

Imbalanced classification

Minería de datos: aspectos avanzados

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The slide features a white background with a large yellow triangle on the right side and two overlapping orange triangles at the bottom left.

1 Introduction

In this report, the problem of imbalanced classification will be addressed. In the first section, we will show a typical workflow to solve the imbalance classification problem, using the dataset *Subclus*. This dataset is an artificially generated two dimensional dataset whose positive class is grouped in a few small subgroups. In the second section, the performance of some SMOTE-based oversampling methods will be tested over that same dataset. Finally, in the third section, we will dig deeper in the classic version of SMOTE, trying to understand how the solution of the problem is influenced by its parameters.

2 Standard imbalanced classification pipeline

In this section, a classical pipeline of imbalanced classification will be shown. We begin by loading the dataset and renaming the variables properly:

```
## Dataset loading and column names setting
dataset <- read.csv("subclus.csv")
colnames(dataset) <- c("Att1", "Att2", "Class")
dataset$Class <- relevel(dataset$Class, "positive")
```

At first, we are interested in knowing about the dataset (variables, types, dimensions...):

```
## DATASET SUMMARY
## Dimensions
dim(dataset)
```

```
## [1] 599    3
```

```
## Structure and type
str(dataset)
```

```
## 'data.frame':    599 obs. of  3 variables:
## $ Att1 : int  187 290 194 204 196 201 289 116 199 174 ...
## $ Att2 : int   34 -57 -80 89 -81 -17 4 -95 38 33 ...
## $ Class: Factor w/ 2 levels "positive","negative": 1 1 1 1 1 1 1 1 1 1 ...
```

```
## First rows of the data
kable(head(dataset))
```

Att1	Att2	Class
187	34	positive
290	-57	positive
194	-80	positive
204	89	positive
196	-81	positive
201	-17	positive

```
## Class levels
levels(dataset$Class)
```

```
## [1] "positive" "negative"
```

As we can see in the output of previous commands, our dataset is composed of 599 examples of 3 variables (two numeric and the class). It is a binary classification problem, with classes named *negative* and *positive*.

```
## Columns summarization
summary(dataset)
```

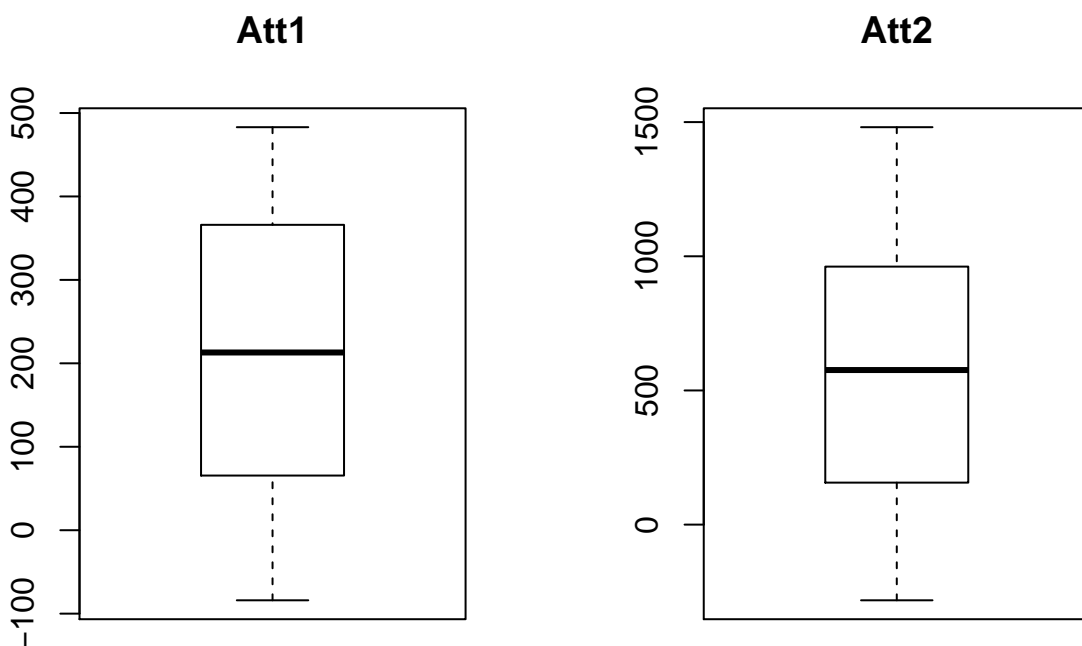
```
##      Att1      Att2      Class
##  Min.   :-84.0   Min.   :-282.0   positive: 99
## 1st Qu.: 65.5   1st Qu.: 156.5   negative:500
## Median :213.0   Median : 576.0
## Mean   :214.2   Mean    : 575.3
## 3rd Qu.:366.0   3rd Qu.: 961.5
## Max.   :483.0   Max.    :1481.0
```

```
## Imbalance ratio  
imbalanceRatio(dataset)
```

```
## [1] 0.198
```

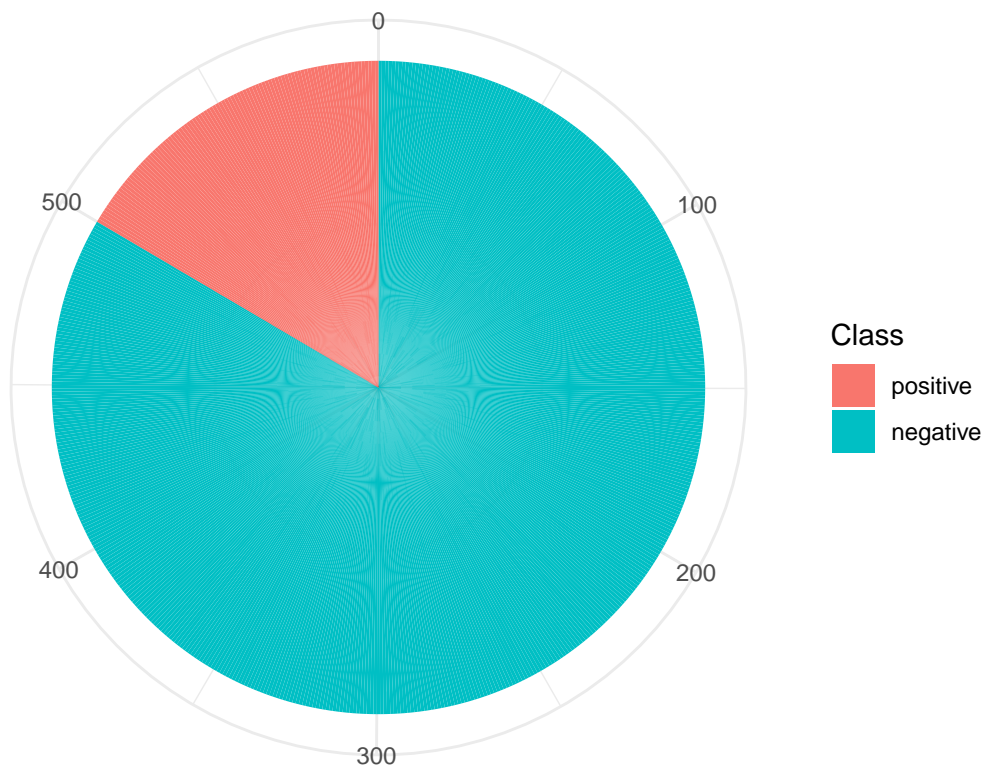
The imbalance ratio of the dataset is not very pronounced (approximately 1 to 5). It is far from the 1 to 40 that we had in other examples. However, it is important enough to be addressed as an imbalanced dataset. Now, we will try and visualize the data. We begin with a boxplot of the attributes and a piechart of the classes distribution:

```
## Dataset visualization  
x <- dataset[,1:2]  
y <- dataset[,3]  
  
## Attributes boxplot  
par(mfrow=c(1,2))  
out <- sapply(1:2, function(i) boxplot(x[,i], main=names(dataset)[i]))
```



