         0
## [18,] 29  0          0         0.0914
## [19,] 192 0.0862     0         0
## [20,] 309 0.0438     0         0
## [21,] 28  0          -0.0426   0
## [22,] 38  0          0         0.0346
## [23,] 18  0          0         0.0189
## [24,] 127 0          0         0.0156
## [25,] 36  0          0         0.0119
```

```
## [1] "ENSG00000019582" "ENSG00000204287"
```

```
paste("Names of the two most contributing genes: ",mydata$genenames[k] )
```

```
## [1] "Names of the two most contributing genes:  ENSG00000019582" "Names of the two most contributing
```

The name of two most contributing genes are, " CD74" and “HLA-DRA”.And both of them are considered as marker genes.

Confusion Matrix. Here we see 73 samples belong to class CD19, 65 sample is classified correctly and 8 are missclassified as CD4. 70 samples belong to CD4. 65 sample is classified correctly and 5 are missclassified as CD8 67 samples belong to CD8, 59 is classified correctly and 8 is missclassified as CD4. This makes an overall error rate 0.1%.

```
pamr.confusion(cvmodel,  threshold = best_Th)
```

```
##      CD19 CD4 CD8 Class Error rate
## CD19   65   8   0       0.10958904
## CD4     0  66   4       0.05714286
## CD8     0   9  58       0.13432836
## Overall error rate= 0.1
```

reporting test error.

```
## [1] "Confusion Matrix for test data :"
```

```
##       pam.diagnosis
## y_test CD19 CD4 CD8
##   CD19   27   0   0
##   CD4     0  26   4
##   CD8     0   6  27
```

```
## ME rate for test data :   0.111111111111111
```

It seems that 27 samples are classified correctly to CD19, 30 samples belong to CD4, in which 4 samples are miss classified. 33 samples belong to CD8,6 samples from them are miss qualified .

task_3

```
library(glmnet)
```

Elastic net with multinomial response :

```
## Loading required package: Matrix
```

```
## Loaded glmnet 4.0-2
```

```
set.seed(12345)
x_e <- as.matrix(train[, -ncol(train)])
y_e <- as.matrix(train[[ncol(train)]])
# fit the elastic net
elastic <- cv.glmnet(x_e, y_e, alpha = 0.5, family = "multinomial")
testx=as.matrix((test[ , -ncol(test)]))
predenet=predict(elastic, newx = testx, s = elastic$lambda.min, type = "class")
cm_elastic_net <- table(y_test, predenet)
cm_elastic_net
```

```
##       predenet
## y_test CD19 CD4 CD8
##   CD19   27   0   0
##   CD4     0  29   1
##   CD8     1   3  29
```

```
test_error_elasic_net <- 1-sum(diag(cm_elastic_net))/sum(cm_elastic_net)
coef1 <-coef(elastic, s="lambda.min")
num_feature<-length(coef1$CD8@x)+length(coef1$CD19@x)+length(coef1$CD4@x)
cat(paste("ME rate for test data :  ", test_error_elasic_net))
```

```
## ME rate for test data :   0.0555555555555556
```

```
paste("Number of feature :",num_feature )
```

```
## [1] "Number of feature : 163"
```

```
library("kernlab")
```

SVM:

```
##
## Attaching package: 'kernlab'

## The following object is masked from 'package:ggplot2':
##
##     alpha
```

```
set.seed(12345)
train.x <-as.matrix(train[, -ncol(train)])
train.y <- as.matrix(train[[ncol(train)]])
svm.trained <- ksvm(train.x, train.y , type = "C-svc", kernel='vanilladot')
```

```
##  Setting default kernel parameters

## Warning in .local(x, ...): Variable(s) '' constant. Cannot scale data.
```

```
svm_pred <- predict(svm.trained, testx)
cm_svm <- table(y_test, svm_pred)
cm_svm
```

```
##       svm_pred
## y_test CD19 CD4 CD8
##   CD19   27   0   0
##   CD4     0  30   0
##   CD8     0   2  31
```

```
test_error_svm = 1-sum(diag(cm_svm))/sum(cm_svm)
paste("number of feature:", (ncol(df)-1))
```

