Case Study 1 - Beers and Breweries in USA

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```
#install.packages("tinytex")
#tinytex::install_tinytex()
```

Prepare Data

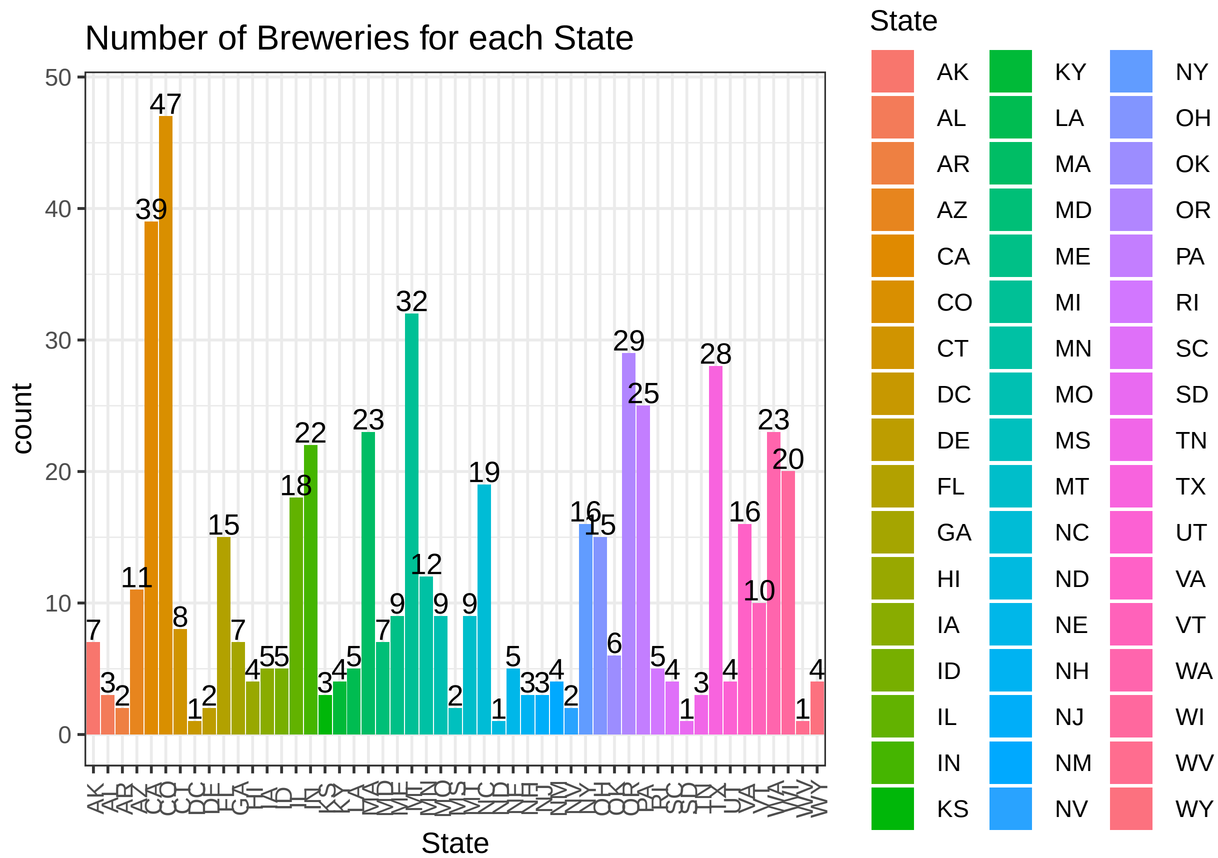
We first prepare data. We import Brew and Breweries data from CSV files and include necessary libraries for our code.

```
library(ggplot2)
library(tidyr)
library(plyr)
library(dplyr)
library(class)
library(caret)
library(e1071)
library(RCurl)
library(httr)
library("RColorBrewer")

x<-getURL('https://raw.githubusercontent.com/yuchrishin/DS6306-GroupProject1/master/data/Beers.csv')
beers =read.csv(text=x)

y<- getURL('https://raw.githubusercontent.com/yuchrishin/DS6306-GroupProject1/master/data/Breweries.csv
breweries = read.csv(text=y)
```

Number of Breweries per state

We want to analyze number of breweries in each states. We count the number of breweries for each state and plot it on top of each bar. From the graph, we can see that Colorado and California have most number of breweries. We see that some states have only 1 breweries such as DC, North and South Dakota. From this graph, we can ask a question why some states have more breweries than others.

```
totalState = count(breweries, State)
breweries %>% arrange() %>% ggplot(aes(x=State, fill = State)) + geom_bar() + geom_text(aes(State, n + 
```



Merge two data

Breweries and Beer data are two separate data. Merging these two datas will give more variables to analyze. For example, we can look into the relationship between states and beers. In order to merge, we need to find if they have key variable that we can join together. Breweries data has Brew_ID and Beer data has Brewery_id which we can merge. Converting the name of column in Beer, two datas are merged as below.

```
colnames(beers)[5] = "Brew_ID"
fullData = merge(beers, breweries, by = "Brew_ID")
head(fullData)
```

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

Missing values

In order to process the analysis, we need to clean up data as there might be some missing data or incorrectly formatted data. Below are the code that we have ran to find out if there is any missing data.

