Case Study 1

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Dear Budweiser Team,

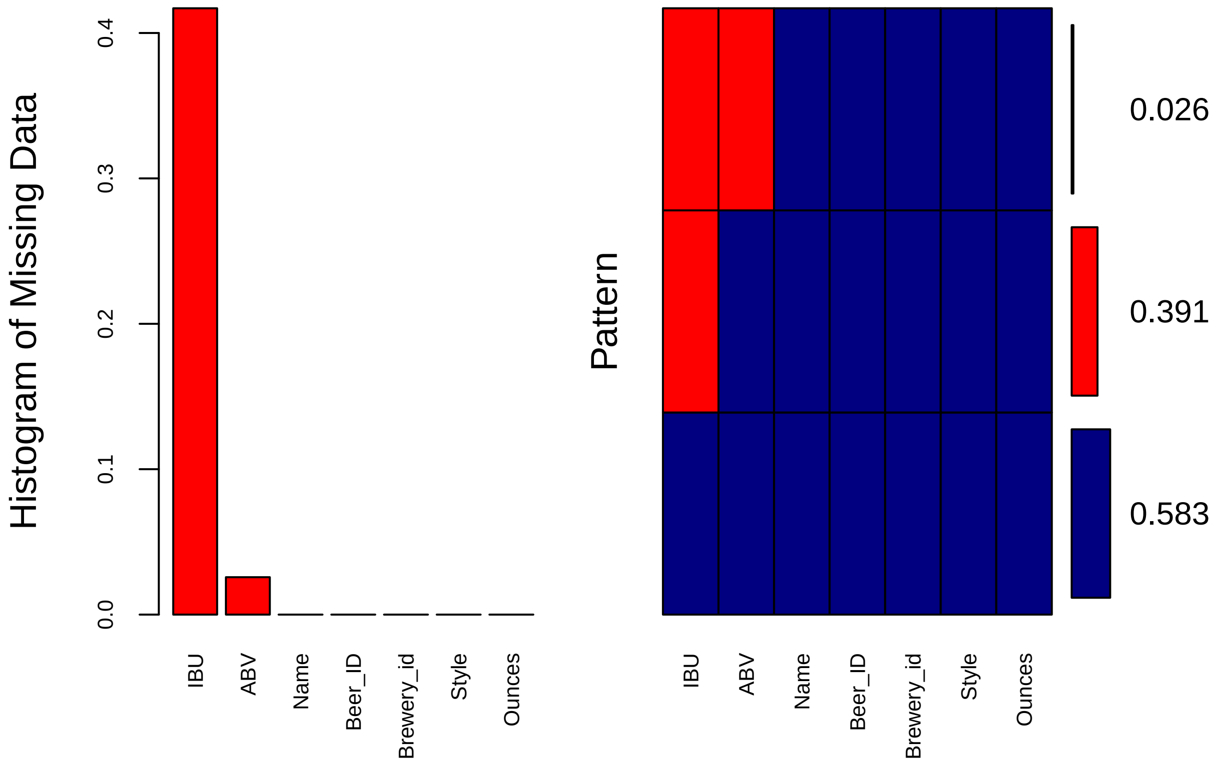
The purpose of this analytics study is to determine the relationship of ABV and IBU between your different types of beers (primarily IPAs and Ales). In this study I will explain how ABV and IBU are distributed between your IPAs and Ales, prove to you that IPAs and Ales have significantly different ABV and IBU ratings, as well as recommend to you an ABV range for future IPAs and Ales you produce which your customers should be satisfied with.

Importing Libraries

```
library(dplyr) #join etc
library(naniar) # check nulls
library(mice) # imputing
library(VIM) # view imputed datas
library(stringi)
library(stringr)
library(rvest) #html_table, html_node
library(purrr)
library(tidyverse) # Data cleaning
library(tidyr) # Data cleaning
library(ggthemes) #Plotting
library(plotly) #Plotting
library(ggplot2) #Plotting
library(reshape2) # melt
library(GGally) # ggpairs
library(caret) #Confution matrix
library(class)
library(caret)
library(e1071)
```

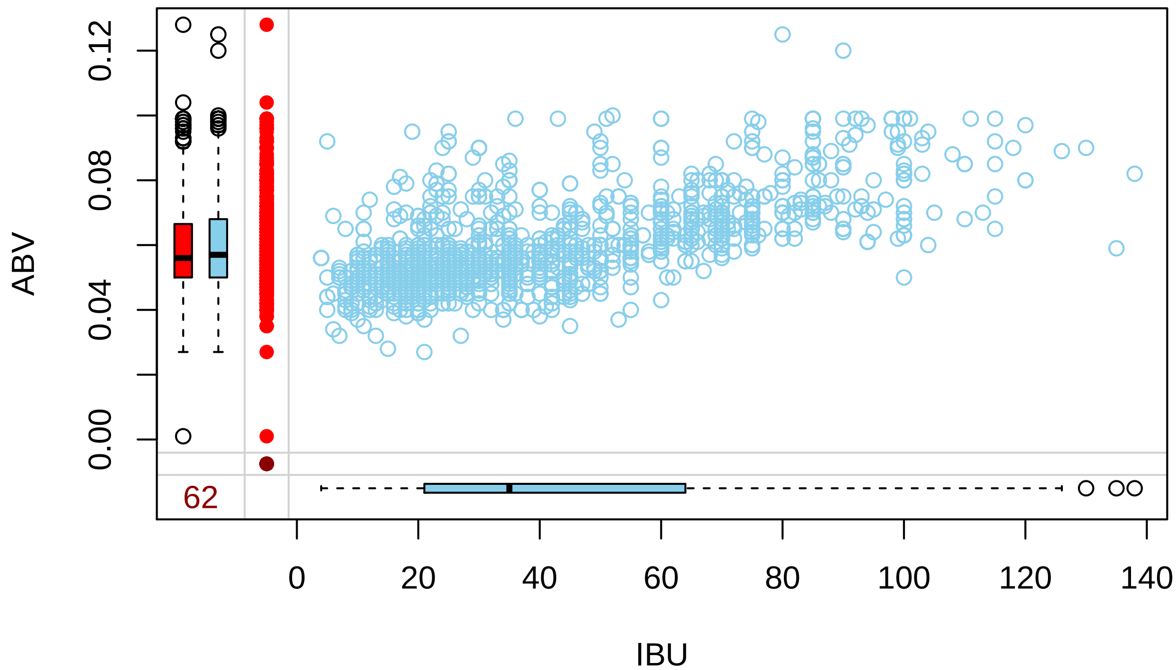
3) We wanted to begint the analysis by addressing all of the missing values. Only the ABV and IBU columns have missing values. They are both continuous random variables. We addressed the missing values with the mice package, using a method called predictive mean matching. Predictive mean matching calculates the predicted value of target variable by forming a small set of complete observations that have predicted values closest to the predicted value for the missing entry. One of the complete observations from the set is randomly drawn and the target variable of the observation is taken to replace the missing value.

```
#Read supplied data
cdw = getwd()
brewwriesData = read.csv("/Users/angelobravo/Downloads/MDS-6306-Doing-Data-Science-Fall-2019-master-4/Un
beerData = read.csv("/Users/angelobravo/Downloads/MDS-6306-Doing-Data-Science-Fall-2019-master-4/Unit 8


# about 58.3% of data are not missing any values
# 40% of IBU and 2.6% of ABV are misisng values
aggr_plot <- aggr(beerData, col=c('navyblue','red'), numbers=TRUE, sortVars=TRUE,
                  labels=names(beerData), cex.axis=.7, gap=3,
                  ylab=c("Histogram of Missing Data","Pattern"))
```




```
##
## Variables sorted by number of missings:
##    Variable      Count
##         IBU 0.41701245
##         ABV 0.02572614
##        Name 0.00000000
##     Beer_ID 0.00000000
##  Brewery_id 0.00000000
##       Style 0.00000000
##      Ounces 0.00000000
```

```
# left box plot to distribution of AVB with and without misisng IBU
#Right shows there are no IBU observations where ABV is missing
marginplot(beerData[c('IBU','ABV')])
```