```
## [1] "number of feature: 2085"
```

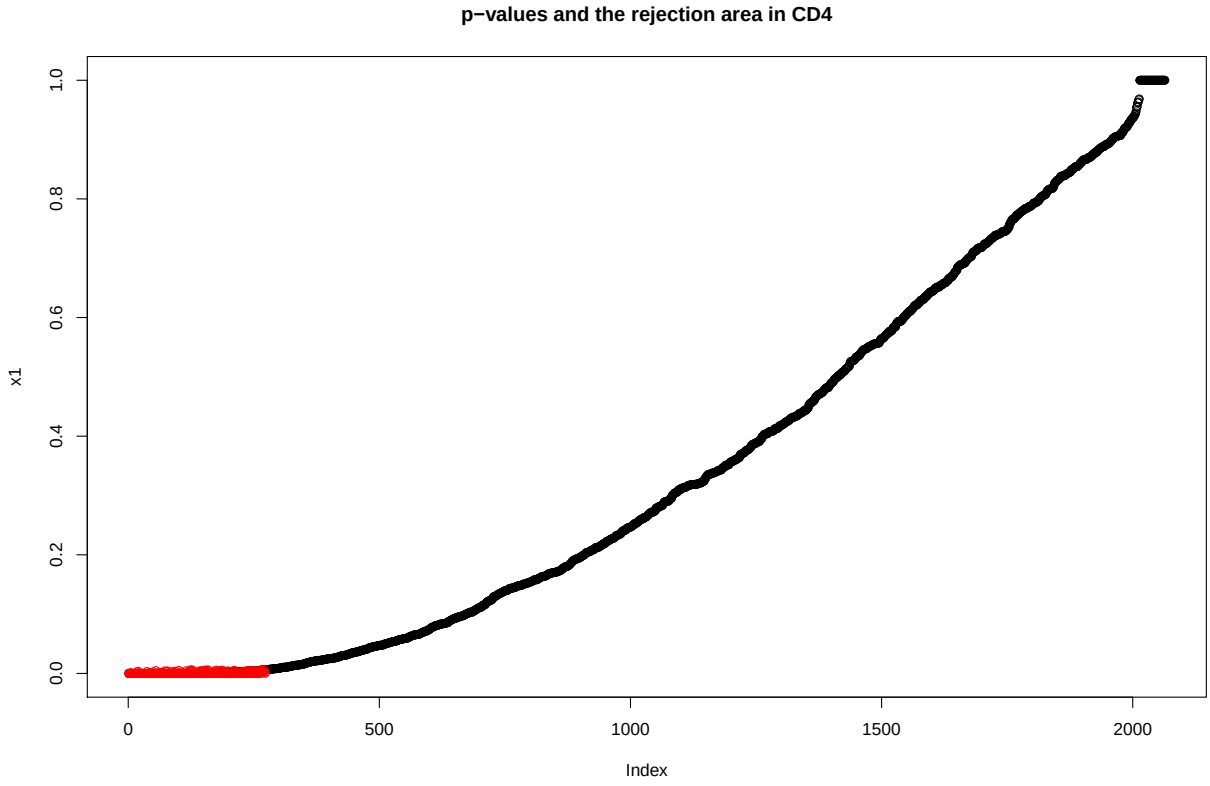
```
cat(paste("ME rate for test data :  ", test_error_svm))
```

