Enrique Otanez Project 2 RMD

Enrique Otanez

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#to work with the dataset you need to use the code on line 15 to retrieve it.  
require(mlbench)

## Loading required package: mlbench

## Warning: package 'mlbench' was built under R version 4.0.4

data(BreastCancer)  
  
#Here you bind the columns you want to work with.  
BreastCancer

## Id Cl.thickness Cell.size Cell.shape Marg.adhesion Epith.c.size  
## 1 1000025 5 1 1 1 2  
## 2 1002945 5 4 4 5 7  
## 3 1015425 3 1 1 1 2  
## 4 1016277 6 8 8 1 3  
## 5 1017023 4 1 1 3 2  
## 6 1017122 8 10 10 8 7  
## 7 1018099 1 1 1 1 2  
## 8 1018561 2 1 2 1 2  
## 9 1033078 2 1 1 1 2  
## 10 1033078 4 2 1 1 2  
## 11 1035283 1 1 1 1 1  
## 12 1036172 2 1 1 1 2  
## 13 1041801 5 3 3 3 2  
## 14 1043999 1 1 1 1 2  
## 15 1044572 8 7 5 10 7  
## 16 1047630 7 4 6 4 6  
## 17 1048672 4 1 1 1 2  
## 18 1049815 4 1 1 1 2  
## 19 1050670 10 7 7 6 4  
## 20 1050718 6 1 1 1 2  
## 21 1054590 7 3 2 10 5  
## 22 1054593 10 5 5 3 6  
## 23 1056784 3 1 1 1 2  
## 24 1057013 8 4 5 1 2  
## 25 1059552 1 1 1 1 2  
## 26 1065726 5 2 3 4 2  
## 27 1066373 3 2 1 1 1  
## 28 1066979 5 1 1 1 2  
## 29 1067444 2 1 1 1 2  
## 30 1070935 1 1 3 1 2  
## 31 1070935 3 1 1 1 1  
## 32 1071760 2 1 1 1 2  
## 33 1072179 10 7 7 3 8  
## 34 1074610 2 1 1 2 2  
## 35 1075123 3 1 2 1 2  
## 36 1079304 2 1 1 1 2  
## 37 1080185 10 10 10 8 6  
## 38 1081791 6 2 1 1 1  
## 39 1084584 5 4 4 9 2  
## 40 1091262 2 5 3 3 6  
## 41 1096800 6 6 6 9 6  
## 42 1099510 10 4 3 1 3  
## 43 1100524 6 10 10 2 8  
## 44 1102573 5 6 5 6 10  
## 45 1103608 10 10 10 4 8  
## 46 1103722 1 1 1 1 2  
## 47 1105257 3 7 7 4 4  
## 48 1105524 1 1 1 1 2  
## 49 1106095 4 1 1 3 2  
## 50 1106829 7 8 7 2 4  
## 51 1108370 9 5 8 1 2  
## 52 1108449 5 3 3 4 2  
## 53 1110102 10 3 6 2 3  
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## 55 1110524 10 5 5 6 8  
## 56 1111249 10 6 6 3 4  
## 57 1112209 8 10 10 1 3  
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## 59 1113483 5 2 3 1 6  
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## 62 1115293 1 1 1 1 2  
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## 64 1116132 6 3 4 1 5  
## 65 1116192 1 1 1 1 2  
## 66 1116998 10 4 2 1 3  
## 67 1117152 4 1 1 1 2  
## 68 1118039 5 3 4 1 8  
## 69 1120559 8 3 8 3 4  
## 70 1121732 1 1 1 1 2  
## 71 1121919 5 1 3 1 2  
## 72 1123061 6 10 2 8 10  
## 73 1124651 1 3 3 2 2  
## 74 1125035 9 4 5 10 6  
## 75 1126417 10 6 4 1 3  
## 76 1131294 1 1 2 1 2  
## 77 1132347 1 1 4 1 2  
## 78 1133041 5 3 1 2 2  
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## 696 1 1 1 1 benign  
## 697 3 8 10 2 malignant  
## 698 4 10 6 1 malignant  
## 699 5 10 4 1 malignant

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BreastCancer

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## 16 4 1047630 7 4 6 4  
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## 693 2 1 1 1 1 benign  
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## 695 3 2 1 1 1 benign  
## 696 2 1 1 1 1 benign  
## 697 7 3 8 10 2 malignant  
## 698 3 4 10 6 1 malignant  
## 699 4 5 10 4 1 malignant

#By identifying the NA's and knowing that they are low in number, complete cases is used to remove entire rows of data.   
sum(is.na(BreastCancer))

## [1] 16

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BreastCancer

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## 2 3 1002945 5 4 4 5  
## 3 3 1015425 3 1 1 1  
## 4 3 1016277 6 8 8 1  
## 5 3 1017023 4 1 1 3  
## 6 9 1017122 8 10 10 8  
## 7 3 1018099 1 1 1 1  
## 8 3 1018561 2 1 2 1  
## 9 1 1033078 2 1 1 1  
## 10 2 1033078 4 2 1 1  
## 11 3 1035283 1 1 1 1  
## 12 2 1036172 2 1 1 1  
## 13 4 1041801 5 3 3 3  
## 14 3 1043999 1 1 1 1  
## 15 5 1044572 8 7 5 10  
## 16 4 1047630 7 4 6 4  
## 17 2 1048672 4 1 1 1  
## 18 3 1049815 4 1 1 1  
## 19 4 1050670 10 7 7 6  
## 20 3 1050718 6 1 1 1  
## 21 5 1054590 7 3 2 10  
## 22 7 1054593 10 5 5 3  
## 23 2 1056784 3 1 1 1  
## 25 3 1059552 1 1 1 1  
## 26 3 1065726 5 2 3 4  
## 27 2 1066373 3 2 1 1  
## 28 2 1066979 5 1 1 1  
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## 50 3 1106829 7 8 7 2  
## 51 2 1108370 9 5 8 1  
## 52 3 1108449 5 3 3 4  
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## 698 3 4 10 6 1 malignant  
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#We can see that we do not need the duplicated column when we cbinded the columns or the ID because of having low predictive value.   
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BreastCancer

## Cl.thickness Cell.size Cell.shape Marg.adhesion Epith.c.size Bare.nuclei  
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## 698 10 6 1 malignant  
## 699 10 4 1 malignant

#Here we run our first model a SVM and we predict our label class.  
library(e1071)

## Warning: package 'e1071' was built under R version 4.0.3

mysvm <- svm(Class ~ ., BreastCancer)  
mysvm.pred <- predict(mysvm, BreastCancer)  
length(mysvm.pred)

## [1] 683

length(BreastCancer$Class)

## [1] 683

table(mysvm.pred,BreastCancer$Class)

##   
## mysvm.pred benign malignant  
## benign 431 8  
## malignant 13 231

#The output shows that we have a classifier that predicts very well.