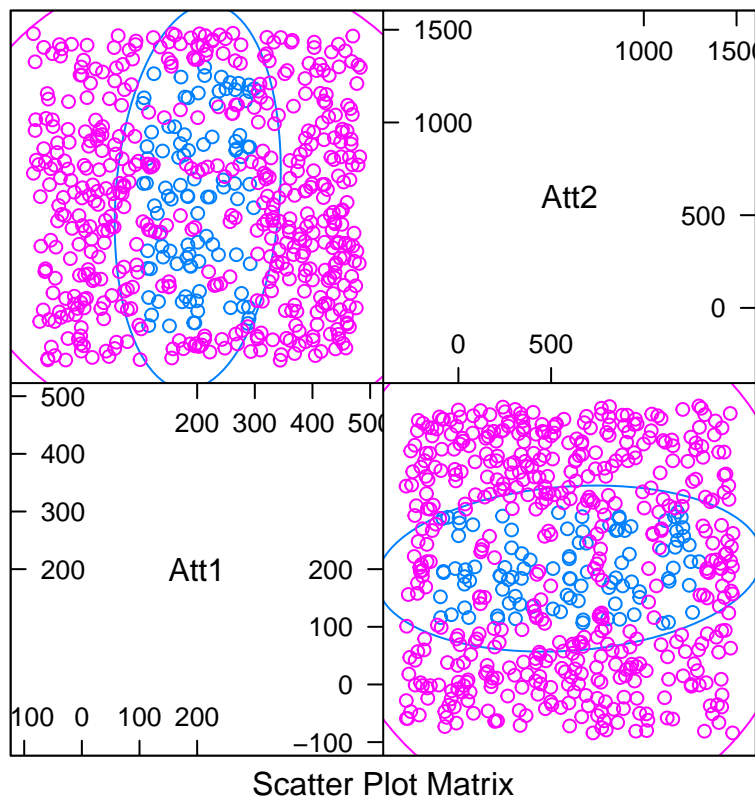
The data distribution along the variables is slightly different. The second attribute is much sparser than the first, with a range three times bigger.

```
## Classes piechart
ggplot(dataset, aes(x="", y=1, fill=Class))+
  geom_bar(width = 1, stat = "identity")+
  coord_polar("y", start=0)+ theme_minimal()+
  theme(axis.title.x=element_blank(), axis.title.y = element_blank())
```

