Multivariate Regression, Logistic and Linear

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Is this fish a Bream?

Affects of Group Prevalence on Logistic Model Accuracy

"When the prevalence within the binary response groups is asymmetric, we must be more careful with our classification threshold." - my teacher
In this analysis I will predict whether a freshwater fish is a *Bream* based on measurements.

```
fish <- read.csv('/Users/gabrielwallon/downloads/Data/fish_data.csv') %>%
  mutate(Bream=ifelse(Species=='Bream',1,0))

colnames(fish)
```

```
## [1] "Species" "Weight"  "Length1" "Length2" "Length3" "Height"  "Width"
## [8] "Bream"
```

How many Bream are in this data set?

```
mean(fish$Bream)
```

```
## [1] 0.2464789
```

Therefore, if we were to guess that a given fish is not a Bream with no information about it at all, we would have around a 75% accuracy. Our model must have a greater accuracy than this.

Let's make a model.

```
model <- glm(Bream~Weight,data=fish,family='binomial')
coefficients(summary(model))
```

```
##                 Estimate   Std. Error   z value     Pr(>|z|)
## (Intercept) -2.604943275 0.4046617509 -6.437335 1.215893e-10
## Weight       0.003420773 0.0006872951  4.977154 6.452600e-07
```

Predicted probabilities of being a Bream:

```
fish_pred <- fish %>%
  cbind(Bream_prob=predict(model,newdata=data.frame(Weight=fish$Weight),type='response'))
```

```
fish_pred %>%
  summarize(Accuracy=mean((Bream_prob>0.5)==Bream))
```

```
##    Accuracy
## 1 0.7042254
```

With a classification threshold of 0.50, this model performs worse than if we were to guess without any information of the fish's weight. Thus we need to choose a new threshold.

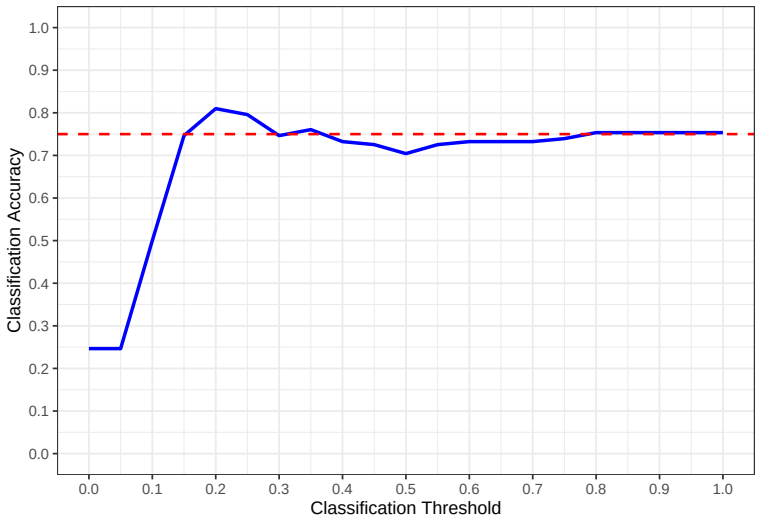
```
#initiate vectors
thresholds <- seq(0,1,0.05)
accuracy <- rep(0,21)
j <- 1

#loop through thresholds and calculate accuracy
for(i in thresholds){

  accuracy[j] <- fish_pred %>%
    summarize(mean((Bream_prob>i)==Bream)) %>%
    pull()

  j <- j+1
}

#graph accuracy versus threshold
data.frame(thresh=thresholds,accur=accuracy) %>%
  ggplot(aes(x=thresh,y=accur)) +
  geom_line(color='blue',size=1) +
  geom_hline(yintercept=0.75,linetype='dashed',
             color='red',size=0.75) +
  labs(x='Classification Threshold',
       y='Classification Accuracy') +
  scale_x_continuous(limits=c(0,1),breaks=seq(0,1,0.1)) +
  scale_y_continuous(limits=c(0,1),breaks=seq(0,1,0.1)) +
  theme_bw()
```



Can see that a classification threshold of around 0.2 allows the model to perform the best.

```
fish_class <- fish_pred %>%
  mutate(Bream_class=if_else(Bream_prob>0.5,1,0))

table(fish_class$Bream,fish_class$Bream_class)
```

```
##
##      0  1
##   0 93 14
##   1 28  7
```

Overall Accuracy = 100/142 = 0.704 True Positive Rate = 7/35 = 0.20 True Negative Rate = 93/107 = 0.869

```
fish_class <- fish_pred %>%
  mutate(Bream_class=if_else(Bream_prob>0.20,1,0))

table(fish_class$Bream,fish_class$Bream_class)
```

```
##
##      0  1
##   0 84 23
##   1  4 31
```

Overall Accuracy = 115/142 = 0.810 True Positive Rate = 31/35 = 0.886 True Negative Rate = 84/107 = 0.785

By sacrificing a little of the true negative accuracy, our true positive accuracy increases dramatically after adjusting the classification threshold to 0.20.