#Here, and for the rest of the models, we do the same thing. Use a different method of classification and then predict with the model.   
#This model here is naive bayes classification.   
library(klaR)

## Warning: package 'klaR' was built under R version 4.0.4

## Loading required package: MASS

mynb <- NaiveBayes(Class ~ ., BreastCancer)  
mynb.pred <- predict(mynb, BreastCancer)

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 2

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 4

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 6

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 13

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 15

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 16

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 21

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 25

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 32

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 38

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 39

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 40

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 42

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 45

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 48

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 52

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 54

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 55

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 56

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 58

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 59

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 62

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 64

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 67

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 70

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 73

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 83

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 84

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 85

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 86

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 97

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 98

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 99

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 100

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 102

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 682

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with  
## observation 683

mynb.df <- data.frame(mynb.pred)  
mynb.df

## class posterior.benign posterior.malignant  
## 1 benign 1.000000e+00 8.495761e-09  
## 2 malignant 8.276441e-05 9.999172e-01  
## 3 benign 1.000000e+00 2.259978e-08  
## 4 malignant 4.928053e-05 9.999507e-01  
## 5 benign 1.000000e+00 2.957752e-08  
## 6 malignant 6.179313e-14 1.000000e+00  
## 7 benign 9.999996e-01 3.834760e-07  
## 8 benign 1.000000e+00 3.216817e-08  
## 9 benign 1.000000e+00 1.043804e-09  
## 10 benign 1.000000e+00 8.892893e-09  
## 11 benign 1.000000e+00 1.358910e-10  
## 12 benign 1.000000e+00 2.164632e-10  
## 13 malignant 1.471544e-02 9.852846e-01  
## 14 benign 1.000000e+00 8.918050e-09  
## 15 malignant 3.076178e-13 1.000000e+00  
## 16 malignant 1.894877e-07 9.999998e-01  
## 17 benign 1.000000e+00 4.458496e-10  
## 18 benign 1.000000e+00 2.806560e-09  
## 19 malignant 7.362316e-11 1.000000e+00  
## 20 benign 1.000000e+00 1.880395e-08  
## 21 malignant 4.633542e-11 1.000000e+00  
## 22 malignant 4.197899e-13 1.000000e+00  
## 23 benign 1.000000e+00 3.246948e-10  
## 25 benign 1.000000e+00 3.456608e-10  
## 26 malignant 7.852285e-02 9.214771e-01  
## 27 benign 1.000000e+00 2.546072e-09  
## 28 benign 1.000000e+00 1.349635e-09  
## 29 benign 1.000000e+00 2.164632e-10  
## 30 benign 1.000000e+00 2.138755e-09  
## 31 benign 1.000000e+00 1.276486e-10  
## 32 benign 1.000000e+00 1.362605e-09  
## 33 malignant 3.810258e-12 1.000000e+00  
## 34 benign 1.000000e+00 9.357782e-09  
## 35 benign 1.000000e+00 7.665345e-09  
## 36 benign 1.000000e+00 2.164632e-10  
## 37 malignant 4.143187e-14 1.000000e+00  
## 38 benign 9.999945e-01 5.546405e-06  
## 39 malignant 5.665836e-06 9.999943e-01  
## 40 malignant 2.333619e-07 9.999998e-01  
## 42 malignant 5.416360e-07 9.999995e-01  
## 43 malignant 2.715995e-12 1.000000e+00  
## 44 malignant 2.384976e-04 9.997615e-01  
## 45 malignant 4.275477e-13 1.000000e+00  
## 46 benign 1.000000e+00 6.051199e-10  
## 47 malignant 3.455690e-08 1.000000e+00  
## 48 benign 1.000000e+00 5.491163e-11  
## 49 benign 1.000000e+00 2.957752e-08  
## 50 malignant 4.141932e-09 1.000000e+00  
## 51 malignant 1.083933e-03 9.989161e-01  
## 52 malignant 1.673265e-02 9.832674e-01  
## 53 malignant 9.983695e-10 1.000000e+00  
## 54 malignant 3.272898e-12 1.000000e+00  
## 55 malignant 2.375524e-10 1.000000e+00  
## 56 malignant 1.473476e-08 1.000000e+00  
## 57 malignant 1.049502e-08 1.000000e+00  
## 58 malignant 1.681246e-05 9.999832e-01  
## 59 malignant 2.344004e-03 9.976560e-01  
## 60 malignant 6.363858e-05 9.999364e-01  
## 61 malignant 6.782602e-07 9.999993e-01  
## 62 benign 1.000000e+00 6.071657e-10  
## 63 malignant 1.936957e-09 1.000000e+00  
## 64 malignant 3.409996e-03 9.965900e-01  
## 65 benign 1.000000e+00 5.491163e-11  
## 66 malignant 3.988211e-06 9.999960e-01  
## 67 benign 1.000000e+00 2.806560e-09  
## 68 malignant 3.403794e-06 9.999966e-01  
## 69 malignant 1.898633e-11 1.000000e+00  
## 70 benign 1.000000e+00 6.592848e-10  
## 71 benign 9.999998e-01 1.779719e-07  
## 72 malignant 1.720288e-10 1.000000e+00  
## 73 benign 9.980853e-01 1.914657e-03  
## 74 malignant 4.701838e-12 1.000000e+00  
## 75 malignant 1.270118e-06 9.999987e-01  
## 76 benign 9.999973e-01 2.731685e-06  
## 77 benign 1.000000e+00 2.439907e-08  
## 78 benign 9.999992e-01 7.917017e-07  
## 79 benign 9.999999e-01 5.273281e-08  
## 80 benign 1.000000e+00 5.619577e-09  
## 81 benign 9.999905e-01 9.488270e-06  
## 82 benign 1.000000e+00 3.061902e-09  
## 83 benign 9.999998e-01 1.694560e-07  
## 84 benign 9.999991e-01 8.501067e-07  
## 85 malignant 4.498826e-13 1.000000e+00  
## 86 malignant 6.099106e-11 1.000000e+00  
## 87 malignant 5.021087e-07 9.999995e-01  
## 88 malignant 4.902032e-11 1.000000e+00  
## 89 benign 1.000000e+00 2.806560e-09  
## 90 benign 1.000000e+00 3.859282e-08  
## 91 benign 1.000000e+00 3.456608e-10  
## 92 benign 1.000000e+00 6.586277e-10  
## 93 benign 1.000000e+00 2.806560e-09  
## 94 benign 1.000000e+00 5.491163e-11  
## 95 benign 1.000000e+00 1.362605e-09  
## 96 benign 1.000000e+00 3.456608e-10  
## 97 benign 1.000000e+00 4.390851e-10  
## 98 benign 1.000000e+00 8.495761e-09  
## 99 malignant 3.368422e-11 1.000000e+00  
## 100 malignant 2.248976e-15 1.000000e+00  
## 101 malignant 5.014012e-09 1.000000e+00  
## 102 malignant 3.004384e-01 6.995616e-01  
## 103 benign 9.999999e-01 6.625682e-08  
## 104 malignant 3.777772e-03 9.962222e-01  
## 105 malignant 1.245201e-14 1.000000e+00  
## 106 malignant 3.379983e-05 9.999662e-01  
## 107 malignant 1.094320e-10 1.000000e+00  
## 108 malignant 6.154105e-10 1.000000e+00  
## 109 benign 1.000000e+00 1.475796e-09  
## 110 malignant 1.724483e-10 1.000000e+00  
## 111 benign 9.830019e-01 1.699812e-02  
## 112 malignant 4.364287e-06 9.999956e-01  
## 113 malignant 9.830023e-10 1.000000e+00  
## 114 