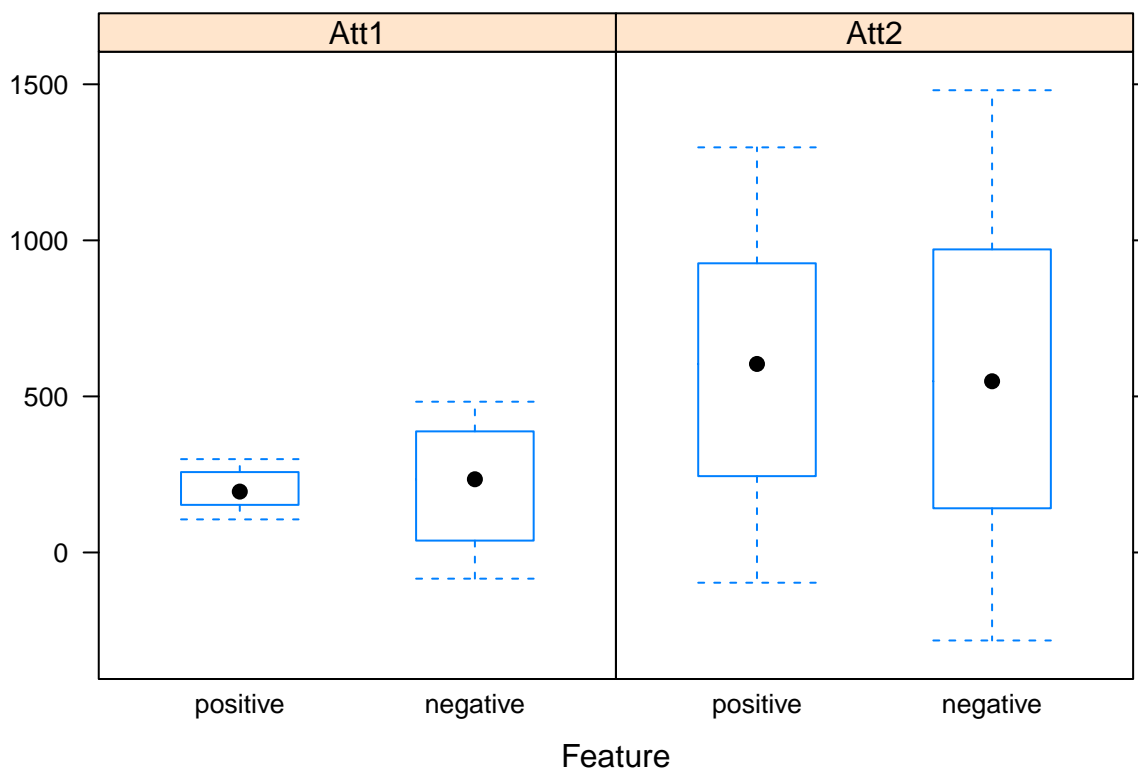


As we said before, in the chart can be seen that there are approximately 5 times more data in the negative class than in the positive one. Now, we will plot the data in

```
## Scatterplot
featurePlot(x=x, y=y, plot="ellipse")
```



```
## Per class boxplot  
featurePlot(x=x, y=y, plot="box")
```



```
set.seed(42) #To ensure the same output
```

```
## An easy way to create split "data partitions":
trainIndex <- createDataPartition(dataset$Class, p = .75,
                                   list = FALSE,
                                   times = 1)
trainData <- dataset[ trainIndex,]
testData  <- dataset[ -trainIndex,]
```

```
## Check IR to ensure a stratified partition
imbalanceRatio(trainData)
```

```
## [1] 0.2
```

```
imbalanceRatio(testData)
```

```
## [1] 0.192
```

```

learn_model <-function(dataset, ctrl, message){
  model.fit <- train(Class ~ ., data = dataset, method = "knn",
    trControl = ctrl, preProcess = c("center","scale"),
    metric="ROC", tuneGrid = expand.grid(k =
      ↪ c(1,3,5,7,9,11)))
  model.pred <- predict(model.fit,newdata = dataset)
  ## Get the confusion matrix to see accuracy value and other parameter
  ↪ values
  model.cm <- confusionMatrix(model.pred, dataset$Class,positive =
  ↪ "positive")
  model.probs <- predict(model.fit,newdata = dataset, type="prob")
  model.roc <- roc(dataset$Class,model.probs[, "positive"],color="green")
  return(model.fit)
}

test_model <-function(dataset, model.fit,message){
  model.pred <- predict(model.fit,newdata = dataset)
  #Get the confusion matrix to see
  ↪ accuracy value and other
  ↪ parameter values
  model.cm <- confusionMatrix(model.pred, dataset$Class,positive =
  ↪ "positive")
  print(model.cm)
  model.probs <- predict(model.fit,newdata = dataset, type="prob")
  model.roc <- roc(dataset$Class,model.probs[, "positive"])
  #print(knn.roc)
  plot(model.roc, type="S", print.thres= 0.5,main=c("ROC
  ↪ Test",message),col="blue")
  #print(paste0("AUC Test
  ↪ ",message, auc(model.roc)))
  return(model.cm)
}

```

```

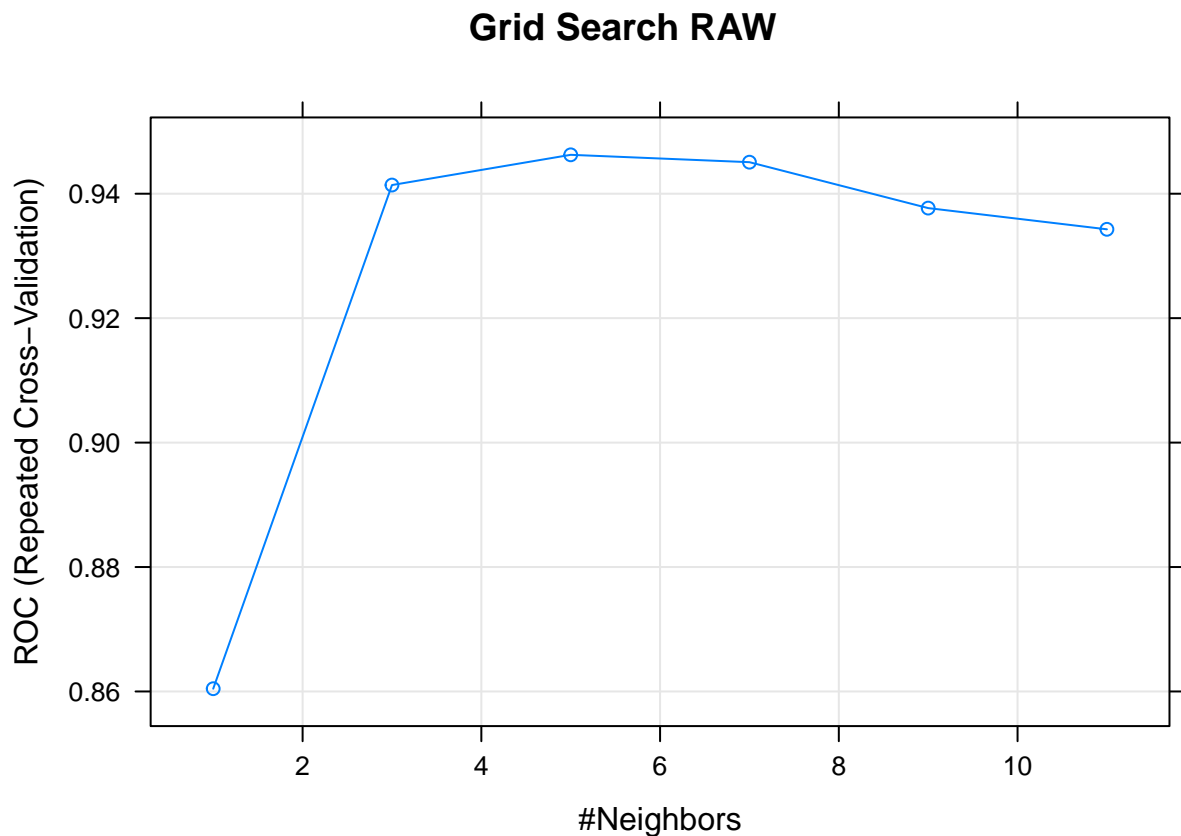
## Execute model ("raw" data)
ctrl <- trainControl(method="repeatedcv",number=5,repeats = 3,
  classProbs=TRUE,summmaryFunction = twoClassSummary)
model.raw <- learn_model(trainData,ctrl,"RAW ")

```

Setting levels: control = positive, case = negative

Setting direction: controls > cases


```
## We may decide to plot the results from the grid search of the  
## model's parameters  
plot(model.raw,main="Grid Search RAW")
```



```
print(model.raw)
```

```
## k-Nearest Neighbors  
##  
## 450 samples  
## 2 predictor  
## 2 classes: 'positive', 'negative'  
##  
## Pre-processing: centered (2), scaled (2)  
## Resampling: Cross-Validated (5 fold, repeated 3 times)  
## Summary of sample sizes: 360, 360, 360, 360, 360, 360, ...  
## Resampling results across tuning parameters:  
##
```

```
##      k   ROC      Sens      Spec
##      1 0.8604444 0.7644444 0.9564444
##      3 0.9413926 0.6977778 0.9502222
##      5 0.9462519 0.6977778 0.9475556
##      7 0.9450667 0.6622222 0.9404444
##      9 0.9376889 0.6488889 0.9288889
##     11 0.9342815 0.6222222 0.9271111
```

```
##
```

```
## ROC was used to select the optimal model using the largest value.
```

```
## The final value used for the model was k = 5.
```

```
cm.raw <- test_model(testData,model.raw,"RAW ")
```

```
## Confusion Matrix and Statistics
```

```
##
```

```
##           Reference
```

```
## Prediction positive negative
```

```
##   positive      14      5
```

```
##   negative     10     120
```

```
##
```

```
##           Accuracy : 0.8993
```

```
##           95% CI : (0.8394, 0.9426)
```

```
##   No Information Rate : 0.8389
```

```
##   P-Value [Acc > NIR] : 0.02414
```

```
##
```

```
##           Kappa : 0.5933
```

```
##
```

```
##   McNemar's Test P-Value : 0.30170
```

```
##
```

```
##           Sensitivity : 0.58333
```

```
##           Specificity : 0.96000
```

```
##   Pos Pred Value : 0.73684
```

```
##   Neg Pred Value : 0.92308
```

```
##           Prevalence : 0.16107
```

```
##   Detection Rate : 0.09396
```

```
##   Detection Prevalence : 0.12752
```

```
##   Balanced Accuracy : 0.77167
```

