Hw12

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11/30/2021

Set up

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.0.2
```

```
## -- Attaching packages ---------------------------------------------------------------------------
```

```
## v ggplot2 3.3.2     v purrr   0.3.4
## v tibble  3.0.1     v dplyr   1.0.2
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.0
```

```
## Warning: package 'ggplot2' was built under R version 4.0.2
```

```
## Warning: package 'tidyr' was built under R version 4.0.2
```

```
## Warning: package 'readr' was built under R version 4.0.2
```

```
## Warning: package 'dplyr' was built under R version 4.0.2
```

```
## Warning: package 'stringr' was built under R version 4.0.2
```

```
## Warning: package 'forcats' was built under R version 4.0.2
```

```
## -- Conflicts ------------------------------------------------------------------------------------
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(palmerpenguins)
```

```
## Warning: package 'palmerpenguins' was built under R version 4.0.2
```

```
library(gridExtra)
```

```
## Warning: package 'gridExtra' was built under R version 4.0.2
```

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

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

```
library(ROCR)
```

```
## Warning: package 'ROCR' was built under R version 4.0.2
```

```
Data<-penguins
##remove penguins with gender missing
```

```
Data<-Data[complete.cases(Data[ , 7]),-c(2,8)]
##80-20 split
set.seed(1)
sample<-sample.int(nrow(Data), floor(.80*nrow(Data)), replace = F)
train<-Data[sample, ]
test<-Data[-sample, ]
head(train)
```

```
## # A tibble: 6 x 6
##   species   bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex
##   <fct>              <dbl>         <dbl>             <int>       <int> <fct>
## 1 Chinstrap           50.2          18.8               202        3800 male
## 2 Gentoo              50.2          14.3               218        5700 male
## 3 Adelie              38.1          17.6               187        3425 female
## 4 Chinstrap           51            18.8               203        4100 male
## 5 Chinstrap           52.7          19.8               197        3725 male
## 6 Gentoo              49.6          16                 225        5700 male
```

1 - A

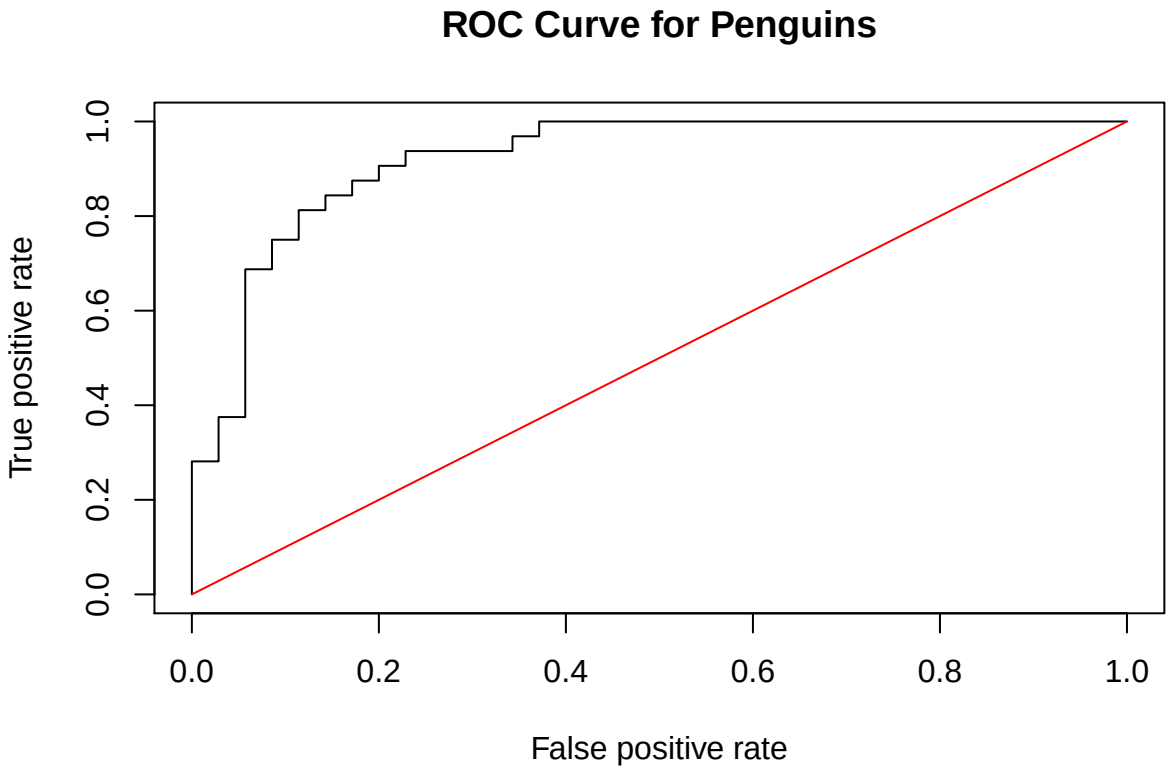
We first need to recreate the model.

