

Project

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Data : Importing and Cleaning

From TidyTuesday URL:<https://github.com/rfordatascience/tidytuesday/tree/master/data/2020/2020-07-07>

Note: within the above link, there was already some pre-processing done to the data with the column and value names.

Quick Overview Summary

```
summary(coffee_ratings)
```

```
## total_cup_points species owner country_of_origin
## Min. : 0.00 Length:1339 Length:1339 Length:1339
## 1st Qu.:81.08 Class :character Class :character Class :character
## Median :82.50 Mode :character Mode :character Mode :character
## Mean :82.09
## 3rd Qu.:83.67
## Max. :90.58
##
## farm_name lot_number mill ico_number
## Length:1339 Length:1339 Length:1339 Length:1339
## Class :character Class :character Class :character Class :character
## Mode :character Mode :character Mode :character Mode :character
##
##
##
## company altitude region producer
## Length:1339 Length:1339 Length:1339 Length:1339
## Class :character Class :character Class :character Class :character
## Mode :character Mode :character Mode :character Mode :character
##
##
##
## number_of_bags bag_weight in_country_partner harvest_year
## Min. : 0.0 Length:1339 Length:1339 Length:1339
## 1st Qu.: 14.0 Class :character Class :character Class :character
## Median : 175.0 Mode :character Mode :character Mode :character
## Mean : 154.2
## 3rd Qu.: 275.0
## Max. :1062.0
```

```

##
## grading_date          owner_1          variety          processing_method
## Length:1339          Length:1339          Length:1339          Length:1339
## Class :character      Class :character      Class :character      Class :character
## Mode  :character      Mode  :character      Mode  :character      Mode  :character
##
##
##
##
##      aroma            flavor            aftertaste            acidity            body
## Min.   :0.000        Min.   :0.00        Min.   :0.000        Min.   :0.000        Min.   :0.000
## 1st Qu.:7.420        1st Qu.:7.33        1st Qu.:7.250        1st Qu.:7.330        1st Qu.:7.330
## Median :7.580        Median :7.58        Median :7.420        Median :7.580        Median :7.500
## Mean   :7.567        Mean   :7.52        Mean   :7.401        Mean   :7.536        Mean   :7.517
## 3rd Qu.:7.750        3rd Qu.:7.75        3rd Qu.:7.580        3rd Qu.:7.750        3rd Qu.:7.670
## Max.   :8.750        Max.   :8.83        Max.   :8.670        Max.   :8.750        Max.   :8.580
##
##      balance          uniformity          clean_cup          sweetness
## Min.   :0.000        Min.   : 0.000        Min.   : 0.000        Min.   : 0.000
## 1st Qu.:7.330        1st Qu.:10.000        1st Qu.:10.000        1st Qu.:10.000
## Median :7.500        Median :10.000        Median :10.000        Median :10.000
## Mean   :7.518        Mean   : 9.835        Mean   : 9.835        Mean   : 9.857
## 3rd Qu.:7.750        3rd Qu.:10.000        3rd Qu.:10.000        3rd Qu.:10.000
## Max.   :8.750        Max.   :10.000        Max.   :10.000        Max.   :10.000
##
##      cupper_points          moisture          category_one_defects          quakers
## Min.   : 0.000        Min.   :0.00000        Min.   : 0.0000        Min.   : 0.0000
## 1st Qu.: 7.250        1st Qu.:0.09000        1st Qu.: 0.0000        1st Qu.: 0.0000
## Median : 7.500        Median :0.11000        Median : 0.0000        Median : 0.0000
## Mean   : 7.503        Mean   :0.08838        Mean   : 0.4795        Mean   : 0.1734
## 3rd Qu.: 7.750        3rd Qu.:0.12000        3rd Qu.: 0.0000        3rd Qu.: 0.0000
## Max.   :10.000        Max.   :0.28000        Max.   :63.0000        Max.   :11.0000
##                                     NA's   :1
##      color            category_two_defects          expiration          certification_body
## Length:1339          Min.   : 0.000        Length:1339          Length:1339
## Class :character      1st Qu.: 0.000        Class :character      Class :character
## Mode  :character      Median : 2.000        Mode  :character      Mode  :character
##                                     Mean   : 3.556
##                                     3rd Qu.: 4.000
##                                     Max.   :55.000
##
##      certification_address          certification_contact          unit_of_measurement
## Length:1339          Length:1339          Length:1339
## Class :character      Class :character      Class :character
## Mode  :character      Mode  :character      Mode  :character
##
##
##
##
##      altitude_low_meters          altitude_high_meters          altitude_mean_meters
## Min.   :      1        Min.   :      1        Min.   :      1
## 1st Qu.:    1100        1st Qu.:    1100        1st Qu.:    1100
## Median :    1311        Median :    1350        Median :    1311
## Mean   :    1751        Mean   :    1799        Mean   :    1775

```

```
## 3rd Qu.: 1600      3rd Qu.: 1650      3rd Qu.: 1600
## Max.    :190164    Max.    :190164    Max.    :190164
## NA's    :230      NA's    :230      NA's    :230
```

Quite a few NA's.

Numerical Columns: 1 within quakers, and 230 in Altitude low/high/mean.

Next, need to check what is happening in the rest of the data set, the character type.

Count of NA's per column

```
#type of data, col = 2, type of function applied
apply(X=is.na(coffee_ratings), MARGIN = 2, FUN = sum)
```

```
##      total_cup_points      species      owner
##              0              0              7
##      country_of_origin      farm_name      lot_number
##              1              359             1063
##              mill           ico_number      company
##             315             151             209
##              altitude           region      producer
##             226             59             231
##      number_of_bags      bag_weight      in_country_partner
##              0              0              0
##      harvest_year      grading_date      owner_1
##             47              0              7
##              variety      processing_method      aroma
##             226             170             0
##              flavor           aftertaste      acidity
##              0              0              0
##              body           balance      uniformity
##              0              0              0
##      clean_cup           sweetness      cupper_points
##              0              0              0
##      moisture      category_one_defects      quakers
##              0              0              1
##              color      category_two_defects      expiration
##             218             0              0
##      certification_body      certification_address      certification_contact
##              0              0              0
##      unit_of_measurement      altitude_low_meters      altitude_high_meters
##              0              230             230
##      altitude_mean_meters
##             230
```

I had to use a quick google search to figure if margin had to be 1 or 2. Site: <https://www.guru99.com/r-apply-sapply-tapply.html>

There are quite a few missing values and many columns have many. I will be just removing some of the columns with too many missing values, for instance `lot_number` and `farm_name`. Additionally, I will be removing columns that do not heavily influence the goals of this project.

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.1 --
```

```
## v ggplot2 3.3.4      v purrr  0.3.4
## v tibble  3.1.2      v dplyr   1.0.7
## v tidyr   1.1.3      v stringr 1.4.0
## v readr   1.4.0      v forcats 0.5.1

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

Removal of columns

```
coffee = coffee_ratings%>%
  select(-farm_name,-lot_number,-mill,-ico_number,-altitude,
        -altitude_low_meters,-altitude_high_meters,-producer,-company,
        -expiration,-certification_address,-owner_1,-grading_date,
        -certification_contact,-unit_of_measurement)
```

```
#Remove Rows Containing Missing Values#
```

```
coffee = na.omit(coffee)
```

```
#Changing Mass to all Imperial Units of Measurements#
```

```
#selecting only items with lbs pattern within column to see how many
```

```
#Nathan F reminded me to the use of grep
```

```
coffee[grepl("lbs",coffee$bag_weight),]
```

```
## # A tibble: 18 x 28
##   total_cup_points species owner      country_of_origin region  number_of_bags
##   <dbl> <chr> <chr> <chr> <chr> <dbl>
## 1      87.2 Arabica the coff~ Costa Rica san ram~      250
## 2      86.3 Arabica francisc~ Costa Rica west an~      250
## 3      85.3 Arabica the coff~ Costa Rica west va~      250
## 4      85.3 Arabica the coff~ Costa Rica san ram~      250
## 5      84.7 Arabica fabian c~ Costa Rica tarrazu      50
## 6      84.5 Arabica fabian c~ Costa Rica tarrazu      250
## 7      83.8 Arabica german n~ United States (Pu~ yauco r~      18
## 8      83.8 Arabica the coff~ Guatemala quetzal~      250
## 9      83.3 Arabica the coff~ Costa Rica san ram~      250
## 10     83.3 Arabica itiah co~ Haiti thiotte~      2
## 11     83 Arabica german n~ United States (Pu~ yauco r~      17
## 12     81.5 Arabica myriam k~ Haiti dondon,~     300
## 13     81.2 Arabica essencec~ Guatemala huehuet~      36
## 14     81.1 Arabica german n~ United States (Pu~ yauco r~      18
## 15     80.9 Arabica chris fi~ Nicaragua matagal~     275
## 16     80.8 Arabica the coff~ Costa Rica san ram~      250
## 17     79.3 Arabica the coff~ Colombia pereira      250
## 18     79.1 Arabica german n~ United States (Pu~ yauco r~      18
## # ... with 22 more variables: bag_weight <chr>, in_country_partner <chr>,
## # harvest_year <chr>, variety <chr>, processing_method <chr>, aroma <dbl>,
## # flavor <dbl>, aftertaste <dbl>, acidity <dbl>, body <dbl>, balance <dbl>,
## # uniformity <dbl>, clean_cup <dbl>, sweetness <dbl>, cupper_points <dbl>,
## # moisture <dbl>, category_one_defects <dbl>, quakers <dbl>, color <chr>,
## # category_two_defects <dbl>, certification_body <chr>,
## # altitude_mean_meters <dbl>
```

```
#separating out the columns based on the value and units associated with it
coffee = separate(data = coffee, col = bag_weight, into = c("weight", "type"), sep = " ")
```

```
#converted string to numeric
coffee$weight = as.numeric(coffee$weight)
```

```
#simple loop to change units
for(i in 1:length(coffee)){
  if(coffee[i,8]=="kg"){
    coffee[i,7] = round(coffee[i,7] * 2.20462,0)
    coffee[i,8] = "lbs"
  }
}
```

```
#remove type column as the weight col is uniform for unit type
coffee = coffee%>%
  select(-type)
```

```
#Changing Length to all Imperial Units of Measurements#
```

```
coffee = coffee%>%
  rename(avg_altitude=altitude_mean_meters)
```

```
coffee$avg_altitude = round(coffee$avg_altitude * 3.28084,0)
```

```
#Altering rows with years with form Year1/Year2 to the initial year (Year1)#
```

```
coffee$harvest_year = substr(coffee$harvest_year,1,4)
coffee$harvest_year = as.numeric(coffee$harvest_year)
```

