lab_08

2023-11-17

Preliminaries

```
## [1] -0.251 0.281
## [1] -0.625 0.626
```

Logs Regression

We perform a logistic regression here, with the intercept term and the FT_PCT_DIFF variable:

```
##
## Call:
## glm(formula = WON ~ FG_PCT_DIFF + FT_PCT_DIFF, family = binomial(),
##
       data = nba2)
##
## Coefficients:
##
                Estimate Std. Error z value Pr(>|z|)
## (Intercept) 0.001455
                          0.078197
                                     0.019
## FG_PCT_DIFF 32.336946
                          1.869744
                                    17.295 < 2e-16 ***
## FT_PCT_DIFF 3.685480
                          0.574464
                                     6.416 1.4e-10 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
##
  (Dispersion parameter for binomial family taken to be 1)
##
                                      degrees of freedom
       Null deviance: 1704.8 on 1229
## Residual deviance: 1011.5 on 1227
                                      degrees of freedom
## AIC: 1017.5
##
## Number of Fisher Scoring iterations: 5
```

Looking at the p-values, we see that the intercept term has a high p-value of 0.985, which is much greater than a 5% significance level. So, there is not enough evidence to reject the null hypothesis that the intercept is 0 when FG_PCT_DIFF and FT_PCT_DIFF have values of 0.

For the FT_PCT_DIFF, there is a very low p-value, of much less than 0.001, so there is enough evidence to reject the null hypothesis that the coefficient associated with FT_PCT_DIFF is 0.

So, we do not want to include the intercept, but we want to include FT_PCT_DIFF.

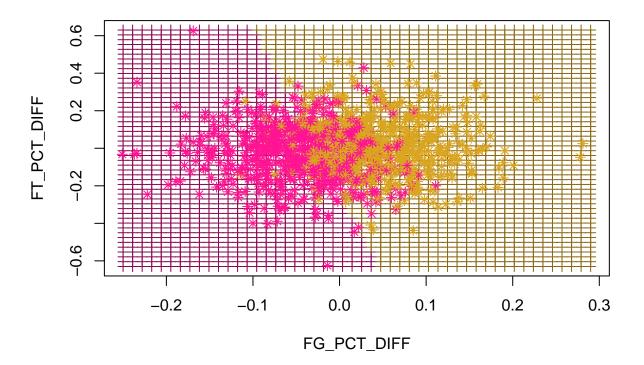
The appropriate equation is: chance of winning = $32.34(FG_PCT_DIFF) + 3.69(FT_PCT_DIFF)$, where the coefficients are rounded up to 2 d.p.

Classifying with Probability

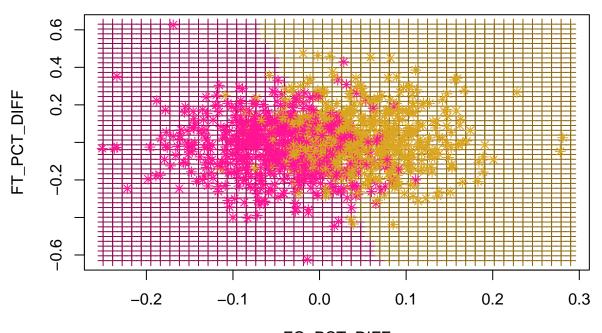
```
p2class <- function(p, threshold) {</pre>
  ifelse(p >= threshold, 1, 0)
Here, we set up the grid and calculate the predicted classes using our grid:
range(nba2$FG_PCT_DIFF)
## [1] -0.251 0.281
range(nba2$FT_PCT_DIFF)
## [1] -0.625 0.626
#setting up the axes
fg_grid <- seq(-0.25, 0.29, length=50)
ft_grid <- seq(-0.63, 0.63, length=50)
#setting up the grid
two_variable_grid <- expand.grid(FG_PCT_DIFF = fg_grid, FT_PCT_DIFF = ft_grid)</pre>
predicted_probabilities <- predict(fit.glm, newdata = two_variable_grid, type = "response")</pre>
classes_0.3 <- p2class(predicted_probabilities, 0.3)</pre>
classes_0.5 <- p2class(predicted_probabilities, 0.5)</pre>
classes_0.7 <- p2class(predicted_probabilities, 0.7)</pre>
```

