

# NBA Shot Prediction

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## ABSTRACT

The use of various predictive metrics in sports has been occurring as long as human beings have watched each other compete. Initially this started out as simple gut feeling or a subjective assessment of the competitors – the bets usually go to the bigger fighter! In more recent times, humanity has refined its predictive power with the advent of statistics and logical decision making (famously put to use in Major League Baseball, as shown in the film Moneyball). With the advent of the information age and the possibility for large-scale data analytics and machine learning, the National Basketball Association has decided to pursue this analysis to better understand player matchups (defender vs offender) and to assess & optimize shooter performance.

## BUSINESS UNDERSTANDING

Detailed statistics are already available to the NBA as these have been tracked for many years, supporting classic statistical decision making. The goal is to run both unsupervised and supervised machine learning algorithms on the statistical data available. In technical terms, we aim to deliver predictive metrics for threat/benefit level at an individual player level, as well as an interactive application that identifies the likelihood of a shot landing from a specific offender shooting from a specific position on the court, against a specific defender located a certain distance away. This will allow coaches to run limited scenarios in the predictive model, to inform both their practice routines and to assist in making strategic decisions during live games.

As an example, consider the matchup of LeBron James on offence and Serge Ibaka on defence. Let's assume that LeBron typically tries to shoot from top of the key, and is being defended by Serge Ibaka, 5 feet away. The model takes these discrete inputs and outputs a real-world percentage success of 10.5% (example). If the average shooting success rate is 30%, we can identify this as a bad shot, and encourage LeBron to pass in these situations.

## DATA UNDERSTANDING

We begin with understanding each feature available in the data. The available data set is data of all shots attempted at NBA games between 2014 and 2015. For each shot attempted, the most important outcome of that attempt, whether the shot was made or missed is available. This is seen in 2 columns SHOT\_RESULTS and FGM. FGM stands for “Field Goal Made”. In support of this outcome, there are a number of other data points to be seen, like the player who attempted the shot and who defended the sho, how far away was the defender, how far away from the basket was the shot attempted, was the match at home or away etc. With that data understanding, let’s look at the “head” of the data.

GAME_ID	MATCHUP	LOCATION	W	FINAL_MARGIN	SHOT_NUMBER	PERIOD	GAME_CLOCK
21400899	MAR 04, 2015 - CHA @ BKN	A	W	24	1	1	1:09
21400899	MAR 04, 2015 - CHA @ BKN	A	W	24	2	1	0:14
21400899	MAR 04, 2015 - CHA @ BKN	A	W	24	3	1	0:00
21400899	MAR 04, 2015 - CHA @ BKN	A	W	24	4	2	11:47
21400899	MAR 04, 2015 - CHA @ BKN	A	W	24	5	2	10:34
21400899	MAR 04, 2015 - CHA @ BKN	A	W	24	6	2	8:15

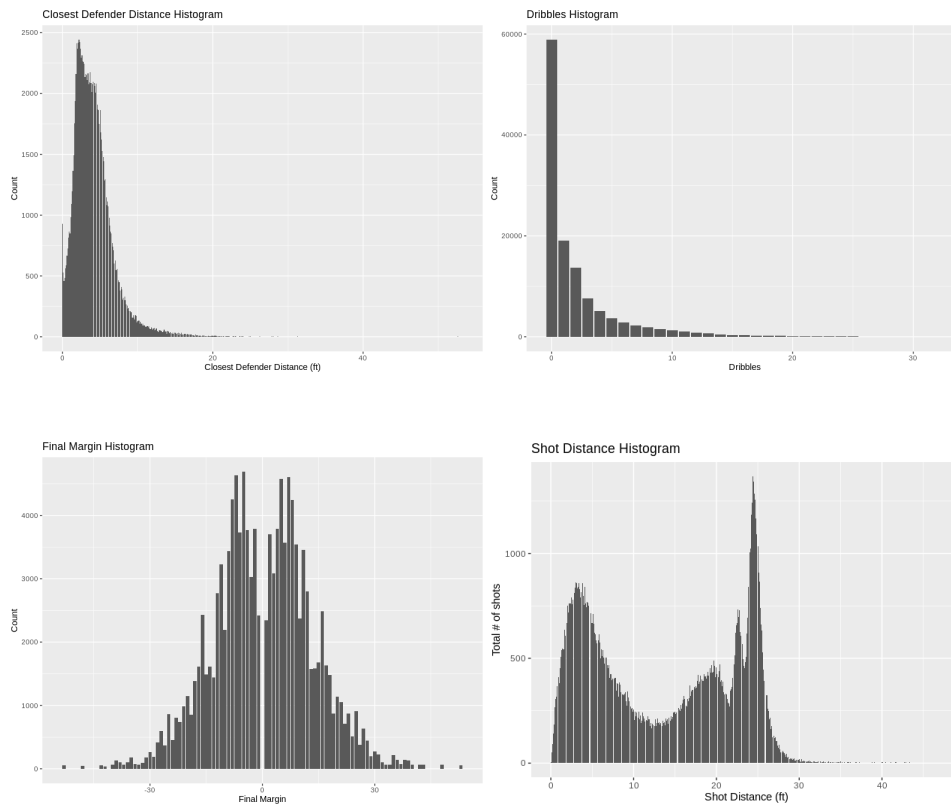
SHOT_CLOCK	DRIBBLES	TOUCH_TIME	SHOT_DIST	PTS_TYPE	SHOT_RESULT	CLOSEST_DEFENDER
10.80	2	1.90	7.70	2	made	Anderson, Alan
3.40	0	0.80	28.20	3	missed	Bogdanovic, Bojan
	3	2.70	10.10	2	missed	Bogdanovic, Bojan
10.30	2	1.90	17.20	2	missed	Brown, Markel
10.90	2	2.70	3.70	2	missed	Young, Thaddeus
9.10	2	4.40	18.40	2	missed	Williams, Deron

Table 1: Data Dictionary - NBA Data

Feature	Feature.Description
GAME_ID	A unique ID for each game
MATCHUP	Shows the date of the match and the teams the match is between
LOCATION	A - Away, H - Home. Shows the location of the match with respect to the first team in the match up column
W	Win or Loss. W means win and L means Loss, with respect to the first team in the match up column
FINAL_MARGIN	Points difference between the teams at the end of the game
SHOT_NUMBER	To be read in conjunction with the PERIOD column. Indicates the shot number in a given game period
PERIOD	Indicates the game period
GAME_CLOCK	Time elapsed since the period commenced. This dataset shows the time at which the shot was attempted. Max 12 minutes per period
SHOT_CLOCK	The length of time for a given shot in seconds. Max - 24 seconds is a rule
DRIBBLES	The number of times the ball was dribbled before the shot was attempted
TOUCH_TIME	The length of time a player touched the ball
SHOT_DIST	The distance from which a shot was attempted. Distance in feet
PTS_TYPE	Points awarded if a shot was made. 2 pointer or 3 pointer shots
SHOT_RESULT	Indicates whether the shot was made or missed
CLOSEST_DEFENDER	Shows the name of the player that was the closest defender
CLOSEST_DEFENDER_PLAYER_ID	Unique ID of the closest defender
CLOSE_DEF_DIST	Distance of the closest defender in feet
FGM	An abbreviation for FIELD GOALS MADE. A proxy for SHOT_RESULT, 0 indicates missed shot and 1 indicates shot made
PTS	Points awarded for shots made
player_name	Name of the player who attempted the shot
player_id	Unique ID of the player who attempted the shot

## Plots

We attempt to further understand the data using the following plots. A histogram of the “closest defender distance” shows that a majority of the shots were defended from within 5 feet of the player attempting the shot and it is safe to say that more than 90% of the shots were defended from within 10 feet. The “dribbles count” shows that most of the shots were attempted soon after getting the ball and that more than 80% of the shots were attempted within 3 dribbles. “Final Margin” histogram shows that most matches were won or lost within a 15 point margin. The “Shot distance” histogram shows that most of the shots were attempted from “top of the key” and followed by 2 to 4 feet range from the basket