The above chunk was done do to the initial inception of that batch of coffee.

```
#Numerical Summary to see the data for potentail outliers#
```

```
summary(coffee[,c(9,12:24,26,28)])
```

```
##   harvest_year      aroma      flavor      aftertaste      acidity
##   Min.   :2011   Min.   :5.080   Min.   :6.170   Min.   :6.170   Min.   :5.250
##   1st Qu.:2012   1st Qu.:7.420   1st Qu.:7.330   1st Qu.:7.170   1st Qu.:7.330
##   Median :2014   Median :7.580   Median :7.500   Median :7.420   Median :7.500
##   Mean   :2014   Mean   :7.559   Mean   :7.504   Mean   :7.374   Mean   :7.515
##   3rd Qu.:2015   3rd Qu.:7.750   3rd Qu.:7.670   3rd Qu.:7.580   3rd Qu.:7.670
##   Max.   :2018   Max.   :8.750   Max.   :8.670   Max.   :8.500   Max.   :8.580
##      body      balance      uniformity      clean_cup
##   Min.   :6.330   Min.   :6.080   Min.   : 6.000   Min.   : 0.000
##   1st Qu.:7.330   1st Qu.:7.330   1st Qu.:10.000   1st Qu.:10.000
##   Median :7.500   Median :7.500   Median :10.000   Median :10.000
##   Mean   :7.494   Mean   :7.488   Mean   : 9.871   Mean   : 9.849
##   3rd Qu.:7.670   3rd Qu.:7.670   3rd Qu.:10.000   3rd Qu.:10.000
##   Max.   :8.420   Max.   :8.580   Max.   :10.000   Max.   :10.000
##      sweetness      cupper_points      moisture      category_one_defects
##   Min.   : 1.33   Min.   :5.170   Min.   :0.00000   Min.   : 0.0000
##   1st Qu.:10.00   1st Qu.:7.250   1st Qu.:0.10000   1st Qu.: 0.0000
##   Median :10.00   Median :7.500   Median :0.11000   Median : 0.0000
##   Mean   : 9.93   Mean   :7.459   Mean   :0.09737   Mean   : 0.4262
##   3rd Qu.:10.00   3rd Qu.:7.670   3rd Qu.:0.12000   3rd Qu.: 0.0000
##   Max.   :10.00   Max.   :8.580   Max.   :0.17000   Max.   :31.0000
##      quakers      category_two_defects      avg_altitude
```

```
## Min.   : 0.0000   Min.   : 0.000   Min.   :    3
## 1st Qu.: 0.0000   1st Qu.: 0.000   1st Qu.: 3609
## Median : 0.0000   Median : 2.000   Median : 4300
## Mean   : 0.1521   Mean   : 3.822   Mean   : 6145
## 3rd Qu.: 0.0000   3rd Qu.: 5.000   3rd Qu.: 5249
## Max.   :11.0000   Max.   :47.000   Max.   :623898
```

The parameters for defects, quakers, and average altitude seem to have quite a range for values. Additionally, it can be seen for these fields that the max points are quite a ways away from the mean.

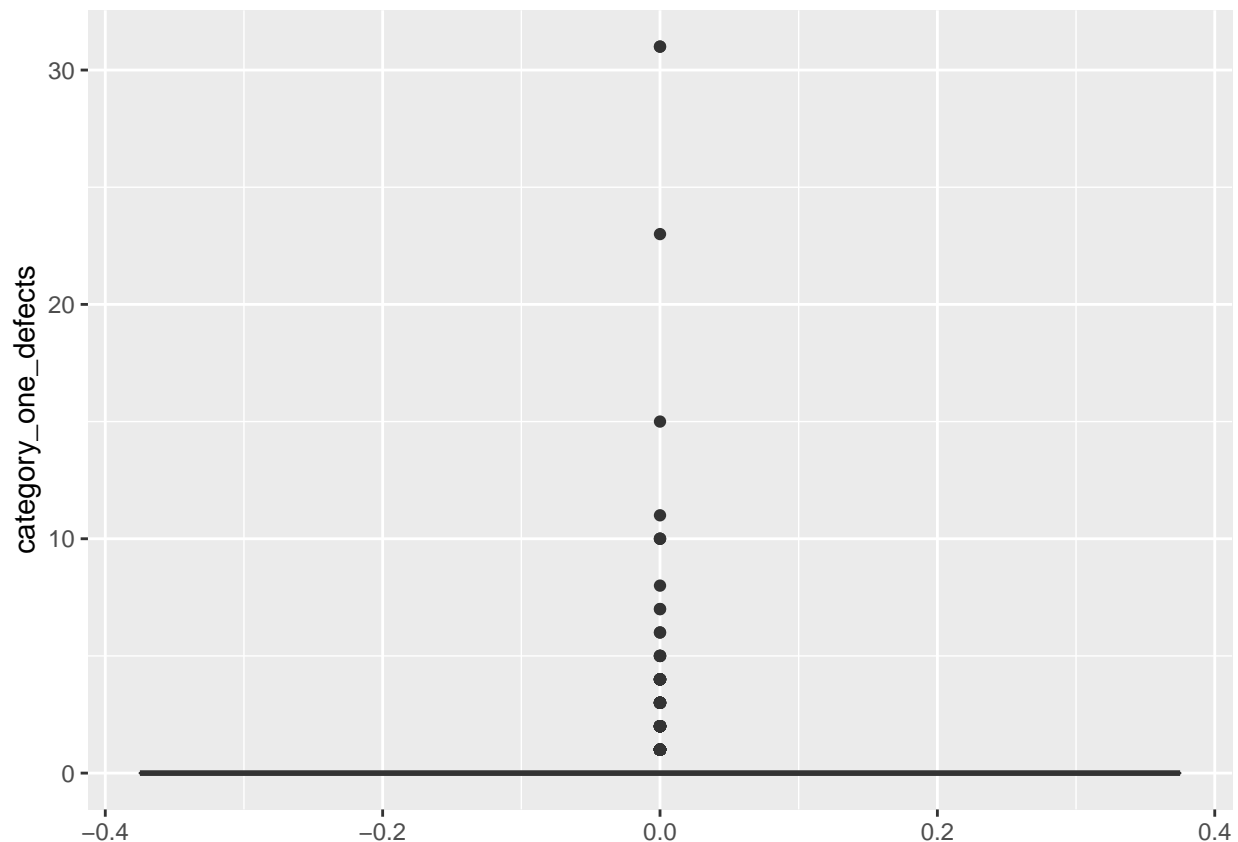
EDA / Visuals

```
library(ggplot2)
```

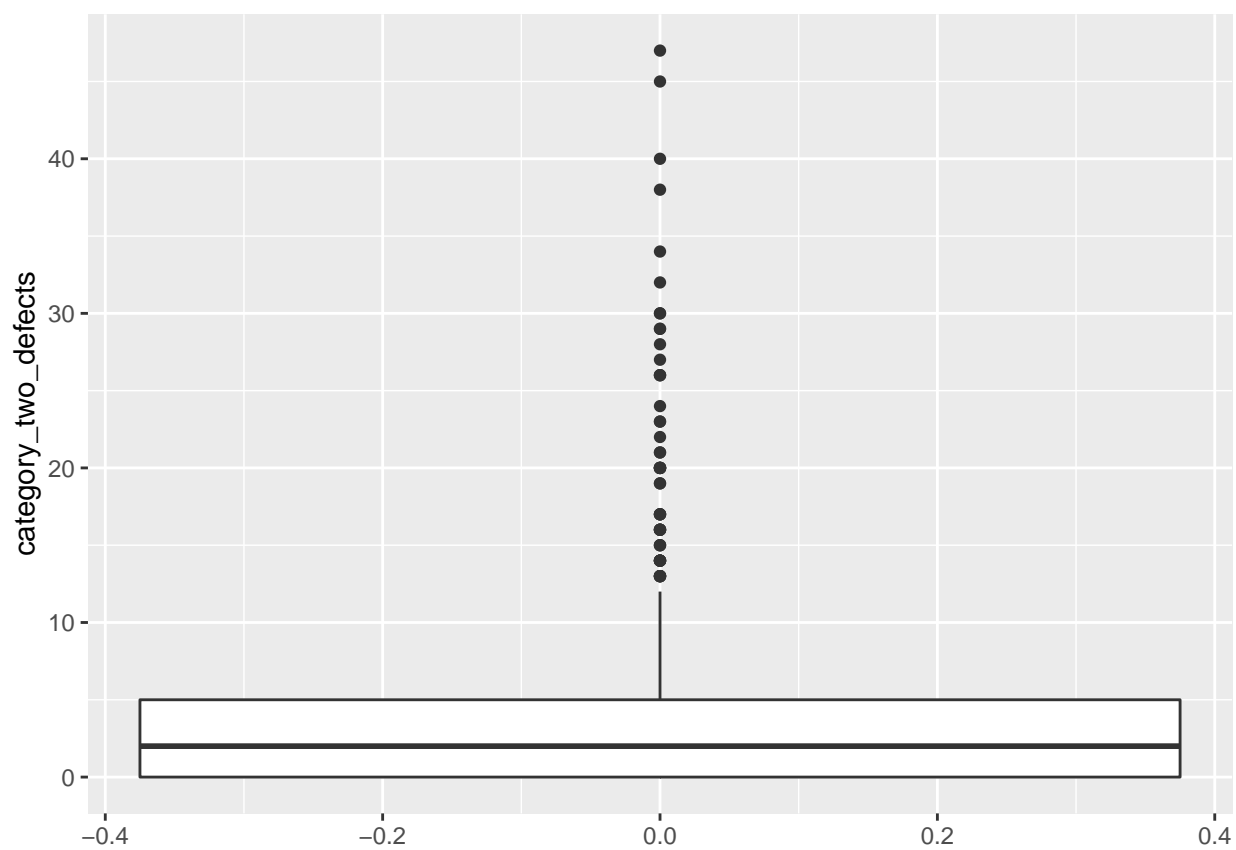
```
#Check for outliers in some of the fields#
```

```
defect1_plt = ggplot(coffee, aes(y=category_one_defects)) +
  geom_boxplot()
defect2_plt = ggplot(coffee, aes(y=category_two_defects)) +
  geom_boxplot()
alt_plt = ggplot(coffee, aes(y=avg_altitude)) +
  geom_boxplot()
quakers = ggplot(coffee, aes(y=quakers)) +
  geom_boxplot()
```

