Oral Cancer Risk Index (OCRI) Test Report

Clinical Information

```
##   DNA_Index  X
## 1  4.707715 NA
## 2  4.106588 NA
## 3  2.408386 NA
## 4  2.393531 NA
## 5  2.380806 NA
## 6  2.353944 NA
```

Name: jjj Sex: o Age: 8 Tel: 000-000-0000 Address: 111 ABC St. City ST 00000 Sample No: 0011 Sampling date: 00/00/0000 Sampling hospital:Some Hospital Sampling physician: Dr. A B OCRI test date: 00/00/0000

```
combino <- params$rda
library(caret)
library(pROC)
library(Metrics)
library(e1071)
library(ranger)
require(compiler)
multiClassSummary <- cmpfun(function (data, lev = NULL, model = NULL)
{
  #Load Libraries
  require(Metrics)
  require(caret)
  #Check data
  if (!all(levels(data[, "pred"]) == levels(data[, "obs"])))
    stop("levels of observed and predicted data do not match")
  #Calculate custom one-vs-all stats for each class
  prob_stats <- lapply(levels(data[, "pred"]), function(class)
  {
    #Grab one-vs-all data for the class
    pred <- ifelse(data[, "pred"] == class, 1, 0)
    obs <- ifelse(data[, "obs"] == class, 1, 0)
    prob <- data[,class]
    #Calculate one-vs-all AUC and logLoss and return
    cap_prob <- pmin(pmax(prob, .000001), .999999)
    prob_stats <- c(auc(obs, prob), logLoss(obs, cap_prob))
    names(prob_stats) <- c("ROC", "logLoss")
    return(prob_stats)
  })
  prob_stats <- do.call(rbind, prob_stats)
  rownames(prob_stats) <- paste( "Class:" , levels(data[, "pred"]))

  #Calculate confusion matrix-based statistics
  CM <- confusionMatrix(data[, "pred"], data[, "obs"])
  #Aggregate and average class-wise stats
  #Todo: add weights
  class_stats <- cbind(CM$byClass, prob_stats)
  class_stats <- colMeans(class_stats)
  #Aggregate overall stats
  overall_stats <- c(CM$overall)
```

```r
  #Combine overall with class-wise stats and remove some stats we don't want
  stats <- c(overall_stats, class_stats)
  stats <- stats[! names(stats) %in% c("AccuracyNull","Prevalence", "Detection Prevalence")]

  #Clean names and return

  names(stats) <- gsub('[[:blank:]] +', '_' , names(stats))
  return(stats)
})

library(ROCR)
set.seed(12345)
inTrainingSet <- createDataPartition(combino$V11, p=.7, list=FALSE)
labelTrain <- combino[ inTrainingSet,]

ctrl <- trainControl(method = "repeatedcv",
                     repeats = 5,
                     summaryFunction = multiClassSummary,
                     classProbs = TRUE)


set.seed(1024)

rfFit <- train(V11 ~ ., data = labelTrain,
               ## training model: svm >>>
               method = "ranger",
               metric = "ROC",
               tuneLength = 10,
               trControl = ctrl)
```

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## note: only 9 unique complexity parameters in default grid. Truncating the grid to 9 .
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## Warning in cbind(CM$byClass, prob_stats): number of rows of result is not a
## multiple of vector length (arg 1)

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## multiple of vector length (arg 1)

## Warning in cbind(CM$byClass, prob_stats): number of rows of result is not a
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## multiple of vector length (arg 1)

## Warning in cbind(CM$byClass, prob_stats): number of rows of result is not a
## multiple of vector length (arg 1)

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## Warning in cbind(CM$byClass, prob_stats): number of rows of result is not a
## multiple of vector length (arg 1)
## Warning in nominalTrainWorkflow(x = x, y = y, wts = weights, info =
## trainInfo, : There were missing values in resampled performance measures.
```

```
peakfunc <- function (x, y){
  return(x[which(diff(sign(diff(y)))==-2)])
}
library(Hmisc)

interval <- c(0.5, 1.5, 2.5, 3.5, 4.5, 5.5, 6.5, 7.5, 8.5, 9.5, 10.5)
interval
```