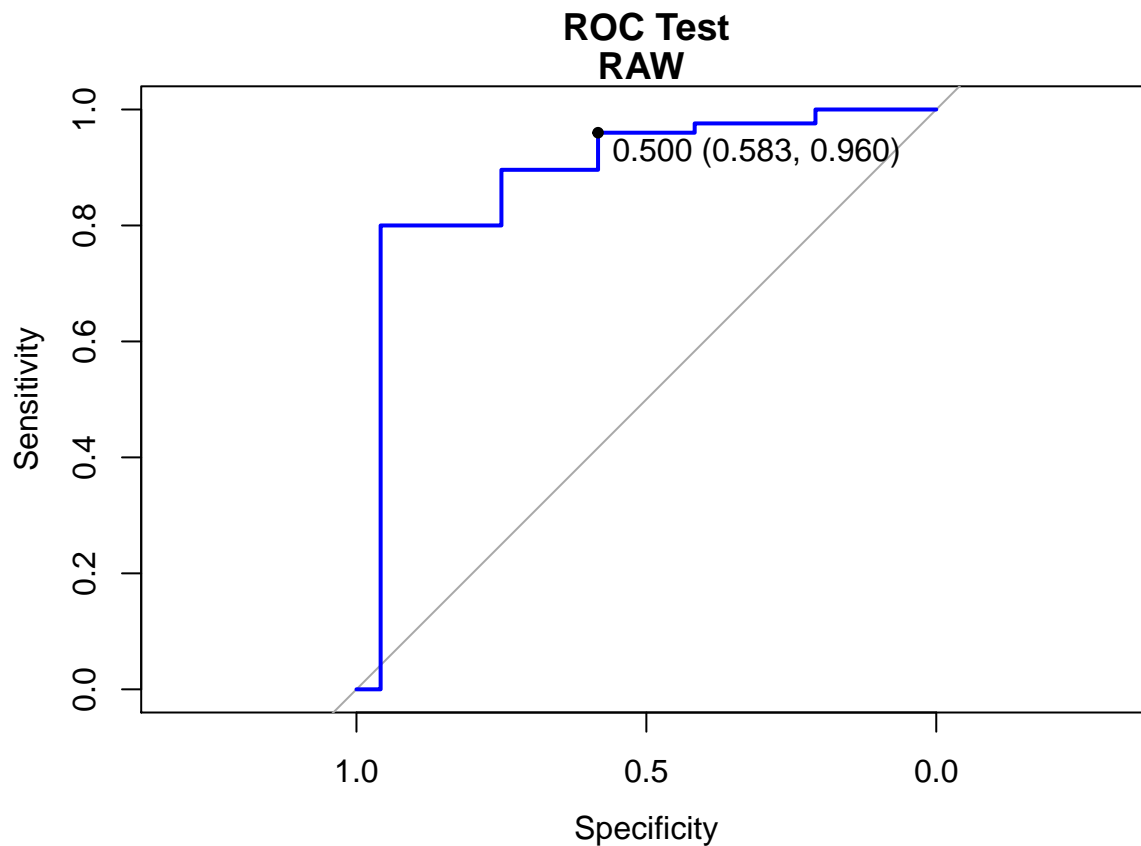
```
##
```

```
##      'Positive' Class : positive
```

```
##
```

```
## Setting levels: control = positive, case = negative
```

```
## Setting direction: controls > cases
```



```
## Execute model ("preprocessed" data)
## Undersampling
ctrl <- trainControl(method="repeatedcv",number=5,repeats = 3,
  classProbs=TRUE,summaryFunction =
    ↪ twoClassSummary,sampling = "down")

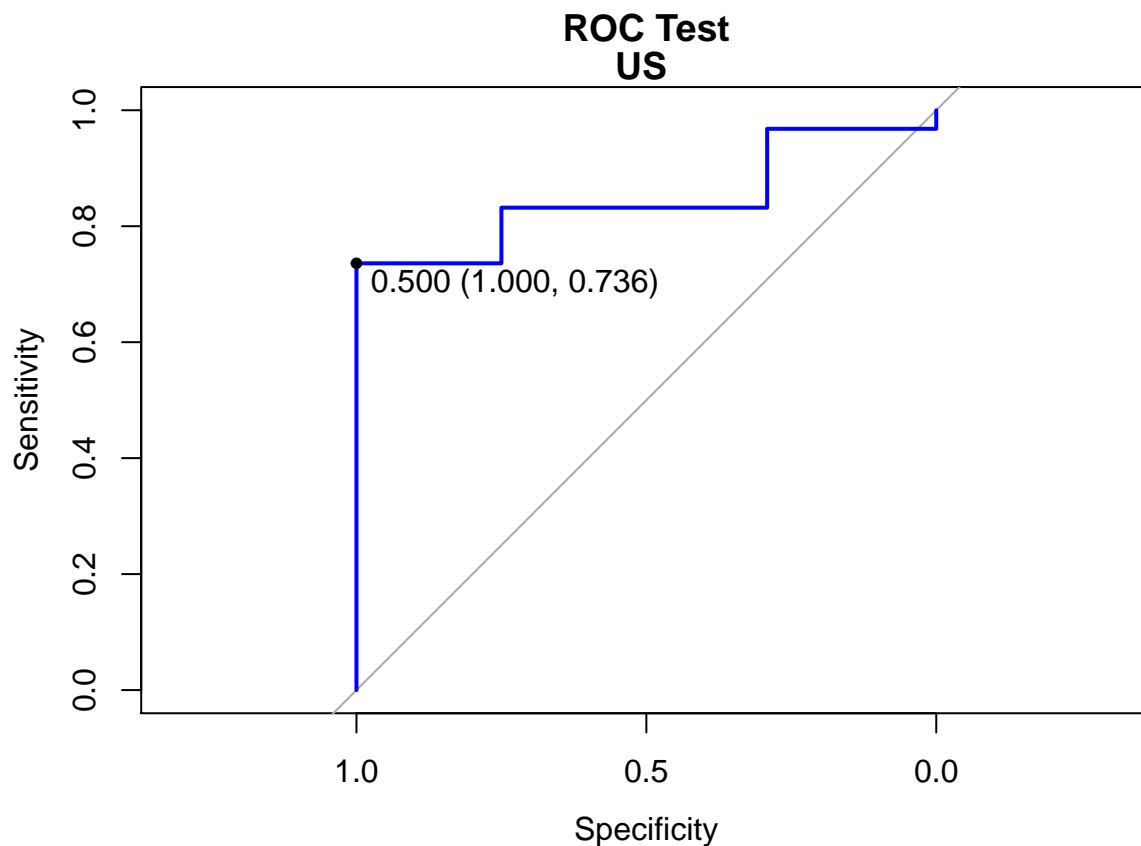
model.us <- learn_model(trainData,ctrl,"US ")
```

```
## Setting levels: control = positive, case = negative
```

```
## Setting direction: controls > cases
```

```
cm.us <- test_model(testData,model.us,"US ")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction positive negative
##   positive      24      33
##   negative       0      92
##
##           Accuracy : 0.7785
##           95% CI : (0.7033, 0.8424)
##   No Information Rate : 0.8389
##   P-Value [Acc > NIR] : 0.9795
##
##           Kappa : 0.4732
##
##  McNemar's Test P-Value : 2.54e-08
##
##           Sensitivity : 1.0000
##           Specificity : 0.7360
##   Pos Pred Value : 0.4211
##   Neg Pred Value : 1.0000
##           Prevalence : 0.1611
##   Detection Rate : 0.1611
##   Detection Prevalence : 0.3826
##   Balanced Accuracy : 0.8680
##
##   'Positive' Class : positive
##
## Setting levels: control = positive, case = negative
## Setting direction: controls > cases
```



```
## Oversampling
ctrl <- trainControl(method="repeatedcv",number=5,repeats = 3,
  classProbs=TRUE,summaryFunction =
    ↪ twoClassSummary,sampling = "up")
model.os <- learn_model(trainData,ctrl,"OS ")
```

```
## Setting levels: control = positive, case = negative
```

```
## Setting direction: controls > cases
```

```
cm.os <- test_model(testData,model.os,"OS ")
```

```
## Confusion Matrix and Statistics
```

```
##
```