malignant 4.577103e-12 1.000000e+00  
## 115 benign 9.998937e-01 1.063246e-04  
## 116 benign 1.000000e+00 8.369041e-10  
## 117 benign 9.641128e-01 3.588717e-02  
## 118 malignant 4.429517e-12 1.000000e+00  
## 119 benign 1.000000e+00 4.143244e-08  
## 120 benign 9.999995e-01 4.507738e-07  
## 121 benign 9.999999e-01 5.604146e-08  
## 122 benign 9.999994e-01 6.189728e-07  
## 123 malignant 9.592840e-15 1.000000e+00  
## 124 malignant 4.283335e-06 9.999957e-01  
## 125 malignant 1.065797e-10 1.000000e+00  
## 126 benign 1.000000e+00 5.491163e-11  
## 127 malignant 1.821739e-12 1.000000e+00  
## 128 benign 1.000000e+00 2.043908e-09  
## 129 malignant 1.510191e-07 9.999998e-01  
## 130 benign 1.000000e+00 8.225386e-09  
## 131 benign 9.999998e-01 1.779719e-07  
## 132 benign 1.000000e+00 1.362605e-09  
## 133 malignant 7.478204e-12 1.000000e+00  
## 134 benign 1.000000e+00 6.192960e-10  
## 135 benign 1.000000e+00 8.429365e-09  
## 136 benign 9.999975e-01 2.524678e-06  
## 137 benign 1.000000e+00 4.458496e-10  
## 138 benign 1.000000e+00 9.590407e-11  
## 139 benign 1.000000e+00 1.052555e-08  
## 141 benign 1.000000e+00 9.590407e-11  
## 142 benign 1.000000e+00 6.393605e-11  
## 143 malignant 1.683792e-11 1.000000e+00  
## 144 benign 1.000000e+00 8.369041e-10  
## 145 benign 1.000000e+00 2.164632e-10  
## 147 malignant 3.111921e-05 9.999689e-01  
## 148 benign 1.000000e+00 1.576256e-08  
## 149 benign 9.943053e-01 5.694709e-03  
## 150 malignant 4.467752e-13 1.000000e+00  
## 151 benign 1.000000e+00 1.358910e-10  
## 152 malignant 2.094298e-09 1.000000e+00  
## 153 malignant 6.302039e-14 1.000000e+00  
## 154 benign 1.000000e+00 3.397581e-09  
## 155 benign 1.000000e+00 1.621907e-11  
## 156 malignant 3.500480e-06 9.999965e-01  
## 157 benign 1.000000e+00 2.585683e-08  
## 158 benign 1.000000e+00 1.362605e-09  
## 160 malignant 2.368948e-14 1.000000e+00  
## 161 malignant 6.203750e-13 1.000000e+00  
## 162 benign 1.000000e+00 5.352999e-09  
## 163 benign 1.000000e+00 2.043908e-09  
## 164 benign 1.000000e+00 2.951091e-08  
## 166 benign 9.999999e-01 5.918887e-08  
## 167 malignant 1.188662e-12 1.000000e+00  
## 168 malignant 1.654479e-10 1.000000e+00  
## 169 benign 1.000000e+00 2.043908e-09  
## 170 benign 1.000000e+00 4.378945e-11  
## 171 benign 1.000000e+00 9.590407e-11  
## 172 benign 1.000000e+00 3.456608e-10  
## 173 benign 1.000000e+00 5.491163e-11  
## 174 malignant 2.774024e-16 1.000000e+00  
## 175 malignant 8.784367e-09 1.000000e+00  
## 176 malignant 5.663530e-11 1.000000e+00  
## 177 benign 1.000000e+00 1.362605e-09  
## 178 malignant 1.309125e-10 1.000000e+00  
## 179 benign 1.000000e+00 2.806560e-09  
## 180 malignant 1.353887e-03 9.986461e-01  
## 181 benign 1.000000e+00 1.358910e-10  
## 182 benign 1.000000e+00 1.621907e-11  
## 183 benign 1.000000e+00 1.880395e-08  
## 184 malignant 5.085644e-11 1.000000e+00  
## 185 malignant 8.538977e-09 1.000000e+00  
## 186 benign 1.000000e+00 5.356864e-10  
## 187 malignant 1.046682e-09 1.000000e+00  
## 188 malignant 2.296409e-16 1.000000e+00  
## 189 malignant 5.211226e-11 1.000000e+00  
## 190 benign 9.999991e-01 9.091582e-07  
## 191 malignant 2.460051e-16 1.000000e+00  
## 192 malignant 5.442245e-17 1.000000e+00  
## 193 benign 1.000000e+00 1.349635e-09  
## 194 benign 1.000000e+00 3.456608e-10  
## 195 benign 1.000000e+00 2.043908e-09  
## 196 benign 1.000000e+00 2.806560e-09  
## 197 malignant 1.532801e-09 1.000000e+00  
## 198 benign 9.999994e-01 5.756724e-07  
## 199 benign 1.000000e+00 1.621907e-11  
## 200 benign 1.000000e+00 3.246948e-10  
## 201 malignant 5.705587e-13 1.000000e+00  
## 202 malignant 4.416311e-12 1.000000e+00  
## 203 benign 1.000000e+00 3.456608e-10  
## 204 benign 1.000000e+00 8.495761e-09  
## 205 benign 1.000000e+00 3.456608e-10  
## 206 malignant 5.964001e-15 1.000000e+00  
## 207 malignant 3.244097e-09 1.000000e+00  
## 208 benign 1.000000e+00 1.358910e-10  
## 209 benign 1.000000e+00 1.358910e-10  
## 210 benign 1.000000e+00 3.339972e-09  
## 211 malignant 3.933053e-17 1.000000e+00  
## 212 malignant 2.469056e-12 1.000000e+00  
## 213 benign 1.000000e+00 3.456608e-10  
## 214 malignant 5.565614e-18 1.000000e+00  
## 215 malignant 1.039412e-14 1.000000e+00  
## 216 malignant 1.105786e-12 1.000000e+00  
## 217 benign 1.000000e+00 5.491163e-11  
## 218 benign 1.000000e+00 3.456608e-10  
## 219 malignant 3.907366e-14 1.000000e+00  
## 220 benign 9.999975e-01 2.479608e-06  
## 221 benign 1.000000e+00 2.373849e-09  
## 222 malignant 2.706758e-13 1.000000e+00  
## 223 benign 9.999999e-01 9.531607e-08  
## 224 malignant 4.900957e-10 1.000000e+00  
## 225 malignant 9.144279e-14 1.000000e+00  
## 226 benign 1.000000e+00 5.491163e-11  
## 227 malignant 5.210324e-14 1.000000e+00  
## 228 malignant 2.639025e-08 1.000000e+00  
## 229 benign 1.000000e+00 1.358910e-10  
## 230 malignant 1.997331e-15 1.000000e+00  
## 231 malignant 6.789999e-09 1.000000e+00  
## 232 malignant 1.228026e-12 1.000000e+00  
## 233 malignant 6.806353e-05 9.999319e-01  
## 234 malignant 3.954614e-09 1.000000e+00  
## 235 benign 9.954292e-01 4.570834e-03  
## 237 malignant 2.900019e-13 1.000000e+00  
## 238 malignant 2.402356e-13 1.000000e+00  
## 239 malignant 6.546295e-16 1.000000e+00  
## 240 malignant 5.900855e-09 1.000000e+00  
## 241 benign 9.994429e-01 5.570596e-04  
## 242 benign 1.000000e+00 8.468165e-09  
## 243 benign 1.000000e+00 1.362605e-09  
## 244 benign 9.999995e-01 4.644815e-07  
## 245 benign 1.000000e+00 3.456608e-10  
## 246 benign 9.999994e-01 6.451309e-07  
## 247 malignant 9.819303e-14 1.000000e+00  
## 248 malignant 2.945124e-03 9.970549e-01  
## 249 benign 9.999999e-01 1.204425e-07  
## 251 benign 1.000000e+00 7.637249e-09  
## 252 malignant 1.040463e-10 1.000000e+00  
## 253 malignant 6.952476e-07 9.999993e-01  
## 254 malignant 2.715995e-12 1.000000e+00  
## 255 malignant 1.936957e-09 1.000000e+00  
## 256 malignant 3.014537e-07 9.999997e-01  
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## 668 benign 1.000000e+00 2.043908e-09  
## 669 malignant 9.863031e-08 9.999999e-01  
## 670 malignant 1.920990e-12 1.000000e+00  
## 671 malignant 1.246835e-10 1.000000e+00  
## 672 benign 9.999997e-01 2.799747e-07  
## 673 benign 1.000000e+00 1.362605e-09  
## 674 benign 9.999791e-01 2.086832e-05  
## 675 benign 1.000000e+00 5.491163e-11  
## 676 benign 9.999999e-01 5.851389e-08  
## 677 benign 1.000000e+00 1.296345e-09  
## 678 benign 1.000000e+00 3.986374e-10  
## 679 benign 1.000000e+00 1.621907e-11  
## 680 benign 1.000000e+00 6.393605e-11  
## 681 malignant 2.992541e-18 1.000000e+00  
## 682 malignant 9.270319e-14 1.000000e+00  
## 683 benign 1.000000e+00 1.620411e-08  
## 684 benign 1.000000e+00 1.621907e-11  
## 685 benign 1.000000e+00 1.621907e-11  
## 686 benign 1.000000e+00 1.621907e-11  
## 687 benign 1.000000e+00 1.621907e-11  
## 688 benign 1.000000e+00 8.726444e-09  
## 689 benign 1.000000e+00 1.316892e-10  
## 690 benign 1.000000e+00 3.707041e-10  
## 691 benign 1.000000e+00 1.709281e-10  
## 692 malignant 4.980136e-10 1.000000e+00  
## 693 benign 1.000000e+00 9.590407e-11  
## 694 benign 1.000000e+00 3.578100e-09  
## 695 benign 1.000000e+00 2.752957e-08  
## 696 benign 1.000000e+00 6.393605e-11  
## 697 malignant 5.850816e-12 1.000000e+00  
## 698 malignant 9.334019e-08 9.999999e-01  
## 699 malignant 4.296095e-09 1.000000e+00

length(mynb.pred$Class)