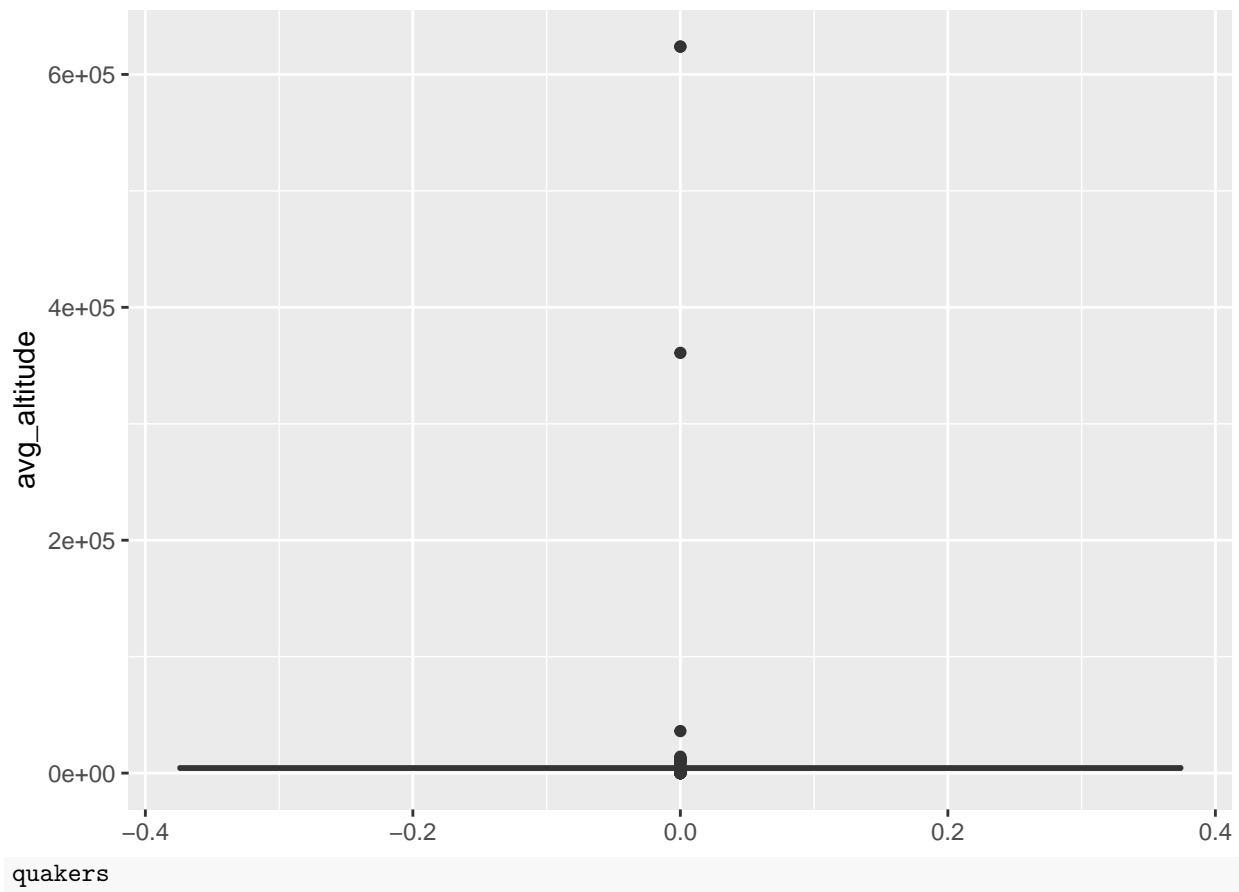
```
defect1_plt
```

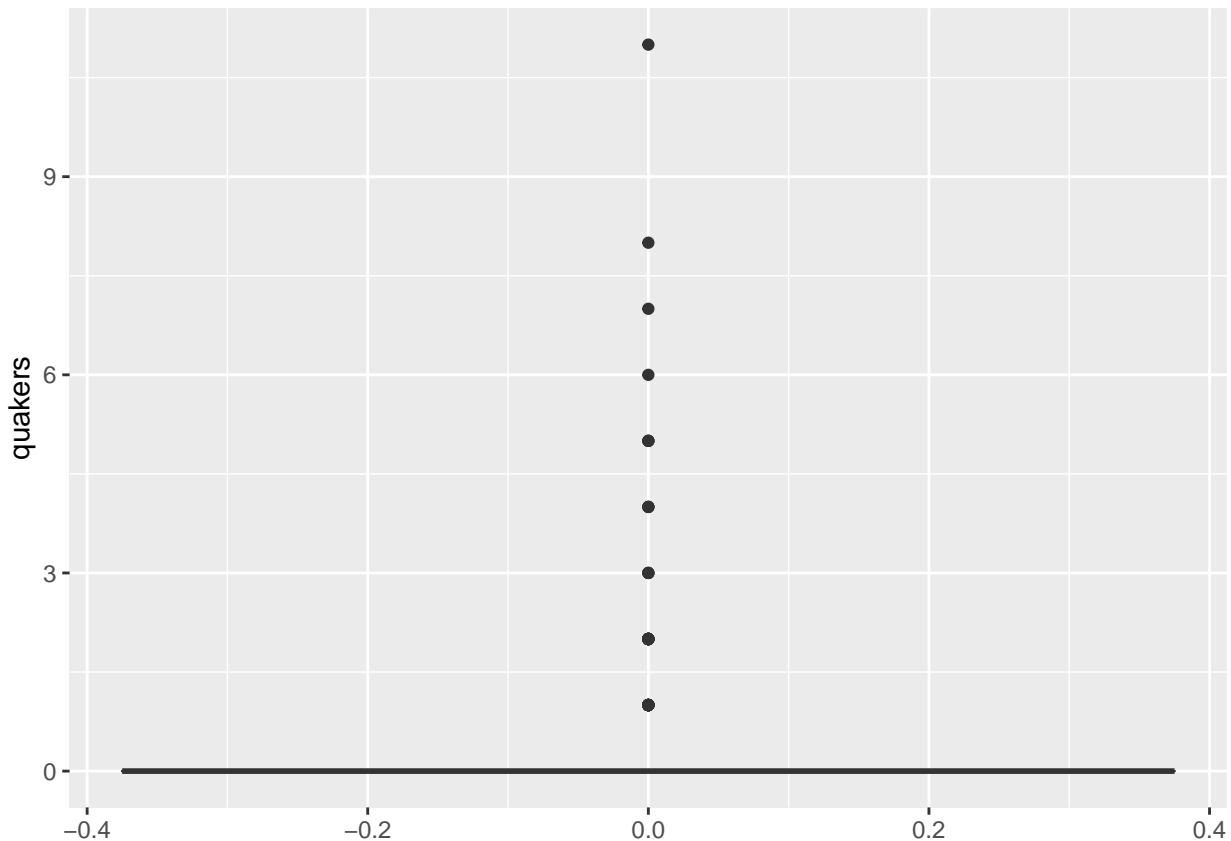


defect2_plt



alt_plt





There are some outliers, but not that many that would result in a concern at this time. These fields may be removed from the current analysis due to the outliers and lack of variance within the data. As the majority of these values are 0. This will be removed in the upcoming data chunks. Additionally, as this project is to have more focus in analysis, there will be additional removal of fields. Specifically, the ownership items and their location details.

#Redfine the Dataset#

```
c = coffee[,c(1:2,4,10:26,28)]
```

#Condense the data#

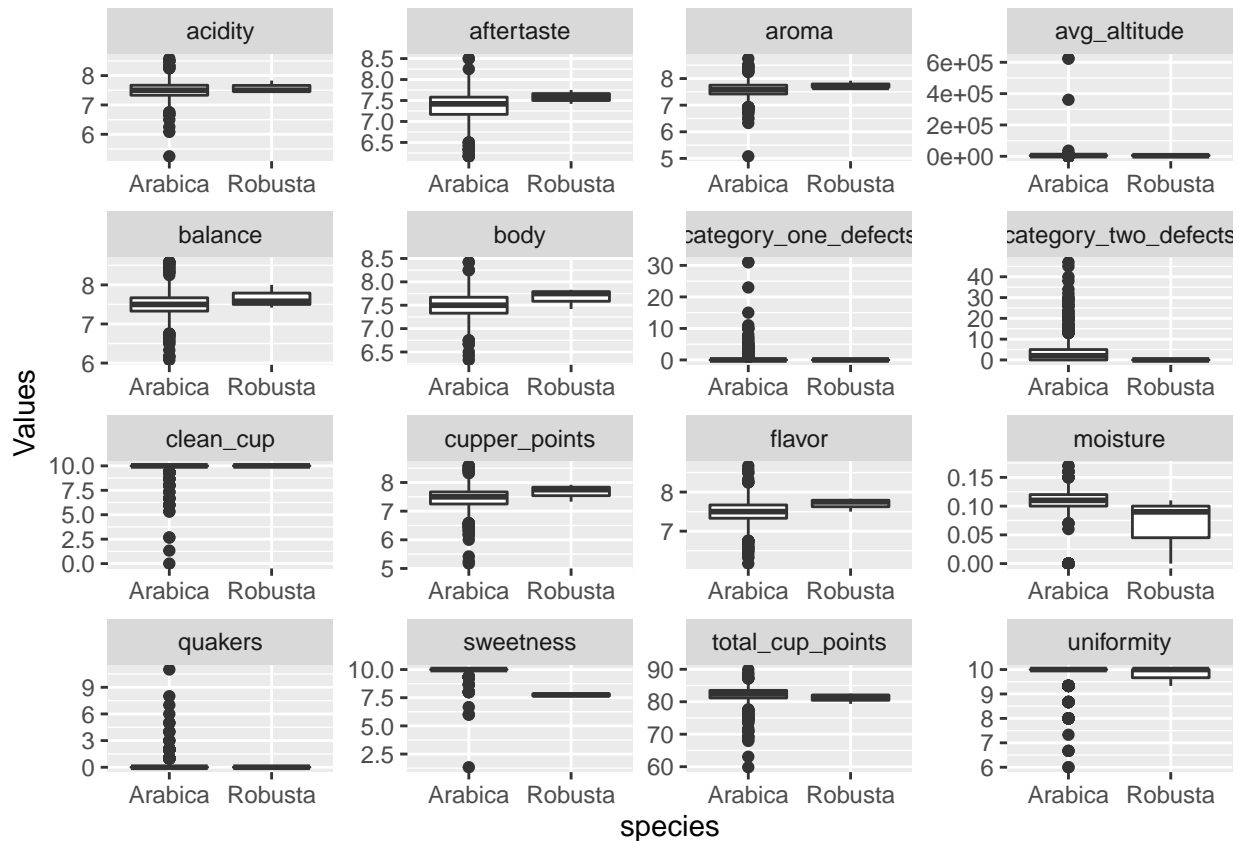
```
c.v1 = c%>%pivot_longer(
  cols = !c(species, country_of_origin,variety,processing_method,color),
  names_to = "Variables",
  values_to = "Values")
```