```
##  [1]  0.5  1.5  2.5  3.5  4.5  5.5  6.5  7.5  8.5  9.5 10.5
```

```
transform1 <- function(bb){
  answers8 <- peakfunc(density(bb$DNA_Index)$x, density(bb$DNA_Index)$y)
  answers8

  interval <- c(0.5, 1.5, 2.5, 3.5, 4.5, 5.5, 6.5, 7.5, 8.5, 9.5, 10.5)
  interval

  matrix2 <- rep(0, 10)
```

```
  z1 <- interval[1:10]
  z2 <- interval[2:11]
  for (i in answers8){
    for (j in 1:10){
      if (i > z1[j] & i < z2[j]){
        matrix2[j] <- matrix2[j] + 1
      }
    }
  }
  matrix2 <- as.data.frame(t(matrix2))
  matrix2$V11 <- "c"
  matrix2$V11 <- as.factor(matrix2$V11)
  matrix2 <- rbind(matrix2, matrix2)
  return(matrix2)
}

plotmatrix2 <- function(bb){
  answers8 <- peakfunc(density(bb$DNA_Index)$x, density(bb$DNA_Index)$y)
  answers8

  interval <- c(0.5, 1.5, 2.5, 3.5, 4.5, 5.5, 6.5, 7.5, 8.5, 9.5, 10.5)
  interval

  matrix2 <- rep(0, 10)
  z1 <- interval[1:10]
  z2 <- interval[2:11]
  for (i in answers8){
    for (j in 1:10){
      if (i > z1[j] & i < z2[j]){
        matrix2[j] <- matrix2[j] + 1
      }
    }
  }
  matrix2 <- as.data.frame(t(matrix2))
  matrix2$V11 <- "c"
  matrix2$V11 <- as.factor(matrix2$V11)
  matrix2 <- rbind(matrix2, matrix2)
  jk <- as.numeric(as.matrix(matrix2[1,1:10]))
  names(jk) = c("0.5-1.5", "1.5-2.5", "2.5-3.5", "3.5-4.5", "4.5-5.5",
                "5.5-6.5", "6.5-7.5", "7.5-8.5", "8.5-9.5", "9.5-10.5")
  barplot(jk, xlab = "intervals", ylab = "peaks")
  text(labels = round(jk, digits = 2), x = seq(0.7, 12, by = 1.2),
       y = rep(1.5, 10))
}

fabaf <- function(bb){
  answers8 <- peakfunc(density(bb$DNA_Index)$x, density(bb$DNA_Index)$y)
  answers8

  interval <- c(0.5, 1.5, 2.5, 3.5, 4.5, 5.5, 6.5, 7.5, 8.5, 9.5, 10.5)
  interval

  matrix2 <- rep(0, 10)
```

```
  z1 <- interval[1:10]
  z2 <- interval[2:11]
  for (i in answers8){
    for (j in 1:10){
      if (i > z1[j] & i < z2[j]){
        matrix2[j] <- matrix2[j] + 1
      }
    }
  }
  matrix2 <- as.data.frame(t(matrix2))
  matrix2$V11 <- "c"
  matrix2$V11 <- as.factor(matrix2$V11)
  matrix2 <- rbind(matrix2, matrix2)
  rfProbs <- predict(rfFit, matrix2, type = "prob")
  return(rfProbs[1,1]*100)

}

suprema <- params$rdaz

rfProbs1 <- predict(rfFit, suprema, type = "prob")
rfProbs1
```

```
##              c           n
## 1   0.86245623 0.1375437693
## 2   0.69401372 0.3059862827
## 3   0.88252897 0.1174710295
## 4   0.95490437 0.0450956321
## 5   0.99626296 0.0037370430
## 6   0.87605167 0.1239483272
## 7   0.87473637 0.1252636341
## 8   0.87749432 0.1225056834
## 9   0.93881163 0.0611883717
## 10  0.99683439 0.0031656145
## 11  0.87833495 0.1216650466
## 12  0.99378677 0.0062132335
## 13  0.98312928 0.0168707154
## 14  0.87182769 0.1281723118
## 15  0.87825990 0.1217400969
## 16  0.86937065 0.1306293521
## 17  0.95422758 0.0457724223
## 18  0.87523913 0.1247608697
## 19  0.99478677 0.0052132335
## 20  0.86749264 0.1325073596
## 21  0.67109098 0.3289090234
## 22  0.68476935 0.3152306456
## 23  0.86651119 0.1334888115
## 24  0.72145996 0.2785400385
## 25  0.94123911 0.0587608903
## 26  0.87121133 0.1287886750
## 27  0.95264661 0.0473533860
## 28  0.88089261 0.1191073931
## 29  0.55900274 0.4409972624
## 30  0.99916800 0.0008320000
```