## DATA PREPARATION

### SHOT\_CLOCK

Looking at the data, some of the NA values need to be dealt with. The “SHOT\_CLOCK” column has some NA values and the assumption is that the SHOT\_CLOCK was equal to the GAME\_CLOCK and therefore it may not be recorded. For such cases, the GAME\_CLOCK is assumed to be equal to SHOT\_CLOCK.

```
cleanData <- initialData
gameClock <- as.vector(second(fast_strptime(cleanData$GAME_CLOCK, "%M:%S"))) +
  as.vector(minute(fast_strptime(cleanData$GAME_CLOCK, "%M:%S"))) * 60
shotClock <- is.na(initialData$SHOT_CLOCK)
for(i in 1:length(gameClock)){
  if(shotClock[i] & gameClock[i] < 25){
    cleanData$SHOT_CLOCK[i] <- gameClock[i]
  }
}
```

## Names

To further handle player names in this exercise, all names are standardized to read as “Last Name,” followed by “First Name”. A custom function was written to achieve this result.

```
nameformatreverse <- function(s) {  
  fname <- str_extract(s, "^\\w+")  
  lname <- str_extract(s, "\\w+$")  
  s <- paste(lname, fname, sep = ", ")  
}
```

All Shooter & Defender names are then put through the function to standardize names

```
shooterName <- cleanNoNADData$player_name  
shooterName <- toupper(shooterName)  
shooterName <- nameformatreverse(shooterName)  
  
cleanNoNADData$player_name <- shooterName  
cleanNoNADData$CLOSEST_DEFENDER <- toupper(cleanNoNADData$CLOSEST_DEFENDER)  
cleanNoNADData$CLOSEST_DEFENDER <- gsub("[.]", "", cleanNoNADData$CLOSEST_DEFENDER)
```

## Game Clock

It makes best sense to have the GAME\_CLOCK expressed in seconds.

```
cleanNoNAScondsClockData <- cleanNoNADData  
cleanNoNAScondsClockData$GAME_CLOCK <-  
  as.vector(second(fast_strptime(cleanNoNADData$GAME_CLOCK, "%M:%S"))) +  
  as.vector(minute(fast_strptime(cleanNoNADData$GAME_CLOCK, "%M:%S"))) * 60
```

## Touch time

Any row that has TOUCH\_TIME less than 0.1 seconds is not right and hence are omitted

```
cleanNoNAScondsClockData <- cleanNoNAScondsClockData[cleanNoNAScondsClockData$TOUCH_TIME > 0, ]
```

# MODELLING

## K-Means Clustering

The Elbow method is a popular, non computation intensive process of determining the most optimal number of clusters for a dataset by looking at a dropoff of variance. The other methods, eg, Bayesian Inference which we ran is more computation intensive, and produced optimal clusters that didnt agree with the visual Elbow method. Therefore, after plotting and analyzing a few different features against each other and highlighting the clusters by colouring the datapoints, we find that 3 clusters is likely the best compromise for the important features, namely, shot distance and closest defender distance.

To perform clustering, only the numeric columns from the data are selected.

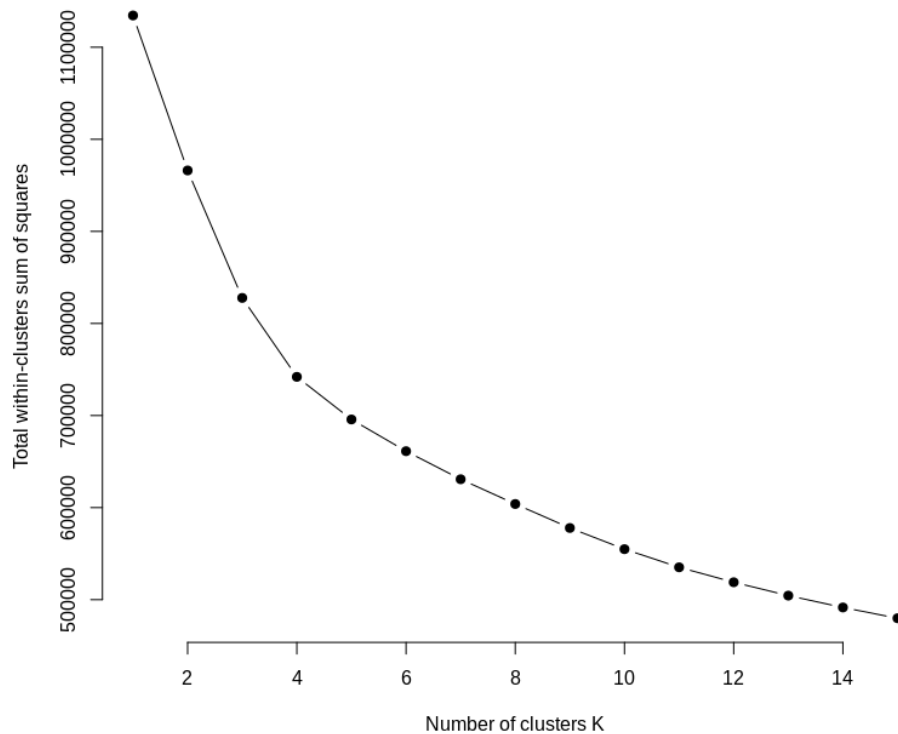
```
kdataunscaled <- cleanNoNAScondsClockData[, c("SHOT_NUMBER", "PERIOD",  
                                              "GAME_CLOCK", "SHOT_CLOCK", "DRIBBLES",  
                                              "TOUCH_TIME", "SHOT_DIST", "CLOSE_DEF_DIST")]  
  
kdata <- scale(kdataunscaled)
```

We use the ‘Elbow’ method to determine the ideal number of clusters

```
set.seed(123)  
# Compute and plot wss for k = 1 to k = 15  
k.max <- 10
```

```
wss <- sapply(1:k.max, function(k){kmeans(kdata, k, nstart=50,iter.max = 15 )$tot.withinss})
wss
plot(1:k.max, wss,
     type="b", pch = 19, frame = FALSE,
     xlab="Number of clusters K",
     ylab="Total within-clusters sum of squares")
```

The “number of clusters” vs “sum of squares” plot helps us identify the ‘Elbow’ and decide on the right number of clusters. From the plot, we will try creating clusters with  $k = 2, 3$  &  $4$



Bayesian Inference Criterion for k means to validate choice from Elbow Method

```
d_clust <- Mclust(as.matrix(kdata), G=1:10,
                 modelNames = mclust.options("emModelNames"))
d_clust$BIC
plot(d_clust)

# Let us apply kmeans for k=2 clusters
kmm.2 <- kmeans(kdata, 2, nstart = 50, iter.max = 15)
# Let us apply kmeans for k=3 clusters
kmm.3 <- kmeans(kdata, 3, nstart = 50, iter.max = 15)
# Let us apply kmeans for k=3 clusters
kmm.4 <- kmeans(kdata, 4, nstart = 50, iter.max = 15)
# We keep number of iter.max=15 to ensure the algorithm converges and nstart=50 to
# Ensure that atleast 50 random sets are choosen
kmm.2
kmm.3
```

```

kmm.4

# Plot the clusters
clusplot(kdataunscaled, kmm.3$cluster, color=TRUE, shade=TRUE, labels=2, lines=0)

# Centroid Plot against 1st 2 discriminant functions
plotcluster(kdataunscaled, kmm.2$cluster)
plotcluster(kdataunscaled, kmm.3$cluster)
plotcluster(kdataunscaled, kmm.4$cluster)

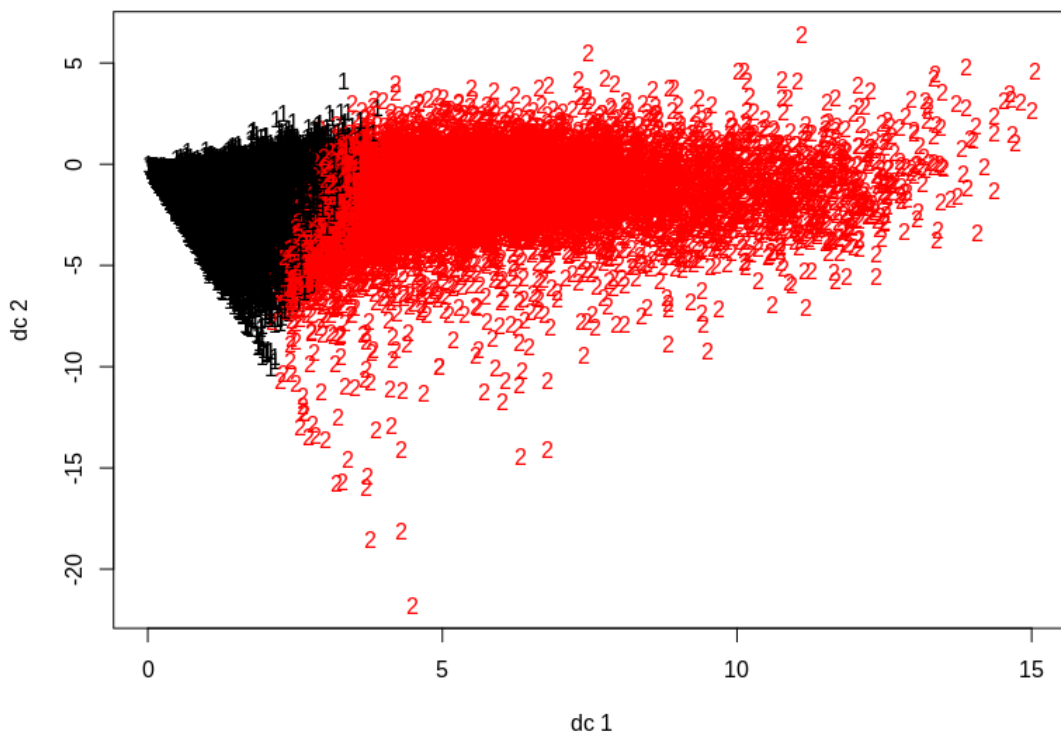
```