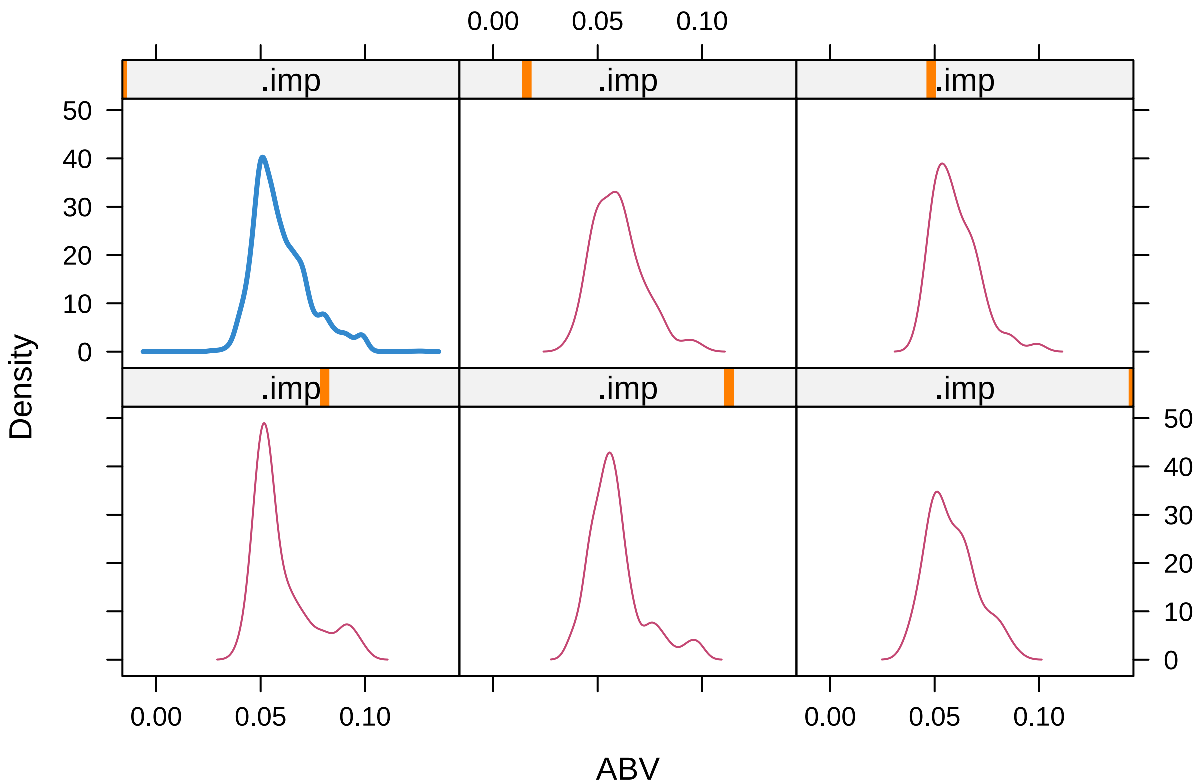

```
# Deal with missing values
#t = beerData %>% head(100)

# We will get all missing vars to build the predictorMatrix to be passed to mice
missVars <- names(beerData)[colSums(is.na(beerData)) > 0]

#Get all the variables names in the dataset
allVars <- names(beerData)

#Code borrwoed from https://rpubs.com/kaz_yos/mice-exclude
#Initialize the matrix witl all row  column having th evar names form above
predictorMatrix <- matrix(0, ncol = length(allVars), nrow = length(allVars))
rownames(predictorMatrix) <- allVars
colnames(predictorMatrix) <- allVars

#List the variables we want to be used for the calculations
imputerVars <- c("ABV","IBU","Style")

## Keep variables that actually exist in dataset
imputerVars <- intersect(unique(imputerVars), allVars)
imputerMatrix <- predictorMatrix
imputerMatrix[,imputerVars] <- 1

#Specify variables to be imputed
imputedOnlyVars <- c("ABV","IBU")
imputedVars <- intersect(unique(c(imputedOnlyVars, imputerVars)), missVars)
imputedMatrix <- predictorMatrix
imputedMatrix[imputedVars,] <- 1

predictorMatrix <- imputerMatrix * imputedMatrix
## Diagonals must be zeros (a variable cannot impute itself)
diag(predictorMatrix) <- 0
```

```r
#Generate 5 sets using 50 iterations using pnm (Predictive mean matching) method
imputedBeer = mice(beerData,m=5,maxit=50,meth='pmm',seed=500, predictorMatrix = predictorMatrix)
```

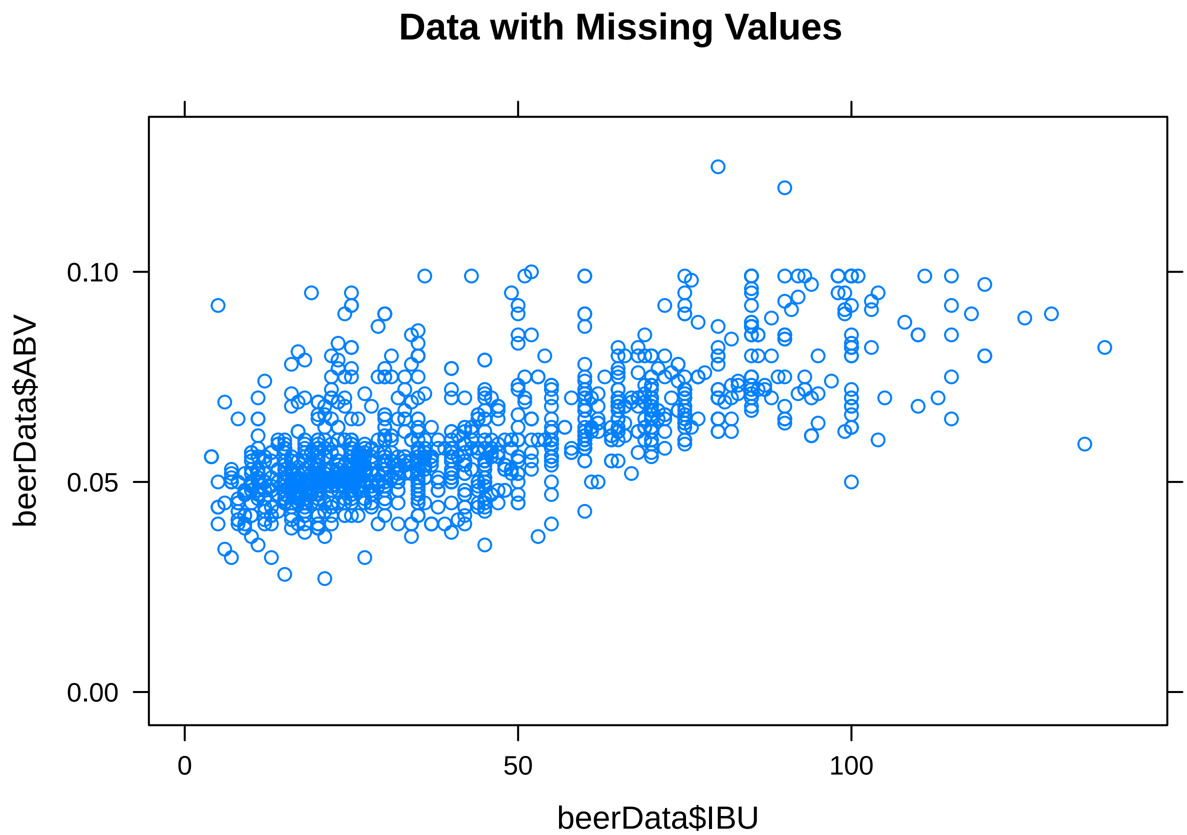
```
## Warning: Number of logged events: 250
```