Since, this data set will be re-used for other visuals. Otherwise the following code chunk could be used to generate a specific visual.

```
c%>%pivot_longer(
  cols = !c(species, country_of_origin,variety,processing_method,color),
  names_to = "Variables",
  values_to = "Values")%>%
  ggplot(aes(x=species,y=Values,color=color))+
  geom_boxplot()+
  facet_wrap(~Variables,scales = "free")
```

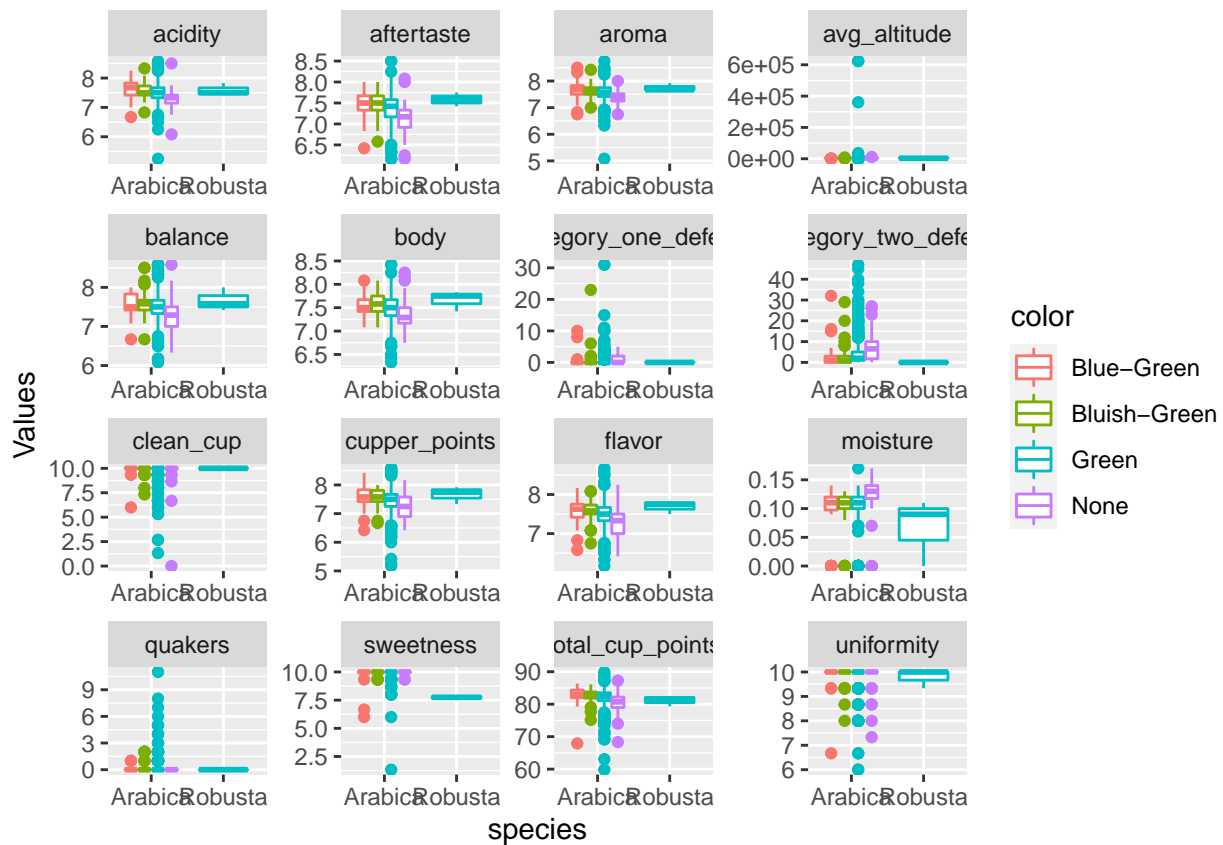
#Plot the data to see overall behavior#

```
ggplot(c.v1,aes(x=species,y=Values))+geom_boxplot()+facet_wrap(~Variables,scales = "free")
```



#Plot the data to see overall behavior for specific field Coffee Color#

```
ggplot(c.v1,aes(x=species,y=Values,color=color))+geom_boxplot()+facet_wrap(~Variables,scales = "free")
```

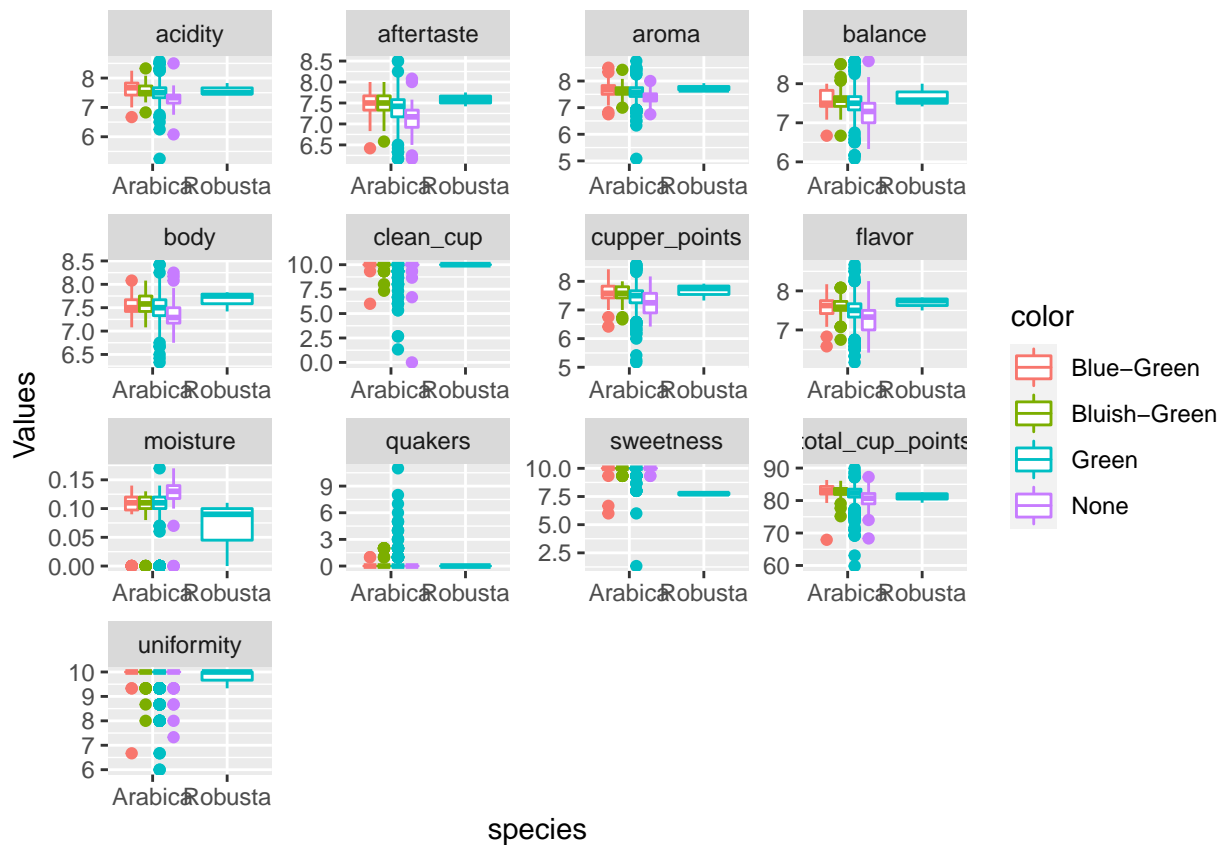


```
#Filter out the items that have known outliers#
```

```
c.v2 = c.v1 %>%
  filter(Variables != 'avg_altitude' & Variables != 'category_one_defects' & Variables != 'category_two_defects')
```

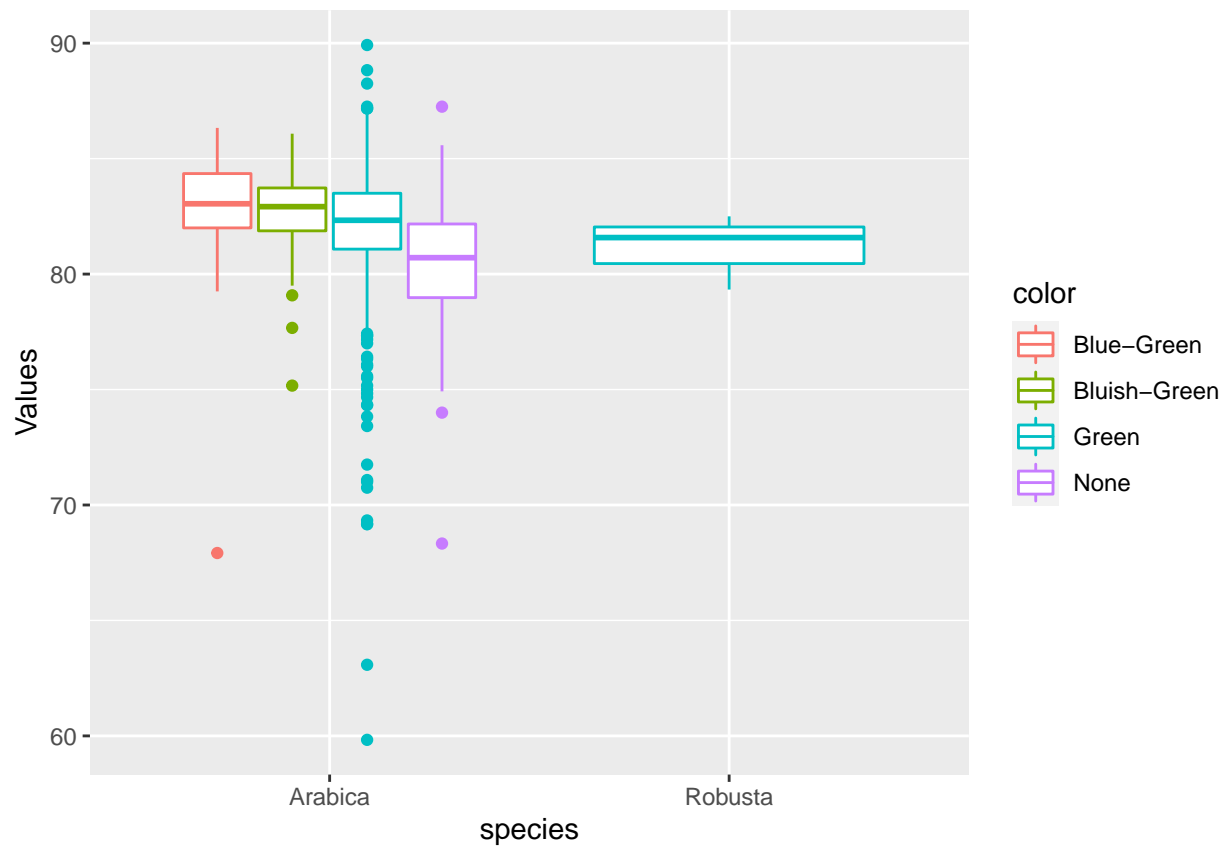
```
#Re-run plot#
```

```
ggplot(c.v2, aes(x=species, y=Values, color=color)) + geom_boxplot() + facet_wrap(~Variables, scales = "free")
```