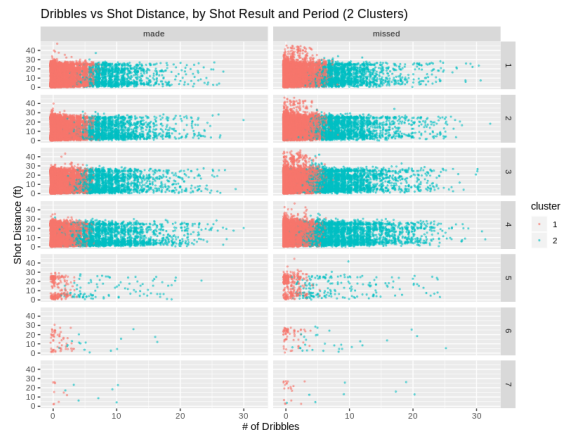
### Clustering Comparison Plots (k=2, k=3, k=4)

For 3 different values of k (# of clusters), k=2, k=3, k=4 we plot the following 5 plots, so that we can compare and choose the best number of clusters.

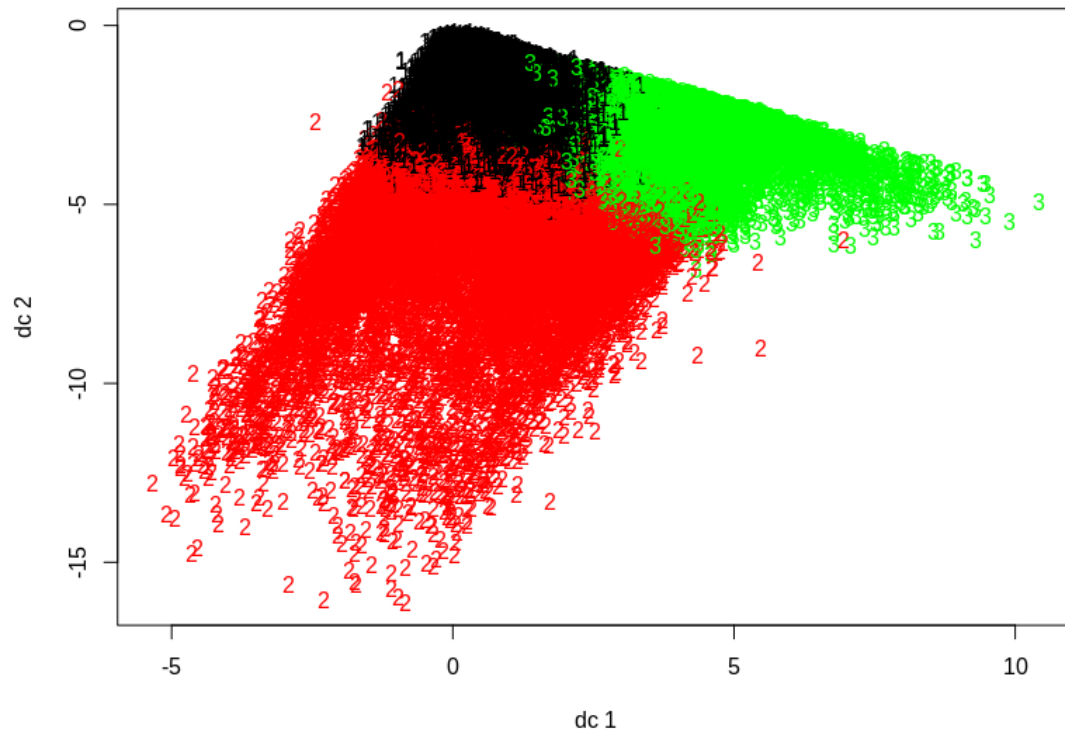
- Plot 1: A simple visual representation of the clusters, based on their principal components
- Plot 2: Dribbles and Shot Distance grouped by Field Goal Made
- Plot 3: Dribbles, Shot Distance, grouped by Field Goal Made and grouped by Periods
- Plot 4: Shot Distance, Closest Defender Distance grouped by Field Goal Made
- Plot 5: Shot Distance, Closest Defender Distance grouped by Field Goal Made and grouped by Periods

k=2 plots

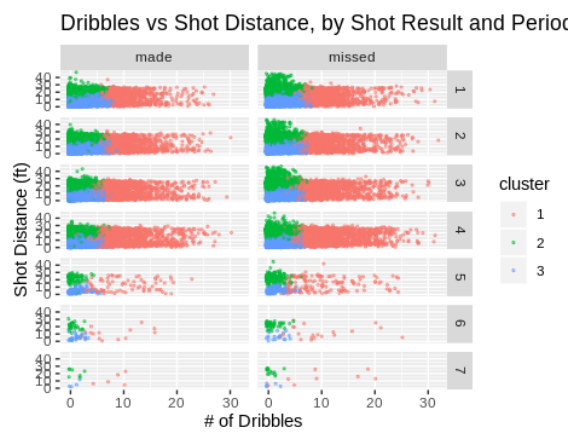
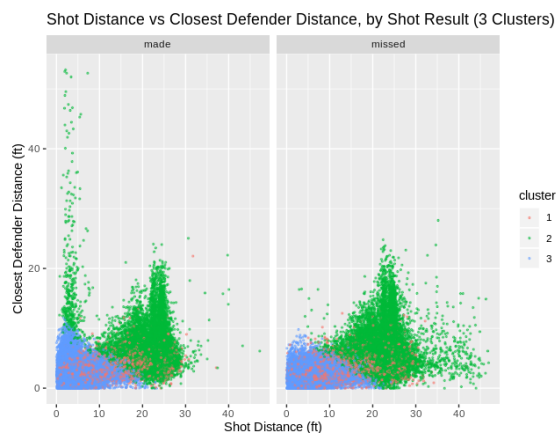
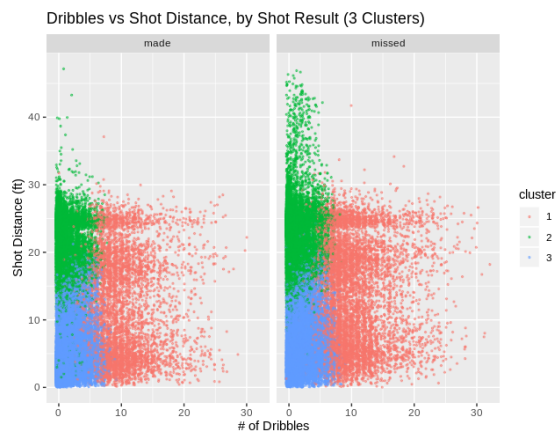