```
## 31  0.99807933 0.0019206743
## 32  0.86471262 0.1352873779
## 33  0.95918987 0.0408101320
## 34  0.68275404 0.3172459590
## 35  0.66179898 0.3382010201
## 36  0.66196612 0.3380338789
## 37  0.85607748 0.1439225188
## 38  0.67290938 0.3270906246
## 39  0.94978571 0.0502142875
## 40  0.86049017 0.1395098343
## 41  0.98553849 0.0144615144
## 42  0.96961355 0.0303864527
## 43  0.87722410 0.1227759009
## 44  0.99000444 0.0099955602
## 45  0.69481499 0.3051850072
## 46  0.98323027 0.0167697257
## 47  0.95191793 0.0480820682
## 48  0.87986981 0.1201301940
## 49  0.70849467 0.2915053273
## 50  0.96873364 0.0312663611
## 51  0.99916800 0.0008320000
## 52  0.95874887 0.0412511299
## 53  0.65149624 0.3485037618
## 54  0.88973996 0.1102600392
## 55  0.87784877 0.1221512334
## 56  0.69489477 0.3051052289
## 57  0.94995162 0.0500483764
## 58  0.99916800 0.0008320000
## 59  0.64378901 0.3562109916
## 60  0.69645898 0.3035410187
## 61  0.97802428 0.0219757165
## 62  0.95928569 0.0407143143
## 63  0.96075052 0.0392494782
## 64  0.86245623 0.1375437693
## 65  0.87766035 0.1223396534
## 66  0.87869859 0.1213014102
## 67  0.87825990 0.1217400969
## 68  0.87210834 0.1278916614
## 69  0.68194554 0.3180544634
## 70  0.95656645 0.0434335510
## 71  0.87568564 0.1243143625
## 72  0.67675669 0.3232433095
## 73  0.69387157 0.3061284337
## 74  0.80098656 0.1990134423
## 75  0.87535553 0.1246444669
## 76  0.99905479 0.0009452075
## 77  0.97222833 0.0277716736
## 78  0.68951907 0.3104809344
## 79  0.99683439 0.0031656145
## 80  0.95918987 0.0408101320
## 81  0.87192811 0.1280718870
## 82  0.95817839 0.0418216055
## 83  0.95207018 0.0479298244
## 84  0.67643174 0.3235682585
```

```
## 85  0.95809253 0.0419074694
## 86  0.99626296 0.0037370430
## 87  0.69103191 0.3089680854
## 88  0.64981741 0.3501825864
## 89  0.87779603 0.1222039711
## 90  0.98456626 0.0154337367
## 91  0.87882474 0.1211752643
## 92  0.86193026 0.1380697417
## 93  0.87932474 0.1206752643
## 94  0.13431518 0.8656848199
## 95  0.19368020 0.8063198035
## 96  0.10167754 0.8983224649
## 97  0.13519336 0.8648066435
## 98  0.13547441 0.8645255896
## 99  0.10334575 0.8966542456
## 100 0.12931195 0.8706880467
## 101 0.18085775 0.8191422487
## 102 0.13415081 0.8658491851
## 103 0.18085775 0.8191422487
## 104 0.12393168 0.8760683210
## 105 0.13547441 0.8645255896
## 106 0.11811274 0.8818872568
## 107 0.12381403 0.8761859681
## 108 0.20078559 0.7992144129
## 109 0.12624425 0.8737557543
## 110 0.09341474 0.9065852555
## 111 0.12362335 0.8763766519
## 112 0.13960426 0.8603957396
## 113 0.10696260 0.8930374010
## 114 0.10173002 0.8982699840
## 115 0.11263223 0.8873677734
## 116 0.10792925 0.8920707536
## 117 0.10791393 0.8920860670
## 118 0.12330556 0.8766944359
## 119 0.19543020 0.8045698035
## 120 0.10505351 0.8949464919
## 121 0.12378446 0.8762155385
## 122 0.10853158 0.8914684199
## 123 0.09556182 0.9044381814
## 124 0.13314871 0.8668512937
## 125 0.20173967 0.7982603313
## 126 0.12509815 0.8749018473
## 127 0.12467205 0.8753279509
## 128 0.12358662 0.8764133820
## 129 0.10173002 0.8982699840
## 130 0.13415081 0.8658491851
## 131 0.12976774 0.8702322638
## 132 0.11503901 0.8849609937
## 133 0.12498051 0.8750194944
## 134 0.12330556 0.8766944359
## 135 0.11671884 0.8832811594
## 136 0.10737855 0.8926214550
## 137 0.10791393 0.8920860670
## 138 0.12358662 0.8764133820
```