```
result<-glm(sex ~ . - flipper_length_mm, family="binomial", data=train)
summary(result)
```

```
##
## Call:
## glm(formula = sex ~ . - flipper_length_mm, family = "binomial",
##     data = train)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.52269  -0.11388   0.00063   0.06524   3.01858
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -1.032e+02  1.706e+01  -6.051 1.44e-09 ***
## speciesChinstrap -1.042e+01  2.544e+00  -4.096 4.20e-05 ***
## speciesGentoo    -1.238e+01  3.383e+00  -3.661 0.000251 ***
## bill_length_mm    9.513e-01  2.210e-01   4.303 1.68e-05 ***
## bill_depth_mm     2.099e+00  4.684e-01   4.481 7.41e-06 ***
## body_mass_g       7.714e-03  1.625e-03   4.746 2.07e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 368.619  on 265  degrees of freedom
## Residual deviance:  70.172  on 260  degrees of freedom
## AIC: 82.172
##
## Number of Fisher Scoring iterations: 8
```

```
##predicted survival rate for test data based on training data
preds<-predict(result,newdata=test, type="response")
```

```
##transform the input data into a format that is suited for the
##performance() function
rates<-prediction(preds, test$sex)
##store the true positive and false positive rates
roc_result<-performance(rates,measure="tpr", x.measure="fpr")
##plot ROC curve and overlay the diagonal line for random guessing
plot(roc_result, main="ROC Curve for Penguins")
lines(x = c(0,1), y = c(0,1), col="red")
```



Since this ROC curve is above the diagonal line, the logistic regression performs better than random guessing.

1 - B

```
##compute the AUC
auc<-performance(rates, measure = "auc")
auc@y.values
```

```
## [[1]]
## [1] 0.9214286
```

The AUC of our ROC curve is 0.9214286, which measn our logitic regressino does better than random guessing.

1 - C

```
table(test$sex, preds>0.5)
```

```
##
##          FALSE TRUE
##   female    28    7
```

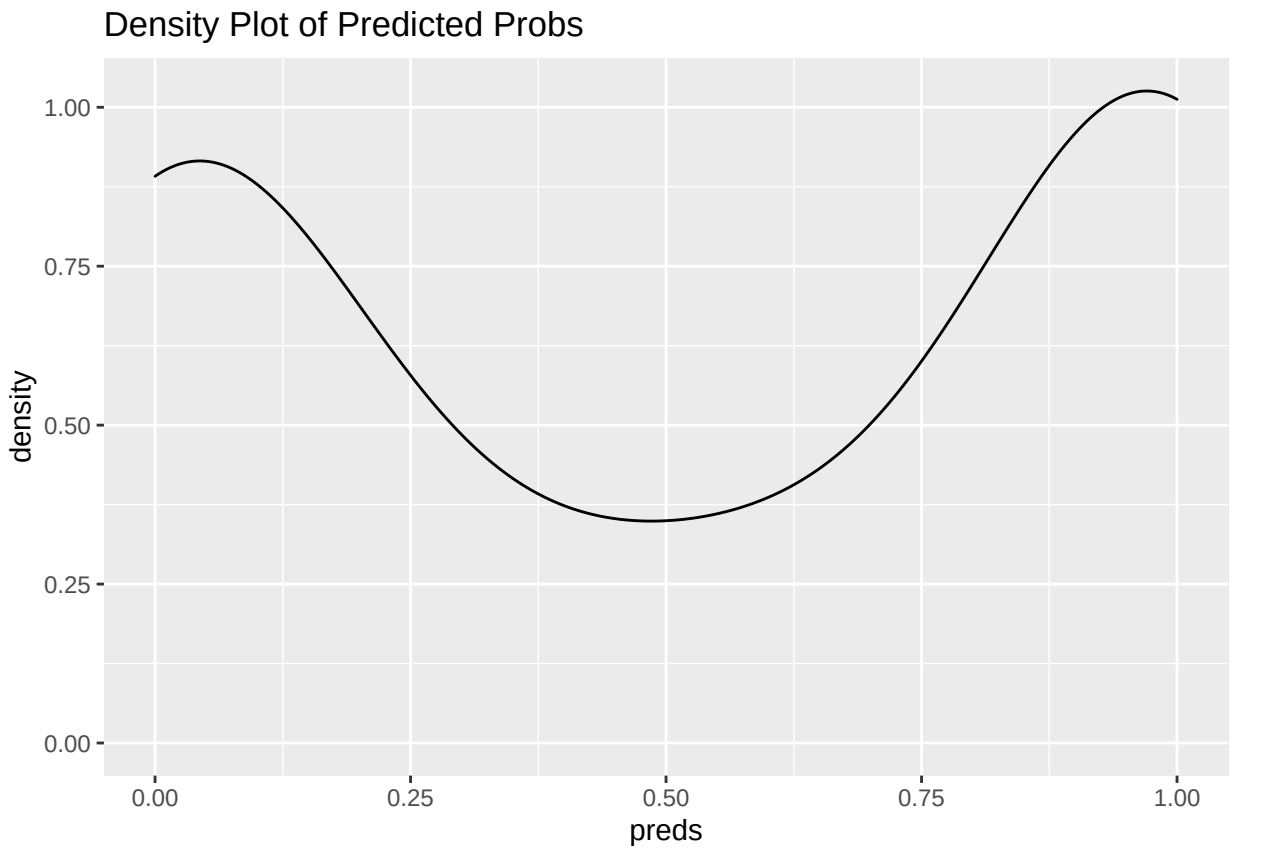
```
##   male       4   28
```

From the table above we can compute the false positive rate, false negative rate, and error rate.

- The false positive rate (FRP) is $\frac{7}{7+28} \rightarrow \frac{7}{35} \rightarrow 0.2$.
- The false negative rate (FNR) is $\frac{4}{4+28} \rightarrow \frac{4}{32} \rightarrow 0.125$
- The error rate is 1 - accuracy $= 1 - \frac{28+28}{28+28+7+4} = 1 - \frac{56}{67} = 1 - 0.8358209 = 0.1641791$

1 - D

```
test<-data.frame(test,preds)
ggplot(test,aes(x=preds))+
geom_density()+
labs(title="Density Plot of Predicted Probs")
```



I personally don't believe the threshold needs to be changed. Sometimes threshold needs to be changed depending on the context of the analysis being done, but in this case increasing and decreasing doesn't make a huge difference in context of the problem. Also the Density plot shows that there is no huge difference in the prediction (probabilities), which means that 0.5 is a decent threshold.