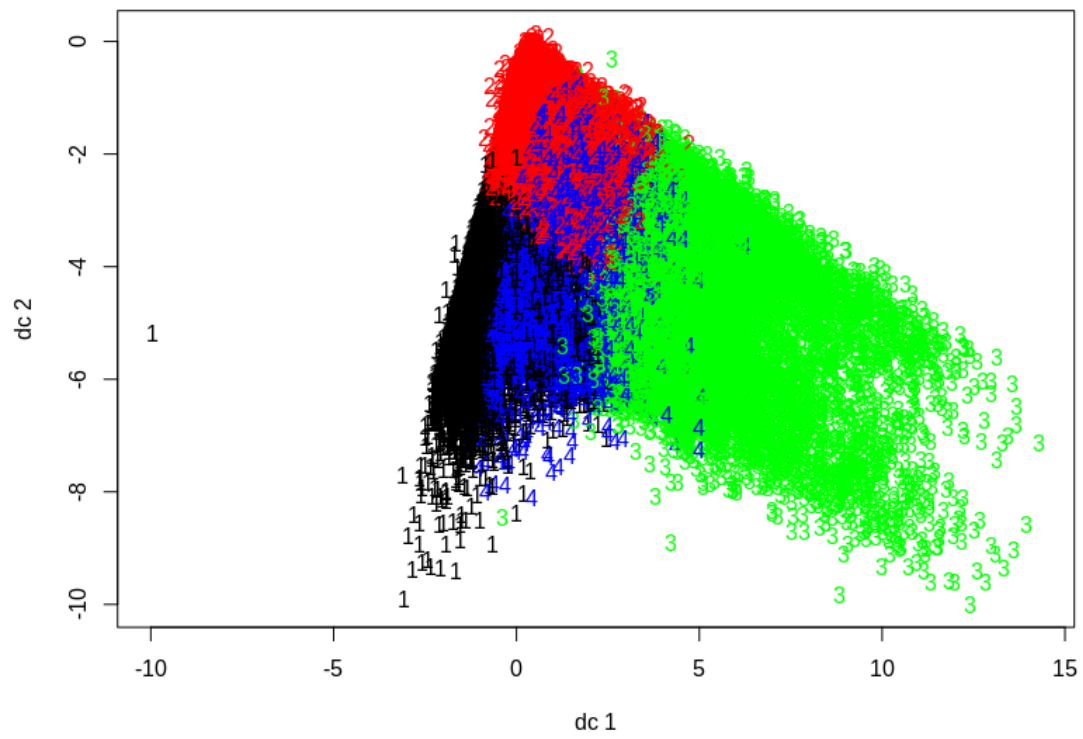
k=3 plots

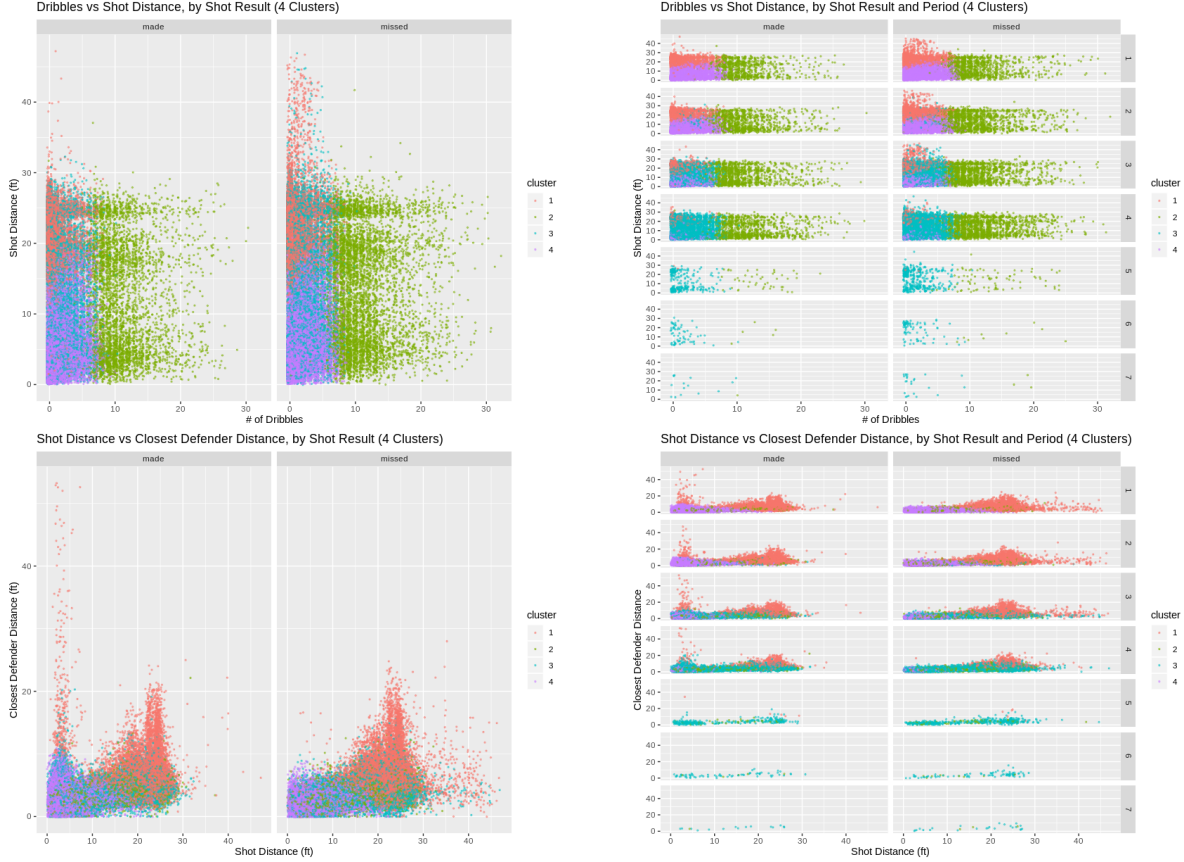






k=4 plots





## Principal Component Analysis

Principle Component Analysis was used to see if there were any features that were highly correlated, so that some of them could be merged into Principle Components without significant data loss. The PCA algorithm identified 8 important numeric features in the dataset. Using PCA to combine these features, we obtained eight principle components (PC1-PC8). Investigating the components further, we determined that the PC1 and PC2 features were responsible for almost 50% of the variance in the data. PC3 through to PC8 were responsible for the other 50%.

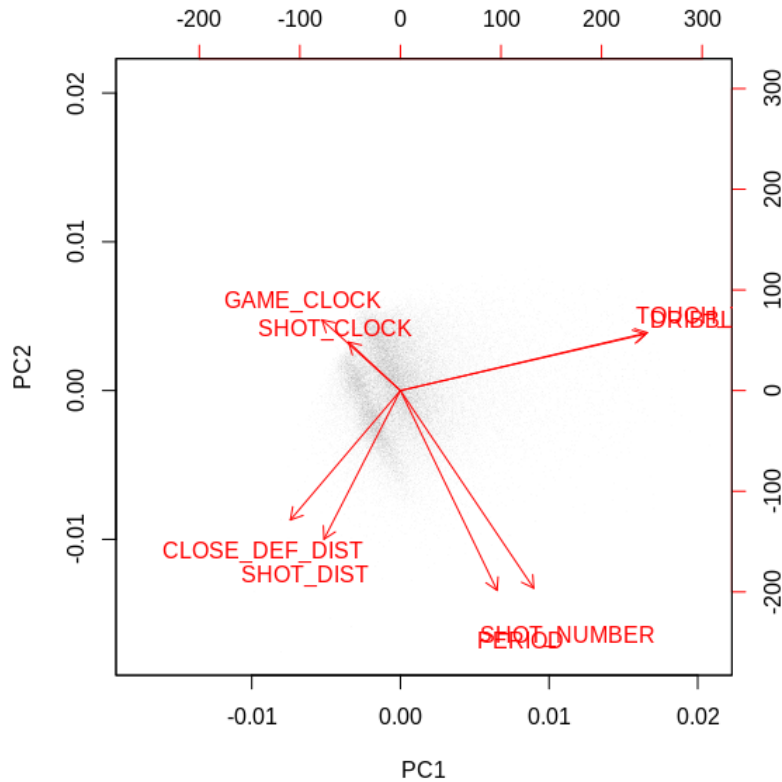
The biplot of PC1 against PC2 (shown below) displays arrow vectors for each feature in the original data set. The length of the arrow indicates the significance of the feature towards the PC1 and PC2 components. The distance from one line to another, explains the correlation of the features in question.