## [1] 0

length(BreastCancer$Class)

## [1] 683

table(mynb.pred$class,BreastCancer$Class)

##   
## benign malignant  
## benign 431 3  
## malignant 13 236

#This model is a neural network classification model.  
library(nnet)  
mynnet <- nnet(Class ~ ., BreastCancer, size=1)

## # weights: 83  
## initial value 447.582951   
## iter 10 value 95.257588  
## iter 20 value 68.783810  
## iter 30 value 64.009485  
## iter 40 value 51.877448  
## iter 50 value 51.410505  
## iter 60 value 51.384843  
## iter 70 value 48.053376  
## iter 80 value 48.028351  
## iter 90 value 48.022562  
## iter 100 value 46.396564  
## final value 46.396564   
## stopped after 100 iterations

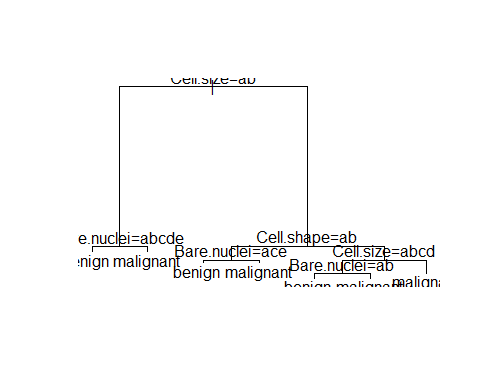
mynnet.pred <- predict(mynnet,BreastCancer,type="class")  
table(mynnet.pred,BreastCancer$Class)

##   
## mynnet.pred benign malignant  
## benign 437 2  
## malignant 7 237

str(mynnet.pred)

## chr [1:683] "benign" "benign" "benign" "benign" "benign" "malignant" ...

library(MASS)  
  
#Here we see a decision tree model for classification, the plot provided helps show the relationships.   
#Decision trees  
library(rpart)  
mytree <- rpart(Class ~ ., BreastCancer)  
plot(mytree); text(mytree) # in "iris\_tree.ps"



summary(mytree)

## Call:  
## rpart(formula = Class ~ ., data = BreastCancer)  
## n= 683   
##   
## CP nsplit rel error xerror xstd  
## 1 0.79079498 0 1.00000000 1.0000000 0.05215335  
## 2 0.05439331 1 0.20920502 0.2468619 0.03071921  
## 3 0.02510460 2 0.15481172 0.1715481 0.02597474  
## 4 0.01255230 3 0.12970711 0.1548117 0.02475192  
## 5 0.01000000 6 0.09205021 0.1506276 0.02443403  
##   
## Variable importance  
## Cell.size Cell.shape Bare.nuclei Epith.c.size Bl.cromatin   
## 21 18 16 15 14   
## Normal.nucleoli Cl.thickness   
## 14 1   
##   
## Node number 1: 683 observations, complexity param=0.790795  
## predicted class=benign expected loss=0.3499268 P(node) =1  
## class counts: 444 239  
## probabilities: 0.650 0.350   
## left son=2 (418 obs) right son=3 (265 obs)  
## Primary splits:  
## Cell.size splits as LLRRRRRRRR, improve=222.3221, (0 missing)  
## Cell.shape splits as LLLRRRRRRR, improve=216.4111, (0 missing)  
## Bare.nuclei splits as LLRRRRRRRR, improve=203.7284, (0 missing)  
## Bl.cromatin splits as LLLRRRRRRR, improve=196.3903, (0 missing)  
## Epith.c.size splits as LLRRRRRRRR, improve=193.1310, (0 missing)  
## Surrogate splits:  
## Cell.shape splits as LLLRRRRRRR, agree=0.917, adj=0.785, (0 split)  
## Epith.c.size splits as LLRRRRRRRR, agree=0.900, adj=0.743, (0 split)  
## Bare.nuclei splits as LLRRRRRRRR, agree=0.880, adj=0.691, (0 split)  
## Normal.nucleoli splits as LLRRRRRRRR, agree=0.877, adj=0.683, (0 split)  
## Bl.cromatin splits as LLLRRRRRRR, agree=0.876, adj=0.679, (0 split)  
##   
## Node number 2: 418 observations, complexity param=0.0251046  
## predicted class=benign expected loss=0.02870813 P(node) =0.6120059  
## class counts: 406 12  
## probabilities: 0.971 0.029   
## left son=4 (410 obs) right son=5 (8 obs)  
## Primary splits:  
## Bare.nuclei splits as LLLLLRRR-R, improve=11.68296, (0 missing)  
## Normal.nucleoli splits as LLLR-RRL-R, improve=11.68296, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=10.32214, (0 missing)  
## Bl.cromatin splits as LLLLR-R---, improve= 8.53307, (0 missing)  
## Epith.c.size splits as LLLRRRRRRR, improve= 4.63208, (0 missing)  
## Surrogate splits:  
## Cl.thickness splits as LLLLLLLLRR, agree=0.988, adj=0.375, (0 split)  
## Normal.nucleoli splits as LLLR-RRL-L, agree=0.988, adj=0.375, (0 split)  
## Mitoses splits as LLRLL-LL-, agree=0.983, adj=0.125, (0 split)  
##   
## Node number 3: 265 observations, complexity param=0.05439331  
## predicted class=malignant expected loss=0.1433962 P(node) =0.3879941  
## class counts: 38 227  
## probabilities: 0.143 0.857   
## left son=6 (23 obs) right son=7 (242 obs)  
## Primary splits:  
## Cell.shape splits as LLRRRRRRRR, improve=20.58158, (0 missing)  
## Cell.size splits as LLLRRRRRRR, improve=18.27650, (0 missing)  
## Bare.nuclei splits as LRRRRRRRRR, improve=16.81493, (0 missing)  
## Bl.cromatin splits as LLRRRRRRRR, improve=13.91034, (0 missing)  
## Marg.adhesion splits as LLRRRRRRRR, improve=11.17148, (0 missing)  
## Surrogate splits:  
## Bl.cromatin splits as LRRRRRRRRR, agree=0.932, adj=0.217, (0 split)  
##   
## Node number 4: 410 observations  
## predicted class=benign expected loss=0.01219512 P(node) =0.6002928  
## class counts: 405 5  
## probabilities: 0.988 0.012   
##   
## Node number 5: 8 observations  
## predicted class=malignant expected loss=0.125 P(node) =0.01171303  
## class counts: 1 7  
## probabilities: 0.125 0.875   
##   
## Node number 6: 23 observations, complexity param=0.0125523  
## predicted class=benign expected loss=0.2173913 P(node) =0.03367496  
## class counts: 18 5  
## probabilities: 0.783 0.217   
## left son=12 (16 obs) right son=13 (7 obs)  
## Primary splits:  
## Bare.nuclei splits as LRLRL----R, improve=4.968944, (0 missing)  
## Bl.cromatin splits as LLLRR-RR--, improve=4.968944, (0 missing)  
## Cl.thickness splits as LLLLRRRRRR, improve=3.381643, (0 missing)  
## Epith.c.size splits as LLRRRRRRRR, improve=1.992754, (0 missing)  
## Cell.shape splits as LRRRRRRRRR, improve=1.397516, (0 missing)  
## Surrogate splits:  
## Bl.cromatin splits as LLLRR-RR--, agree=0.913, adj=0.714, (0 split)  
## Cl.thickness splits as LLLLLRRRRR, agree=0.870, adj=0.571, (0 split)  
## Mitoses splits as LRLR----R, agree=0.870, adj=0.571, (0 split)  
## Marg.adhesion splits as LLLLLLLRRR, agree=0.826, adj=0.429, (0 split)  
## Normal.nucleoli splits as LLRRLL-L--, agree=0.826, adj=0.429, (0 split)  
##   
## Node number 7: 242 observations, complexity param=0.0125523  
## predicted class=malignant expected loss=0.08264463 P(node) =0.3543192  
## class counts: 20 222  
## probabilities: 0.083 0.917   
## left son=14 (68 obs) right son=15 (174 obs)  
## Primary splits:  
## Cell.size splits as LLLLRRRRRR, improve=5.297663, (0 missing)  
## Bare.nuclei splits as LLRRRRRRRR, improve=4.093695, (0 missing)  
## Cell.shape splits as LLLLRRRRRR, improve=2.958548, (0 missing)  
## Bl.cromatin splits as LLLLRLRRRR, improve=2.838336, (0 missing)  
## Marg.adhesion splits as LLLLLRRRRR, improve=2.754821, (0 missing)  
## Surrogate splits:  
## Cell.shape splits as LLLLRRRRRR, agree=0.789, adj=0.250, (0 split)  
## Epith.c.size splits as LLRRRRRRRR, agree=0.777, adj=0.206, (0 split)  
## Marg.adhesion splits as LRRRRRRRRR, agree=0.744, adj=0.088, (0 split)  
## Bl.cromatin splits as LLRRRRRRRR, agree=0.736, adj=0.059, (0 split)  
## Bare.nuclei splits as RRRRRRLRRR, agree=0.723, adj=0.015, (0 split)  
##   
## Node number 12: 16 observations  
## predicted class=benign expected loss=0 P(node) =0.02342606  
## class counts: 16 0  
## probabilities: 1.000 0.000   
##   
## Node number 13: 7 observations  
## predicted class=malignant expected loss=0.2857143 P(node) =0.0102489  
## class counts: 2 5  
## probabilities: 0.286 0.714   
##   
## Node number 14: 68 observations, complexity param=0.0125523  
## predicted class=malignant expected loss=0.25 P(node) =0.09956076  
## class counts: 17 51  
## probabilities: 0.250 0.750   
## left son=28 (14 obs) right son=29 (54 obs)  
## Primary splits:  
## Bare.nuclei splits as LLRRR-RRRR, improve=7.600529, (0 missing)  
## Cl.thickness splits as LLLLLLRRRR, improve=3.558824, (0 missing)  
## Normal.nucleoli splits as LLRRRLLLRR, improve=2.951389, (0 missing)  
## Marg.adhesion splits as LLLLLRRRRR, improve=2.615385, (0 missing)  
## Bl.cromatin splits as LLLLRLLR-R, improve=1.640351, (0 missing)  
##   
## Node number 15: 174 observations  
## predicted class=malignant expected loss=0.01724138 P(node) =0.2547584  
## class counts: 3 171  
## probabilities: 0.017 0.983   
##   
## Node number 28: 14 observations  
## predicted class=benign expected loss=0.2857143 P(node) =0.0204978  
## class counts: 10 4  
## probabilities: 0.714 0.286   
##   
## Node number 29: 54 observations  
## predicted class=malignant expected loss=0.1296296 P(node) =0.07906296  
## class counts: 7 47  
## probabilities: 0.130 0.870