```
## 139 0.11133337 0.8886666259
## 140 0.10749619 0.8925038079
## 141 0.13547441 0.8645255896
## 142 0.10321070 0.8967893002
## 143 0.11430112 0.8856988840
## 144 0.13519336 0.8648066435
## 145 0.10211097 0.8978890316
## 146 0.12976774 0.8702322638
## 147 0.13431518 0.8656848199
## 148 0.11951706 0.8804829443
## 149 0.13431518 0.8656848199
## 150 0.12372099 0.8762790080
## 151 0.13572797 0.8642720346
## 152 0.12976774 0.8702322638
## 153 0.09303379 0.9069662079
## 154 0.11811274 0.8818872568
## 155 0.10739386 0.8926061416
## 156 0.12854959 0.8714504072
## 157 0.12393168 0.8760683210
## 158 0.12455440 0.8754455979
## 159 0.11753687 0.8824631283
## 160 0.11739512 0.8826048818
## 161 0.10942428 0.8905757168
## 162 0.12598862 0.8740113848
## 163 0.19580771 0.8041922868
## 164 0.11016662 0.8898333793
## 165 0.12902304 0.8709769609
## 166 0.10739386 0.8926061416
## 167 0.13110741 0.8688925875
## 168 0.19720317 0.8027968275
## 169 0.12770559 0.8722944123
## 170 0.12498051 0.8750194944
## 171 0.12393168 0.8760683210
## 172 0.59374292 0.4062570831
## 173 0.12467205 0.8753279509
## 174 0.12322904 0.8767709588
## 175 0.12498051 0.8750194944
## 176 0.13110741 0.8688925875
## 177 0.11739512 0.8826048818
## 178 0.11379664 0.8862033642
## 179 0.11739512 0.8826048818
## 180 0.12931195 0.8706880467
## 181 0.12800949 0.8719905142
## 182 0.10522392 0.8947760842
## 183 0.12482483 0.8751751698
## 184 0.12726296 0.8727370377
## 185 0.10696260 0.8930374010
## 186 0.10696260 0.8930374010
## 187 0.10769915 0.8923008480
## 188 0.12482483 0.8751751698
## 189 0.10545290 0.8945470987
## 190 0.12329080 0.8767091998
## 191 0.12498051 0.8750194944
## 192 0.11670712 0.8832928830
```

```
## 193 0.09206909 0.9079309077
## 194 0.10579585 0.8942041544
## 195 0.13519336 0.8648066435
## 196 0.10545290 0.8945470987
## 197 0.13076739 0.8692326136
## 198 0.10497424 0.8950257595
## 199 0.67420507 0.3257949273
## 200 0.11263223 0.8873677734
## 201 0.10853158 0.8914684199
## 202 0.11811274 0.8818872568
## 203 0.11379664 0.8862033642
## 204 0.12582428 0.8741757193
## 205 0.10791393 0.8920860670
## 206 0.11958419 0.8804158079
## 207 0.11133337 0.8886666259
## 208 0.10792925 0.8920707536
## 209 0.18085775 0.8191422487
## 210 0.12901739 0.8709826136
## 211 0.13547441 0.8645255896
## 212 0.87932474 0.1206752643
## 213 0.11753687 0.8824631283
## 214 0.11263223 0.8873677734
## 215 0.10792925 0.8920707536
## 216 0.09303379 0.9069662079
## 217 0.12598862 0.8740113848
## 218 0.11133337 0.8886666259
## 219 0.10853158 0.8914684199
## 220 0.10696260 0.8930374010
## 221 0.19736948 0.8026305178
## 222 0.11263223 0.8873677734
## 223 0.12378446 0.8762155385
## 224 0.11739512 0.8826048818
## 225 0.81160278 0.1883972226
## 226 0.95422758 0.0457724223
## 227 0.12361866 0.8763813416
## 228 0.87844859 0.1215514102
## 229 0.12480952 0.8751904832
## 230 0.12612065 0.8738793521
## 231 0.61165884 0.3883411630
## 232 0.87182769 0.1281723118
## 233 0.82869098 0.1713090228
## 234 0.10993034 0.8900696590
## 235 0.11586865 0.8841313476
## 236 0.86382230 0.1361777004
## 237 0.13297510 0.8670249015
## 238 0.13285838 0.8671416208
## 239 0.12376915 0.8762308519
## 240 0.13541537 0.8645846285
## 241 0.12610533 0.8738946655
## 242 0.10505351 0.8949464919
## 243 0.12370269 0.8762973066
## 244 0.67960288 0.3203971193
## 245 0.87722410 0.1227759009
## 246 0.12358505 0.8764149536
```

