RF for TBI

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```
library(ranger)
library(ggplot2)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(sampling)
```

```
## Warning: package 'sampling' was built under R version 4.1.2
```

```
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
```

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

```
tbidata <- read.csv("tbi_flattened.csv")
#  ciTBI and outcome are the same, we only need one.
tbidata <- subset(tbidata,select=-c(ciTBI))
# make age invariant
tbidata <- subset(tbidata,select=-c(GCSEye,GCSVerbal,GCSMotor,FontBulg,Amnesia_verb_0.0,Amnesia_verb_1.0
tbidata$outcome <- as.factor(tbidata$outcome)
# create ID value
tbidata$id = 1:34739

set.seed(2112)
```

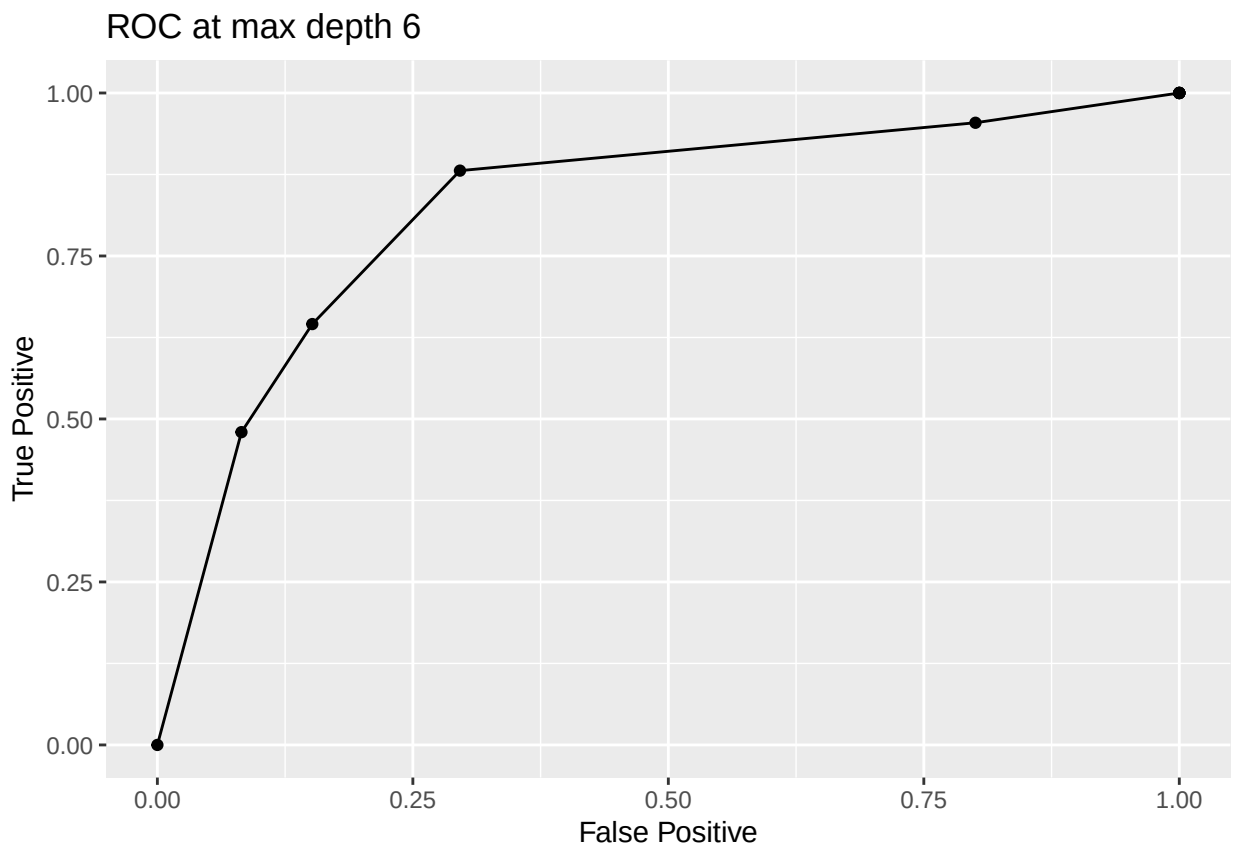
```r
# proportion of overall data that has TBI
p <- mean(tbidata$outcome==1)
# Create our validation set via stratified samples.