mytree.pred <- predict(mytree,BreastCancer,type="class")  
table(mytree.pred,BreastCancer$Class)

##   
## mytree.pred benign malignant  
## benign 431 9  
## malignant 13 230

#Here is a leave-1-out cross validation model.   
# Leave-1-Out Cross Validation (LOOCV)  
ans <- numeric(length(BreastCancer[,1]))  
for (i in 1:length(BreastCancer[,1])) {  
 mytree <- rpart(Class ~ ., BreastCancer[-i,])  
 mytree.pred <- predict(mytree,BreastCancer[i,],type="class")  
 ans[i] <- mytree.pred  
}  
ans <- factor(ans,labels=levels(BreastCancer$Class))  
table(ans,BreastCancer$Class)

##   
## ans benign malignant  
## benign 430 20  
## malignant 14 219

#This model lis marginally better than the previous model.

#Here is a quadratic discriminant analysis.  
#Quadratic Discriminant Analysis  
library(MASS)  
str(BreastCancer)

## 'data.frame': 683 obs. of 10 variables:  
## $ Cl.thickness : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 5 5 3 6 4 8 1 2 2 4 ...  
## $ Cell.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 4 1 8 1 10 1 1 1 2 ...  
## $ Cell.shape : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 4 1 8 1 10 1 2 1 1 ...  
## $ Marg.adhesion : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 5 1 1 3 8 1 1 1 1 ...  
## $ Epith.c.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 2 7 2 3 2 7 2 2 2 2 ...  
## $ Bare.nuclei : Factor w/ 10 levels "1","2","3","4",..: 1 10 2 4 1 10 10 1 1 1 ...  
## $ Bl.cromatin : Factor w/ 10 levels "1","2","3","4",..: 3 3 3 3 3 9 3 3 1 2 ...  
## $ Normal.nucleoli: Factor w/ 10 levels "1","2","3","4",..: 1 2 1 7 1 7 1 1 1 1 ...  
## $ Mitoses : Factor w/ 9 levels "1","2","3","4",..: 1 1 1 1 1 1 1 1 5 1 ...  
## $ Class : Factor w/ 2 levels "benign","malignant": 1 1 1 1 1 2 1 1 1 1 ...

for (i in 1:ncol(BreastCancer)){  
 BreastCancer[,i] <- as.numeric(BreastCancer[,i])  
}  
BreastCancer$Class <- as.factor(BreastCancer$Class)  
BreastCancer <- data.frame(BreastCancer)  
str(BreastCancer)

## 'data.frame': 683 obs. of 10 variables:  
## $ Cl.thickness : num 5 5 3 6 4 8 1 2 2 4 ...  
## $ Cell.size : num 1 4 1 8 1 10 1 1 1 2 ...  
## $ Cell.shape : num 1 4 1 8 1 10 1 2 1 1 ...  
## $ Marg.adhesion : num 1 5 1 1 3 8 1 1 1 1 ...  
## $ Epith.c.size : num 2 7 2 3 2 7 2 2 2 2 ...  
## $ Bare.nuclei : num 1 10 2 4 1 10 10 1 1 1 ...  
## $ Bl.cromatin : num 3 3 3 3 3 9 3 3 1 2 ...  
## $ Normal.nucleoli: num 1 2 1 7 1 7 1 1 1 1 ...  
## $ Mitoses : num 1 1 1 1 1 1 1 1 5 1 ...  
## $ Class : Factor w/ 2 levels "1","2": 1 1 1 1 1 2 1 1 1 1 ...

myqda <- qda(Class ~ ., BreastCancer)  
myqda.pred <- predict(myqda, BreastCancer)  
table(myqda.pred$class,BreastCancer$Class)

##   
## 1 2  
## 1 422 6  
## 2 22 233

# A regularised Discriminant Analysis  
library(klaR)  
myrda <- rda(Class ~ ., BreastCancer)  
myrda.pred <- predict(myrda, BreastCancer)  
table(myrda.pred$class,BreastCancer$Class)

##   
## 1 2  
## 1 430 6  
## 2 14 233

#Lastly, a random forest.   
#Random Forests  
library(randomForest)

## Warning: package 'randomForest' was built under R version 4.0.3

## randomForest 4.6-14

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

myrf <- randomForest(Class ~ .,BreastCancer)  
myrf.pred <- predict(myrf, BreastCancer)  
table(myrf.pred, BreastCancer$Class)

##   
## myrf.pred 1 2  
## 1 444 0  
## 2 0 239

# myrf.pred setosa versicolor virginica  
# setosa 50 0 0  
# versicolor 0 50 0  
# virginica 0 0 50  
# (Suspiciously correct! - need to read the manual)