- Looking at the graph, we can see that GAME\_CLOCK and SHOT\_CLOCK are highly correlated but have minimal effect on PC1 and PC2.
- We see correlation between CLOSE\_DEF\_DIST and SHOT\_DIST. Both of these features have a medium impact on both PC1 and PC2.
- Some correlation is seen between SHOT\_NUMBER and PERIOD. Both of these features have a significant effect on both PC1 and PC2.
- Lastly, the highly correlated TOUCH\_TIME and DRIBBLE have a significant effect on the combined features.

Having conducted this analysis, we have learned a bit more about the individual features and how they impact our data, and therefore our prediction. We will use this information to choose what features we expose to the user through our application. For instance, exposing either TOUCH\_TIME or DRIBBLE would likely have similar effect, so we may simply pick one of them. This is also a good rough measure of the significance of each feature.

Importance of components:

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Standard deviation	1.483	1.2860	1.1858	0.9954	0.9659	0.66435	0.55532	0.25781
Proportion of Variance	0.275	0.2067	0.1758	0.1239	0.1166	0.05517	0.03855	0.00831
Cumulative Proportion	0.275	0.4817	0.6575	0.7813	0.8980	0.95314	0.99169	1.00000



## Supervised Learning Models

We chose a number of supervised machine learning models to predict the number of field goals made. We ran, evaluated, and compared the performance of the following models:

- Decision Tree
- Logistic Regression
- GBM
- GBM with PCA

Before running the models, we converted the predictors and response variable to their correct data type. For example, numeric factors such as SHOT\_DIST were explicitly converted into numeric, while categorical factors such as FGM were explicitly converted into categorical factors. Because the binary response variables of, 0 and 1, showcased a relatively balanced dataset, with the split being roughly 55%/45%, we did not need to undersample or oversample the data.

We also split the dataset into a training, and testing set. The split was set at 70% testing, and 30% training, ensuring a balanced split.

## Decision Tree

The Decision tree algorithm is an algorithm that uses a tree-like data structure to make either predictions for regression, or classification problems. Given the business problem and context, a categorical variable decision tree was chosen as we wanted to classify, given the available data, whether or not an attempted shot made became a FGM (Field Goal Made); in this particular situation, there would be two categories for the response variable: either 0, denoting an attempted shot that missed, or 1, denoting an attempted shot that resulted in a field goal. A decision tree is suitable supervised machine learning algorithm because it is fairly easy to explain and visualize. For example, the following figure below is the generated decision tree diagram. Shot Distance, titled as SHOT\_DIST, as well as the distance to the closest defender, titled as CLOSE\_DEF\_DIST, were the two most important variables in the decision tree, and of which the decisions are based upon.

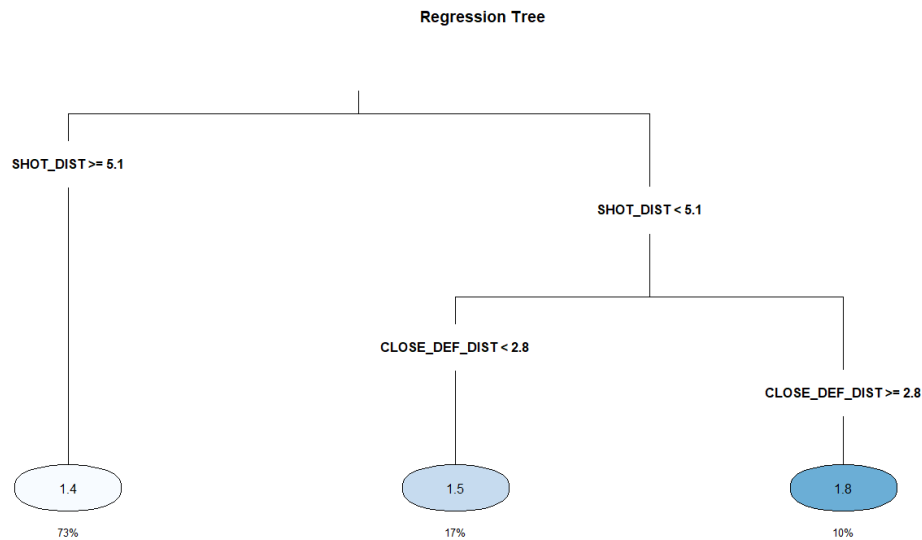


Figure 1: Decision Tree Visual

The ROC curve, and AUC of the decision tree algorithm showed similar results to the other models, as seen in the figure below. Nevertheless, it was decided not to use the decision tree algorithm as the model only showed 3 raw probabilities given the different permutations of SHOT\_DIST and CLOSE\_DEF\_DIST. This would not have looked good on the Shiny app, as we wanted to show more probabilities on a more granular level, as there were other predictor variables that were not being used in the final model.

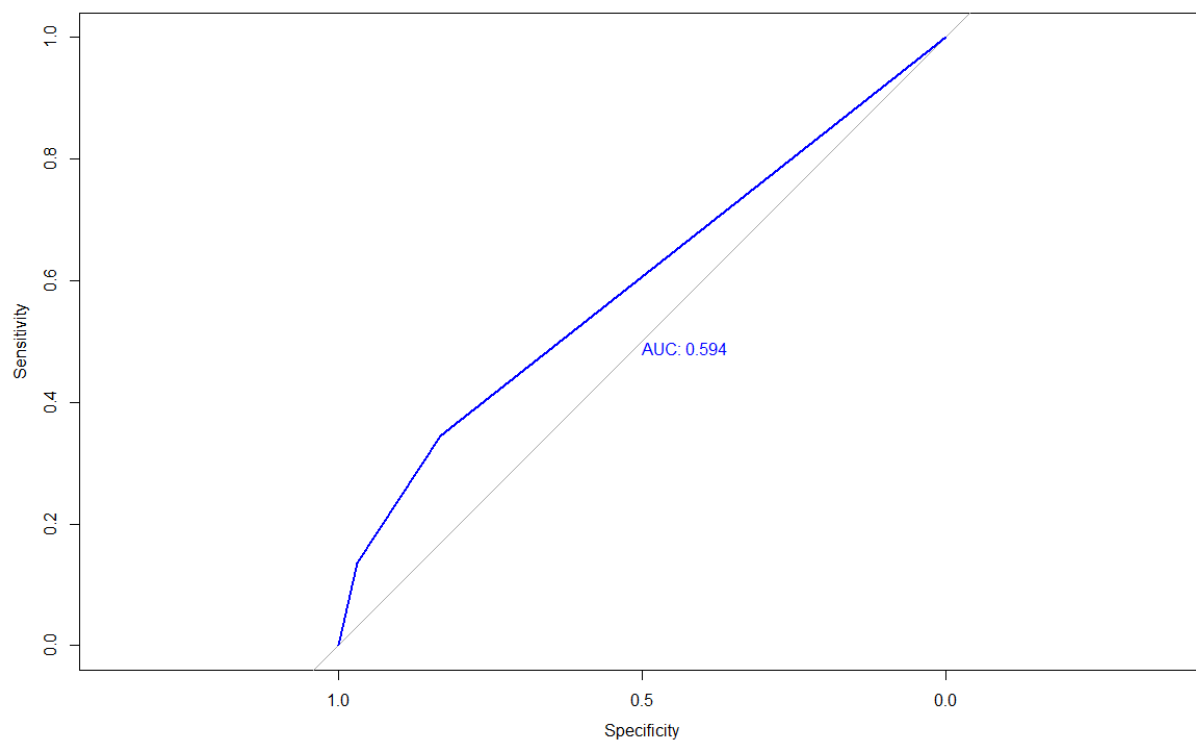


Figure 2: Decision Tree AUC

## Logistic Regression

Logistic Regression is a parametric model used for binary classification, and it is based off the logit (logistic) function, hence the name. There are a few assumptions that were made with logistic regression: \* There is a large enough dataset to make accurate predictions \* Observations are independent of one another \* Response variable is binary (0 or 1). \* Predictor variables are related to logit function \* Minimal multicollinearity among the predictor variables All assumptions except (4) and (5) are true, and due to the lack of time on our part, we were unable to ascertain whether the last two assumptions were, indeed, true. The results for the logistic regression showed similar results to other models. Listed below is the ROC curve/AUC results of the logistic regression model.