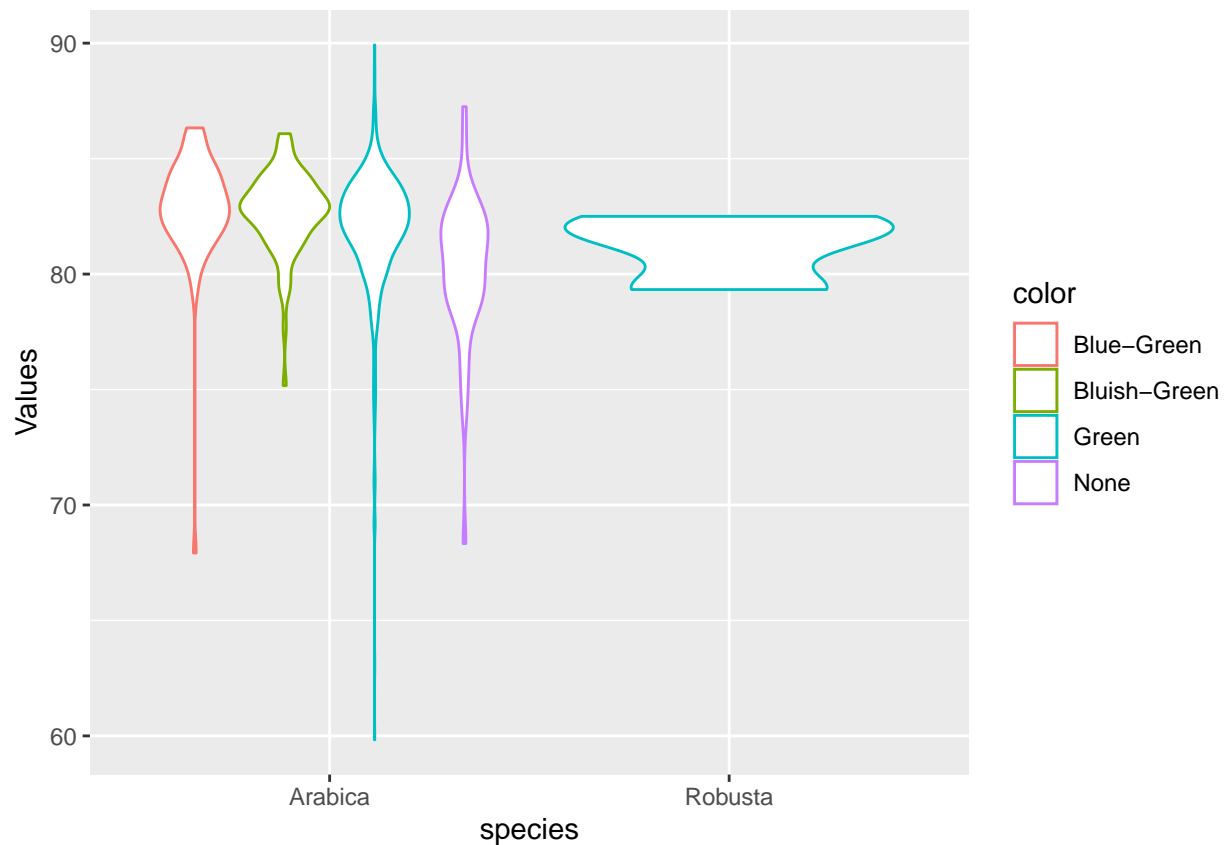


#How are the cup points distributed and where the 'weight' it is at by the Species and Coffee Color#

```
c.v2 %>%
  filter(Variables == 'total_cup_points')%>%
  ggplot(aes(x=species,y=Values,color=color))+geom_boxplot()
```

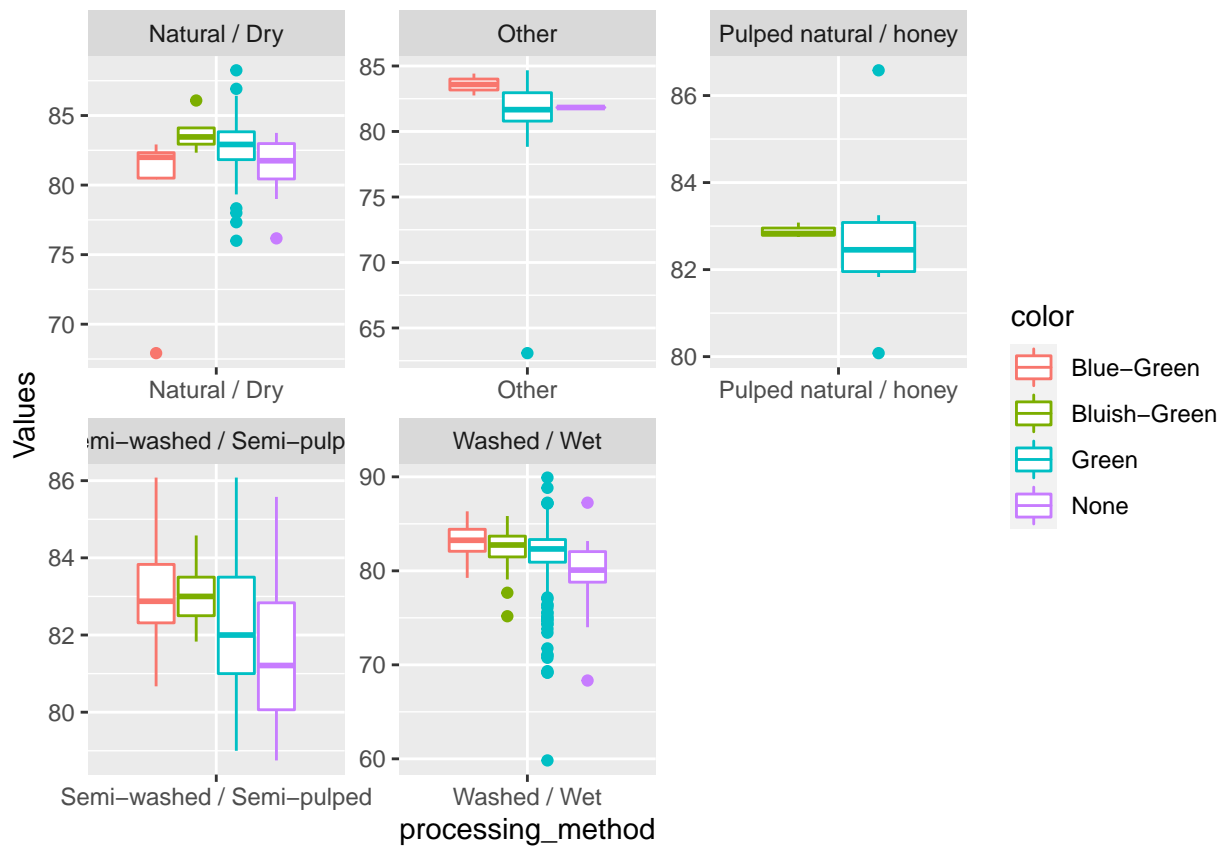


```
c.v2 %>%
  filter(Variables == 'total_cup_points')%>%
  ggplot(aes(x=species,y=Values,color=color))+geom_violin()
```