#Here we are combining the predictions of each model except mypda.pred. There is some error here and the results without including the model are well enough.   
combine.classes<-data.frame(myrf.pred, myrda.pred$class,#myqda.pred,  
mytree.pred,mynnet.pred,mysvm.pred, mynb.pred$class)  
  
#We take a look at the data.   
head(combine.classes)

## myrf.pred myrda.pred.class mytree.pred mynnet.pred mysvm.pred mynb.pred.class  
## 1 1 1 malignant benign benign benign  
## 2 1 2 malignant benign malignant malignant  
## 3 1 1 malignant benign benign benign  
## 4 1 2 malignant benign malignant malignant  
## 5 1 1 malignant benign benign benign  
## 6 2 2 malignant malignant malignant malignant

head(myrf.pred)

## 1 2 3 4 5 6   
## 1 1 1 1 1 2   
## Levels: 1 2

head(myrda.pred)

## $class  
## [1] 1 2 1 2 1 2 2 1 1 1 1 1 1 1 2 2 1 1 2 1 2 2 1 1 2 1 1 1 1 1 1 2 1 1 1 2 1  
## [38] 2 2 2 2 2 2 1 2 1 1 2 2 1 2 2 2 2 2 2 2 2 2 1 2 2 1 2 1 2 2 1 1 2 1 2 2 1  
## [75] 1 1 1 1 1 1 1 1 2 2 2 2 1 1 1 1 1 1 1 1 1 1 2 2 2 2 1 2 2 2 2 2 1 2 1 2 2  
## [112] 2 1 1 1 2 1 1 1 1 2 2 2 1 2 1 2 1 1 1 2 1 1 1 1 1 1 1 1 2 1 1 2 1 2 2 1 2  
## [149] 2 1 1 2 1 1 2 2 1 1 1 1 2 2 1 1 1 1 1 2 2 2 1 2 1 2 1 1 1 2 2 1 2 2 2 1 2  
## [186] 2 1 1 1 1 2 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 1 2 2 2 1 1 2 1 1 2 1 2 2 1 2 2  
## [223] 1 2 2 2 2 2 1 2 2 2 2 1 1 1 1 1 1 2 2 1 1 2 2 2 2 2 1 1 1 2 2 2 2 2 2 1 2  
## [260] 2 2 1 2 1 2 1 1 1 1 1 2 1 1 2 2 2 2 2 1 2 2 1 1 2 2 2 1 2 2 1 2 1 2 2 1 1  
## [297] 2 1 1 1 2 1 1 2 2 1 2 2 1 2 1 1 2 1 2 2 2 1 1 2 2 1 2 1 1 2 2 1 1 1 2 1 1  
## [334] 1 2 2 1 1 2 2 1 1 1 2 2 2 2 2 1 1 1 1 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1  
## [371] 1 1 2 1 1 1 1 2 1 1 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 2 1 2 1 2 1 1 1 1 2  
## [408] 1 1 1 2 1 2 1 1 1 1 1 1 2 2 2 1 1 1 2 1 1 1 1 1 1 1 1 2 1 1 1 2 1 2 2 2 1  
## [445] 1 1 1 1 1 1 2 2 2 1 1 1 1 1 1 1 1 1 1 1 2 1 1 2 2 1 1 1 2 2 1 1 2 1 2 2 1  
## [482] 1 1 1 1 1 1 1 1 1 1 2 1 1 1 1 1 1 1 2 2 1 1 1 2 1 1 2 2 1 1 1 1 1 1 2 1 1  
## [519] 1 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 2 2  
## [556] 2 2 1 1 2 1 1 1 1 1 1 2 2 1 1 1 2 1 2 1 2 2 2 1 2 1 1 1 1 1 1 1 1 2 2 2 1  
## [593] 1 2 1 2 2 2 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 1 1 1 1 2 1 1 2 1 1 1 1 1 1 1 1  
## [630] 1 1 1 2 1 1 1 1 1 1 1 1 2 2 1 1 1 1 1 1 1 1 1 2 2 2 1 1 1 1 1 1 1 1 1 2 2  
## [667] 1 1 1 1 1 1 1 1 1 2 1 1 1 1 2 2 2  
## Levels: 1 2  
##   
## $posterior  
## 1 2  
## [1,] 1.000000e+00 1.427567e-08  
## [2,] 1.947520e-13 1.000000e+00  
## [3,] 1.000000e+00 4.123055e-09  
## [4,] 3.501914e-14 1.000000e+00  
## [5,] 1.000000e+00 2.258496e-08  
## [6,] 8.057674e-48 1.000000e+00  
## [7,] 3.195278e-03 9.968047e-01  
## [8,] 1.000000e+00 2.144185e-09  
## [9,] 1.000000e+00 3.620704e-08  
## [10,] 1.000000e+00 3.985552e-09  
## [11,] 1.000000e+00 8.629979e-10  
## [12,] 1.000000e+00 4.561139e-10  
## [13,] 9.926815e-01 7.318534e-03  
## [14,] 1.000000e+00 1.248851e-08  
## [15,] 1.662353e-30 1.000000e+00  
## [16,] 3.955623e-05 9.999604e-01  
## [17,] 1.000000e+00 1.714891e-09  
## [18,] 1.000000e+00 3.675464e-09  
## [19,] 7.415920e-25 1.000000e+00  
## [20,] 9.999999e-01 8.823238e-08  
## [21,] 2.075919e-22 1.000000e+00  
## [22,] 6.630427e-26 1.000000e+00  
## [23,] 1.000000e+00 7.011024e-10  
## [24,] 1.000000e+00 1.018453e-09  
## [25,] 6.715594e-05 9.999328e-01  
## [26,] 1.000000e+00 1.400046e-09  
## [27,] 1.000000e+00 6.674808e-09  
## [28,] 1.000000e+00 4.561139e-10  
## [29,] 1.000000e+00 2.843693e-09  
## [30,] 1.000000e+00 5.961758e-10  
## [31,] 1.000000e+00 9.817127e-10  
## [32,] 1.533137e-22 1.000000e+00  
## [33,] 1.000000e+00 1.923370e-09  
## [34,] 1.000000e+00 1.526663e-09  
## [35,] 1.000000e+00 4.561139e-10  
## [36,] 1.073053e-40 1.000000e+00  
## [37,] 9.995326e-01 4.673651e-04  
## [38,] 3.097450e-20 1.000000e+00  
## [39,] 7.976721e-10 1.000000e+00  
## [40,] 1.653203e-07 9.999998e-01  
## [41,] 3.746687e-35 1.000000e+00  
## [42,] 8.027153e-11 1.000000e+00  
## [43,] 2.974638e-40 1.000000e+00  
## [44,] 1.000000e+00 7.157179e-10  
## [45,] 1.906279e-20 1.000000e+00  
## [46,] 1.000000e+00 4.721851e-10  
## [47,] 1.000000e+00 2.258496e-08  
## [48,] 2.808369e-21 1.000000e+00  
## [49,] 2.941191e-09 1.000000e+00  
## [50,] 9.310429e-01 6.895715e-02  
## [51,] 9.003257e-18 1.000000e+00  
## [52,] 7.582679e-28 1.000000e+00  
## [53,] 1.605655e-22 1.000000e+00  
## [54,] 3.737987e-14 1.000000e+00  
## [55,] 2.767582e-29 1.000000e+00  
## [56,] 2.980343e-03 9.970197e-01  
## [57,] 4.761832e-09 1.000000e+00  
## [58,] 2.275638e-04 9.997724e-01  
## [59,] 6.786282e-11 1.000000e+00  
## [60,] 1.000000e+00 1.304424e-09  
## [61,] 7.019593e-34 1.000000e+00  
## [62,] 1.935542e-06 9.999981e-01  
## [63,] 1.000000e+00 4.721851e-10  
## [64,] 2.256937e-10 1.000000e+00  
## [65,] 1.000000e+00 3.675464e-09  
## [66,] 3.399956e-20 1.000000e+00  
## [67,] 1.846402e-32 1.000000e+00  
## [68,] 1.000000e+00 2.209936e-09  
## [69,] 9.999999e-01 5.034638e-08  
## [70,] 1.696168e-36 1.000000e+00  
## [71,] 9.992659e-01 7.341004e-04  
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## [446,] 1.000000e+00 3.121562e-08  
## [447,] 9.999994e-01 5.526119e-07  
## [448,] 9.999998e-01 1.920044e-07  
## [449,] 1.000000e+00 2.821075e-09  
## [450,] 1.000000e+00 1.301790e-09  
## [451,] 2.115188e-36 1.000000e+00  
## [452,] 2.274500e-29 1.000000e+00  
## [453,] 2.528087e-22 1.000000e+00  
## [454,] 1.000000e+00 1.301790e-09  
## [455,] 1.000000e+00 1.041210e-09  
## [456,] 1.000000e+00 5.961758e-10  
## [457,] 9.999998e-01 1.920044e-07  
## [458,] 1.000000e+00 2.697082e-08  
## [459,] 1.000000e+00 1.301790e-09  
## [460,] 1.000000e+00 5.077628e-09  
## [461,] 1.000000e+00 5.310900e-10  
## [462,] 1.000000e+00 2.826095e-09  
## [463,] 1.000000e+00 1.301790e-09  
## [464,] 1.000000e+00 1.178787e-08  
## [465,] 1.532082e-31 1.000000e+00  
## [466,] 1.000000e+00 4.332892e-09  
## [467,] 9.999971e-01 2.903040e-06  
## [468,] 2.064332e-63 1.000000e+00  
## [469,] 2.063624e-38 1.000000e+00  
## [470,] 1.000000e+00 1.095404e-08  
## [471,] 1.000000e+00 2.363839e-08  
## [472,] 1.000000e+00 5.961758e-10  
## [473,] 4.115410e-49 1.000000e+00  
## [474,] 2.398945e-10 1.000000e+00  
## [475,] 9.992001e-01 7.999120e-04  
## [476,] 1.000000e+00 3.561750e-10  
## [477,] 3.129617e-24 1.000000e+00  
## [478,] 1.000000e+00 1.462442e-09  
## [479,] 1.644652e-41 1.000000e+00  
## [480,] 1.012017e-06 9.999990e-01  
## [481,] 1.000000e+00 5.961758e-10  
## [482,] 1.000000e+00 3.004576e-10  
## [483,] 1.000000e+00 3.037754e-09  
## [484,] 1.000000e+00 1.714891e-09  
## [485,] 1.000000e+00 1.714891e-09  
## [486,] 9.999999e-01 8.823238e-08  
## [487,] 1.000000e+00 1.714891e-09  
## [488,] 1.000000e+00 3.337492e-09  
## [489,] 1.000000e+00 3.675464e-09  
## [490,] 1.000000e+00 3.561750e-10  
## [491,] 1.000000e+00 4.777021e-09  
## [492,] 1.155273e-43 1.000000e+00  
## [493,] 1.000000e+00 3.219094e-08  
## [494,] 1.000000e+00 5.077628e-09  
## [495,] 1.000000e+00 3.447802e-10  
## [496,] 1.000000e+00 3.561750e-10  