```
## 247 0.12482483 0.8751751698
## 248 0.12381403 0.8761859681
## 249 0.12378446 0.8762155385
## 250 0.11753687 0.8824631283
## 251 0.12381403 0.8761859681
## 252 0.95888569 0.0411143143
## 253 0.12329080 0.8767091998
## 254 0.11811274 0.8818872568
## 255 0.09556182 0.9044381814
## 256 0.12455440 0.8754455979
## 257 0.79743165 0.2025683496
## 258 0.18085775 0.8191422487
## 259 0.59552917 0.4044708341
## 260 0.61360431 0.3863956883
## 261 0.68674325 0.3132567492
## 262 0.12467205 0.8753279509
## 263 0.12598862 0.8740113848
## 264 0.10792925 0.8920707536
## 265 0.20173967 0.7982603313
## 266 0.11133337 0.8886666259
## 267 0.66429331 0.3357066880
## 268 0.20078559 0.7992144129
## 269 0.12446990 0.8755301014
## 270 0.13415081 0.8658491851
## 271 0.12509815 0.8749018473
## 272 0.11739512 0.8826048818
## 273 0.69323784 0.3067621577
## 274 0.12916459 0.8708354107
## 275 0.10791393 0.8920860670
## 276 0.12467205 0.8753279509
## 277 0.94995162 0.0500483764
```

```
ploty1 <- function(bb){

  answers8 <- peakfunc(density(bb$DNA_Index)$x, density(bb$DNA_Index)$y)
  answers8

  interval <- c(0.5, 1.5, 2.5, 3.5, 4.5, 5.5, 6.5, 7.5, 8.5, 9.5, 10.5)
  interval

  matrix2 <- rep(0, 10)
  z1 <- interval[1:10]
  z2 <- interval[2:11]
  for (i in answers8){
    for (j in 1:10){
      if (i > z1[j] & i < z2[j]){
        matrix2[j] <- matrix2[j] + 1
      }
    }
  }
  matrix2 <- as.data.frame(t(matrix2))
  matrix2$V11 <- "c"
  matrix2$V11 <- as.factor(matrix2$V11)
  matrix2 <- rbind(matrix2, matrix2)
```

```
  rfProbs <- predict(rfFit, matrix2, type = "prob")

  par(mfrow=c(1,2), pin = c(2,2))
  labels <- c(rep("OSCC", 93), rep("Normal", 102), rep("OLK", 82))
  dts <- c(rfProbs1$c)
  dt2plot <- as.data.frame (list (lab = labels, dt = dts))
  boxplot(dt ~ lab, data = dt2plot, ylab = "OCRI", outline = FALSE,ylim = c(0,1))
  stripchart(dt ~ lab, vertical = TRUE, data = dt2plot
             , add = TRUE, pch = 20, col = "green")
  if(rfProbs[1,1] > 0.5){
    plot(rfProbs[1,1], ylim = c(0,1), xaxt='n', xlab = "Patient", ylab = "OCRI", col = "red", pch = 20)
  }
  else{
    plot(rfProbs[1,1], ylim = c(0,1), xaxt='n', xlab = "Patient", ylab = "OCRI", col = "blue", pch = 20)
  }
}

ploty2 <- function(bb){

  answers8 <- peakfunc(density(bb$DNA_Index)$x, density(bb$DNA_Index)$y)
  #answers8

  interval <- c(0.5, 1.5, 2.5, 3.5, 4.5, 5.5, 6.5, 7.5, 8.5, 9.5, 10.5)
  #interval

  matrix2 <- rep(0, 10)
  z1 <- interval[1:10]
  z2 <- interval[2:11]
  for (i in answers8){
    for (j in 1:10){
      if (i > z1[j] & i < z2[j]){
        matrix2[j] <- matrix2[j] + 1
      }
    }
  }
  matrix2 <- as.data.frame(t(matrix2))
  matrix2$V11 <- "c"
  matrix2$V11 <- as.factor(matrix2$V11)
  matrix2 <- rbind(matrix2, matrix2)
  rfProbs <- predict(rfFit, matrix2, type = "prob")


  if(rfProbs[1,1] > 0.5){
    plot(rfProbs[1,1], ylim = c(0,1), xaxt='n', xlab = "Patient", ylab = "OCRI", type='n')
    text(1,rfProbs[1,1],label=rfProbs[1,1],col='red')
  }
  else{
    plot(rfProbs[1,1], ylim = c(0,1), xaxt='n', xlab = "Patient", ylab = "OCRI", type='n')
    text(1,rfProbs[1,1],label=rfProbs[1,1],col='blue')
  }
}
```