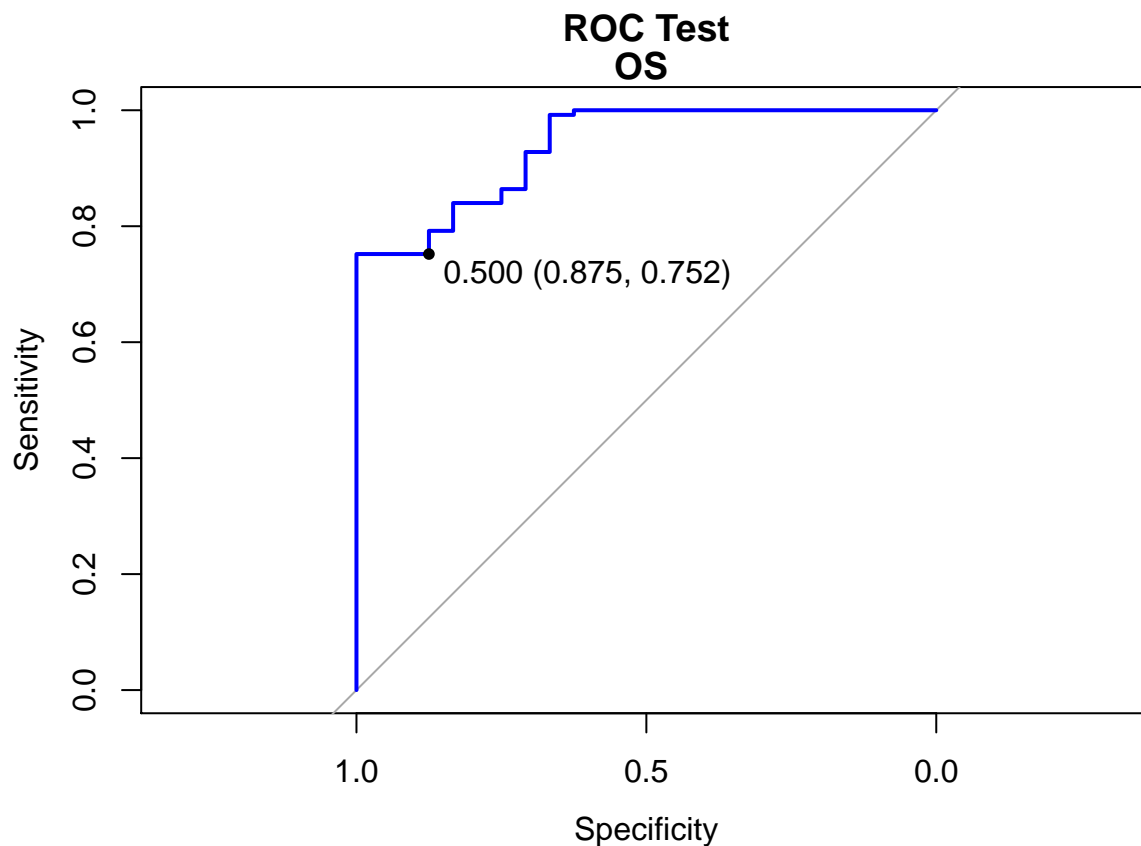
```
##           Reference
```

```
## Prediction positive negative
```

```
## positive           21          31
```

```
##      negative          3          94
##
##              Accuracy : 0.7718
##              95% CI : (0.696, 0.8365)
##      No Information Rate : 0.8389
##      P-Value [Acc > NIR] : 0.9877
##
##              Kappa : 0.4261
##
##      McNemar's Test P-Value : 3.649e-06
##
##              Sensitivity : 0.8750
##              Specificity : 0.7520
##              Pos Pred Value : 0.4038
##              Neg Pred Value : 0.9691
##              Prevalence : 0.1611
##              Detection Rate : 0.1409
##      Detection Prevalence : 0.3490
##      Balanced Accuracy : 0.8135
##
##      'Positive' Class : positive
##

## Setting levels: control = positive, case = negative
## Setting direction: controls > cases
```



```
## SMOTE
ctrl <- trainControl(method="repeatedcv",number=5,repeats = 3,
                     classProbs=TRUE,summaryFunction =
                       ↪ twoClassSummary,sampling = "smote")
model.smt <- learn_model(trainData,ctrl,"SMT ")
```

```
## Loading required package: grid
```

```
## Registered S3 method overwritten by 'xts':
```

```
##   method      from
```

```
##   as.zoo.xts zoo
```

```
## Registered S3 method overwritten by 'quantmod':
```

```
##   method      from
```

```
##   as.zoo.data.frame zoo
```

```
## Setting levels: control = positive, case = negative
```

```
## Setting direction: controls > cases
```

```
cm.smt <- test_model(testData,model.smt,"SMT ")
```

```
## Confusion Matrix and Statistics
```

```
##
```

```
##           Reference
```

```
## Prediction positive negative
```

```
##   positive      22      14
```

```
##   negative       2     111
```

```
##
```

```
##           Accuracy : 0.8926
```

```
##           95% CI : (0.8315, 0.9374)
```

```
##   No Information Rate : 0.8389
```

```
##   P-Value [Acc > NIR] : 0.04215
```

```
##
```

```
##           Kappa : 0.6694
```

```
##
```

```
##   McNemar's Test P-Value : 0.00596
```

```
##
```

```
##           Sensitivity : 0.9167
```

```
##           Specificity : 0.8880
```

```
##   Pos Pred Value : 0.6111
```

```
##   Neg Pred Value : 0.9823
```

```
##           Prevalence : 0.1611
```

```
##   Detection Rate : 0.1477
```

```
##   Detection Prevalence : 0.2416
```

```
##   Balanced Accuracy : 0.9023
```

