features

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finding discriminative features

The features are going to be selected based on different models. To find the significant features permutation test is applied.

```
data <- t(read.table("C:/Users/nz1413/Desktop/dataTAC/sputum_508genes.txt",                    head
dataScaled = scale(data)
```

```
library(mclust)
```

```
## Package 'mclust' version 5.4
## Type 'citation("mclust")' for citing this R package in publications.
```

```
mbc<-Mclust(dataScaled)
summary(mbc)
```

```
## ----------------------------------------------------
## Gaussian finite mixture model fitted by EM algorithm
## ----------------------------------------------------
##
## Mclust VII (spherical, varying volume) model with 4 components:
##
##  log.likelihood   n   df       BIC       ICL
##       -63604.42 104 2039 -136678.7 -136678.8
##
## Clustering table:
##  1  2  3  4
## 24 23 28 29
```

```
#clusters
library(CMA)
```

```
## Loading required package: Biobase
## Loading required package: BiocGenerics
## Loading required package: parallel
##
## Attaching package: 'BiocGenerics'
## The following objects are masked from 'package:parallel':
##
##     clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##     clusterExport, clusterMap, parApply, parCapply, parLapply,
##     parLapplyLB, parRapply, parSapply, parSapplyLB
## The following objects are masked from 'package:stats':
##
##     IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
```

```
##
##     anyDuplicated, append, as.data.frame, cbind, colMeans,
##     colnames, colSums, do.call, duplicated, eval, evalq, Filter,
##     Find, get, grep, grepl, intersect, is.unsorted, lapply,
##     lengths, Map, mapply, match, mget, order, paste, pmax,
##     pmax.int, pmin, pmin.int, Position, rank, rbind, Reduce,
##     rowMeans, rownames, rowSums, sapply, setdiff, sort, table,
##     tapply, union, unique, unsplit, which, which.max, which.min

## Welcome to Bioconductor
##
##     Vignettes contain introductory material; view with
##     'browseVignettes()'. To cite Bioconductor, see
##     'citation("Biobase")', and for packages 'citation("pkgname")'.
```

```
set.seed(321)
options(warn=-1)
varsel_ftest <- GeneSelection(X = dataScaled, y=mbc$classification,
                              method = "f.test")
```

```
## GeneSelection: iteration 1
```

```
varsel_kruskaltest <- GeneSelection(X = dataScaled, y=mbc$classification,
                                    method = "kruskal.test")
```

```
## GeneSelection: iteration 1
```

```
varsel_rf <- GeneSelection(X = dataScaled, y=mbc$classification,
                           method = "rf")
```

```
## GeneSelection: iteration 1

## randomForest 4.6-12

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

##
## Attaching package: 'randomForest'

## The following object is masked from 'package:Biobase':
##
##     combine

## The following object is masked from 'package:BiocGenerics':
##
##     combine
```

```
varsel_boosting <- GeneSelection(X = dataScaled, y=mbc$classification,
                                 method = "boosting", mstop = 1000)
```

```
## GeneSelection: iteration 1
```

```
options(warn=0)
```

```
library(CMA)
options(warn=-1)
set.seed(113)
numberOfResampling = 1000
nvars = dim(dataScaled)[2]
nSamples = dim(dataScaled)[1]
varImportanceftest = matrix(0,numberOfResampling,nvars)
```

```
varImportancekruskaltest = matrix(0,numberOfResampling,nvars)
varImportancerf = matrix(0,numberOfResampling,nvars)
varImportanceboosting = matrix(0,numberOfResampling,nvars)
for(i in 1:numberOfResampling)
{
  labels_permutated = sample(mbc$classification)
  varsel_ftest <- GeneSelection(X = dataScaled, y=labels_permutated,
                               method = "f.test")
  varsel_kruskaltest <- GeneSelection(X = dataScaled, y=labels_permutated,
                                     method = "kruskal.test")
  varsel_rf <- GeneSelection(X = dataScaled, labels_permutated,
                            mtry= ceiling(10*sqrt(nvars)), nodesize = 8,                          meth
  varsel_boosting <- GeneSelection(X = dataScaled, y=labels_permutated,
                                  method = "boosting", mstop = 1000)
  varImportanceftest[i,varsel_ftest@rankings[[1]][1:nvars]] = varsel_ftest@importance[[1]][1:nvars]
  varImportancekruskaltest[i,varsel_kruskaltest@rankings[[1]][1:nvars]] = varsel_kruskaltest@importance
  varImportancerf[i,varsel_rf@rankings[[1]][1:nvars]] = varsel_rf@importance[[1]][1:nvars]
  varImportanceboosting[i,varsel_boosting@rankings[[1]][1:nvars]] = varsel_boosting@importance[[1]][1:n
}
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```