```
## ME rate for test data :   0.0222222222222223
```

Table 1: Comparsion of Three models

	Nearest Shrunken Centroid Model	Elastic_Net Model	SVM Model
Number of Features	25.0000000	163.0000000	2.08500e+03
Error rate	0.1111111	0.0555556	2.22222e-02

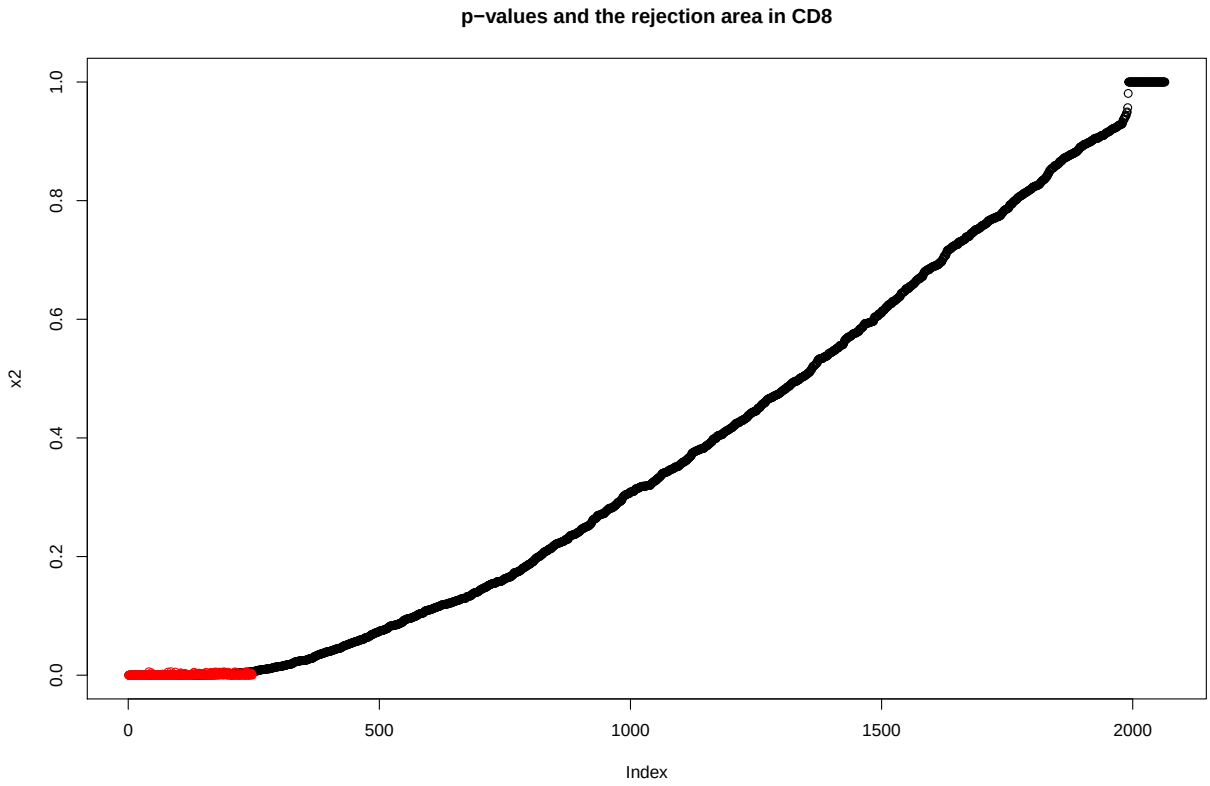
Analysis: By comparison three different models, we can see the SVM has the lowest error rate compare two other models, but the this model select 2085 features for classifying three different classes. The error rate in Elastic net model is lower than NSC.but number of features in three classes are more than NSC. As the difference between error rate in NSC and Elastic net could be ignored, by considering number of features, NSC could be a good model for classification. #### task4: Benjamin Hochberg

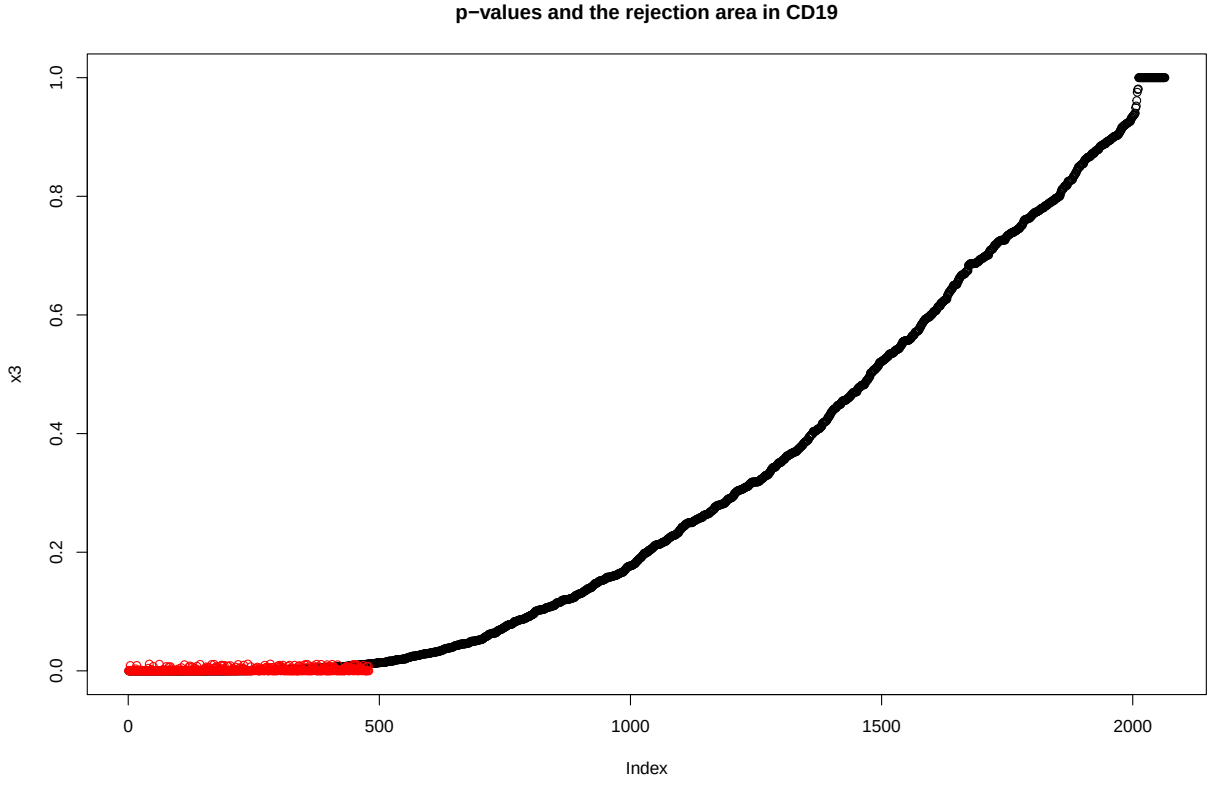