Visualizng Imputed Dataset

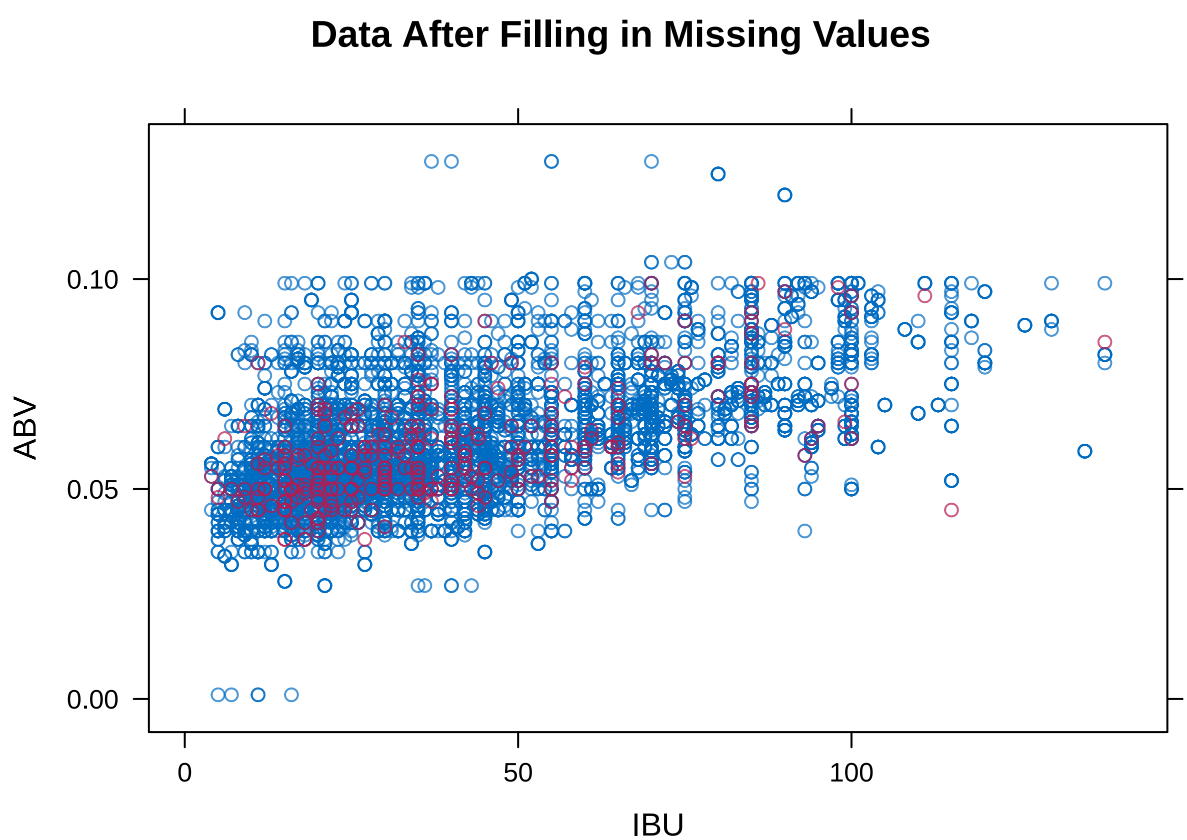
```r
densityplot(imputedBeer,IBU~ABV|.imp)
```




```r
completedData = mice::complete(imputedBeer,4)
xyplot(beerData$ABV ~ beerData$IBU,data = beerData, main = "Data with Missing Values")
```




```r
xyplot(imputedBeer,ABV ~ IBU, main = "Data After Filling in Missing Values")
```



1) Here is brewery count for each state.

```
brewwriesData %>% count(State)
```

```
## # A tibble: 51 x 2
##    State     n
##    <fct> <int>
##  1 " AK"     7
##  2 " AL"     3
##  3 " AR"     2
##  4 " AZ"    11
##  5 " CA"    39
##  6 " CO"    47
##  7 " CT"     8
##  8 " DC"     1
##  9 " DE"     2
## 10 " FL"    15
## # ... with 41 more rows
```

2) We merged the data and printed the first 6 and last 6 observations

```
beerBrewries = merge(completedData, brewwriesData, by.x = "Brewery_id", by.y = "Brew_ID")
head(beerBrewries,6)
```

```
##   Brewery_id        Name.x Beer_ID   ABV IBU
## 1          1  Get Together    2692 0.045  50
## 2          1 Maggie's Leap    2691 0.049  26
## 3          1    Wall's End    2690 0.048  19
## 4          1       Pumpion    2689 0.060  38
## 5          1    Stronghold    2688 0.060  25
## 6          1   Parapet ESB    2687 0.056  47
##                                Style Ounces             Name.y
## 1                     American IPA     16 NorthGate Brewing
## 2               Milk / Sweet Stout     16 NorthGate Brewing
## 3                English Brown Ale     16 NorthGate Brewing
## 4                      Pumpkin Ale     16 NorthGate Brewing
## 5                  American Porter     16 NorthGate Brewing
## 6 Extra Special / Strong Bitter (ESB)     16 NorthGate Brewing
##          City State
## 1 Minneapolis    MN
## 2 Minneapolis    MN
## 3 Minneapolis    MN
## 4 Minneapolis    MN
## 5 Minneapolis    MN
## 6 Minneapolis    MN
```