## [497,] 1.000000e+00 6.674808e-09  
## [498,] 1.000000e+00 5.077628e-09  
## [499,] 1.000000e+00 5.961758e-10  
## [500,] 1.387826e-38 1.000000e+00  
## [501,] 5.684716e-37 1.000000e+00  
## [502,] 1.000000e+00 3.004576e-10  
## [503,] 1.000000e+00 3.992147e-10  
## [504,] 1.000000e+00 2.265717e-09  
## [505,] 4.720535e-23 1.000000e+00  
## [506,] 1.000000e+00 6.901845e-10  
## [507,] 1.000000e+00 2.500892e-09  
## [508,] 1.071117e-11 1.000000e+00  
## [509,] 9.817147e-25 1.000000e+00  
## [510,] 1.000000e+00 7.011024e-10  
## [511,] 1.000000e+00 1.040755e-09  
## [512,] 1.000000e+00 1.301790e-09  
## [513,] 1.000000e+00 3.675464e-09  
## [514,] 9.999995e-01 4.535990e-07  
## [515,] 1.000000e+00 1.462442e-09  
## [516,] 5.330778e-21 1.000000e+00  
## [517,] 1.000000e+00 8.541419e-09  
## [518,] 1.000000e+00 8.629979e-10  
## [519,] 1.000000e+00 7.011024e-10  
## [520,] 1.000000e+00 4.561139e-10  
## [521,] 1.000000e+00 1.568543e-08  
## [522,] 1.000000e+00 1.427567e-08  
## [523,] 1.000000e+00 3.059693e-08  
## [524,] 1.000000e+00 1.714891e-09  
## [525,] 1.000000e+00 4.134166e-08  
## [526,] 1.000000e+00 1.824713e-08  
## [527,] 1.000000e+00 5.310900e-10  
## [528,] 1.000000e+00 4.474053e-08  
## [529,] 1.000000e+00 1.714891e-09  
## [530,] 1.000000e+00 6.967319e-09  
## [531,] 1.000000e+00 6.674808e-09  
## [532,] 3.087870e-49 1.000000e+00  
## [533,] 1.000000e+00 2.916832e-10  
## [534,] 1.000000e+00 4.505952e-10  
## [535,] 1.339005e-20 1.000000e+00  
## [536,] 1.000000e+00 7.011024e-10  
## [537,] 1.000000e+00 1.018453e-09  
## [538,] 9.999999e-01 1.063728e-07  
## [539,] 9.997240e-01 2.760499e-04  
## [540,] 1.000000e+00 5.310900e-10  
## [541,] 6.368600e-01 3.631400e-01  
## [542,] 9.999999e-01 5.479707e-08  
## [543,] 1.000000e+00 3.121562e-08  
## [544,] 1.000000e+00 4.561139e-10  
## [545,] 1.000000e+00 6.674808e-09  
## [546,] 1.000000e+00 1.427567e-08  
## [547,] 1.000000e+00 1.427567e-08  
## [548,] 1.000000e+00 1.018453e-09  
## [549,] 1.000000e+00 7.011024e-10  
## [550,] 1.000000e+00 7.880338e-09  
## [551,] 1.657200e-48 1.000000e+00  
## [552,] 1.000000e+00 3.268289e-09  
## [553,] 1.000000e+00 2.085229e-08  
## [554,] 5.658322e-15 1.000000e+00  
## [555,] 1.914482e-39 1.000000e+00  
## [556,] 3.840069e-30 1.000000e+00  
## [557,] 8.997288e-39 1.000000e+00  
## [558,] 1.000000e+00 7.011024e-10  
## [559,] 1.000000e+00 4.721851e-10  
## [560,] 2.108301e-22 1.000000e+00  
## [561,] 1.000000e+00 3.059693e-08  
## [562,] 1.000000e+00 6.674808e-09  
## [563,] 1.000000e+00 4.721851e-10  
## [564,] 1.000000e+00 4.721851e-10  
## [565,] 1.000000e+00 1.018453e-09  
## [566,] 1.000000e+00 1.435278e-08  
## [567,] 6.150938e-30 1.000000e+00  
## [568,] 3.597068e-33 1.000000e+00  
## [569,] 1.000000e+00 5.310900e-10  
## [570,] 9.999651e-01 3.494028e-05  
## [571,] 1.000000e+00 3.561750e-10  
## [572,] 3.206604e-57 1.000000e+00  
## [573,] 1.000000e+00 1.433034e-08  
## [574,] 2.346975e-22 1.000000e+00  
## [575,] 1.000000e+00 5.077628e-09  
## [576,] 7.992079e-21 1.000000e+00  
## [577,] 1.048011e-21 1.000000e+00  
## [578,] 1.267730e-15 1.000000e+00  
## [579,] 1.000000e+00 1.095404e-08  
## [580,] 7.677836e-19 1.000000e+00  
## [581,] 1.000000e+00 6.674808e-09  
## [582,] 1.000000e+00 3.710788e-09  
## [583,] 9.999999e-01 1.069778e-07  
## [584,] 1.000000e+00 7.011024e-10  
## [585,] 9.999996e-01 4.342301e-07  
## [586,] 1.000000e+00 7.011024e-10  
## [587,] 1.000000e+00 3.992147e-10  
## [588,] 1.000000e+00 1.714891e-09  
## [589,] 2.772986e-20 1.000000e+00  
## [590,] 5.236870e-18 1.000000e+00  
## [591,] 3.636680e-31 1.000000e+00  
## [592,] 1.000000e+00 2.539555e-09  
## [593,] 1.000000e+00 3.561750e-10  
## [594,] 2.196617e-50 1.000000e+00  
## [595,] 1.000000e+00 5.077628e-09  
## [596,] 3.465677e-26 1.000000e+00  
## [597,] 1.248277e-32 1.000000e+00  
## [598,] 1.365284e-64 1.000000e+00  
## [599,] 1.000000e+00 4.111663e-09  
## [600,] 1.000000e+00 3.867380e-10  
## [601,] 1.000000e+00 1.309877e-08  
## [602,] 1.000000e+00 7.011024e-10  
## [603,] 1.000000e+00 1.714891e-09  
## [604,] 1.000000e+00 6.674808e-09  
## [605,] 1.000000e+00 7.011024e-10  
## [606,] 9.751053e-01 2.489468e-02  
## [607,] 9.999948e-01 5.162532e-06  
## [608,] 1.000000e+00 3.561750e-10  
## [609,] 1.000000e+00 1.110040e-08  
## [610,] 9.999993e-01 6.714165e-07  
## [611,] 2.075405e-18 1.000000e+00  
## [612,] 9.999996e-01 3.625310e-07  
## [613,] 1.000000e+00 3.447802e-10  
## [614,] 1.000000e+00 1.301790e-09  
## [615,] 9.999995e-01 5.352861e-07  
## [616,] 1.000000e+00 6.674808e-09  
## [617,] 1.000000e+00 3.561750e-10  
## [618,] 6.073675e-18 1.000000e+00  
## [619,] 1.000000e+00 5.310900e-10  
## [620,] 1.000000e+00 2.403843e-08  
## [621,] 2.284967e-42 1.000000e+00  
## [622,] 9.999973e-01 2.707118e-06  
## [623,] 1.000000e+00 1.301790e-09  
## [624,] 1.000000e+00 3.121562e-08  
## [625,] 1.000000e+00 8.075694e-09  
## [626,] 1.000000e+00 7.011024e-10  
## [627,] 1.000000e+00 7.011024e-10  
## [628,] 1.000000e+00 3.561750e-10  
## [629,] 1.000000e+00 3.447802e-10  
## [630,] 1.000000e+00 7.011024e-10  
## [631,] 1.000000e+00 1.849442e-09  
## [632,] 1.000000e+00 2.270312e-09  
## [633,] 3.335334e-57 1.000000e+00  
## [634,] 1.000000e+00 7.011024e-10  
## [635,] 9.999998e-01 1.723337e-07  
## [636,] 1.000000e+00 7.015088e-09  
## [637,] 1.000000e+00 1.433034e-08  
## [638,] 1.000000e+00 1.714891e-09  
## [639,] 1.000000e+00 1.505826e-09  
## [640,] 1.000000e+00 7.011024e-10  
## [641,] 1.000000e+00 6.674808e-09  
## [642,] 1.491422e-05 9.999851e-01  
## [643,] 3.393665e-28 1.000000e+00  
## [644,] 1.000000e+00 3.561750e-10  
## [645,] 1.000000e+00 4.721851e-10  
## [646,] 1.000000e+00 3.675464e-09  
## [647,] 1.000000e+00 3.745409e-09  
## [648,] 1.000000e+00 3.745409e-09  
## [649,] 1.000000e+00 4.367996e-09  
## [650,] 1.000000e+00 3.561750e-10  
## [651,] 9.999999e-01 7.347182e-08  
## [652,] 1.000000e+00 1.505826e-09  
## [653,] 2.934080e-16 1.000000e+00  
## [654,] 1.522651e-37 1.000000e+00  
## [655,] 3.116717e-27 1.000000e+00  
## [656,] 1.000000e+00 6.806430e-09  
## [657,] 1.000000e+00 9.817127e-10  
## [658,] 9.999998e-01 1.786279e-07  
## [659,] 1.000000e+00 4.721851e-10  
## [660,] 9.999999e-01 5.782057e-08  
## [661,] 1.000000e+00 1.041210e-09  
## [662,] 1.000000e+00 5.077628e-09  
## [663,] 1.000000e+00 3.561750e-10  
## [664,] 1.000000e+00 3.447802e-10  
## [665,] 1.968828e-63 1.000000e+00  
## [666,] 1.279897e-40 1.000000e+00  
## [667,] 1.000000e+00 3.048554e-08  
## [668,] 1.000000e+00 3.561750e-10  
## [669,] 1.000000e+00 3.561750e-10  
## [670,] 1.000000e+00 3.561750e-10  
## [671,] 1.000000e+00 3.561750e-10  
## [672,] 1.000000e+00 5.345951e-09  
## [673,] 1.000000e+00 1.301790e-09  
## [674,] 9.997706e-01 2.293795e-04  
## [675,] 1.000000e+00 2.270312e-09  
## [676,] 8.582291e-22 1.000000e+00  
## [677,] 1.000000e+00 5.310900e-10  
## [678,] 1.000000e+00 1.063270e-09  
## [679,] 1.000000e+00 2.810069e-09  
## [680,] 1.000000e+00 3.447802e-10  
## [681,] 7.962980e-34 1.000000e+00  
## [682,] 5.334273e-18 1.000000e+00  
## [683,] 3.524630e-21 1.000000e+00