```
## [1] "number of features in CD4:  273"
```

```
## [1] "number of features in CD8:  247"
```

```
## [1] "number of features in CD19:  479"
```





The Benjamin_Hochberg method is implemented. By using t.test, varoius p_value are calculated for three

different classes.The number of features that are not related to three classes are more than three other models.

Appendix:

```
knitr::opts_chunk$set(echo = TRUE)
library(kknn)
library(ggplot2)

library(randomForest)
set.seed(1234)

x1<-runif(1000)
x2<-runif(1000)
tedataA<-cbind(x1,x2)
y<-as.numeric(x1<x2)
telabelsA<-as.factor(y)
plot(x1,x2,col=(y+1))


forestsize = c(1,10,100)
results = matrix(0,100,3)

for (i in 1:3){
  ntree = forestsize[i]

  for(j in 1:100){
    x1<-runif(100)
    x2<-runif(100)
    trdata<-cbind(x1,x2)
    y<-as.numeric(x1<x2)
    trlabels<-as.factor(y)

    fitA = randomForest(trdata, trlabels, ntree=ntree, nodesize = 25, keep.forest = TRUE)
    predA = predict(fitA, tedataA)
    results[j,i] = sum(as.numeric(predA != telabelsA))/length(telabelsA)
  }
}

resdataA = matrix(0,3,2)
dimnames(resdataA) = list(c("[1]","[10]","[100]"),c("Mean","Variance"))
for(i in 1:3){
  resdataA[i,1] = mean(results[,i])
  resdataA[i,2] = var(results[,i])
}

set.seed(1234)

x1<-runif(1000)
x2<-runif(1000)
tedataB<-cbind(x1,x2)
```

```
y<-as.numeric(x1<0.5)
telabelsB<-as.factor(y)
plot(x1,x2,col=(y+1))

forestsize = c(1,10,100)
results = matrix(0,100,3)

for (i in 1:3){
  ntree = forestsize[i]