Below, we see the three required plots:

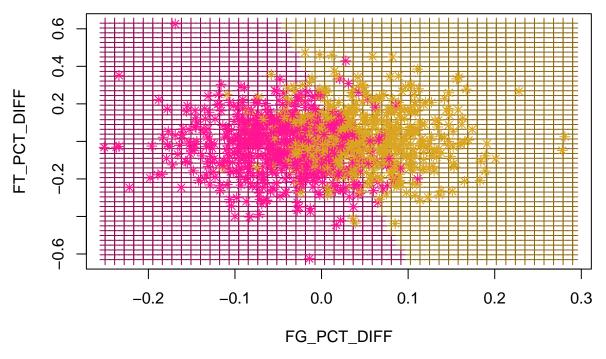
Decision Boundaries with T = 0.3



Decision Boundaries with T = 0.5



FG_PCT_DIFF **Decision Boundaries with T = 0.7**



Looking at the three plots above, it seems like the decision boundary looks pretty linear on all three plots, and by eyeballing, they seem to have similar slopes. However, as the threshold increases, for each value of FG_PCT_DIFF, a higher value of FT_PCT_DIFF is necessary for the model to class a point as 1, so the boundary "moves to the right" as the threshold increases.

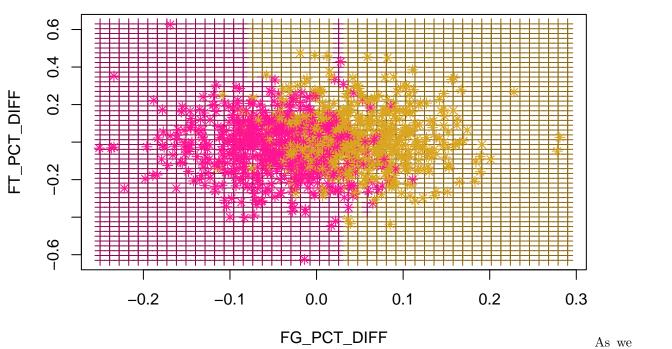
Helping Stop Deforestation

Now, we grow a forest:

```
set.seed(2000)
T <- 1000
m <-2
nba2$WON <- as.factor(nba2$WON)</pre>
forest <- randomForest(WON ~ FG_PCT_DIFF + FT_PCT_DIFF, data = nba2, ntree = T, mtry = m)
forest
##
## Call:
    randomForest(formula = WON ~ FG_PCT_DIFF + FT_PCT_DIFF, data = nba2, ntree = T, mtry = m)
##
                  Type of random forest: classification
                        Number of trees: 1000
##
## No. of variables tried at each split: 2
##
##
           OOB estimate of error rate: 22.6%
## Confusion matrix:
##
       0
           1 class.error
## 0 488 137
               0.2192000
## 1 141 464
               0.2330579
```

The estimated accuracy of the forest is 77.8%.

Decision Boundaries of the Forest



can see, the decision boundary no longer looks linear, compared to the plots from earlier. The boundary also looks less clean, as we can see two sections of pink in the yellow part of the grid near the top of the plot.

```
m <-1
forest_1 <- randomForest(WON ~ FG_PCT_DIFF + FT_PCT_DIFF, data = nba2, ntree = T, mtry = m)
forest_1</pre>
```

```
##
## Call:
  randomForest(formula = WON ~ FG_PCT_DIFF + FT_PCT_DIFF, data = nba2, ntree = T, mtry = m)
##
##
                 Type of random forest: classification
##
                       Number of trees: 1000
## No. of variables tried at each split: 1
          OOB estimate of error rate: 22.2%
##
## Confusion matrix:
##
      0
          1 class.error
## 0 491 134
              0.2144000
## 1 139 466
              0.2297521
```

Repeating with only one variable tried at every split, we have a higher accuracy rate of 78.13%. We should do a hypothesis test to see if this increase in accuracy is significantly higher.