```r
sapply(fullData, function(x) sum(is.na(x)))
```

```
## Brew_ID  Name.x Beer_ID     ABV     IBU   Style  Ounces  Name.y    City   State
##       0       0       0      62    1005       0       0       0       0       0
```

```r
cleanData = fullData %>% filter(!is.na(ABV) & !is.na(IBU))
```

There are 1005 rows of data that do not have IBU value. We need a IBU data in order to make an analysis so we decided to drop the rows that are missing IBU and ABV data.

Median ABV and IBU per states

We want to look at the median values for each state. In order to get median for each states, we collecte the data grouping by state and summarize them. With the data we calculated, we draw a bar charts with median ABV and IBU of all states.

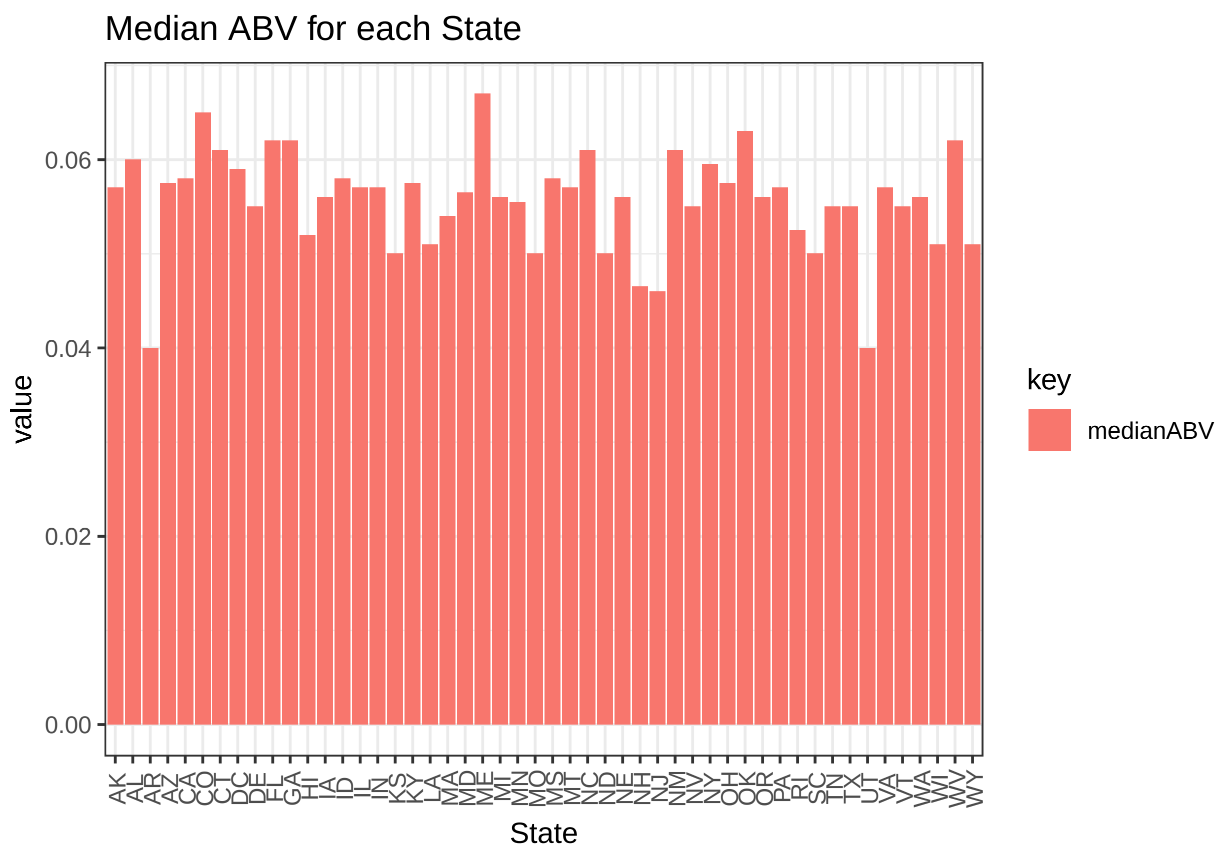
```r
cleanData %>% group_by(State) %>% summarize(medianABV = median(ABV), medianIBU = median(IBU), count = n
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 50 x 4
##    State medianABV medianIBU count
##    <fct>     <dbl>     <dbl> <int>
##  1 " AK"    0.057       46      17
##  2 " AL"    0.06        43       9
##  3 " AR"    0.04        39       1
##  4 " AZ"    0.0575      20.5    24
##  5 " CA"    0.058       42     135
##  6 " CO"    0.065       40     146
##  7 " CT"    0.061       29       6
##  8 " DC"    0.059       47.5     4
##  9 " DE"    0.055       52       1
## 10 " FL"    0.062       55      37
## # ... with 40 more rows
```

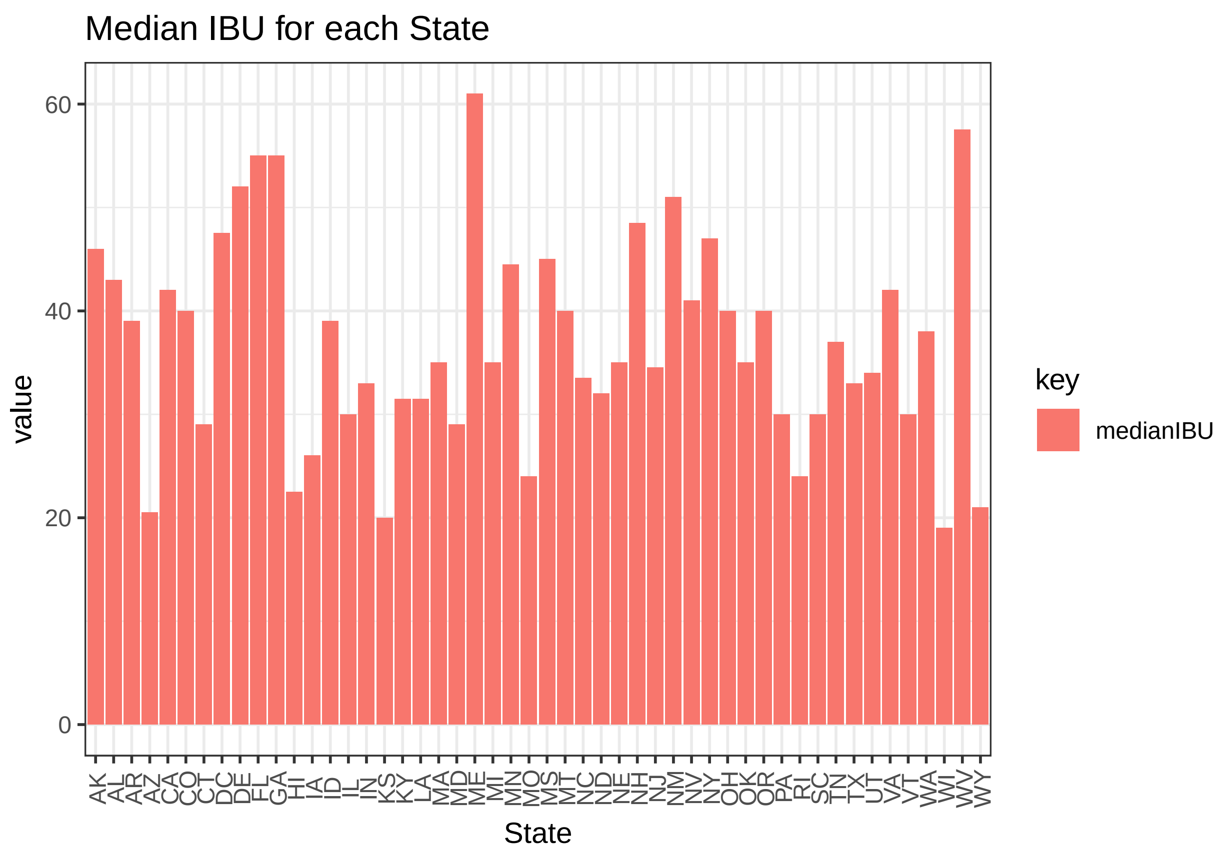
```r
cleanData %>%
  group_by(State) %>%
  summarise(medianABV = median(ABV)) %>%
  gather(key, value, -State) %>%
  ggplot(aes(State, value, fill = key)) + geom_bar(stat = "identity", position = "dodge") + ggtitle("Me
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```




```r
cleanData %>%
  group_by(State) %>%
  summarise(medianIBU = median(IBU)) %>%
  gather(key, value, -State) %>%
  ggplot(aes(State, value, fill = key)) + geom_bar(stat = "identity", position = "dodge") + ggtitle("Med
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```