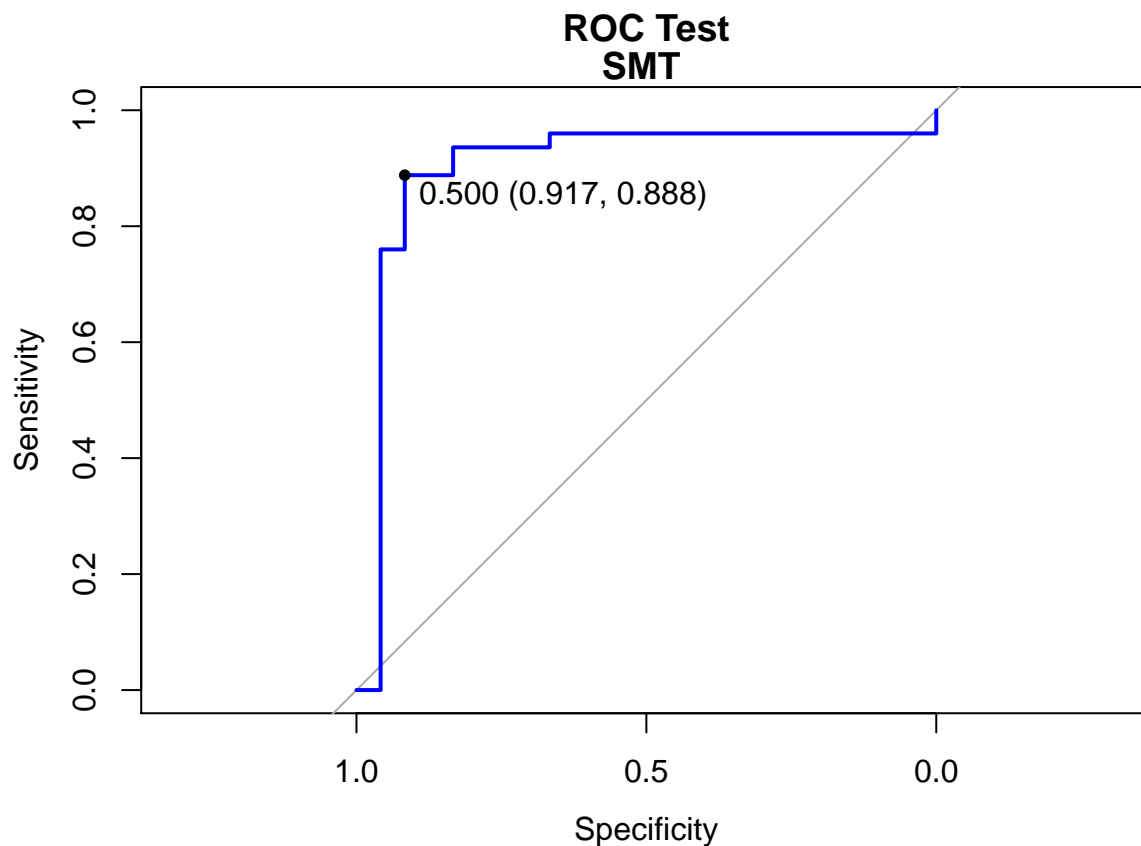
```
##
```

```
##   'Positive' Class : positive
```

```
##
```

```
## Setting levels: control = positive, case = negative
```

```
## Setting direction: controls > cases
```