#We make sure that the data types will run.  
str(combine.classes)

## 'data.frame': 683 obs. of 6 variables:  
## $ myrf.pred : Factor w/ 2 levels "1","2": 1 1 1 1 1 2 1 1 1 1 ...  
## $ myrda.pred.class: Factor w/ 2 levels "1","2": 1 2 1 2 1 2 2 1 1 1 ...  
## $ mytree.pred : Factor w/ 2 levels "benign","malignant": 2 2 2 2 2 2 2 2 2 2 ...  
## $ mynnet.pred : chr "benign" "benign" "benign" "benign" ...  
## $ mysvm.pred : Factor w/ 2 levels "benign","malignant": 1 2 1 2 1 2 1 1 1 1 ...  
## $ mynb.pred.class : Factor w/ 2 levels "benign","malignant": 1 2 1 2 1 2 1 1 1 1 ...

#Here we start to change each of the predictions by changing it to either 0 or 1.   
combine.classes$myrf.pred<-ifelse(combine.classes$myrf.pred=="benign", 0, 1)  
combine.classes[,2]<-ifelse(combine.classes[,2]=="benign", 0, 1)  
combine.classes[,3]<-ifelse(combine.classes[,3]=="benign", 0, 1)  
combine.classes[,4]<-ifelse(combine.classes[,4]=="benign", 0, 1)  
combine.classes[,5]<-ifelse(combine.classes[,5]=="benign", 0, 1)  
combine.classes[,6]<-ifelse(combine.classes[,6]=="benign", 0, 1)  
  
#Here, we take the majority vote rule by using the rowSums function on the combine.classes.  
majority.vote=rowSums(combine.classes)  
head(majority.vote)

## 1 2 3 4 5 6   
## 3 5 3 5 3 6

#We do the rowSums on the last two columns in the data.frame, this is because their output was slightly different than the other models and as such needed to be   
#treated differently.  
combine.classes[,7]<-rowSums(combine.classes)  
combine.classes[,8]<-ifelse(combine.classes[,7]>=4, "malignant", "benign")  
  
#Here we have the ensemble table.  
table(combine.classes[,8], BreastCancer$Class)

##   
## 1 2  
## benign 430 1  
## malignant 14 238