  for(j in 1:100){
    x1<-runif(100)
    x2<-runif(100)
    trdata<-cbind(x1,x2)
    y<-as.numeric(x1<0.5)
    trlabels<-as.factor(y)

    fitB = randomForest(trdata, trlabels, ntree=ntree, nodesize = 25, keep.forest = TRUE)
    predB = predict(fitB, tedataB)
    results[j,i] = sum(as.numeric(predB != telabelsB))/length(telabelsB)
  }
}

resdataB = matrix(0,3,2)
dimnames(resdataB) = list(c("[1]","[10]","[100]"),c("Mean","Variance"))
for(i in 1:3){
  resdataB[i,1] = mean(results[,i])
  resdataB[i,2] = var(results[,i])
}

set.seed(1234)

x1<-runif(1000)
x2<-runif(1000)
tedataC<-cbind(x1,x2)
y<-as.numeric((x1<0.5 & x2<0.5) | (x1>0.5 & x2>0.5))
telabelsC<-as.factor(y)
plot(x1,x2,col=(y+1))

forestsize = c(1,10,100)
results = matrix(0,100,3)

for (i in 1:3){
  ntree = forestsize[i]

  for(j in 1:100){
    x1<-runif(100)
    x2<-runif(100)
    trdata<-cbind(x1,x2)
    y<-as.numeric( (x1<0.5 & x2<0.5) | (x1>0.5 & x2>0.5) )
    trlabels<-as.factor(y)

    fitC = randomForest(trdata, trlabels, ntree=ntree, nodesize = 12, keep.forest = TRUE)
```

```
    predC = predict(fitC, tedataC)
    results[j,i] = sum(as.numeric(predC != telabelsC))/length(telabelsC)
  }
}

resdataC = matrix(0,3,2)
dimnames(resdataC) = list(c("[1]","[10]","[100]"),c("Mean","Variance"))
for(i in 1:3){
  resdataC[i,1] = mean(results[,i])
  resdataC[i,2] = var(results[,i])
}

print("Task A results:", quote = FALSE)
print(resdataA)

print("Task B results:", quote = FALSE)
print(resdataB)

print("Task B results:", quote = FALSE)
print(resdataC)
EM_algo <- function(k_num){
set.seed(1234567890)
max_it <- 100 # max number of EM iterations
min_change <- 0.1 # min change in log likelihood between two consecutive EM iterations
N=1000 # number of training points
D=10 # number of dimensions
x <- matrix(nrow=N, ncol=D) # training data

true_pi <- vector(length = 3) # true mixing coefficients
true_mu <- matrix(nrow=3, ncol=D) # true conditional distributions
true_pi=c(1/3, 1/3, 1/3)
true_mu[1,]=c(0.5,0.6,0.4,0.7,0.3,0.8,0.2,0.9,0.1,1)
true_mu[2,]=c(0.5,0.4,0.6,0.3,0.7,0.2,0.8,0.1,0.9,0)
true_mu[3,]=c(0.5,0.5,0.5,0.5,0.5,0.5,0.5,0.5,0.5,0.5)

# Producing the training data
for(n in 1:N) {
  k <- sample(1:3,1,prob=true_pi)
  for(d in 1:D) {
    x[n,d] <- rbinom(1,1,true_mu[k,d])
  }
}

K <- k_num# number of guessed components
z <- matrix(nrow=N, ncol=K) # fractional component assignments
pi <- vector(length = K) # mixing coefficients
mu <- matrix(nrow=K, ncol=D) # conditional distributions
llik <- vector(length = max_it) # log likelihood of the EM iterations

# Random initialization of the paramters
pi <- runif(K,0.49,0.51)
pi <- pi / sum(pi)
for(k in 1:K) {
```

```
  mu[k,] <- runif(D,0.49,0.51)
}

#pi
#mu

for(it in 1:max_it) {
  #plot(mu[1,], type="o", col="blue", ylim=c(0,1))
  #points(mu[2,], type="o", col="red")
  #points(mu[3,], type="o", col="green")
  #points(mu[4,], type="o", col="yellow")
  Sys.sleep(0.5)