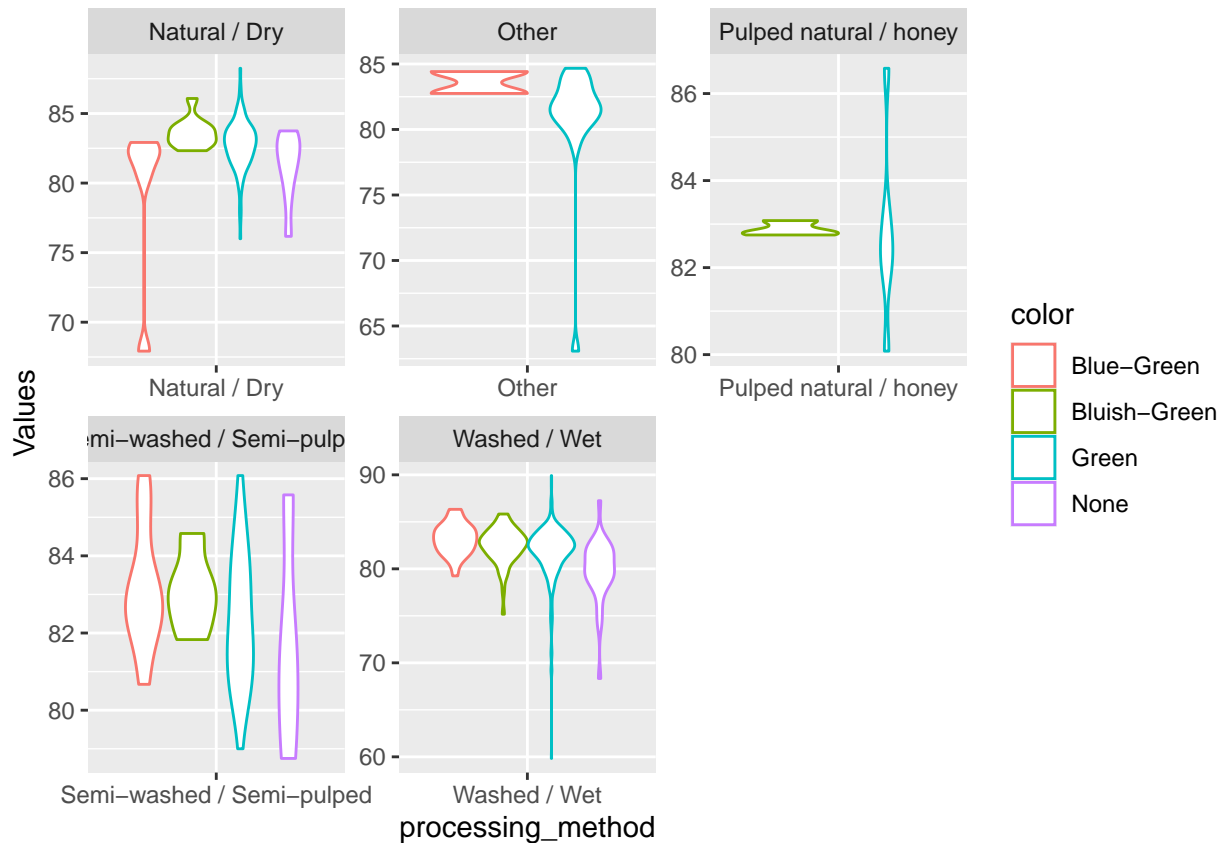


#How are the cup points distributed and where the 'weight' it is at by the Coffee Color and Processing Method#

```
c.v2 %>%
  filter(Variables == 'total_cup_points')%>%
  ggplot(aes(x=processing_method,y=Values,color=color))+geom_boxplot()+
  facet_wrap(~processing_method,scales = "free")
```



```
c.v2 %>%
  filter(Variables == 'total_cup_points')%>%
  ggplot(aes(x=processing_method,y=Values,color=color))+geom_violin()+
  facet_wrap(~processing_method,scales = "free")
```



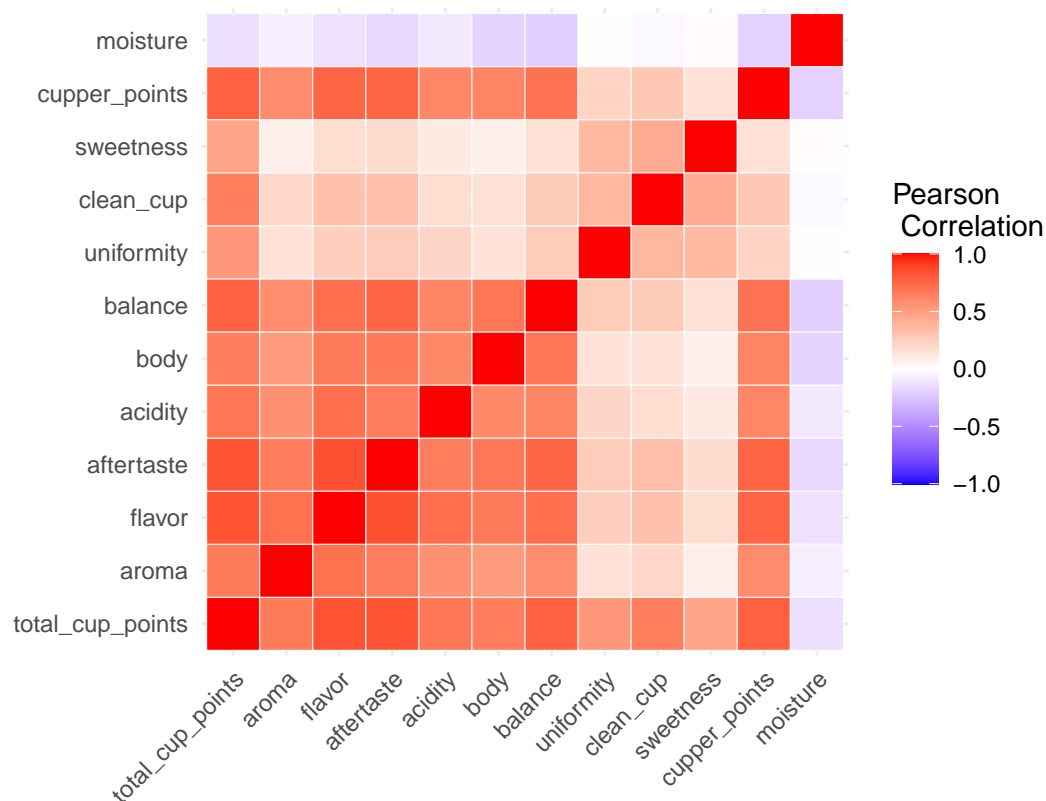
```
#Heatmap of Correlations#
```

```
library(reshape)
```

```
##
## Attaching package: 'reshape'
## The following object is masked from 'package:dplyr':
##
##   rename
## The following objects are masked from 'package:tidyr':
##
##   expand, smiths
c = c[,c(1,6:16)]
cormat = cor(c)
melted = melt(cormat, varnames = c("ParameterX", "ParameterY"))
```

```
#Heatmap#
```

```
ggplot(data = melted, aes(x=ParameterX, y=ParameterY, fill=value)) +
  geom_tile(color = "white")+
  scale_fill_gradient2(low = "blue", high = "red", mid = "white",
    midpoint = 0, limit = c(-1,1), space = "Lab",
    name="Pearson \n Correlation") +
  labs(x = "", y = "")+
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5), axis.text.x = element_text(angle = 45, vjust = 1, size = 12),
    coord_fixed())
```

This took quite a bit of using ggplot2 to aid in creating this visual. I used quite a few site for reference. ~1 https://ggplot2.tidyverse.org/reference/geom_tile.html ~2 <https://r-charts.com/correlation/heat-map-ggplot2/> ~3 <https://stackoverflow.com/questions/1330989/rotating-and-spacing-axis-labels-in-ggplot2>

#See the data make-up in a numerical summary#

```
library(formattable)
```

#Function for Calculating Frequency#

```
freq = function(df,col_i,col_j){
  a = df %>%
    group_by({{col_i}},{{col_j}}) %>%
    summarise(count = n()) %>%
    mutate(freq = formattable::percent(count / sum(count)))
  return(a)
}
```

#Overall Frequency all Countries#

```
freqq(c.v1,Variables,Values)
```

`summarise()` has grouped output by 'Variables'. You can override using the `.groups` argument.

A tibble: 611 x 4

Groups: Variables [16]

	Variables	Values	count	freq
	<chr>	<dbl>	<int>	<formttbl>
##	1 acidity	5.25	1	0.11%
##	2 acidity	6.08	1	0.11%
##	3 acidity	6.25	1	0.11%
##	4 acidity	6.5	1	0.11%

```
## 5 acidity      6.67      3 0.34%
## 6 acidity      6.75      2 0.22%
## 7 acidity      6.83      6 0.67%
## 8 acidity      6.92      7 0.78%
## 9 acidity      7        23 2.57%
## 10 acidity     7.08     25 2.80%
## # ... with 601 more rows

#Overall Frequency for Brazil#
freqq(c.v1%>%filter(country_of_origin=="Brazil"),Variables,Values)

## `summarise()` has grouped output by 'Variables'. You can override using the `.groups` argument.
## # A tibble: 216 x 4
## # Groups:   Variables [16]
##   Variables Values count freq
##   <chr>      <dbl> <int> <formttbl>
## 1 acidity    6.92      1 1.05%
## 2 acidity    7        1 1.05%
## 3 acidity    7.08      3 3.16%
## 4 acidity    7.17      4 4.21%
## 5 acidity    7.25      5 5.26%
## 6 acidity    7.33      8 8.42%
## 7 acidity    7.42      7 7.37%
## 8 acidity    7.5      26 27.37%
## 9 acidity    7.58      9 9.47%
## 10 acidity   7.67     13 13.68%
## # ... with 206 more rows

##Analysis Preparation##

#Format new label (total_cup_points) to be categorical#
coffee$tcp = coffee$total_cup_points

#Creating Bins for the Cup Points#
for(i in 1:894){
  if(coffee[i,29] >= 80){
    coffee[i,29] = 80
  }
  else if(coffee[i,29] >= 70 & coffee[i,29] < 80){
    coffee[i,29] = 70
  }
  else if(coffee[i,29] >= 60 & coffee[i,29] < 70){
    coffee[i,29] = 60
  }
  else{
    coffee[i,29] = 50
  }
}
coffee$tcp = round(coffee$tcp,0)
```

While the bins could be more specific and look at every 2 or 5 points, it made more sense to use broader bins. This is due to trying to understand what makes a coffee from a specific bean have higher or lower overall cup points (i.e., what is the difference between 70s and 80s cup of coffee).

```
#Accuracy table for comparison between models#
```

```
table_accuracy = matrix(nrow=6,ncol=1)
colnames(table_accuracy) = c('Accuracy')
rownames(table_accuracy) = c('DTree','NB','SVM-Linerar','SVM-Polynomial','ANN','KNN')
table_accuracy
```

```
##              Accuracy
## DTree              NA
## NB                 NA
## SVM-Linerar        NA
## SVM-Polynomial     NA
## ANN               NA
## KNN               NA
```

This is to help determining which model or models is better than the others. If there are many with similar accuracy, then the model that is the easiest to interpret and explain to a general audience.

#Set seed so analysis is repeatable#

```
set.seed(1)
```

For analysis

```
df = coffee[,c(9:22,25,29)]
for(i in 4 : 13){
  df[,i]=round(df[,i],2)
}
```

If the data was processing a bit slowly for initial predicting, as it was too granular so this step was helpful to making the ML run quicker.

#Fix issue with the Data#

```
df$processing_method= as.factor(df$processing_method)
df$variety = as.factor(df$variety)
df = df[,c(1:16)]
df$tcp = as.factor(df$tcp)
df$moisture = round(df$moisture,1)
```

This was missed earlier in the summary, but the fields that are characters, need to be changed to type factor for the analysis.

Simple k-fold cross validation(cv)

```
set.seed(1)
n = nrow(df)
folds = 10
tail = n%%folds

rnd = runif(n)
rank = rank(rnd)

#block/chunk from cv
blk = (rank-1)%/%tail+1
blk = as.factor(blk)

#to see formation of folds
print(summary(blk))
```

```
##  1  2  3  4  5  6  7  8  9 10 11
```

```
## 89 89 89 89 89 89 89 89 89 89 4
```

Could turn the above into a more personalized cross validation method than one of the packages in an R library.