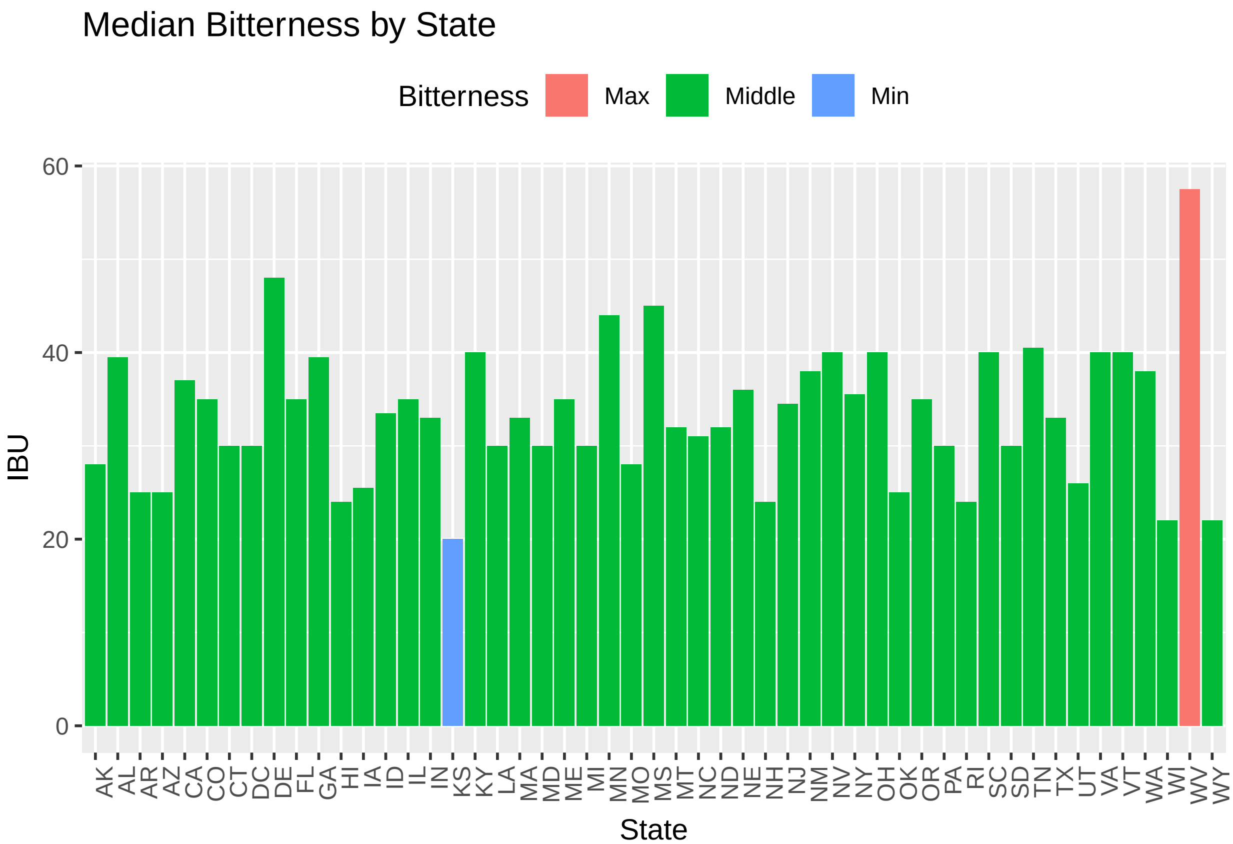
```
tail(beerBrewries,6)
```

```
##      Brewery_id                    Name.x Beer_ID   ABV IBU
## 2405        556             Pilsner Ukiah      98 0.055  23
## 2406        557  Heinnieweisse Weissebier      52 0.049  27
## 2407        557           Snapperhead IPA      51 0.068  65
## 2408        557         Moo Thunder Stout      50 0.049  22
## 2409        557         Porkslap Pale Ale      49 0.043  45
## 2410        558 Urban Wilderness Pale Ale      30 0.049  22
##                         Style Ounces                        Name.y
## 2405          German Pilsener     12         Ukiah Brewing Company
```

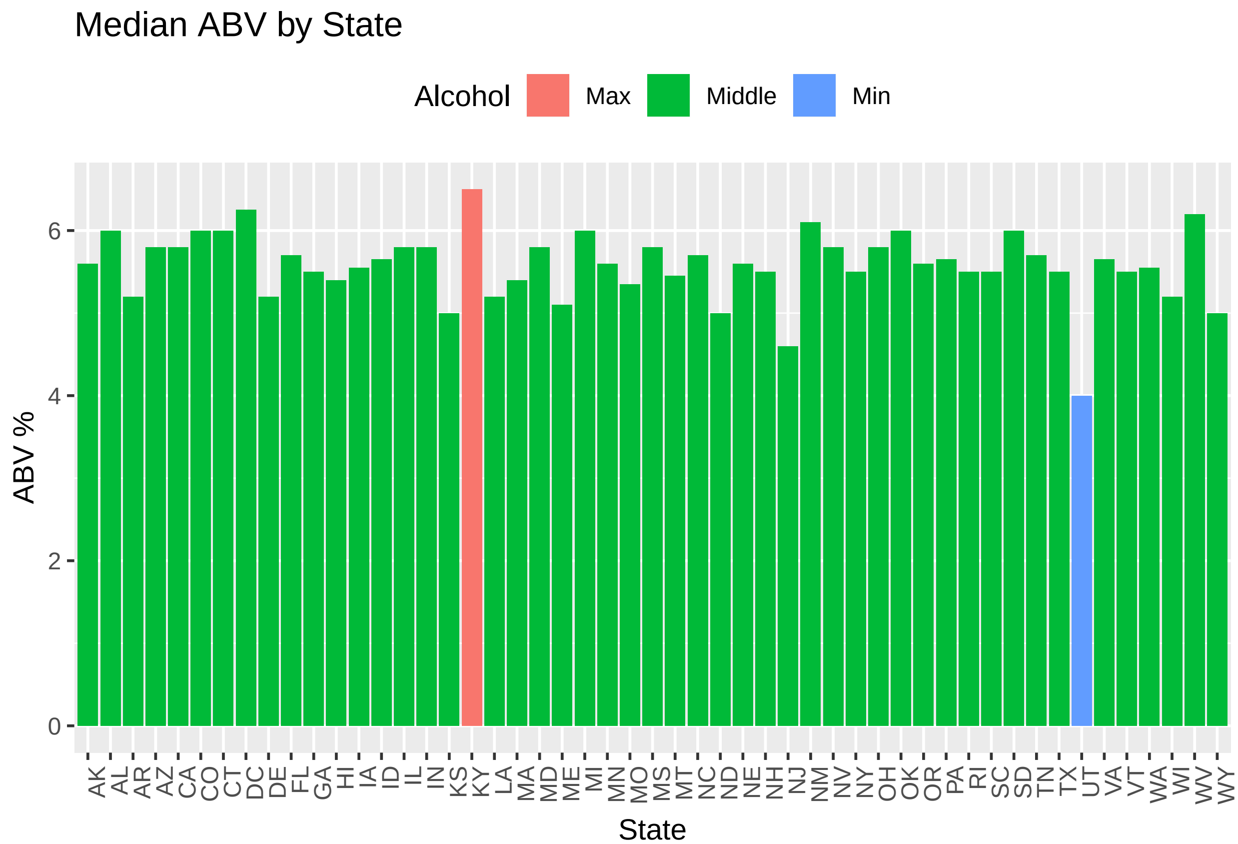
```
## 2406             Hefeweizen     12       Butternuts Beer and Ale
## 2407            American IPA     12       Butternuts Beer and Ale
## 2408      Milk / Sweet Stout     12       Butternuts Beer and Ale
## 2409 American Pale Ale (APA)     12       Butternuts Beer and Ale
## 2410        English Pale Ale     12 Sleeping Lady Brewing Company
##               City State
## 2405         Ukiah    CA
## 2406 Garrattsville    NY
## 2407 Garrattsville    NY
## 2408 Garrattsville    NY
## 2409 Garrattsville    NY
## 2410     Anchorage    AK
```

4) Here we will demonstrate the median alcohol content (ABV) and bitterness (IBU) for each state

```
abByState = beerBrewries %>% group_by(State) %>%
  summarize(medianIBU = median(IBU), medianABV = median(ABV))
abByState = abByState %>% mutate(Bitterness = 'Middle')
abByState[which.max(abByState$medianIBU),]$Bitterness = "Max"
abByState[which.min(abByState$medianIBU),]$Bitterness = "Min"
abByState = abByState %>% mutate(Alcohol = 'Middle')
abByState[which.max(abByState$medianABV),]$Alcohol = "Max"
abByState[which.min(abByState$medianABV),]$Alcohol = "Min"

#Comparision bar chart per state
p = ggplot(abByState,aes(x = State,y = medianIBU)) +
    geom_bar(aes(fill = Bitterness),stat = "identity") +
  labs(title="Median Bitterness by State", y = "IBU", x="State" ) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1))
p + theme(legend.position = "top")
```




```
p =ggplot(abByState,aes(x = State,y = medianABV*100)) +
    geom_bar(aes(fill = Alcohol),stat = "identity") +
  labs(title="Median ABV by State", y = "ABV %", x="State" ) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1))
p + theme(legend.position = "top")
```




```r
#Identify beer Categories by Lager//Ale/Other
beerBrewries = beerBrewries %>% mutate(bClass = 'Other')
beerBrewries = beerBrewries %>% mutate(ABVpercent = ABV*100)
beerBrewries[grepl('IPA',beerBrewries$Style, ignore.case = TRUE),]$bClass = "IPA"
beerBrewries[grepl('Ale',beerBrewries$Style, ignore.case = TRUE),]$bClass = "Ale"
#beerBrewries[grepl('lager',beerBrewries$Style, ignore.case = TRUE),]$bClass = "Lager"
```