```
medABV <- cleanData %>% group_by(State) %>% summarize(medianABV = median(ABV), medianIBU = median(IBU),
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
medABV <- medABV %>% select(State, medianABV)

medIBU <- cleanData %>% group_by(State) %>% summarize(medianABV = median(ABV), medianIBU = median(IBU),
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
medIBU <- medIBU %>% select(State, medianIBU)

head(medABV)
```

```
## # A tibble: 6 x 2
##   State medianABV
##   <fct>     <dbl>
## 1 " ME"     0.067
## 2 " CO"     0.065
## 3 " OK"     0.063
## 4 " FL"     0.062
## 5 " GA"     0.062
## 6 " WV"     0.062
```

```r
tail(medABV)
```

```
## # A tibble: 6 x 2
##   State medianABV
##   <fct>     <dbl>
## 1 " ND"    0.05
## 2 " SC"    0.05
## 3 " NH"    0.0465
## 4 " NJ"    0.046
## 5 " AR"    0.04
## 6 " UT"    0.04
```

```r
head(medIBU)
```

```
## # A tibble: 6 x 2
##   State medianIBU
##   <fct>     <dbl>
## 1 " ME"      61
## 2 " WV"      57.5
## 3 " FL"      55
## 4 " GA"      55
## 5 " DE"      52
## 6 " NM"      51
```

```r
tail(medIBU)
```

```
## # A tibble: 6 x 2
##   State medianIBU
##   <fct>     <dbl>
## 1 " RI"      24
## 2 " HI"      22.5
## 3 " WY"      21
## 4 " AZ"      20.5
## 5 " KS"      20
## 6 " WI"      19
```

In median ABV bar chart, we can see it quite evenly spread out except for Arizona and Utah that it has significatly lower medians than others. We see that Maine and Colorado has much higher median ABV than other states. For median IBU bar chart, results come out to be distributed wider than median ABV. We see there is dramatic differences for each states. We found Maine and West Virgina have highest median IBU, and Kansas and Wisconsin have lowest median IBU.

Max ABV and IBU of state

In order to get the max ABV and IBU value, we followed two approaches. One is to get max values for each state by grouping state and summarizing each state. Another appropach is to get max values among all states.

```r
cleanData %>% group_by(State) %>% summarize(maxABV = max(ABV), maxIBU = max(IBU))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 50 x 3
##    State maxABV maxIBU
##    <fct>  <dbl>  <int>
##  1 " AK"  0.065     71
##  2 " AL"  0.093    103
##  3 " AR"  0.04      39
##  4 " AZ"  0.095     99
##  5 " CA"  0.099    115
##  6 " CO"  0.099    104
##  7 " CT"  0.088     85
##  8 " DC"  0.092    115
##  9 " DE"  0.055     52
## 10 " FL"  0.082     82
## # ... with 40 more rows
```

```r
maxABV = max(cleanData$ABV)
maxIBU = max(cleanData$IBU)

cleanData %>% filter(ABV == maxABV)
```

```
##   Brew_ID         Name.x Beer_ID   ABV IBU              Style Ounces                    Name.y
## 1       2 London Balling    2685 0.125  80 English Barleywine     16 Against the Grain Brewery Louis
```