stratsample <- function(data,n){
 stratas <- strata(data, c("outcome"),size = c(round(n*(1-p)),round(n*p)), method = "srswor")
 return(getdata(data,stratas)[,1:88])
}

valid <- stratsample(tbidata,4739)
cvdata <- setdiff(tbidata,valid)

# Randomly generate our folds from the remainder of the data:
fold1 <- stratsample(cvdata,10000)
fold23 <- setdiff(cvdata,fold1)
fold2 <- stratsample(fold23,10000)
fold3<- setdiff(fold23,fold2)
fold12 <- rbind(fold1,fold2)
fold13 <- rbind(fold1,fold3)
```

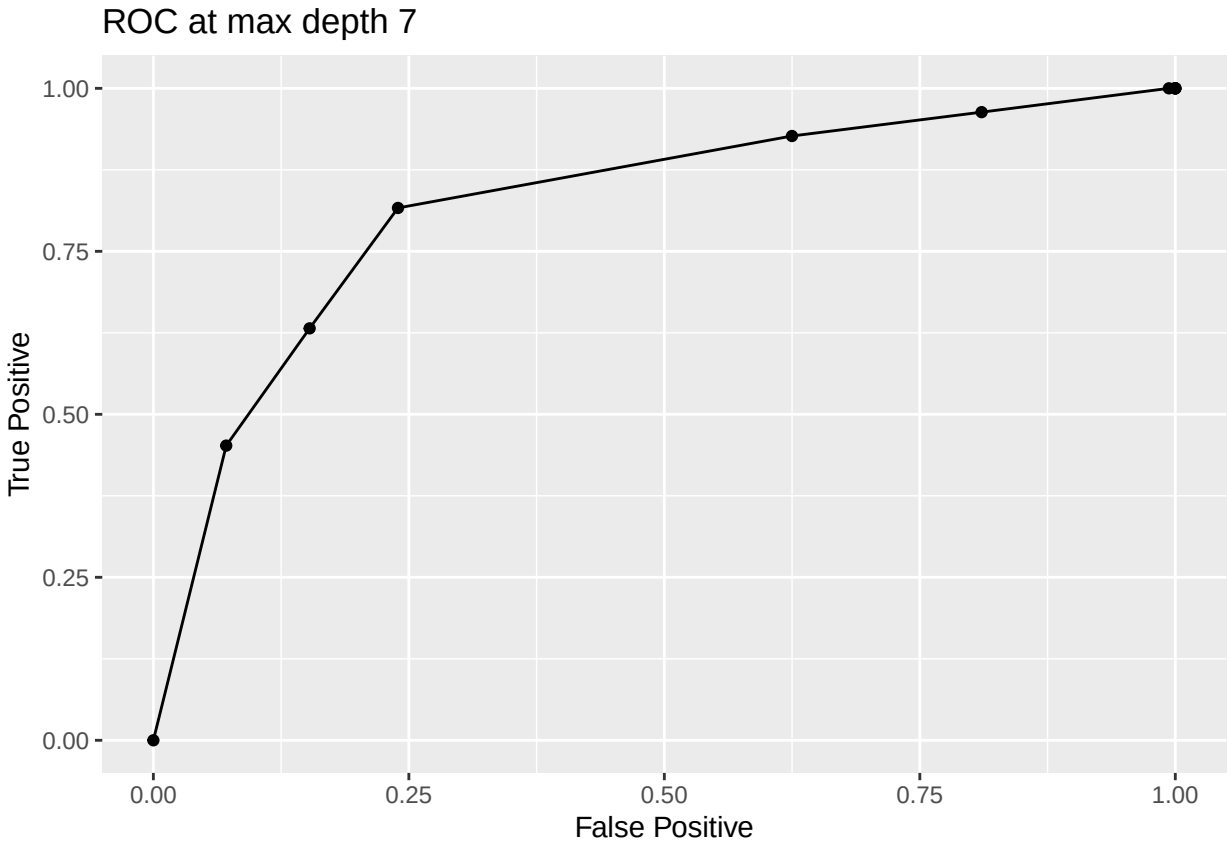
Now that our folds are set up, we can tune our model's hyperparameters. From exploratory work with the forests, we stick with a