5) The states with maximum ABV and maximum IBU, which were Colorado and Oregon, respectively.

```r
#State with max ABV
beerBrewries$State[which.max(beerBrewries$ABV)]
```

```
## [1]  CO
## 51 Levels:  AK  AL  AR  AZ  CA  CO  CT  DC  DE  FL  GA  HI  IA  ID ...  WY
```

```r
#State with max IBU
beerBrewries$State[which.max(beerBrewries$IBU)]
```

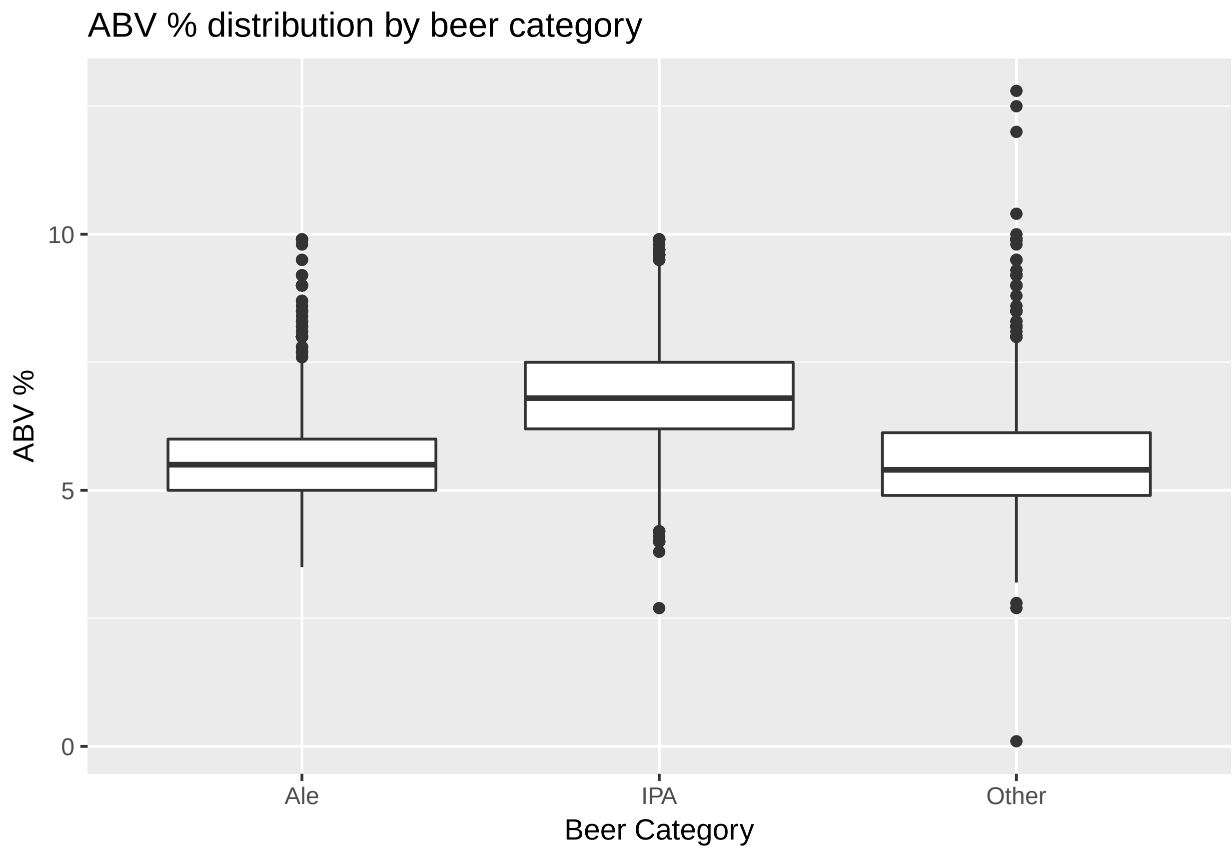
```
## [1]  OR
## 51 Levels:  AK  AL  AR  AZ  CA  CO  CT  DC  DE  FL  GA  HI  IA  ID ...  WY
```

6) We will now comment on the summary statistics and distribution of the ABV variable: ABV in our dataset ranges from 0.10% to 12.80%. ABV has a median of 5.65% and mean of 5.98%. According to our boxplot, IPA have the highest median ABV. IPAs, Ales, and all other categories (combined) all have different median ABVs. IPA ABV appears to most closely resemble a normal distribution, while Ales and Others appear to be more positively skewed.

```r
beerBrewries = beerBrewries %>% mutate(bClass = as.factor(bClass))
summary(beerBrewries$ABVpercent)
```

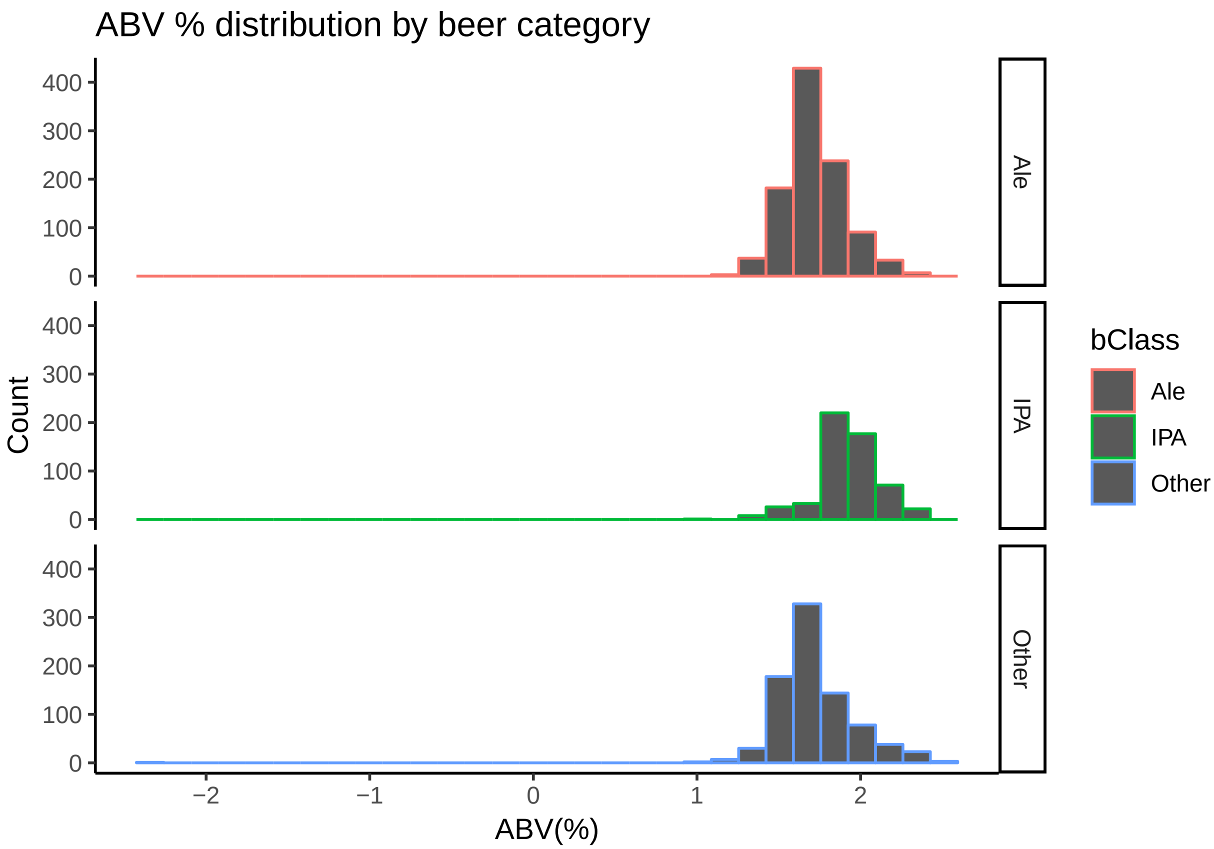
```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.100   5.000   5.600   5.974   6.700  12.800
```

```
beerBrewries %>% ggplot(aes(x = bClass, y = ABVpercent)) +
  geom_boxplot() +
  labs(title="ABV % distribution by beer category", y = "ABV %", x="Beer Category" )
```