```r
cleanData %>% filter(IBU == maxIBU)
```

```
##   Brew_ID                     Name.x Beer_ID   ABV IBU                          Style Ounces
## 1     375 Bitter Bitch Imperial IPA     980 0.082 138 American Double / Imperial IPA     12 Astoria 
```

First chart display max ABV and IBU for each state. From the data, we found that London Balling has ABV of 0.125 and it has maximum ABV among all beers. We also found Bitter Bitch Imperial IPA contains IBU of 138 which is the maximum among all beers.

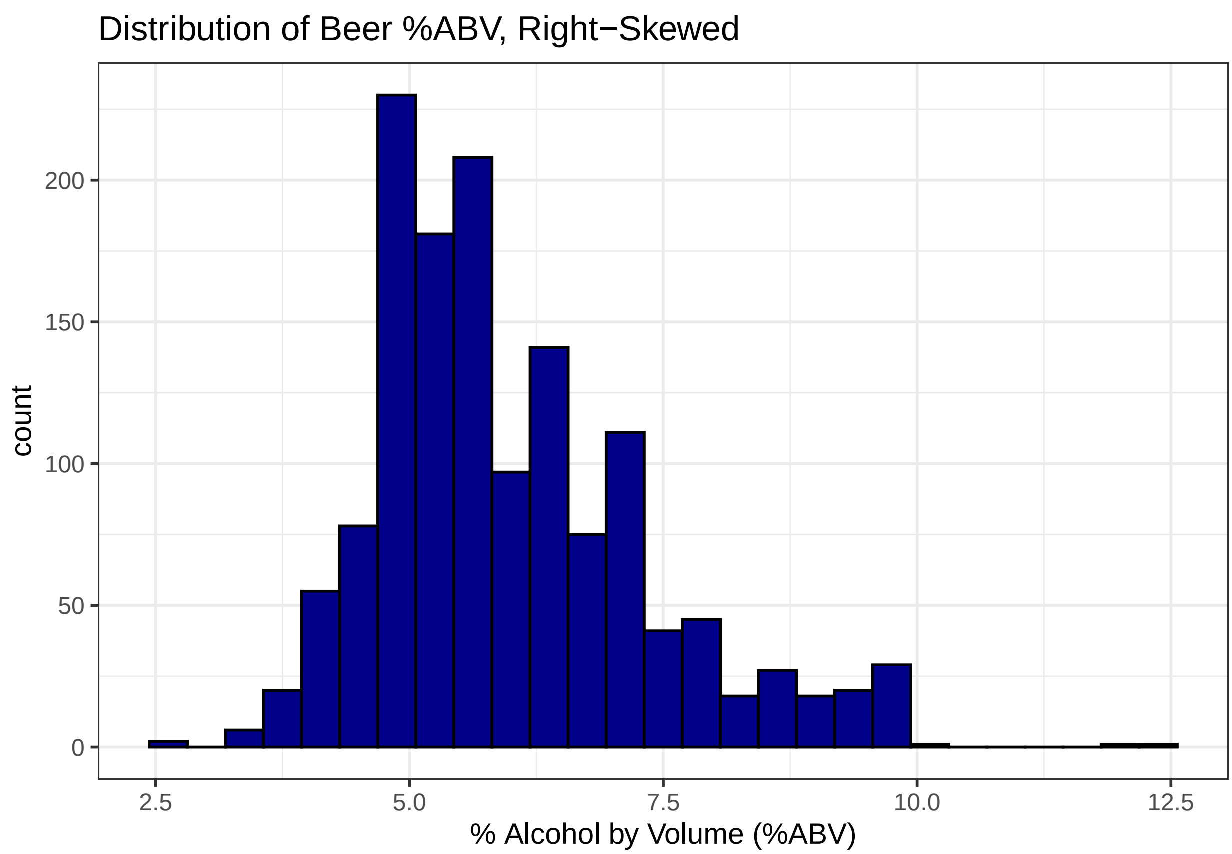
Summarize ABV

Checking distribution of the data is one of key part of EDA. We plot several distributions graphs of ABV to check its normality.

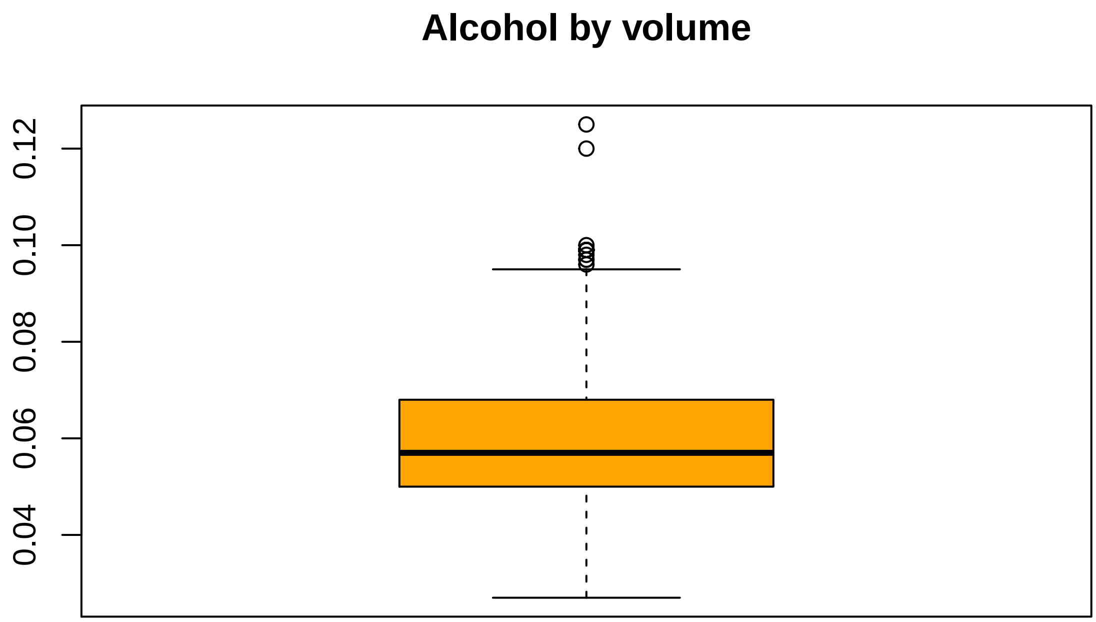
```r
summary(cleanData$ABV)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.02700 0.05000 0.05700 0.05991 0.06800 0.12500
```

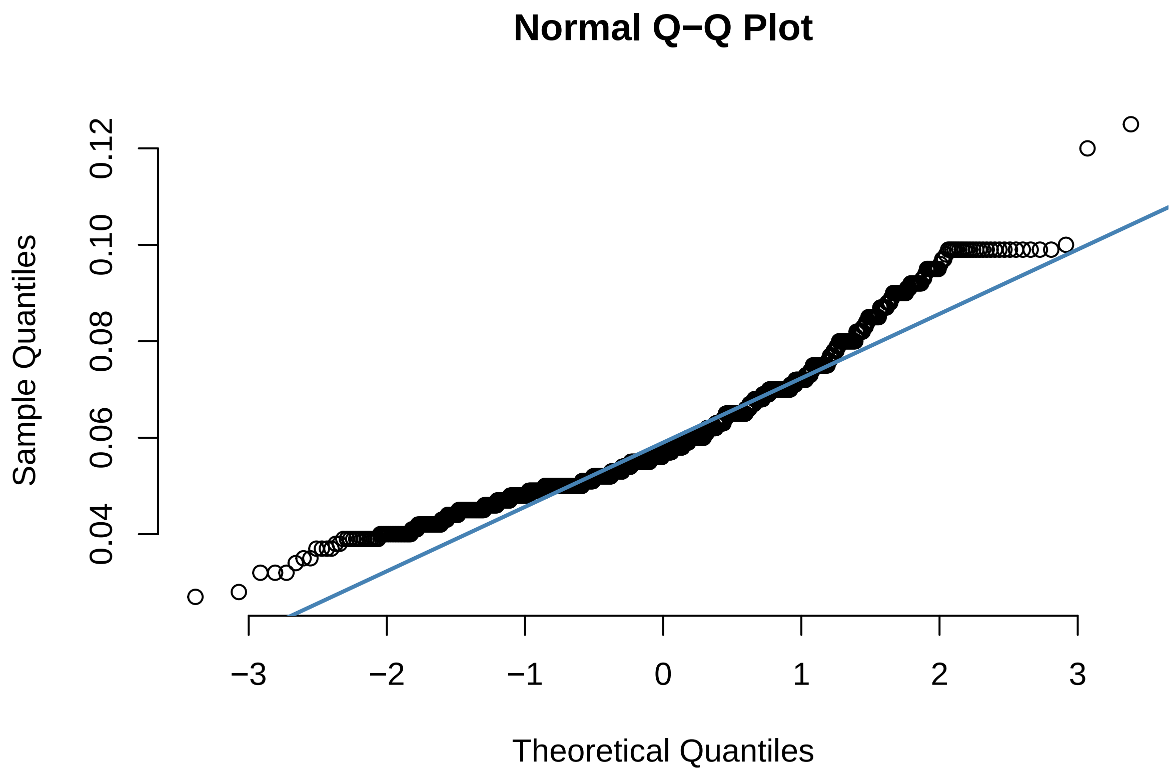
```r
# Histogram of ABV Percentage
cleanData  %>% ggplot(aes(ABV*100)) + geom_histogram(fill="darkblue",color="black", binwidth= 0.375) + 
```