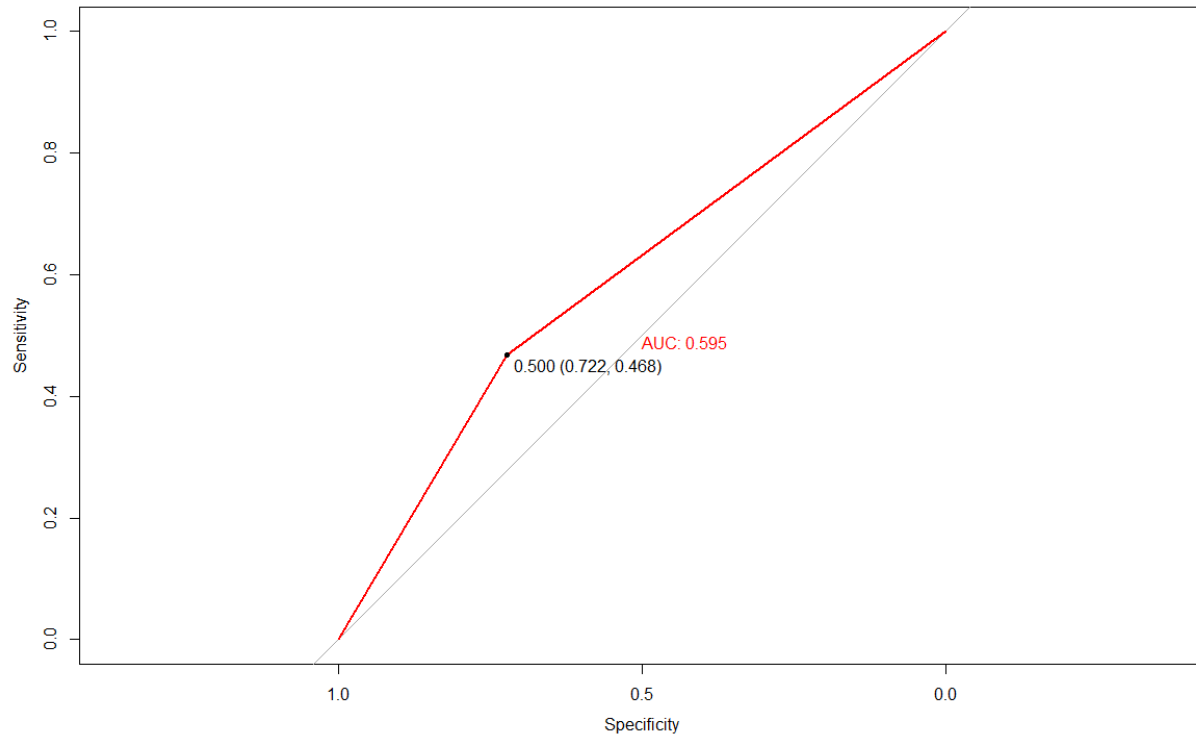


Figure 3: GLM AUC

In terms of other metrics like accuracy, balanced accuracy, sensitivity, and specificity, the logistic regression model also showed similar results to the other models. Unfortunately, logistic regression took the longest amount of time to train compared to all the other models, at 2.5 hours. Listed below are the other metrics, as well as the runtime of the logistic regression model.

### Confusion Matrix and Statistics

	Reference	
Prediction	no	yes
no	15018	9051
yes	5695	8053

Accuracy : 0.6101  
95% CI : (0.6051, 0.615)  
No Information Rate : 0.5477  
P-Value [Acc > NIR] : < 2.2e-16

Kappa : 0.1993

Mcnemar's Test P-Value : < 2.2e-16

Sensitivity : 0.7251

Specificity : 0.4708

Pos Pred Value : 0.6240

Neg Pred Value : 0.5858

Prevalence : 0.5477

Detection Rate : 0.3971

Detection Prevalence : 0.6365

Balanced Accuracy : 0.5979

'Positive' Class : no



## Stochastic Gradient Boosting (GBM)

Stochastic Gradient Boosting is a relatively complex supervised learning algorithm. The algorithm continuously iterates through several trees, at one at a time, so that it can boost the performance of its weakest learners.

When initially training the GBM model, we first decided to keep CLOSEST\_DEFENDER\_PLAYER\_ID, and player\_name, when training the GBM model, but the model itself was fairly big, and in terms of variable importance, both features were not that important unless if the players had a large enough data sample to draw meaningful conclusions from. For example, looking at the figure of output variable importance, one could see the top CLOSEST\_DEFENDER and player\_name names were highly regarded players from the 2015 season, or at least players who had a lot of playtime.

### Confusion Matrix and Statistics

```

      Reference
Prediction  no  yes
no      17477 11287
yes      2703 5362

      Accuracy : 0.6201
      95% CI : (0.6152, 0.6251)
No Information Rate : 0.5479
P-Value [Acc > NIR] : < 2.2e-16

      Kappa : 0.197

McNemar's Test P-Value : < 2.2e-16

      Sensitivity : 0.8661
      Specificity : 0.3221
Pos Pred Value : 0.6076
Neg Pred Value : 0.6648
Prevalence : 0.5479
Detection Rate : 0.4745
Detection Prevalence : 0.7810
Balanced Accuracy : 0.5941

'Positive' Class : no
```

Also, including the features CLOSEST\_DEFENDER\_PLYAER\_ID and player\_name made the model size unnecessarily big for little to no improvement in the prediction of FGM. In relation to the size of the models, it also took a lot longer to train the model as well, at about 4 hours instead of the usual 1 hour. For hyper parameter optimization, we found that GBM produced the best results at with an interaction depth of 5, 40 trees, minimum of 10 observations in each node, and a shrinkage of 0.1. Using such hyper parameters offered a relatively fast training time of around 10 minutes

Listed below is the ROC curve, and AUC value for GBM without CLOSEST\_DEFENDER\_PLAYER\_ID, and player\_name predictor variables. Also listed below is the console output of training the GBM model, showing some of the metrics from the test dataset. Overall, the GBM model did the best compared to the other models, although not by a huge margin. It had an accuracy of 62.01%, a sensitivity of 0.8661 which were the highest of all the models. Unfortunately, its specificity was at the lower end compared to other models at 0.3221