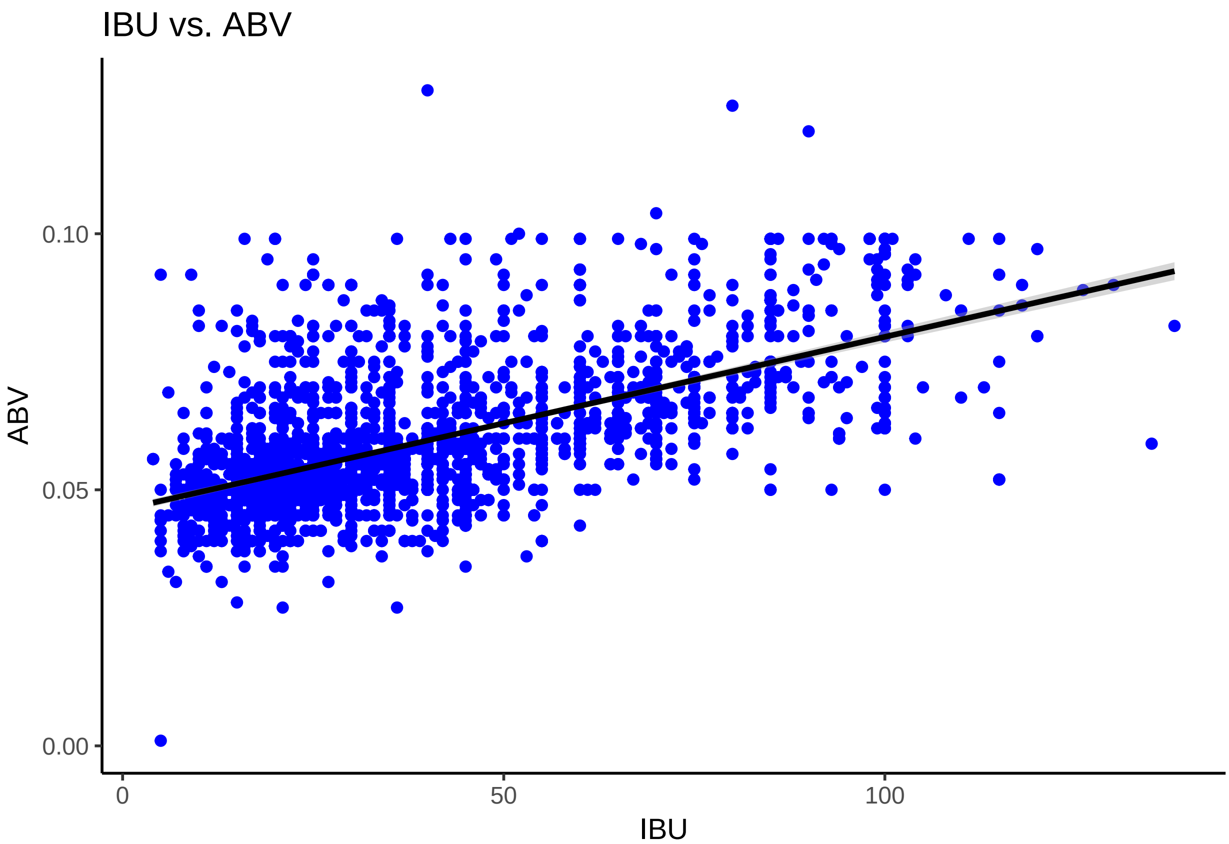

```
beerBrewries %>%

ggplot(aes(x = log(ABVpercent), color = bClass)) +
  geom_histogram() + facet_grid(rows = vars(bClass)) +
  labs(title="ABV % distribution by beer category", y = "Count", x="ABV(%)" ) +
  theme_classic()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



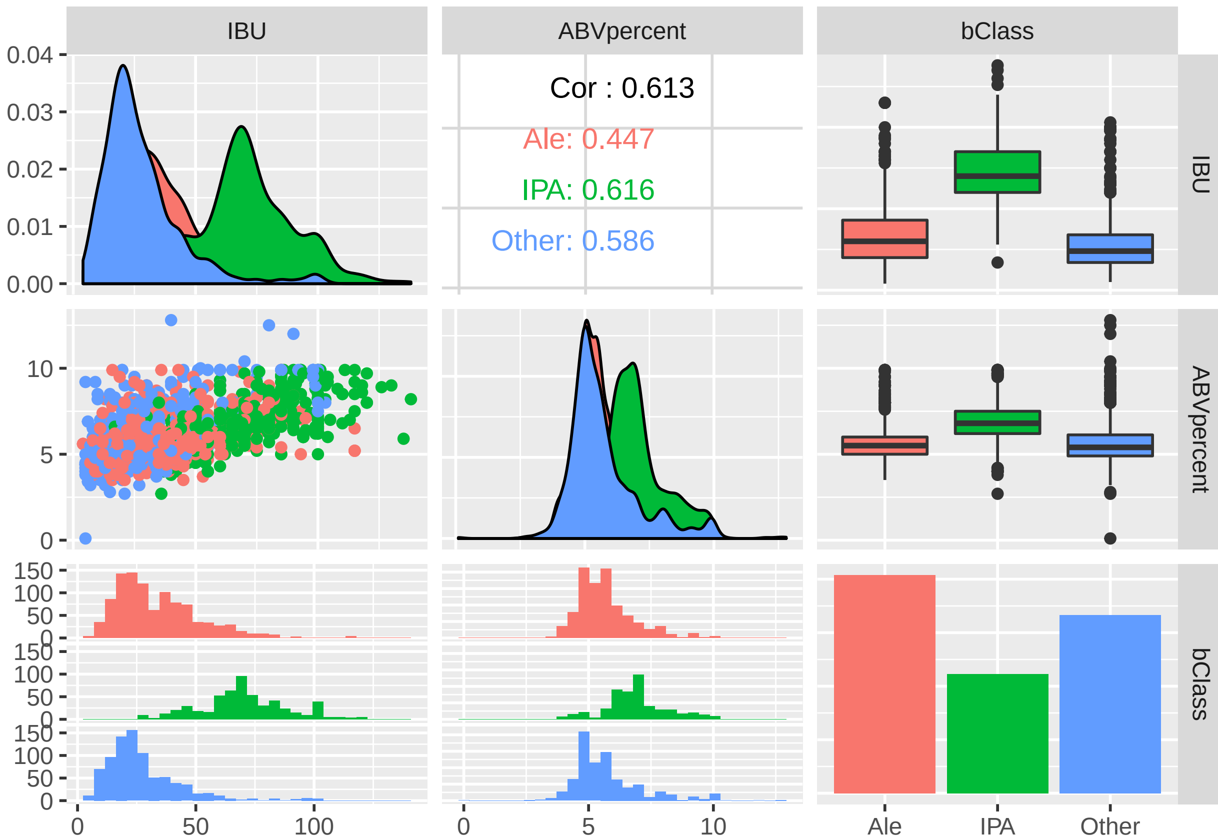
7) We will now demonstrate the relationship between ABV and IBU. It is evident that there is a moderately positive correlation between IBU and ABV regardless of beer type. As IBU increases, ABV tends to increase.