```
# Box Plot
boxplot(cleanData$ABV, col='orange',main = 'Alcohol by volume')
```




```r
# QQ plot for normality check
qqnorm(cleanData$ABV, pch = 1, frame = FALSE)
qqline(cleanData$ABV, col = "steelblue", lwd = 2, main = 'Alcohol by volume')
```

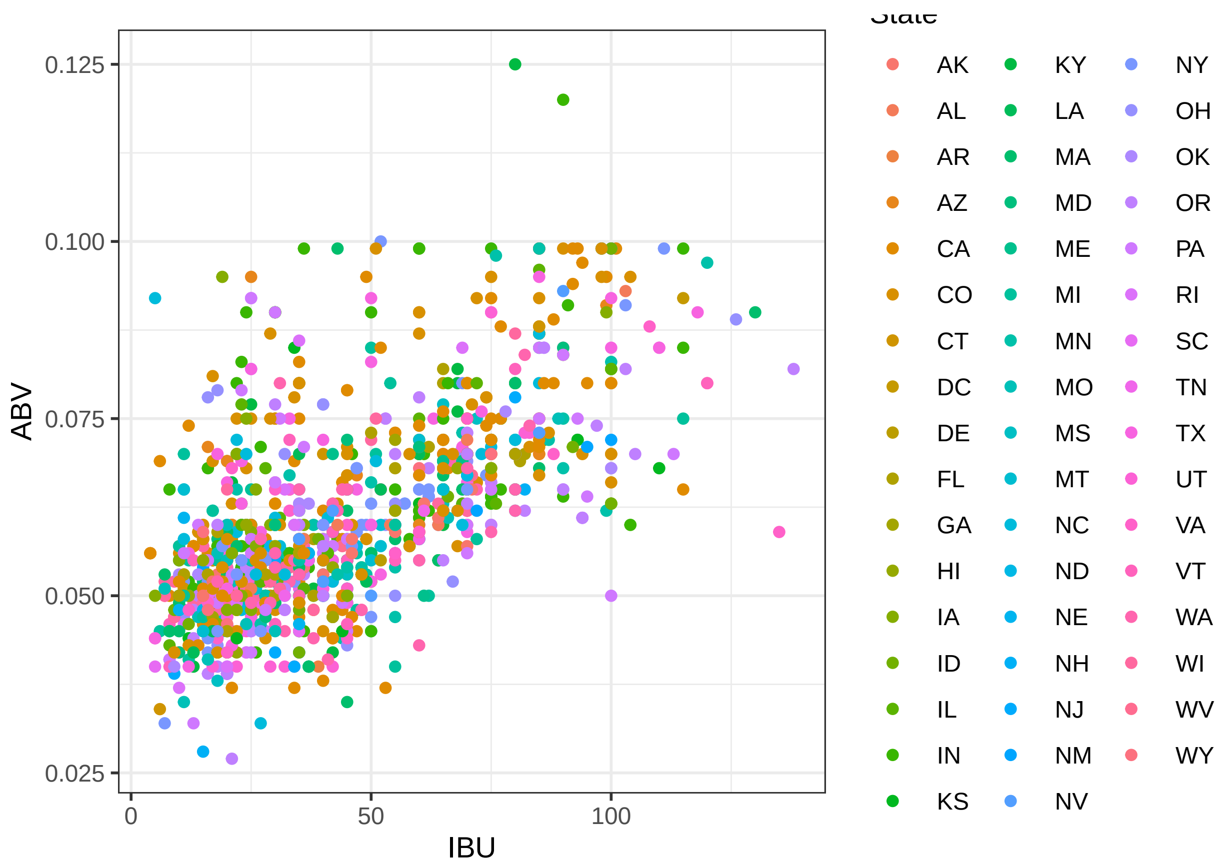


We see it's quite right skewed from its histogram. QQ plot also showed that this is not normally distributed data as it has some curve at upper quantiles. In the box plot, we clearly see there are some outliers. such as London Balling beer we found from MAX ABV.

Relationship between ABV and IBU

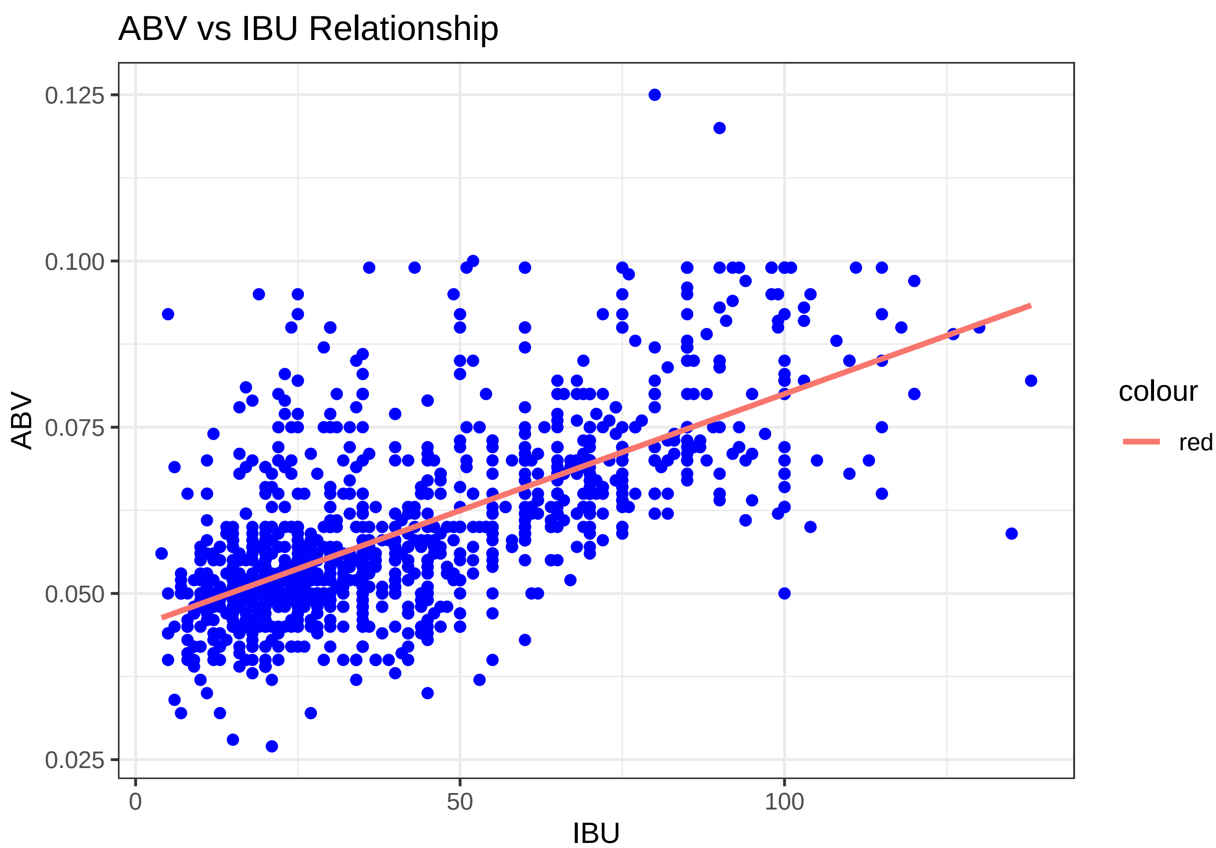
We made scatter plot between ABV and IBU to see what is the relationship, and we see that it has some positive relationship that as ABV Value goes up IBU tend to go up as well.