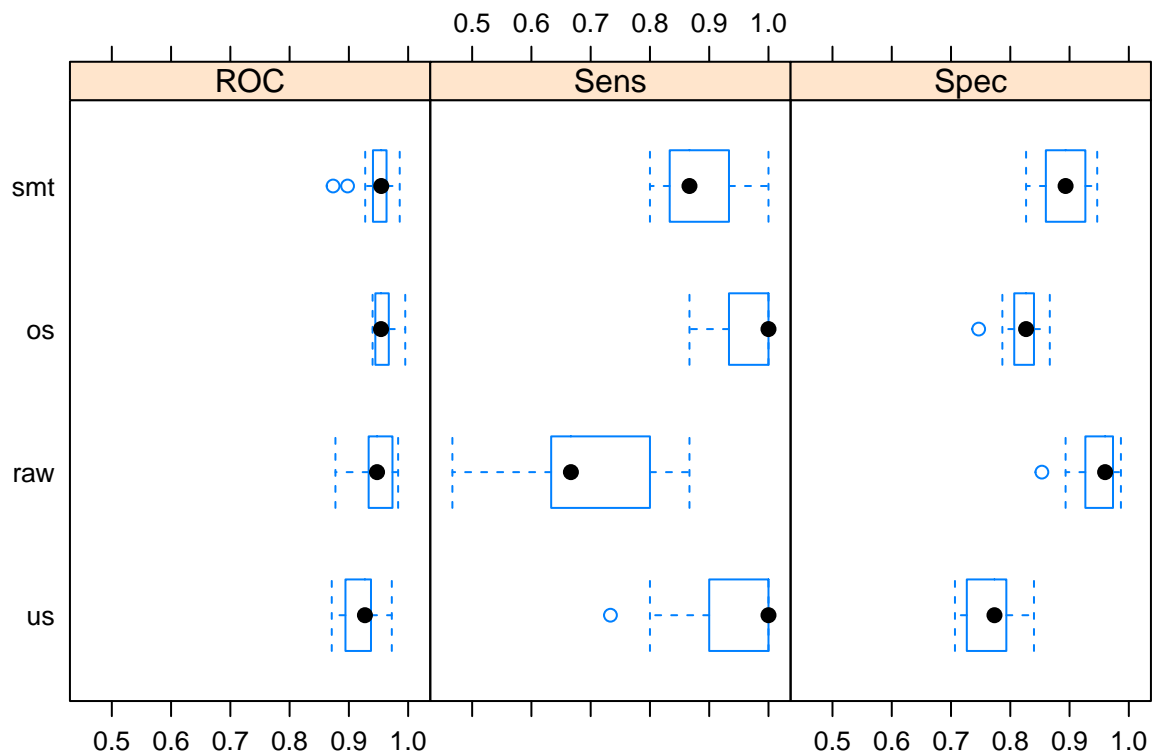
```
## summarize accuracy of models
models <- list(raw = model.raw, us = model.us, os = model.os, smt = model.smt)
results <- resamples(models)
summary(results)
```

```
##
## Call:
## summary.resamples(object = results)
##
## Models: raw, us, os, smt
## Number of resamples: 15
##
## ROC
##           Min.   1st Qu.   Median     Mean   3rd Qu.     Max. NA's
## raw 0.8773333 0.9333333 0.9475556 0.9462519 0.9735556 0.9831111    0
## us  0.8711111 0.8942222 0.9271111 0.9188444 0.9373333 0.9724444    0
## os  0.9400000 0.9446667 0.9542222 0.9590815 0.9673333 0.9951111    0
```

```
## smt 0.8733333 0.9406667 0.9546667 0.9480593 0.9635556 0.9857778    0
##
## Sens
##      Min.   1st Qu.   Median     Mean   3rd Qu.   Max. NA's
## raw 0.4666667 0.6333333 0.6666667 0.6977778 0.8000000 0.8666667    0
## us  0.7333333 0.9000000 1.0000000 0.9333333 1.0000000 1.0000000    0
## os  0.8666667 0.9333333 1.0000000 0.9733333 1.0000000 1.0000000    0
## smt 0.8000000 0.8333333 0.8666667 0.8800000 0.9333333 1.0000000    0
##
## Spec
##      Min.   1st Qu.   Median     Mean   3rd Qu.   Max. NA's
## raw 0.8533333 0.9266667 0.9600000 0.9475556 0.9733333 0.9866667    0
## us  0.7066667 0.7266667 0.7733333 0.7688889 0.7933333 0.8400000    0
## os  0.7466667 0.8066667 0.8266667 0.8222222 0.8400000 0.8666667    0
## smt 0.8266667 0.8600000 0.8933333 0.8915556 0.9266667 0.9466667    0
```

```
## Compare accuracy of models
```

```
bwplot(results)
```



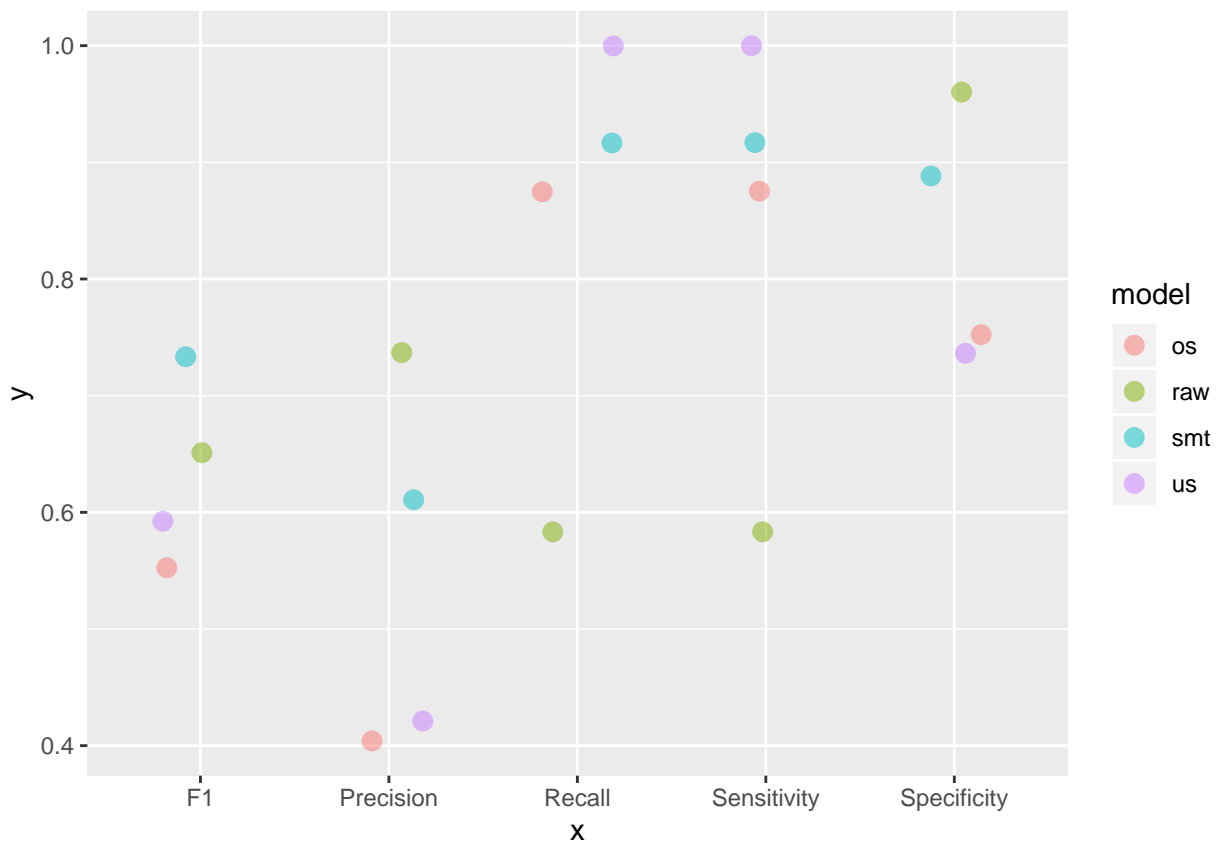
```
#dotplot(results)
```

```
## Carry out a comparison over all imbalanced metrics
comparison <- data.frame(model = names(models),
                        Sensitivity = rep(NA, length(models)),
                        Specificity = rep(NA, length(models)),
                        Precision = rep(NA, length(models)),
                        Recall = rep(NA, length(models)),
                        F1 = rep(NA, length(models)))

for (name in names(models)) {
  cm_model <- get(paste0("cm.", name))

  comparison[comparison$model == name, ] <- filter(comparison, model ==
  ↪ name) %>%
  mutate(Sensitivity = cm_model$byClass["Sensitivity"],
         Specificity = cm_model$byClass["Specificity"],
         Precision = cm_model$byClass["Precision"],
         Recall = cm_model$byClass["Recall"],
         F1 = cm_model$byClass["F1"])
}

comparison %>%
  gather(x, y, Sensitivity:F1) %>%
  ggplot(aes(x = x, y = y, color = model)) +
  geom_jitter(width = 0.2, alpha = 0.5, size = 3)
```