```
beerBrewries %>%
  ggplot(aes(x = IBU, y = ABV)) + geom_point(color = "blue") +
  labs(title="IBU vs. ABV", y = "ABV", x="IBU" ) +
  geom_smooth(method = "lm", color = "black") +
  theme_classic()
```




```r
beerBrewries %>%  select( IBU, ABVpercent,bClass) %>% ggpairs(aes(color = bClass))
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



Preparing dataset for KNN Creating IPA/Ale only dataframe

```
ipa_ale_df <- beerBrewries %>% filter(bClass %in% c("IPA", "Ale"))
ipa_df <- beerBrewries %>% filter(bClass %in% c("IPA"))
ale_df <- beerBrewries %>% filter(bClass %in% c("Ale"))
ipa_ale_df$bClass <-  droplevels(ipa_ale_df$bClass)
ipa_ale_df$bClass <- factor(ipa_ale_df$bClass, levels = c("IPA", "Ale"))

#removing ale,other levels
ipa_df$bClass <- droplevels(ipa_df$bClass)
#adding ale level to ipa_df
ipa_df$bClass <- factor(ipa_df$bClass,
                        levels = c(levels(ipa_df$bClass), "Ale"))
#same process to ale_df
ale_df$bClass <- droplevels(ale_df$bClass)
#adding ale level to ipa_df
ale_df$bClass <- factor(ale_df$bClass,
                        levels = c(levels(ale_df$bClass), "IPA"))
```

8) We will now be using KNN in order to show that there is a significant difference in ABV and IBU between IPAs and Ales by fitting 100 models for 100 Ks and getting the mean accuracy for each K.

In order to demonstrate that ABV and IBU values are significantly different from each other between Ales and IPAs, we wanted to show that we can attain a predictive accuracy greater than 50% (random guess) when classifying only between IPAs and Ales. We did this by: *Gathering a subset of the data which only contained IPA or ALE as a factor.* Performing 100 iterations of 50/50 Ale/IPA splits for the train data, and running KNN on each iteration for 100 Ks using only IPAs and Ales in our test set.

Results: Our maximum accuracy was 93.3% with K=11, with a sensitity of 93.3% and specificity 94.3%.

Our accuracies from all models range from 74.0% (k = 1) to 94.0% (k = 11). Our overall best performing average K for 100 iterations was K = 61, with a mean accuracy of 84.9%, mean sensitivity of 83.6%, and mean specificity 85.3%. All of our predictive accuracy results for 10,000 models fitted were significantly greater than 50%, showing that there is a significant distinction in ABV and IBU between Ales and IPAs.

```r
#IPA,ALE VS IPA,ALE (50/50 split)
set.seed(100)
n = 1
accuracydf <- data.frame(accuracy = numeric(10000), k = numeric(10000),
                         sensitivity = numeric(10000), specificity = numeric(10000))
for(i in 1:100) {
  #Get dataset with evenly distributed IPAs and Ales (50/50)
  ipa_test_ind <- sample(1:nrow(ipa_df), nrow(ipa_df)-250)
  ale_df_ind <- sample(1:nrow(ale_df), 250)
  #building train set
  ipa_ale_train <- rbind(ipa_df[-ipa_test_ind,], ale_df[ale_df_ind,])
  ipa_ale_overall_test <- ipa_ale_df[sapply(ipa_ale_df$Name.x,
                               function(x) x %in% ipa_ale_train$Name.x) == FALSE,]
  ipa_ale_test_ind <- sample(1:nrow(ipa_ale_overall_test),
                               round(.2 * nrow(ipa_ale_train)))
  ipa_ale_test <- ipa_ale_overall_test[ipa_ale_test_ind,]


  #storing accuracy data in data frame
  for(j in 1:100) {
    classifications <- knn(ipa_ale_train[c("ABV", "IBU")],
                           ipa_ale_test[c("ABV", "IBU")],
                           cl = ipa_ale_train$bClass, k = j, prob = F)
    CM = confusionMatrix(table(classifications, ipa_ale_test$bClass))
    accuracydf$accuracy[n] = CM$overall[1]
    accuracydf$sensitivity[n] = CM$byClass["Sensitivity"]
    accuracydf$specificity[n] = CM$byClass["Specificity"]
    accuracydf$k[n] = j
    n = n + 1
  }
}



#grabbing lowest accuracy and respective k
accuracydf[which.min(accuracydf$accuracy), ]
```

```
##     accuracy k sensitivity specificity
## 201     0.74 1    0.826087   0.7142857
```

```r
#grabbing highest accuracy and respective k
accuracydf[which.max(accuracydf$accuracy), ]
```

```
##      accuracy  k sensitivity specificity
## 2911     0.94 11   0.9333333   0.9428571
```