  # E-step: Computation of the fractional component assignments
  for (j in 1:k) {
    for (i in 1:n) {
      z[i,j] <- pi[j]*prod((mu[j,]^x[i,])*((1-mu[j,])^(1-x[i,])))
    }
  }
  for(j in 1:nrow(z)) {
    z[j,] <- z[j,]/sum(z[j,])
  }

  #Log likelihood computation.
  for(i in 1:n ){
    for(j in 1:k){
      llik[it] <- llik[it] + z[i,j] * (log(pi[j]) + sum(x[i,] * log(mu[j,]) + (1- x[i,])*log(1- mu[j,]))
    }
  }

  cat("iteration: ", it, "log likelihood: ", llik[it], "\n")
  flush.console()
  # Stop if the lok likelihood has not changed significantly
  if(it > 1 ){
    if(( abs(llik[it]- llik[it-1])  < min_change)){
      break
    }
  }
  #M-step: ML parameter estimation from the data and fractional component assignments
  row_sum_z <- c(rep(NA, ncol(z)))
  for (i in 1:ncol(z)) {
    row_sum_z[i] <- sum(z[,i])
  }
  pi <- row_sum_z/N
  mu <- t(z) %*% x /row_sum_z

}
return(list(pi = pi))
}
  # E-step: Computation of the fractional component assignments
  for (j in 1:k) {
    for (i in 1:n) {
      z[i,j] <- pi[j]*prod((mu[j,]^x[i,])*((1-mu[j,])^(1-x[i,])))
```

```
    }
  }
  for(j in 1:nrow(z)) {
    z[j,] <- z[j,]/sum(z[j,])
  }
  #Log likelihood computation.
  for(i in 1:n ){
    for(j in 1:k){
      llik[it] <- llik[it] + z[i,j] * (log(pi[j]) + sum(x[i,] * log(mu[j,]) + (1- x[i,])*log(1- mu[j,]))
    }
  }


  #M-step: ML parameter estimation from the data and fractional component assignments
  row_sum_z <- c(rep(NA, ncol(z)))
  for (i in 1:ncol(z)) {
    row_sum_z[i] <- sum(z[,i])
  }
EM_algo(2)
EM_algo(3)
EM_algo(4)
setwd("D:/Linkoping university/first semester/Machine Learning/lab/block2")

new_df <- read.csv("geneexp.csv")

df = new_df[,-1]  # the first and the last are factor
set.seed(12345)
m <- nrow(df)
# divide data to train and test(70:30)
id <- sample(1:m, floor(m*0.7))
train <- df[id,]
test <- df[-id,]

### train ###
rownames(train) = 1:nrow(train)
x = t(train[, -ncol(train)])
y = train[[ncol(train)]]
mydata <- list(x=x, y=as.factor(y),geneid=as.character(1:nrow(x)),genenames=rownames(x))

### test ###
rownames(test) = 1:nrow(test)
x_test = t(test[, -ncol(test)])
y_test = test[[ncol(test)]]
test_mydata <- list(x=x_test, y=as.factor(y_test),geneid=as.character(1:nrow(x_test)),genenames=rowname

library(pamr)
model = pamr.train(mydata)

# choice the threshold by cv
cvmodel = pamr.cv(model,mydata)
model
cvmodel
```

```
pamr.plotcv(cvmodel)

min_Error <- which.min(cvmodel$error)
best_Th <- cvmodel$threshold[min_Error]
paste("Best threshold equals: ", best_Th)
numberofgen <- model$nonzero[min_Error]
paste("Number of features: ", numberofgen)
pamr.plotcen(model, mydata, threshold = best_Th)