forest size of 200 trees, as it maintains sufficient accuracy without large computational burdens. Thus, maximum depth would seem to be left as our main hyperparameter of interest.

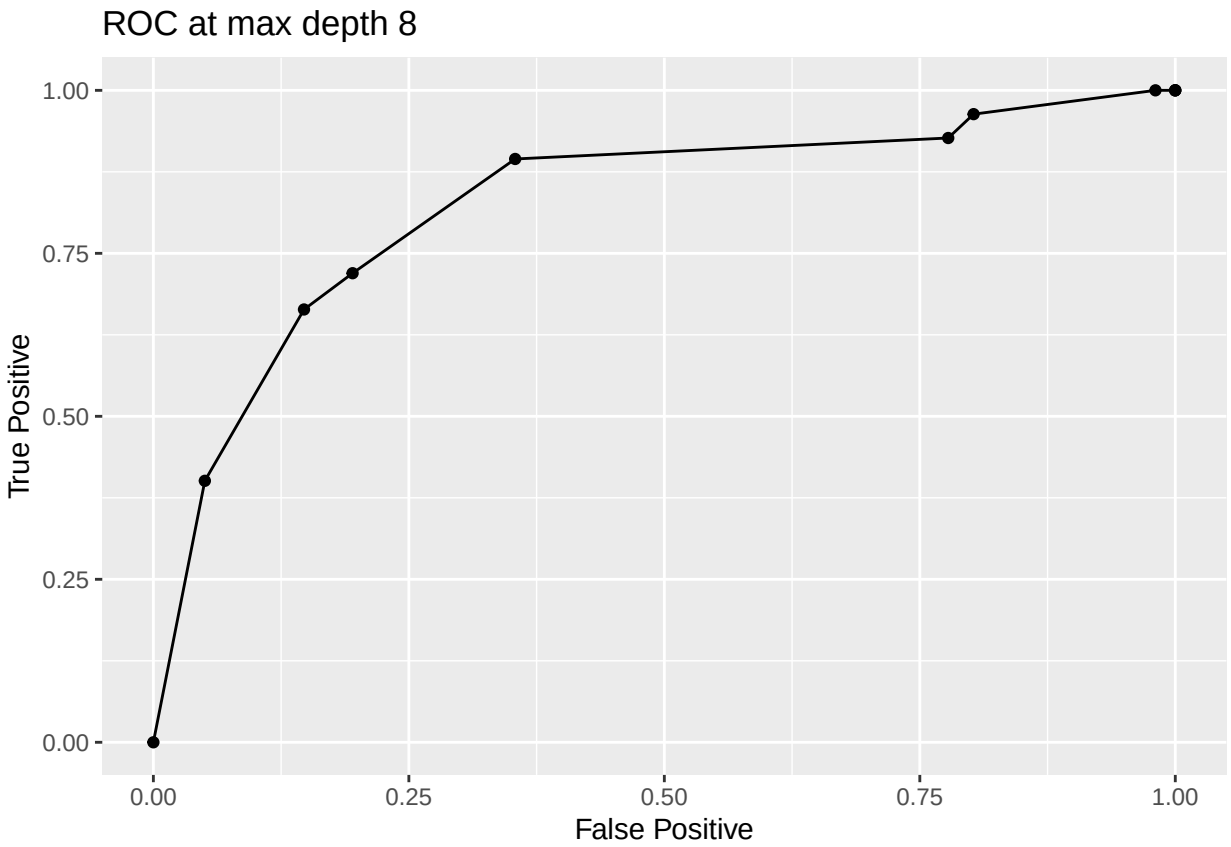
However, due to the unbalanced nature of our outputs (around 0.7% of children have a TBI, the remaining 99.3% do not), simply fitting a random forest classifier would predict non-TBI every single time, and be more than 99% accurate. Thus we need to add a second hyperparameter: that of weight attached to positive results. This will be our main way of tweaking the balance between sensitivity and specificity; the greater the weight of outcome 