```
# Scatter Plot for ABV vs IBU for each State
cleanData %>% ggplot(aes(x=IBU, y=ABV, color=State)) + geom_point()
```




```
#7 Scatter Plot for ABV vs IBU relationship
theme_set(theme_bw())  # pre-set the bw theme.
g <- ggplot(cleanData, aes(IBU, ABV, color='red'))
g + geom_point(color='blue') +
  geom_smooth(method="lm", se=F) +
  labs(y="ABV",
       x="IBU",
       title="ABV vs IBU Relationship")
```

```
## `geom_smooth()` using formula 'y ~ x'
```

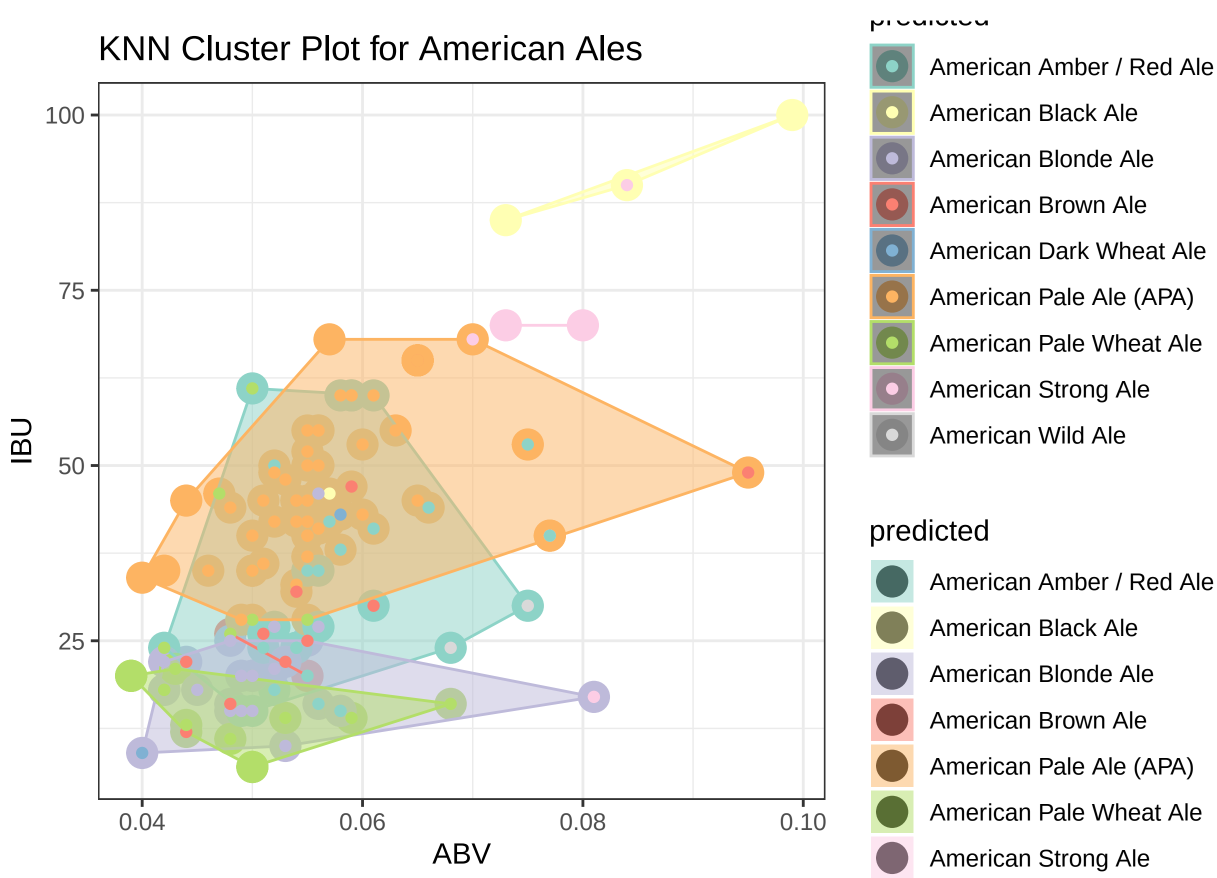


KNN Cluster Plot for American Ales

From the KNN cluster plot of Ale vs IPA, we found beers with high ABV and IBU are most likely IPA and beers with low ABV and IBU are most likely Ale. We want to know why there are some Ales on upper side of plot and IPAs on low IBU/ABV. To get in deeper, we made a KNN cluster plot just for Ale, especially American to reduce number of variables.

```
set.seed(4)
splitPerc = .70
aleData = cleanData %>% filter(grepl("Ale", Style) & grepl("American", Style))
trainIndices = sample(1:dim(aleData)[1],round(splitPerc * dim(aleData)[1]))
trainAle = aleData[trainIndices,]
testAle = aleData[-trainIndices,]
fit = knn(trainAle[,c(4,5)],testAle[,c(4,5)],trainAle$Style, k=6)

predAleDF = data.frame(testAle, predicted = fit)

predAleBoundary = data.frame(x = predAleDF$ABV,
                             y = predAleDF$IBU,
                             predicted = predAleDF$predicted)

find_hull = function(df) df[chull(df$x, df$y), ]
boundary = ddply(predAleBoundary, .variables = "predicted", .fun = find_hull)
```