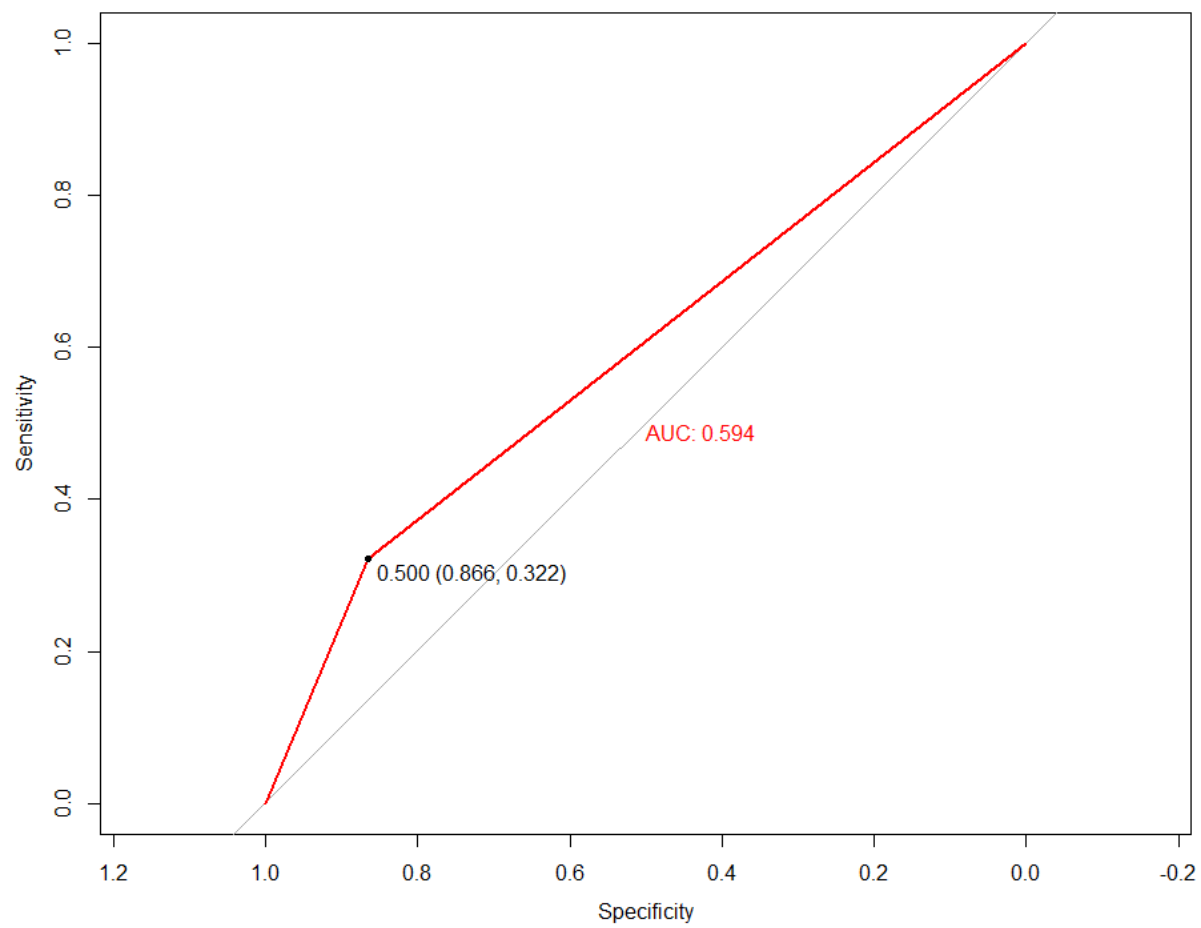


Figure 4: GBM AUC

### Stochastic Gradient Boosting (GBM) with PCA

We also chose to perform GBM with the results generated from PCA. We used all 8 of the components for the GBM model. Listed below was the variable importance of each component:

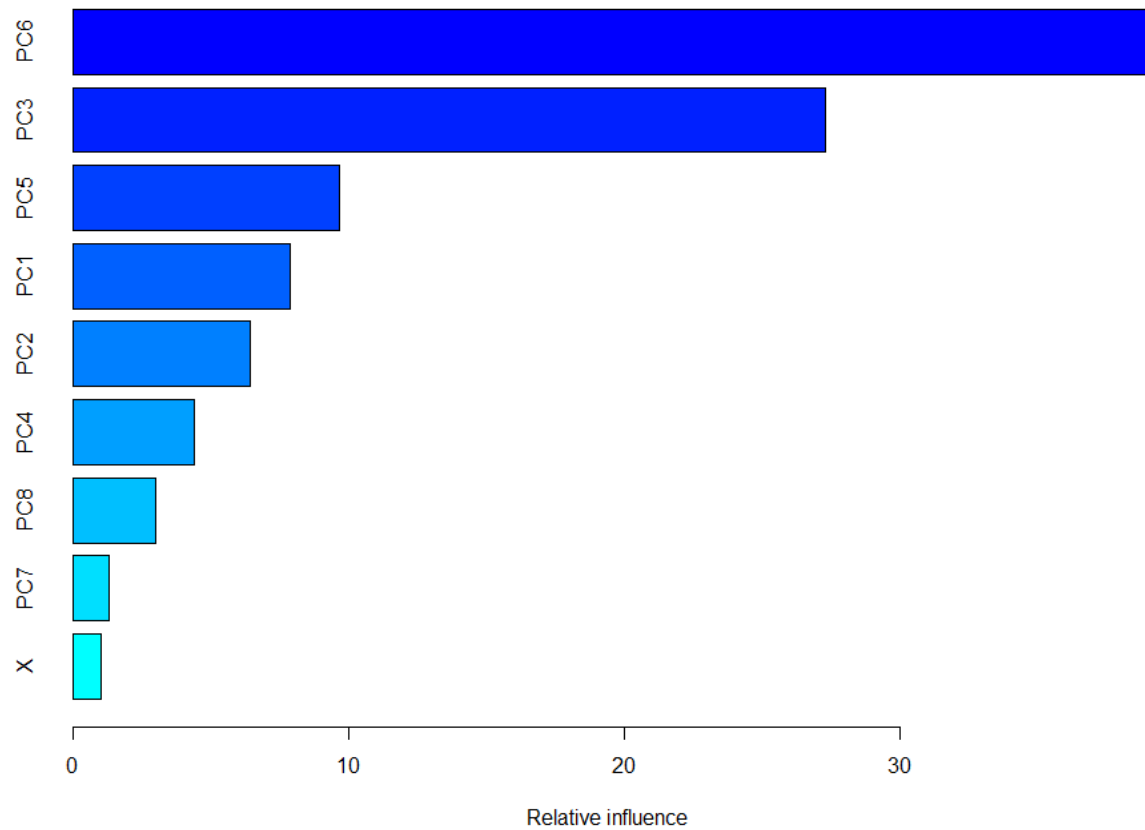
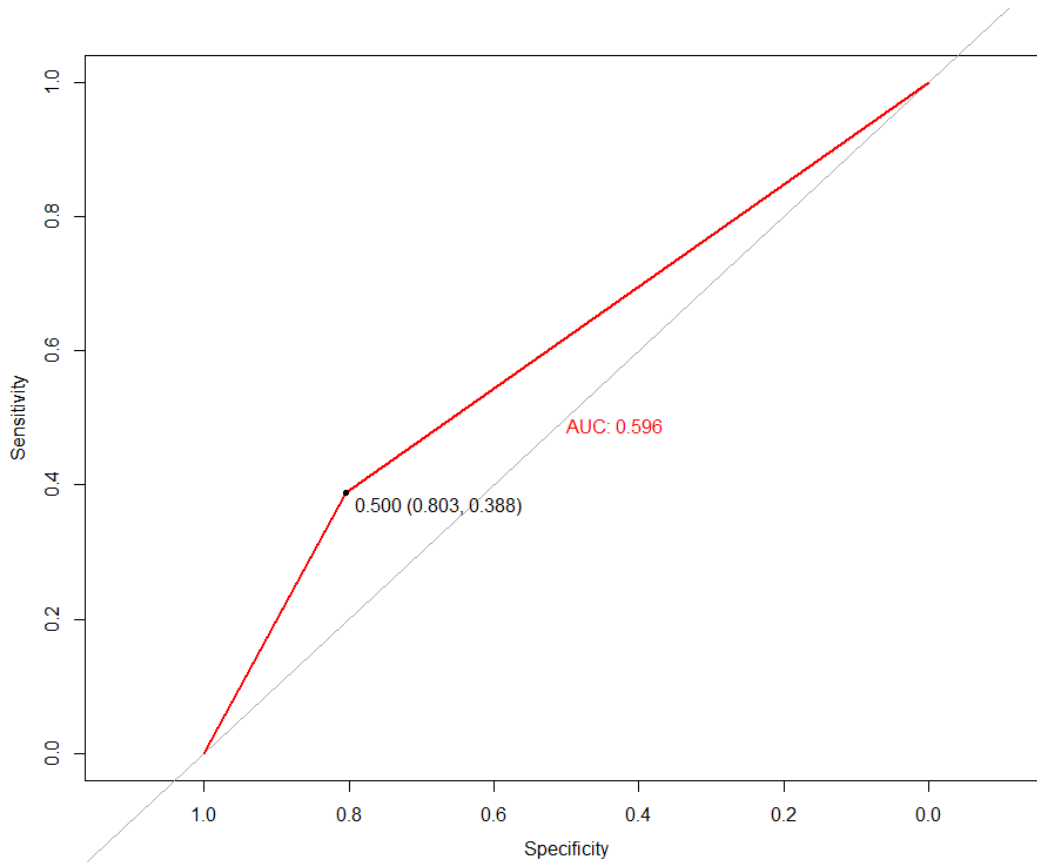


Figure 5: GBM with PCA AUC

Listed below are the metrics of the GBM with PCA. Overall the GBM with PCA model was fairly competitive with the previous GBM model, as it scored 61.58% accuracy, and a 0.8035 sensitivity. Its specificity was a bit better than the previous GBM model at 0.3884. In terms of runtime both GBM models were fairly similar with a training duration of around 10 minutes.