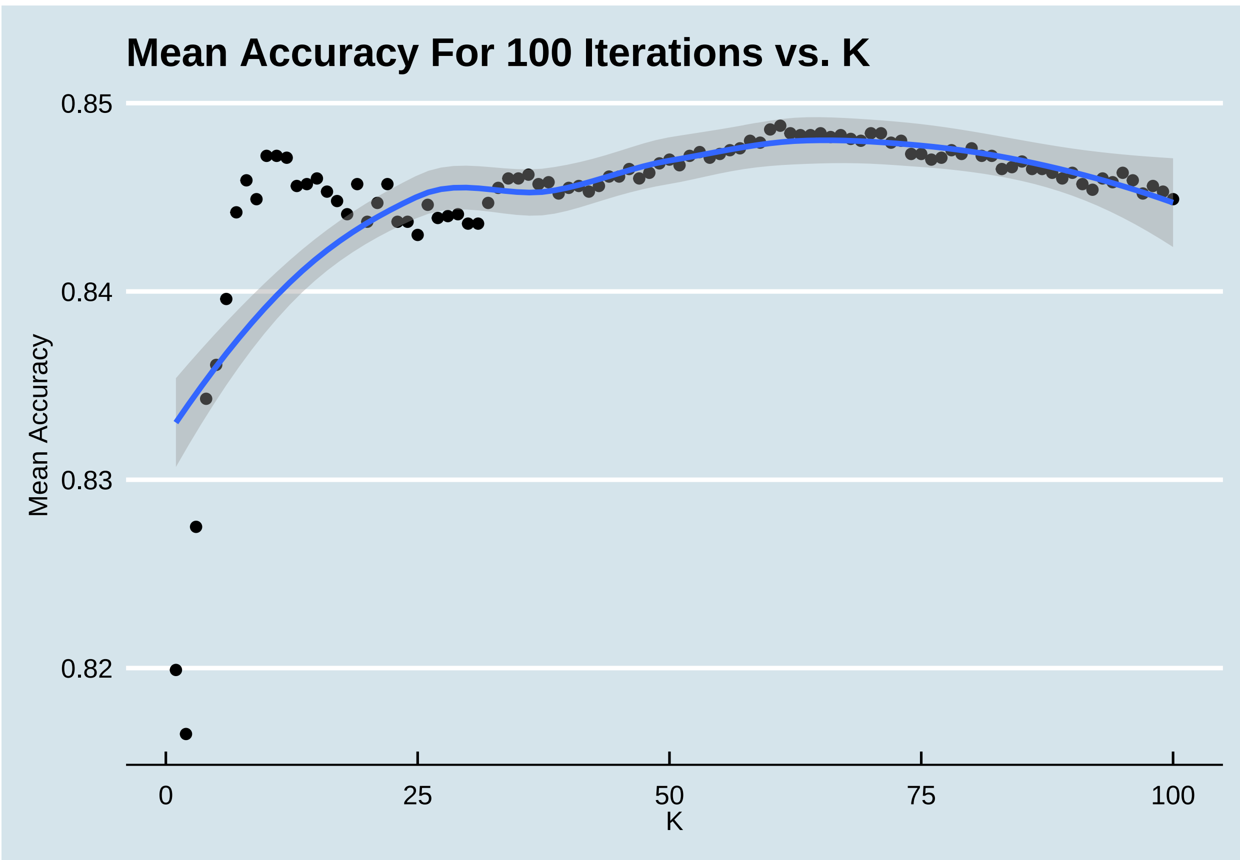
```r
summary_acc_df <- accuracydf %>% group_by(k) %>%
  summarise(mean_accuracy = mean(accuracy),
  mean_sensitivity = mean(sensitivity),
  mean_specificity = mean(specificity, na.rm = T))
```

```r
#overall_mean_accuracy
overall_mean_accuracy <- summary_acc_df[which.max(summary_acc_df$mean_accuracy),]
acc_df <- as.data.frame(summary_acc_df)

#Grabbing maximum average mean accuracy and respective k
overall_mean_accuracy
```

```
## # A tibble: 1 x 4
##       k mean_accuracy mean_sensitivity mean_specificity
##   <dbl>         <dbl>            <dbl>            <dbl>
## 1    61         0.849            0.836            0.853
```

```r
library(ggthemes)
acc_df %>% ggplot(aes(x = k, y = mean_accuracy)) + geom_point() +
  geom_smooth() + theme_economist() +
  ggtitle("Mean Accuracy For 100 Iterations vs. K") +
  xlab("K") + ylab("Mean Accuracy")
```

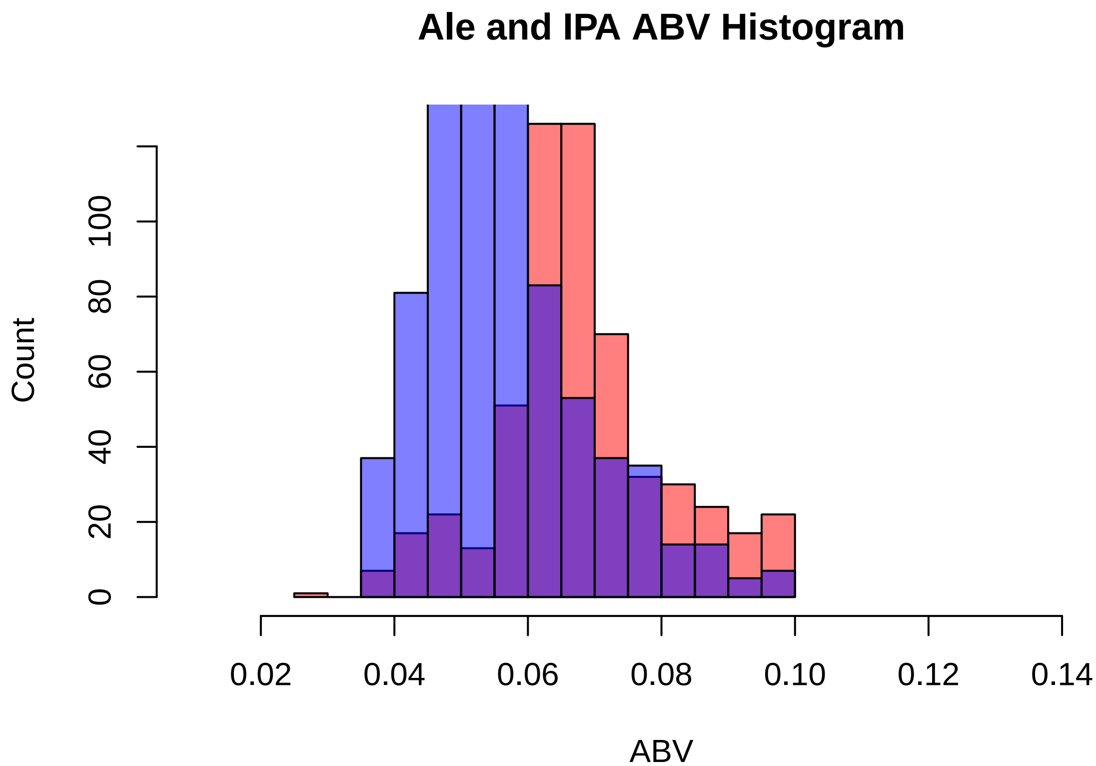
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



9) We will now get ABV 95% confidence intervals for IPAs and Ales to help Budweiser determine what ABV levels to produce their IPAs and Ales. ALES: *We can say with 95% confidence that the true mean ABV for all Ales lies within 5.59% - 5.73%. IPAs:* We can say with 95% confidence that the true mean ABV for all Ales lies within 6.79% - 7.01%. Takeaways: *Producing IPAs or Ales with ABVs within their respective ranges provides a guarantee that consumers will be comfortable with that ABV when purchasing your IPAs or Ales.* Knowing that ABV is positively correlated with IBU, your consumers

should be comfortable with IBU levels of beers with an ABV within their respective mean ranges.

```r
#ABV Distribution of Ales and IPAs
hist(ipa_ale_df$ABV[ipa_ale_df$bClass=="IPA"], col=rgb(1,0,0,0.5),
     xlim = range(.01,.15), main="Ale and IPA ABV Histogram",
     xlab = "ABV", ylab = "Count")
hist(ipa_ale_df$ABV[ipa_ale_df$bClass=="Ale"], col=rgb(0,0,1,0.5), add=T)
```




```r
#run a two-sample to test if the groups have significantly different ABVs
t.test(ipa_ale_df$ABV[ipa_ale_df$bClass=="IPA"], ipa_ale_df$ABV[ipa_ale_df$bClass=="Ale"])
```

```
##
##  Welch Two Sample t-test
##
## data:  ipa_ale_df$ABV[ipa_ale_df$bClass == "IPA"] and ipa_ale_df$ABV[ipa_ale_df$bClass == "Ale"]
## t = 19.513, df = 1034.3, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.01114313 0.01363483
## sample estimates:
##  mean of x  mean of y
## 0.06902330 0.05663431
```

```r
#run a ttest on each group in order to determine a 95% CI of abv for each group
t.test(ipa_ale_df$ABV[ipa_ale_df$bClass=="IPA"])
```

```
##
##  One Sample t-test
##
## data:  ipa_ale_df$ABV[ipa_ale_df$bClass == "IPA"]
## t = 130, df = 557, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
```

```
## 95 percent confidence interval:
##  0.06798038 0.07006622
## sample estimates:
## mean of x
## 0.0690233
```

```r
t.test(ipa_ale_df$ABV[ipa_ale_df$bClass=="Ale"])
```

```
##
##  One Sample t-test
##
## data:  ipa_ale_df$ABV[ipa_ale_df$bClass == "Ale"]
## t = 162.68, df = 1019, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  0.05595119 0.05731744
## sample estimates:
##  mean of x
## 0.05663431
```