1, the more false negatives are penalized and the greater the sensitivity of the model. Given TBI's rarity, we use weights ranging from 100 to 1000.

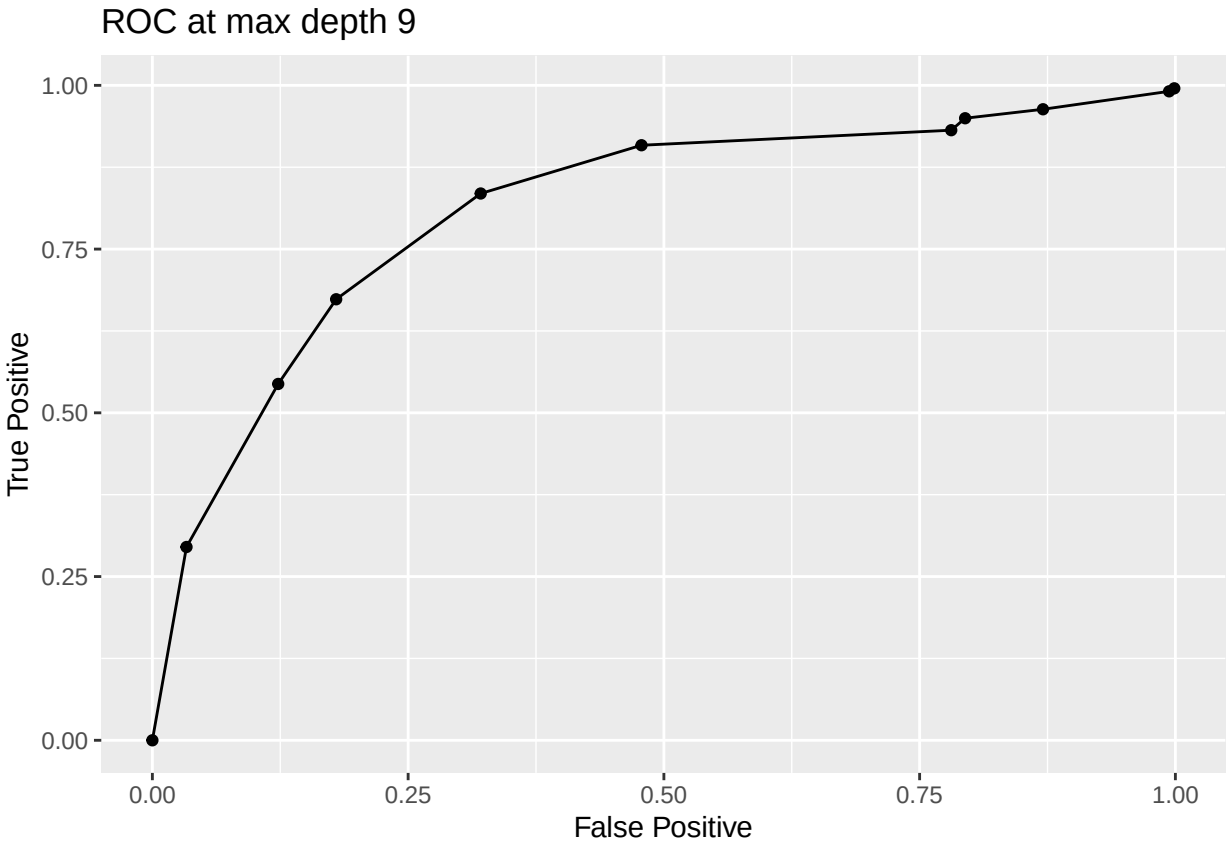
```r
pred_rf_sens <- function(train,test,trees=200,depth=5,weight=1){
  # Gives the sensitivity of a random forest prediction on the TBI data. Increasing the weight of posit
    fit <- ranger(outcome ~ .-Race-Gender-AgeinYears-id, data = train, num.trees=trees, max.depth = dep
    pred <- ranger:::predict.ranger(fit,subset(test,select=c(-Race,-Gender,-AgeinYears,-outcome,-id)))
    return(sum(pred$predictions==test$outcome & test$outcome==1)/sum(test$outcome==1))
}