```
set.seed(113)
options(warn=-1)
varsel_ftest <- GeneSelection(X = dataScaled, y=mbc$classification,
                              method = "f.test")
```

```
## GeneSelection: iteration 1
```

```
varsel_kruskaltest <- GeneSelection(X = dataScaled, y=mbc$classification,
                                    method = "kruskal.test")
```

```
## GeneSelection: iteration 1
```

```
varsel_rf <- GeneSelection(X = dataScaled, y=mbc$classification,
                           mtry= ceiling(10*sqrt(nvars)), nodesize =8 , method = "rf")
```

```
## GeneSelection: iteration 1
```

```
varsel_boosting <- GeneSelection(X = dataScaled, y=mbc$classification,
                                 method = "boosting", mstop = 1000)
```

```
## GeneSelection: iteration 1
```

```
options(warn=0)
pValueftest = matrix(0,1,nvars)
pValuekruskaltest = matrix(0,1,nvars)
pValuerf = matrix(0,1,nvars)
pValueboosting = matrix(0,1,nvars)
for(i in 1:nvars)
{
  temp = which(varsel_ftest@rankings[[1]]==i)
  pValueftest[1,i] = length(which(varImportanceftest[,i]>
                                    varsel_ftest@importance[[1]][temp]))
```

```
  temp = which(varsel_kruskaltest@rankings[[1]]==i)
  pValuekruskaltest[1,i] = length(which(varImportancekruskaltest[,i]>
                                        varsel_kruskaltest@importance[[1]][temp]))
  temp = which(varsel_rf@rankings[[1]]==i)
  pValuerf[1,i] = length(which(varImportancerf[,i]>
                               varsel_rf@importance[[1]][temp]))
  temp = which(varsel_boosting@rankings[[1]]==i)
  pValueboosting[1,i] = length(which(varImportanceboosting[,i]>
                                     varsel_boosting@importance[[1]][temp]))
}

ftestPvalue = t(pValueftest)/1000
kruskalPvalue = t(pValuekruskaltest)/1000
boostingPvalue = t(pValueboosting)/1000
rfPvalue = t(pValuerf)/1000

# adjustment
indeces = order(ftestPvalue)
ftestPvalue[indeces] = p.adjust(ftestPvalue[indeces],
                                method = "bonferroni")
indeces = order(kruskalPvalue)
kruskalPvalue[indeces] = p.adjust(kruskalPvalue[indeces],
                                method = "bonferroni")
indeces = order(boostingPvalue)
boostingPvalue[indeces] = p.adjust(boostingPvalue[indeces],
                                method = "bonferroni")
indeces = order(rfPvalue)
rfPvalue[indeces] = p.adjust(rfPvalue[indeces],
                                method = "bonferroni")

result = cbind(varsel_ftest@importance[[1]][varsel_ftest@rankings[[1]][1:nvars]],
               ftestPvalue,
               varsel_kruskaltest@importance[[1]][varsel_kruskaltest@rankings[[1]][1:nvars]],
               kruskalPvalue,
               varsel_rf@importance[[1]][varsel_rf@rankings[[1]][1:nvars]],
               rfPvalue,
               varsel_boosting@importance[[1]][varsel_boosting@rankings[[1]][1:nvars]],
               boostingPvalue)

nvars = dim(dataScaled)[2]
library(gtools)
foldChange = 1:nvars
for (i in 1:nvars)
{
  foldChange[i] = foldchange(mean(dataScaled[which(mbc$classification==1 | mbc$classification==2),i]), m
}

FinalSelection = matrix(0,nvars,4 )
colnames(FinalSelection) = c("f.test", "kruskal.test", "component boosting","random Forst")
rownames(FinalSelection) = colnames(dataScaled)
for(i in seq(1,8,2))
{
```

```
  quantTemp = quantile(result[,i], 0.95)
  FinalSelection[,(floor(i/2)+1)] = as.numeric(c(result[,i]>= quantTemp & result[,(i+1)]<= 0.01))
}

FinalSelection = cbind(FinalSelection, foldChange)
rownames(FinalSelection) = colnames(dataScaled)

result = cbind(result, foldChange)
rownames(result) = colnames(dataScaled)

write.table(result, file = 'C:/Users/nz1413/Desktop/AnalysisTag/Final/data/featuresFor4Classes.txt' )

write.table(FinalSelection, file = 'C:/Users/nz1413/Desktop/AnalysisTag/Final/data/DesicionfeaturesFor4
```