2.1 Package imbalance utilization

```
## Oversampling using classic SMOTE
trainData.smote <- oversample(trainData, ratio=0.4, method="SMOTE")

## TrainControl without
ctrl <- trainControl(method="repeatedcv", number=5, repeats = 3,
                     classProbs=TRUE, summaryFunction = twoClassSummary)

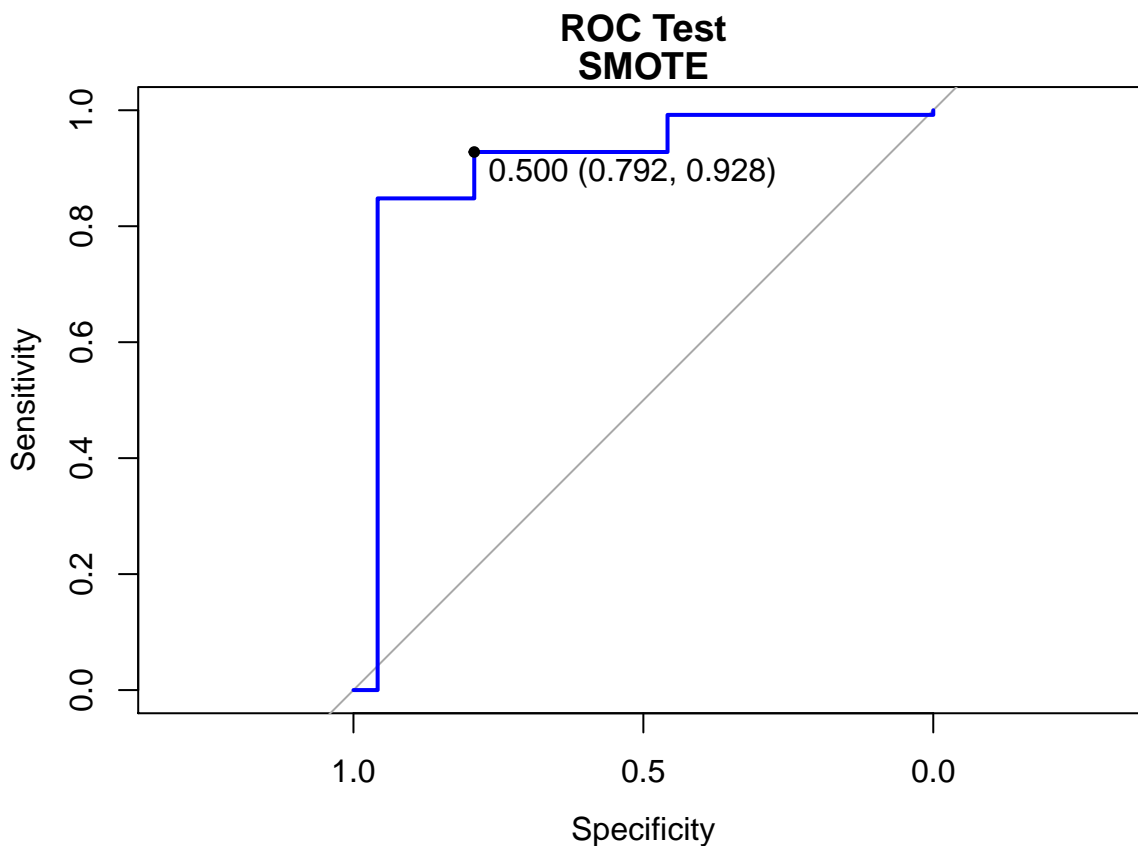
model.smt <- learn_model(trainData.smote, ctrl, "SMOTE")
```

```
## Setting levels: control = positive, case = negative
```

```
## Setting direction: controls > cases
```

```
cm.smt <- test_model(testData, model.smt, "SMOTE")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction positive negative
##   positive      19        9
##   negative       5       116
##
##           Accuracy : 0.906
##           95% CI : (0.8474, 0.9477)
##   No Information Rate : 0.8389
##   P-Value [Acc > NIR] : 0.01295
##
##           Kappa : 0.6743
##
##  McNemar's Test P-Value : 0.42268
##
##           Sensitivity : 0.7917
##           Specificity : 0.9280
##   Pos Pred Value : 0.6786
##   Neg Pred Value : 0.9587
##           Prevalence : 0.1611
##   Detection Rate : 0.1275
##   Detection Prevalence : 0.1879
##   Balanced Accuracy : 0.8598
##
##   'Positive' Class : positive
##
## Setting levels: control = positive, case = negative
## Setting direction: controls > cases
```



```
## Oversampling using classic
trainData.smote <- oversample(trainData, ratio=0.6, method="MWMOTE")

## TrainControl without
ctrl <- trainControl(method="repeatedcv", number=5, repeats = 3,
                     classProbs=TRUE, summaryFunction = twoClassSummary)

model.smt <- learn_model(trainData.smote, ctrl, "SMOTE")
```

```
## Setting levels: control = positive, case = negative
```

```
## Setting direction: controls > cases
```

```
cm.smt <- test_model(testData, model.smt, "SMOTE")
```

```
## Confusion Matrix and Statistics
```

```
##
##           Reference
## Prediction positive negative
##   positive      21      13
##   negative       3     112
##
##           Accuracy : 0.8926
##           95% CI : (0.8315, 0.9374)
##   No Information Rate : 0.8389
##   P-Value [Acc > NIR] : 0.04215
##
##           Kappa : 0.6599
##
##   McNemar's Test P-Value : 0.02445
##
##           Sensitivity : 0.8750
##           Specificity : 0.8960
##           Pos Pred Value : 0.6176
##           Neg Pred Value : 0.9739
##           Prevalence : 0.1611
##           Detection Rate : 0.1409
##           Detection Prevalence : 0.2282
##           Balanced Accuracy : 0.8855
##
##           'Positive' Class : positive
##

## Setting levels: control = positive, case = negative
## Setting direction: controls > cases
```