a<-pamr.listgenes(model, mydata, threshold = best_Th, genenames=FALSE)
nrow(a)
paste("Number of genes selected by this model : ", nrow(a))
a<-(pamr.listgenes(model, mydata, threshold = best_Th))
top_2 = a[1:2,1]
k <- as.numeric(top_2)
mydata$genenames[k]
paste("Names of the two most contributing genes: ",mydata$genenames[k] )
pamr.confusion(cvmodel,  threshold = best_Th)
pam.diagnosis <- pamr.predict(model, x_test, threshold = best_Th)
new_matrix <- table(y_test, pam.diagnosis)
paste("Confusion Matrix for test data :")
new_matrix
test_ME <- 1-(sum(diag(new_matrix)))/sum(new_matrix)
cat(paste("ME rate for test data :  ", test_ME))
library(glmnet)
set.seed(12345)
x_e <- as.matrix(train[, -ncol(train)])
y_e <- as.matrix(train[[ncol(train)]])
# fit the elastic net
elastic <- cv.glmnet(x_e, y_e, alpha = 0.5, family = "multinomial")
testx=as.matrix((test[ , -ncol(test)]))
predenet=predict(elastic, newx = testx, s = elastic$lambda.min, type = "class")
cm_elastic_net <- table(y_test, predenet)
cm_elastic_net
test_error_elasic_net <- 1-sum(diag(cm_elastic_net))/sum(cm_elastic_net)
coef1 <-coef(elastic, s="lambda.min")
num_feature<-length(coef1$CD8@x)+length(coef1$CD19@x)+length(coef1$CD4@x)
cat(paste("ME rate for test data :  ", test_error_elasic_net))
paste("Number of feature :",num_feature )

library("kernlab")
set.seed(12345)
train.x <-as.matrix(train[, -ncol(train)])
train.y <- as.matrix(train[[ncol(train)]])
svm.trained <- ksvm(train.x, train.y , type = "C-svc", kernel='vanilladot')
svm_pred <- predict(svm.trained, testx)
cm_svm <- table(y_test, svm_pred)
cm_svm
test_error_svm = 1-sum(diag(cm_svm))/sum(cm_svm)
paste("number of feature:", (ncol(df)-1))
cat(paste("ME rate for test data :  ", test_error_svm))
final_result <- cbind(numberofgen, num_feature, (ncol(df)-1))
```

```
feature_count <- cbind(test_ME, test_error_elasic_net,test_error_svm)
final_matrix <- rbind(final_result,feature_count)
colnames(final_matrix) <- c("Nearest Shrunken Centroid Model", "Elastic_Net Model","SVM Model")
rownames(final_matrix) <- c("Number of Features", "Error rate")
knitr::kable(final_matrix, caption = "Comparsion of Three models")
df = new_df[,-1]
y_1 <- ifelse(df$CellType=="CD4",1,0)
y_2 <- ifelse(df$CellType=="CD8",1,0)
y_3 <- ifelse(df$CellType=="CD19",1,0)
p1 <- sapply(1:(ncol(df)-1), function(x) t.test(df[,x] ~ y_1, data = df)$p.val)
p2 <- sapply(1:(ncol(df)-1), function(x) t.test(df[,x] ~ y_2, data = df)$p.val)
p3 <- sapply(1:(ncol(df)-1), function(x) t.test(df[,x] ~ y_3, data = df)$p.val)

pvall_1 <- as.data.frame(p1)
pvall_2 <- as.data.frame(p2)
pvall_3 <- as.data.frame(p3)

x1 <- sort(as.numeric(p1))
x2 <- sort(as.numeric(p2))
x3 <- sort(as.numeric(p3))


get_p_rej <- function(x1){
  l = 1
  while (x1[l] < (0.05* l / length(x1))) {
    l=l+1
  }
  p_rej <- x1[l]
  return(p_rej)
}

plot(x1, main="p-values and the rejection area in CD4")
points(pvall_1$p1[which(p1 < get_p_rej(x1))],col= "red")




no_CD4 <-length(pvall_1$p1[which(p1 < get_p_rej(x1))])

paste("number of features in CD4: ", no_CD4)
no_CD8 <-length(pvall_2$p2[which(p2 < get_p_rej(x2))])
paste("number of features in CD8: ", no_CD8)
no_CD19 <-length(pvall_3$p3[which(p3 < get_p_rej(x3))])
paste("number of features in CD19: ", no_CD19)

plot(x2, main="p-values and the rejection area in CD8")
points(pvall_2$p2[which(p2 < get_p_rej(x2))],col= "red")

plot(x3, main="p-values and the rejection area in CD19")
points(pvall_3$p3[which(p3 < get_p_rej(x3))],col= "red")
```