Predictive Analysis

```
#Decision Tree#
```

```
library(rpart)
set.seed(1)

all.acc = numeric(0)
for(i in 1:folds){
  tree = rpart(tcp~.,df[blk != i,],method="class")
  pred = predict(tree,df[blk==i,],type="class")
  confMat = table(pred,df$tcp[blk==i])
  acc = (confMat[1,1]+confMat[2,2]+confMat[3,3]+confMat[4,4])/sum(confMat)
  all.acc = rbind(all.acc,acc)
}

print(mean(all.acc))
```

```
## [1] 0.9516854
```

```
table_accuracy[1,1] = mean(all.acc)
```

A 95% overall accuracy is really good! This indicates if following this tree, with details on a bean one could reasonable figure out what its overall score will be prior to evaluation. It also indicates what are the more important parameters are for a coffee scoring.

Example of a table matrix of predicted(rows) and actual(columns)

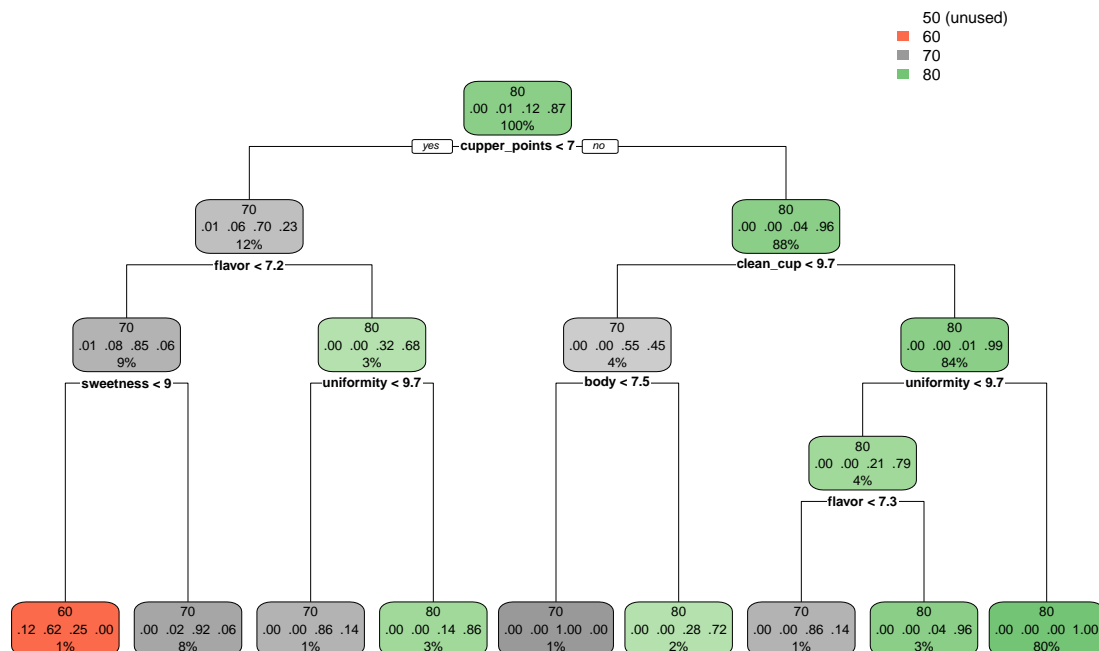
```
confMat
```

```
##
## pred 50 60 70 80
## 50 0 0 0 0
## 60 0 0 0 0
## 70 0 0 13 0
## 80 0 0 3 73
```

This indicates, for the given run, there were 3 miss classifications. Where the tree suggested that the bean should have been in the 80s, but was actually in the 70s.

Visual of Decision Tree

```
rpart.plot::rpart.plot(tree)
```



From this plot, I could just bin 50s with the 60sw group. This will help with future evaluations where re-binning the classifier would be a potential option to get more granular information.

Naive Bayes

```
library(e1071)
set.seed(1)

all.acc = numeric(0)
for(i in 1:folds){
  model = naiveBayes(tcp~.,df[blk != i,],method="class")
  pred = predict(model,df[blk==i,],type="class")
  confMat = table(pred,df$tcp[blk==i])
  acc = (confMat[1,1]+confMat[2,2]+confMat[3,3]+confMat[4,4])/sum(confMat)
  all.acc = rbind(all.acc,acc)
}

print(mean(all.acc))
```

```
## [1] 0.9550562
```

```
table_accuracy[2,1] = mean(all.acc)
```

Another nice and high accuracy for this PA!

#Lineat Support Vector Machine (SVM)#

```
set.seed(1)
```

```
all.acc = numeric(0)
for(i in 1:folds){
  model = svm(tcp~. ,df[blk != i,],kernel="linear",type="C")
  pred = predict(model,df[blk==i,],type="class")
  confMat = table(pred,df$tcp[blk==i])
```

```

    acc = (confMat[1,1]+confMat[2,2]+confMat[3,3]+confMat[4,4])/sum(confMat)
    all.acc = rbind(all.acc,acc)
  }

print(mean(all.acc))

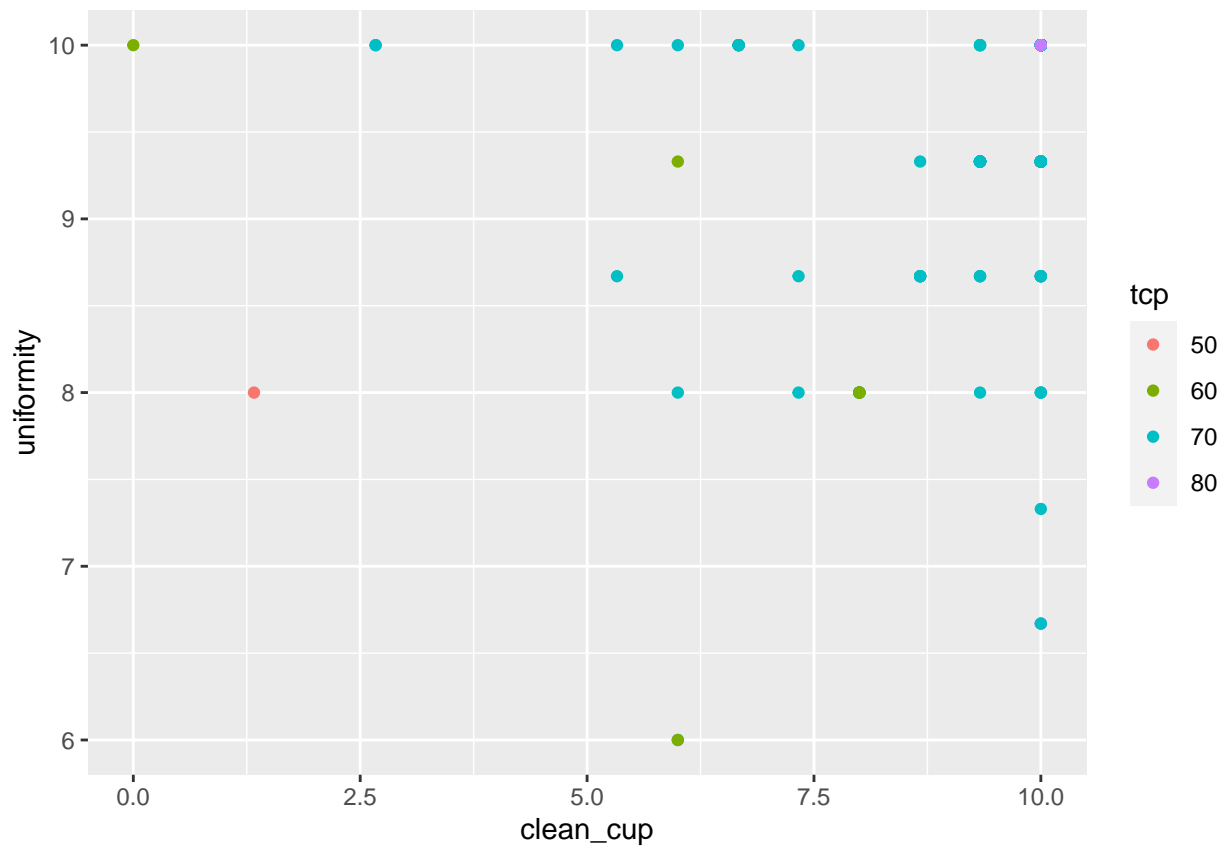
```

```
## [1] 0.9865169
```

```
table_accuracy[3,1] = mean(all.acc)
```

This makes sense as the data has many types of fields, and not all of the fields are continuous.

```
ggplot(df,aes(x=clean_cup,y=uniformity,color=tcp))+geom_point()
```



```
##+ facet_wrap(~processing_method,scales = "free")
```

From the decision tree, taking the top two parameters and placing them in a scatter plot and giving color to the points based on their classifier. It is very easy to see where the lines could be to separate the 70s and 80s bins.

Polynomial SVM

```

set.seed(1)
all.acc = numeric(0)
for(i in 1:folds){
  model = svm(tcp~.,df[blk != i,],kernel="polynomial",type="C")
  pred = predict(model,df[blk==i,],type="class")
}

```

```

confMat = table(pred,df$tcp[blk==i])
acc = (confMat[1,1]+confMat[2,2]+confMat[3,3]+confMat[4,4])/sum(confMat)
all.acc = rbind(all.acc,acc)
}

print(mean(all.acc))

## [1] 0.9404494
table_accuracy[4,1] = mean(all.acc)

```

Wierd R Issue

```

#switch the classifier to numerical
df$tcp = round(as.numeric(df$tcp),0)
#them switch it back to a factor
df$tcp = as.factor(df$tcp)

```

This was a very weird issue. I knew that this was a factor was needed for the classifier. However, it was throwing a NaN for an accuracy value and just by switching the format back and forth corrected it.