```
palettes = brewer.pal(n = 9, name = "Set3")
colors = c("American Amber / Red Ale" = palettes[1], "American Black Ale" = palettes[2], "American Blond
ggplot() +
  geom_point(data=predAleDF,aes(ABV, IBU, color=predicted, fill=predicted), size = 5) +
  geom_polygon(data = boundary, aes(x,y, color=predicted, fill=predicted), alpha = 0.5)+
  geom_point(aes(ABV, IBU, color=Style), data=testAle) + ggtitle("KNN Cluster Plot for American Ales")
```



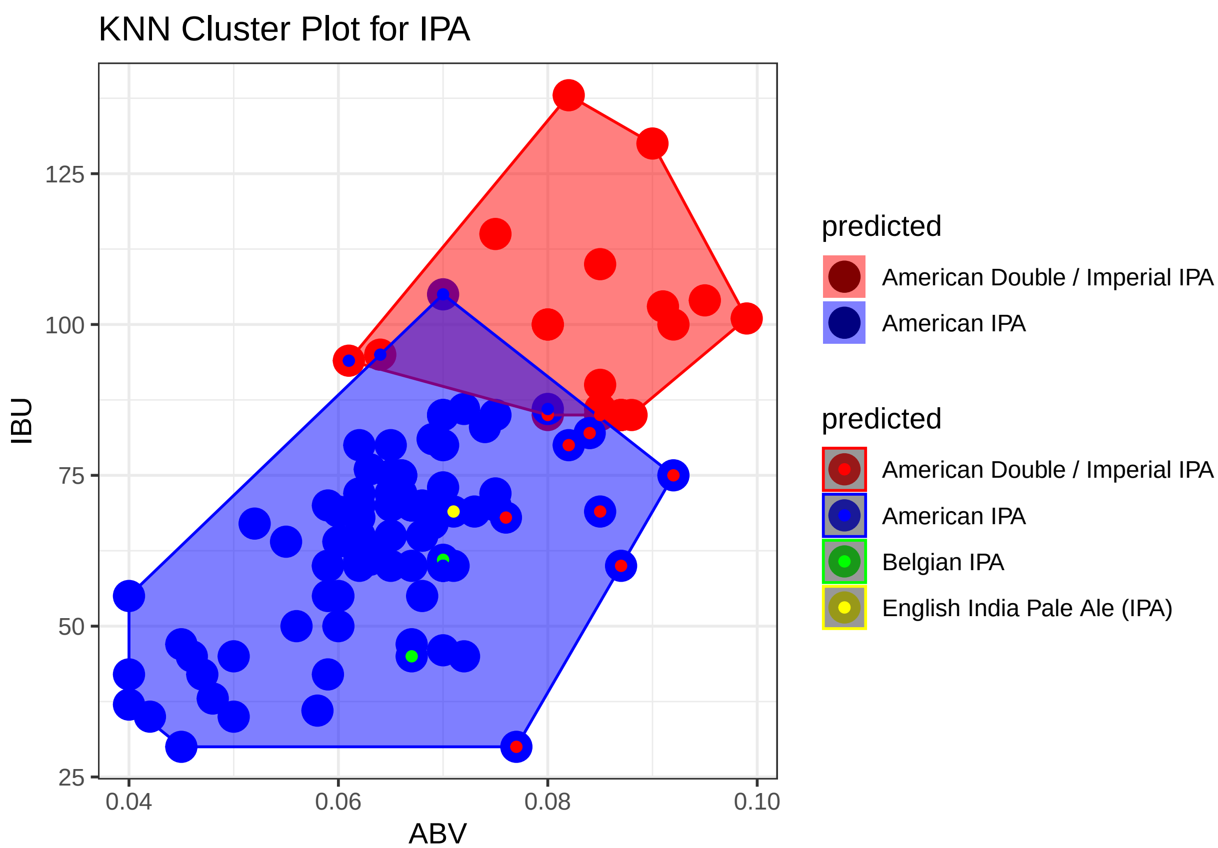
Looking at the plot, we see the some types of Ale have high IBU and ABV even though it's not an IPA. American black Ale is one the type, which sometimes called as Black IPA. If we set this type as IPA, we could have gotten better classfication results than before.

KNN Cluster Plot for IPA

We made another KNN cluster plot just for IPA.

```
set.seed(4)
splitPerc = .70
ipaData  = cleanData %>% filter(grepl("IPA", Style))
trainIndices = sample(1:dim(ipaData)[1],round(splitPerc * dim(ipaData)[1]))
trainIPA = ipaData[trainIndices,]
testIPA = ipaData[-trainIndices,]
fit = knn(trainIPA[,c(4,5)],testIPA[,c(4,5)],trainIPA$Style, k=6)
predIpaDF = data.frame(testIPA, predicted = fit)
```

```r
predIpaBoundary = data.frame(x = predIpaDF$ABV,
                             y = predIpaDF$IBU,
                             predicted = predIpaDF$predicted)

find_hull = function(df) df[chull(df$x, df$y), ]
boundary = ddply(predIpaBoundary, .variables = "predicted", .fun = find_hull)

colors = c("American Double / Imperial IPA" = "red", "American IPA" = "blue", "Belgian IPA" = "green",
ggplot() +
  geom_point(data=predIpaDF, aes(ABV, IBU, color=predicted, fill=predicted), size = 5) +
  geom_polygon(data = boundary, aes(x,y, color=predicted, fill=predicted), alpha = 0.5)+
  geom_point(aes(ABV, IBU, color=Style), data=testIPA) + ggtitle("KNN Cluster Plot") + ggtitle("KNN Clu
```



We found American IPA have much broader range of IBU and ABV that they contains. With just two information, IBU and ABV, it is not enough to understand the relationship of ABV and IBU against its style. For IPA, we may need additional feature variables such as hop ratio or type of ingredients to get better classification model.

From the above chart, we found that Colarado and Orgeon have more high ABV and IBU Ales than other states. Thus we can make a question that why these states have more Ales that have high bitterness and alcohol level.