pred_rf_spec <- function(train,test,trees=200,depth=5,weight=1){
  # As before, but with specificity this time.
    fit <- ranger(outcome ~ .-Race-Gender-AgeinYears-id, data = train, num.trees=trees, max.depth = dep
    pred <- ranger:::predict.ranger(fit,subset(test,select=c(-Race,-Gender,-AgeinYears,-outcome,-id)))
    return(sum(pred$predictions==test$outcome & test$outcome==0)/sum(test$outcome==0))
}

# Function to generate and plot ROC curves for a given max depth.
rocplot <- function(depth){
  sens <- c()
  spec <- c()
  for(i in 0:10){
    # Take sensitivity and specificity for each fold, then average.
    sens1 <- pred_rf_sens(train=fold23,test=fold1,depth=depth,weight=i*100)
    sens2 <- pred_rf_sens(train=fold13,test=fold2,depth=depth,weight=i*100)
    sens3 <- pred_rf_sens(train=fold12,test=fold3,depth=depth,weight=i*100)
```

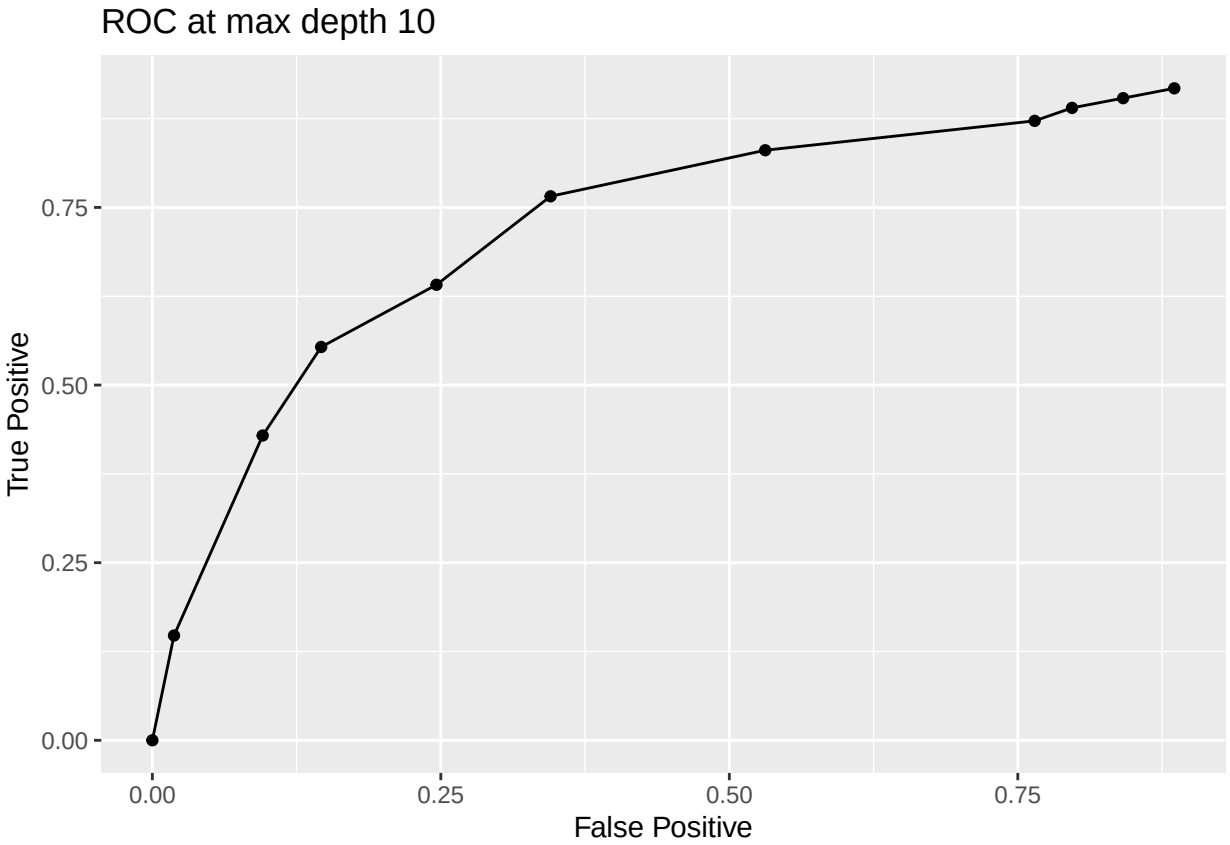
```
    sens <- c(sens,mean(c(sens1,sens2,sens3)))
    spec1 <- pred_rf_spec(train=fold23,test=fold1,depth=depth,weight=i*100)
    spec2 <- pred_rf_spec(train=fold13,test=fold2,depth=depth,weight=i*100)
    spec3 <- pred_rf_spec(train=fold12,test=fold3,depth=depth,weight=i*100)
    spec <- c(spec,mean(c(spec1,spec2,spec3)))
  }
  # Create ROC plot
  print(ggplot(mapping=aes(x=1-spec,y=sens)) + geom_line() + geom_point() + xlab("False Positive") + yla
}