- Fold5: shrinkage=0.1, interaction.depth=10, n.minobsinnode=10, n.trees=200

Aggregating results

Selecting tuning parameters

Fitting n.trees = 100, interaction.depth = 5, shrinkage = 0.1, n.minobsinnode = 10 on full training set

Iter	TrainDeviance	ValidDeviance	StepSize	Improve
1	1.3695	nan	0.1000	0.0037
2	1.3625	nan	0.1000	0.0035
3	1.3568	nan	0.1000	0.0028
4	1.3518	nan	0.1000	0.0025
5	1.3474	nan	0.1000	0.0021
6	1.3440	nan	0.1000	0.0017
7	1.3408	nan	0.1000	0.0015
8	1.3378	nan	0.1000	0.0013
9	1.3350	nan	0.1000	0.0013
10	1.3328	nan	0.1000	0.0010
20	1.3178	nan	0.1000	0.0004
40	1.3046	nan	0.1000	0.0001
60	1.2993	nan	0.1000	0.0000
80	1.2965	nan	0.1000	0.0000
100	1.2944	nan	0.1000	-0.0000

```
> proc.time() - ptm_rf
  user system elapsed
217.28   0.20  217.50
>
```

## Stochastic Gradient Boosting

Tuning parameter 'shrinkage' was held constant at a value of 0.1

Tuning parameter 'n.minobsinnode' was held constant at a value of 10

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

The final values used for the model were n.trees = 100, interaction.depth = 5, shrinkage = 0.1 and n.minobsinnode = 10.

## Confusion Matrix and Statistics

	Reference	
Prediction	no	yes
no	16214	10182
yes	3966	6467

Accuracy : 0.6158  
95% CI : (0.6109, 0.6208)  
No Information Rate : 0.5479  
P-Value [Acc > NIR] : < 2.2e-16

Kappa : 0.1984

Mcnemar's Test P-Value : < 2.2e-16

Sensitivity : 0.8035  
Specificity : 0.3884  
Pos Pred Value : 0.6143  
Neg Pred Value : 0.6199  
Prevalence : 0.5479  
Detection Rate : 0.4403  
Detection Prevalence : 0.7167  
Balanced Accuracy : 0.5960

'Positive' Class : no

```
>
> #summary of model
> summary(model_gbm)
      var  rel.inf
PC6 PC6 39.162726
PC3 PC3 27.261858
PC5 PC5  9.652336
PC1 PC1  7.877662
PC2 PC2  6.407543
PC4 PC4  4.380920
PC8 PC8  2.955187
PC7 PC7  1.287303
X    X  1.014465
```

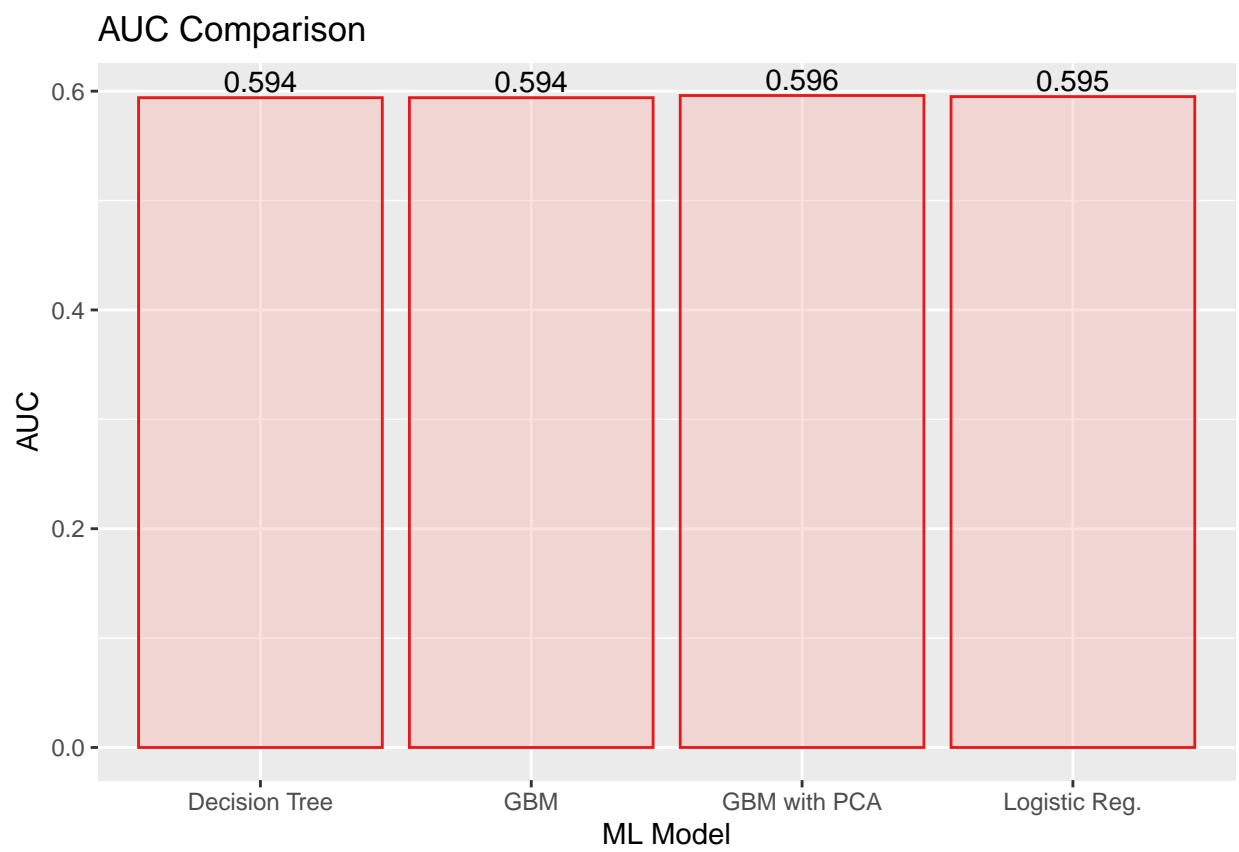


Figure 6: AUC Comparison

## EVALUATION AND CONCLUSION

All models performed fairly similarly in terms of metrics, such as ROC, AUC, Accuracy, Balanced Accuracy, Sensitivity, and Specificity. In terms of overall performance, the models were not spectacular: they showed an accuracy, balanced accuracy, and AUC of around 0.60, sensitivity of around 70% to 80%, and a specificity of 30% to 40%. Nevertheless, there were some positives to be noted: although the model was only 10% better than chance, the sensitivity of all models was quite high at 70% to 80%. This meant that the model was fairly good at correctly predicting the percentage of actual positive cases (i.e FGM); on the flip side, all models had fairly poor specificity, meaning the models were not so good at correctly predicting the percentage of actual negative cases (i.e. shots that missed).

## ETHICAL CONSIDERATIONS

As with any dataset that includes specific data on real people - we must carefully consider the impact of our predictions on individuals. We have specifically chosen to exclude player name and defender from our application in consideration of possible discrimination against individual players. Instead, we present our application as a generic tool to be used for any kind of basketball decision making (i.e. determining the best positioning, post-game review, testing new strategies, etc.)- not to judge specific players.

When using our application to predict shot percentages, it is important to remember the data set on which it is based. As a purely NBA dataset, it is only applicable to NBA players and should be used to generalize to other leagues such as the NCAA or WNBA where player characteristics, court specifics, rules, etc. may be different. There is risk in this predictive model being applied incorrectly, which is why we have tried to explicitly specify that this is an NBA predictor only.