# Lab3 block2 732A95

Anton Persson antpe404
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## Assignment 1 High dimensional methods

The first assignment is about different methods to deal with wide data.

### Assignment 1.1

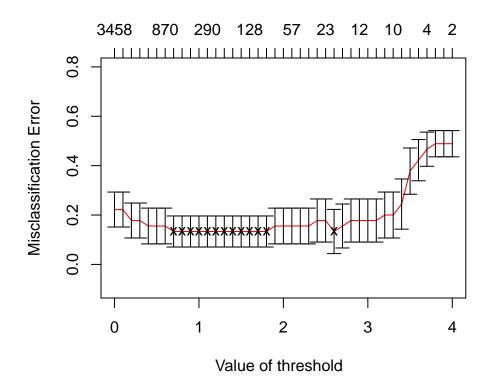
I divided the data into training and test according to the instruction. The nearest shrunken centroid classification was done and the required results are presented below.

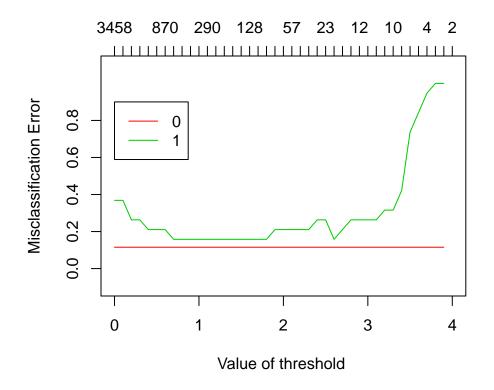
```
## Call:
## pamr.cv(fit = model, data = mydata)
##
      threshold nonzero errors
## 1
                 3458
                         10
      0.0
## 2
      0.1
                 3428
                          10
## 3
      0.2
                 3110
                         8
## 4
      0.3
                 3042
                         8
## 5
      0.4
                 3025
                         7
## 6
      0.5
                         7
                 1977
## 7
      0.6
                  870
                         7
## 8 0.7
                  850
                         6
## 9
      0.8
                  673
                         6
## 10 0.9
                  671
                         6
## 11 1.0
                  295
                         6
## 12 1.1
                  290
                         6
## 13 1.2
                  269
                         6
## 14 1.3
                  234
                         6
## 15 1.4
                  154
                         6
## 16 1.5
                  151
                         6
## 17 1.6
                  128
                          6
## 18 1.7
                  100
                          6
## 19 1.8
                   97
                         6
## 20 1.9
                   73
                         7
## 21 2.0
                   64
                         7
                   57
                         7
## 22 2.1
## 23 2.2
                   42
                         7
## 24 2.3
                   37
                         7
## 25 2.4
                   35
                         8
## 26 2.5
                   23
                         8
## 27 2.6
                   21
                         6
## 28 2.7
                   20
                         7
## 29 2.8
                   14
                         8
## 30 2.9
                   12
                         8
## 31 3.0
                   11
                         8
## 32 3.1
                   10
                         8
## 33 3.2
                   10
                         9
```

##	34	3.3	10	9
##	35	3.4	9	11
##	36	3.5	4	17
##	37	3.6	4	19
##	38	3.7	4	21
##	39	3.8	4	22
##	40	3.9	3	22
##	41	4.0	2	22

From the table above, I conclude that a threshold between 0.7-1.8 or 2.6 generates the lowest error. I choose 2.6 as threshold because of simplicity. This will generate 21 selected features, notated as nonzero in the output above. The figure below visualizes the table above. The plot on top in the figure below says that above mentioned thresholds minimizes the error.

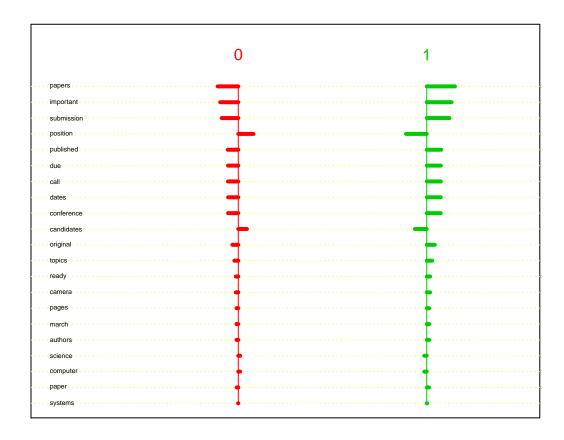
# Number of genes





The ten most important features for the model with 2.6 as threshold is visualized in a cendriod plot below.

#### ## 1



The deafult plot in pamr doesn't have a brilliant layout, why it's kind of hard to read which variables are actually chosen. For clarity I decided to list them in a more proper way. The ten most contributing features are thus listed below.

## papers
## important
## submission
## position
## published
## call
## due
## conference
## dates
## candidates

I'd say that the words are reasonable. I can see why you'd mention words like *paper*, *submission*, *candidates*, *published*, *dates* and *conference* in a mail about conferences. Finally, the test error is presented below.

#### ## [1] 0.1052632

### Assignment 1.2

In this assignment I'm supposed to compute the error rate and number of contributing features for two more methods, elastic net and support vector machine. I start off with elastic net.

#### Assignment 1.2a

The instructions defines the type of response and value of  $\alpha$  for me. I do use the function cv.glmnet to decide penalty by cross validation. The number of features and test error rate is presented below.

```
## $test_error_rate_elastic
## [1] 0.1578947
##
## $number_of_features_elastic
## [1] 12
```

#### Assignment 1.2b

The test error and number of contributing features for a SVM with vanilladot kernel are presented below.

```
## Setting default kernel parameters
## $test_error_rate_svm
## [1] 0.05263158
##
## $number_of_features_svm
## [1] 44
```

Finally I compare the three methods used above, nearest shrunken centroid method, elastic net and support vector machine, by arranging a table with all the results. Watch it below!

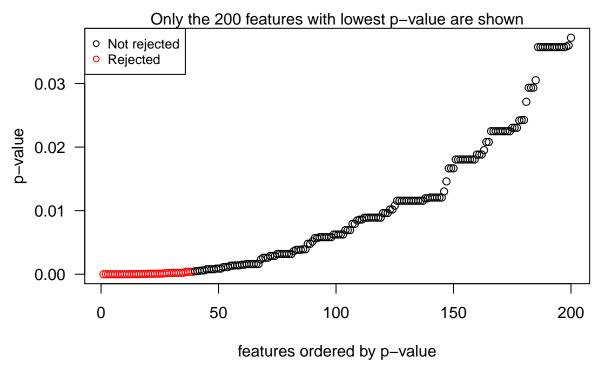
```
## NSC Elastic SVM
## Number of features 21.0000000 12.0000000 44.00000000
## test_error_rate 0.1052632 0.1578947 0.05263158
```

From the table I conclude that I'd probably choose the SVM. It uses the most number of features (44) but also get the best error rate.

## Assignment 1.3

In this assignment I implemented the Benjamini Hochberg method on the complete original data, not the training set only. To begin with, the result is visualized by the plot below.

## Rejected hypotheses by Benjamini Hochberg method



Notice that in the plot above, only the first 200 features of the ordered data frame are plotted. That means that the features visualized in the plot only corresponds to the about 4% of all features in the data. I did this because of the 4702 features tested, only 39 gets rejected. Those 39 rejected features are thus the features that are most useful for describing the feature Conference.