for(i in 6:11){
  rocplot(i)
}
```

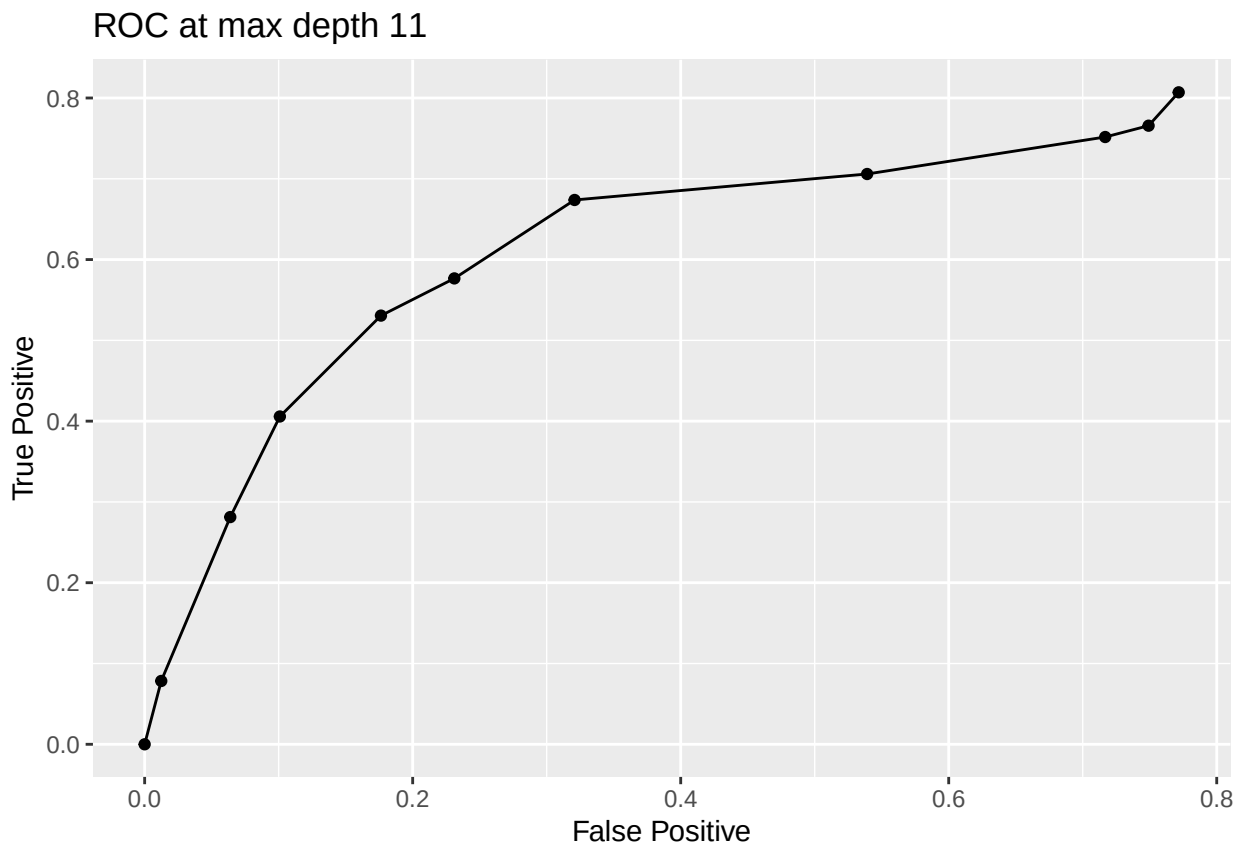



ROC at max depth 7
1.00
0.75
0.50
0.25
0.00
True Positive
0.00
0.25
0.50
0.75
1.00
False Positive


ROC at max depth 8
True Positive
False Positive
0.00
0.25
0.50
0.75
1.00


ROC at max depth 9
1.00
0.75
0.50
0.25
0.00
True Positive
0.00
0.25
0.50
0.75
1.00
False Positive


ROC at max depth 10
True Positive
False Positive
0.00
0.25
0.50
0.75
0.00
0.25
0.50
0.75



Overall, random forest in general does not do as well as other classifiers, with any decent level of sensitivity generally coming alongside a significant amount of false positives. Overall it seems like the best model is depth 8 with weight 400, with a sensitivity around 0.9 and a specificity around 0.65. Let's see how it does on the validation set, and what variables are important:

```
pred_rf_sens(cvdata,valid,depth=8,weight=400)
```

```
## [1] 0.8823529
```

```
pred_rf_spec(cvdata,valid,depth=8,weight=400)
```

```
## [1] 0.5802338
```

```
rf_final <- ranger(outcome ~ .-Race-Gender-AgeinYears-id, data = tbidata, num.trees=200, max.depth = 8,
imp <- importance(rf_final)
head(sort(imp,decreasing=T))
```

```
##          SFxBasHem            ActNorm           AMSSlow           ClavPar
##          1553.0189           631.1648          540.9274          523.3459
##       AMSAgitated SFxPalpDepress_2.0
##          487.7688           465.4740
```

As it turns out, the model's sensitivity goes up to a respectable 97% when applied to the validation set, though its specificity decreases to a still-decent 62%; probably good given that we would rather give an unnecessary test than miss a TBI.

The highest importance factor by far is the basilar hemorrhage, which makes sense given its high prevalence in other classifiers. Other important rules include whether or not the child acts normal, whether they had parietal (scalp) trauma, and whether or not they appeared to be responding slower than normal. Unfortunately, random forests do not give coefficients in the traditional sense, so we cannot exactly determine the direction each predictor's association with TBI goes, but we can infer the direction of most of these splits from domain knowledge and common sense.