Neural Network

```

library(nnet)
set.seed(1)

all.acc = numeric(0)
for(i in 1:folds){
  model = nnet(tcp~.,df[blk != i,], size = 11, trace=FALSE, rang=.06, decay=.006,maxit=500)
  pred = predict(model, df[blk==i,],type="class")
  confMat = table(factor(pred,levels=1:4),factor(df$tcp[blk==i],levels=1:4))
  acc = (confMat[1,1]+confMat[2,2]+confMat[3,3]+confMat[4,4])/sum(confMat)
  all.acc = rbind(all.acc,acc)
}
print(mean(all.acc))

## [1] 0.8876404
table_accuracy[5,1] = mean(all.acc)

```

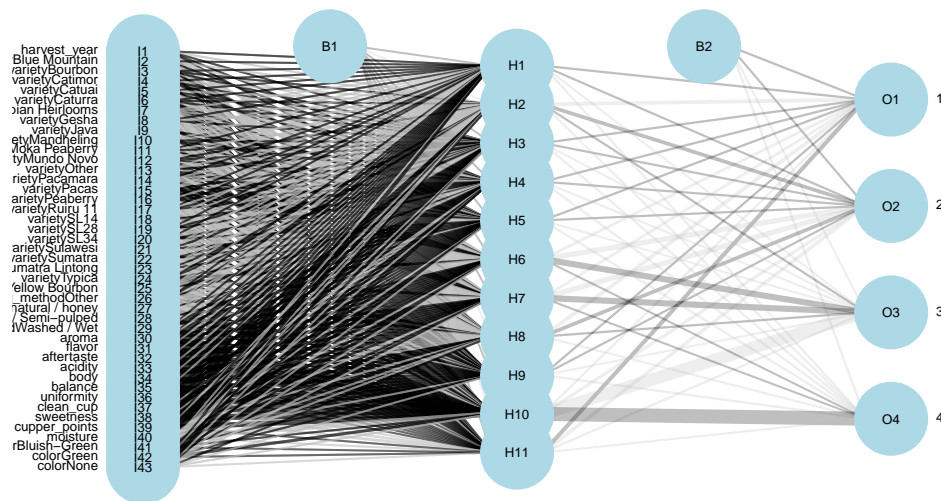
Not the best not the worst NN that I have seen. If there was more time, I would have liked to increased the classifiers and used a different library that allowed for more hidden layers.

Neural Network Visual

```

library("NeuralNetTools")
plotnet(model,circle_cex=5,cex_val=.4,max_sp=TRUE,alpha_val=.25,skip=TRUE)

```



The above code was applied

from then following link:

<chrome-extension://efaidnbmnnnibpcajpcgiclfendmkaj/viewer.html?pdfurl=https%3A%2F%2Fcran.r-project.org%2Fweb%2Fpackages%2FNeuralNetTools%2FNeuralNetTools.pdf&clen=142691&chunk=true>

to be able to visualize a neural network.

Note

An issue I ran in to:

I re-formatted the label/target field and went from a binary (good [>74]/bad [<75]) classifier to what is it currently; 50s,60s,70s, and 80s. However, when running the all of the PAs prior to neural network there were no strange issues. When running the NN I recieved an output accuracy of 0.003 an knew there was an issue.

There was an (un)interesting issue with NN table (well, all tables), as it was dropping the first two rows as it was not forward feeding into those nodes. The following is the work around to resolve this issue.

#Before#

```
set.seed(1)
i=1
model = nnet(tcp~.,df[blk != i,], size = 10, trace=FALSE, wgt=.05)
pred = predict(model, df[blk==i,],type="class")
confMat = table(pred,df$tcp[blk==i])
confMat
```

##

```
## pred  1  2  3  4
##      3  1  0 16 72
```

#After#

```
set.seed(1)
i=1
model = nnet(tcp~.,df[blk != i,], size = 10, trace=FALSE, wgt=.05)
pred = predict(model, df[blk==i,],type="class")
confMat = table(factor(pred,levels=1:4),factor(df$tcp[blk==i],levels=1:4))
confMat
```

##


```
##      1  2  3  4
##    1  0  0  0  0
##    2  0  0  0  0
##    3  1  0 16 72
##    4  0  0  0  0
```

This was then applied to all of the PAs.

K-Nearest Neighbor Preparation

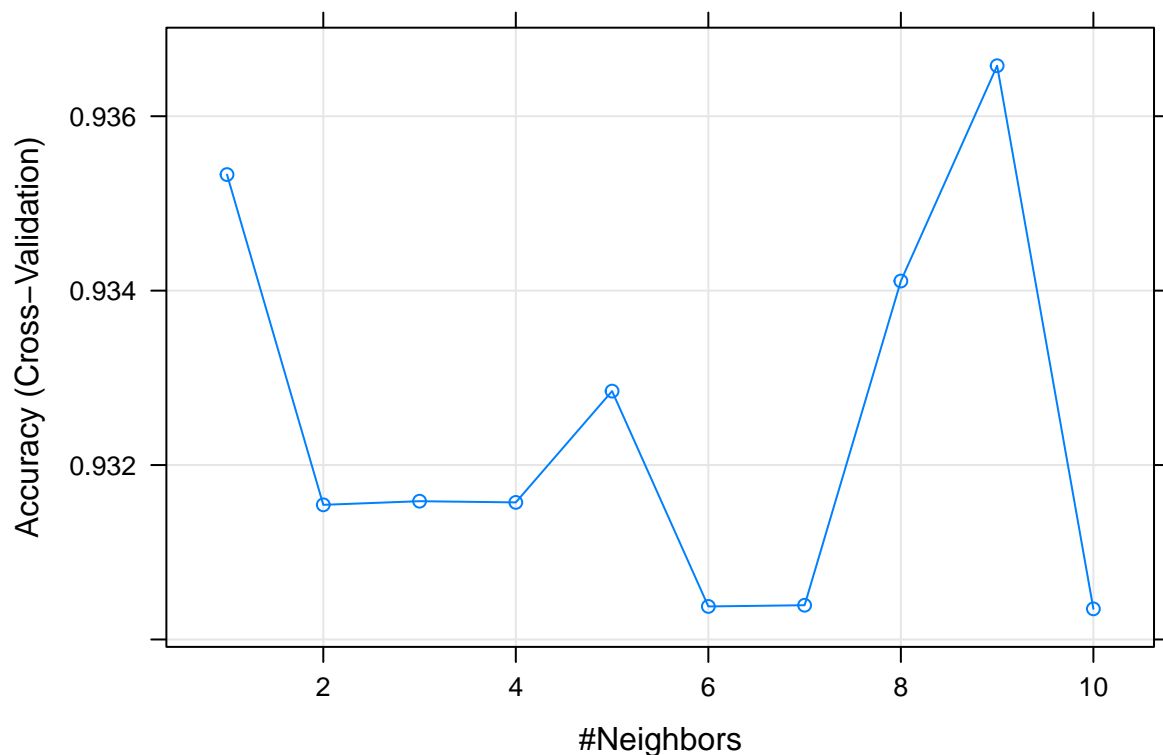
```
set.seed(1)
df$tcp = as.factor(df$tcp)
library(caret)

## Loading required package: lattice
##
## Attaching package: 'caret'
## The following object is masked from 'package:purrr':
##
##      lift
trControl <- trainControl(method = "cv", number = 10)
knn = df[,]
```

KNN

```
set.seed(1)
model <- train(tcp ~ .,
               method = "knn",
               tuneGrid = expand.grid(k = 1:10),
               trControl = trControl,
               data = knn)
acc = mean(model$results$Accuracy)
table_accuracy[6,1] = acc

plot(model)
```



This is a visual to see how many neighbors the KNN will be running. From this visual it could possibly run at 9 groups due to the accuracy level.

#View Accuracy Table#

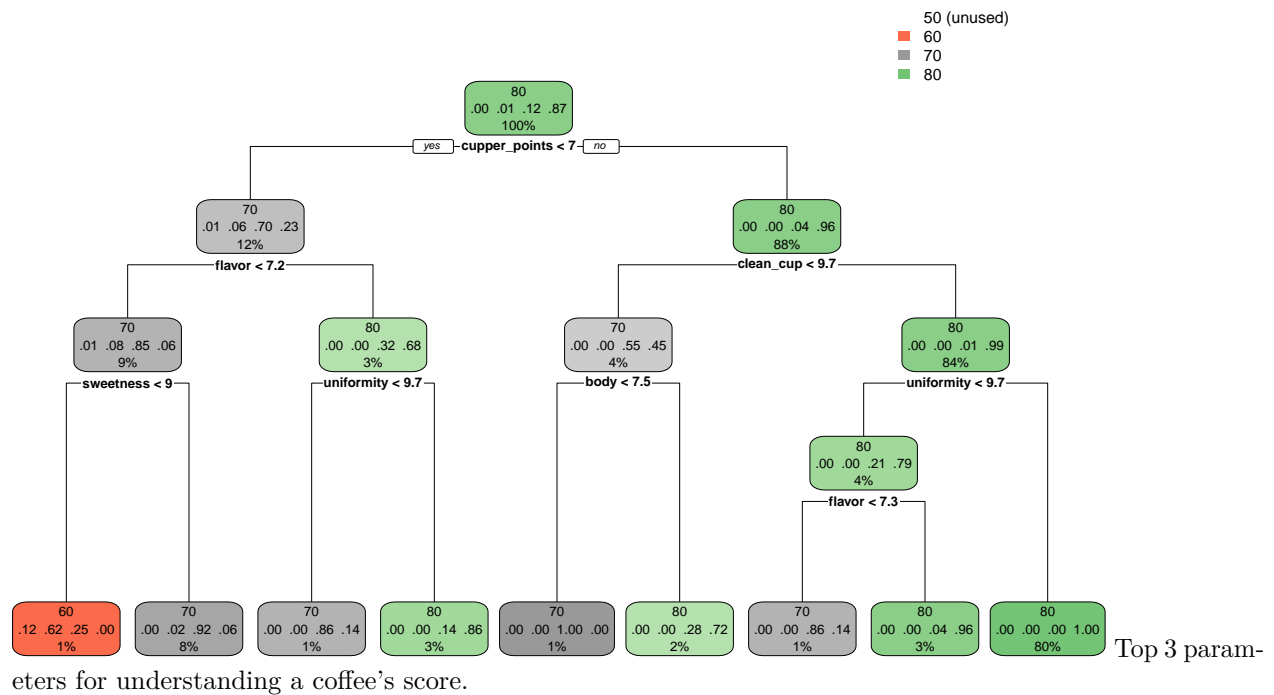
```
tab = round(table_accuracy,4)
tab
```

##	Accuracy
## DTree	0.9517
## NB	0.9551
## SVM-Linerar	0.9865
## SVM-Polynomial	0.9404
## ANN	0.8876
## KNN	0.9325

Most of these predictive techniques did really well! Linear SVM having the highest accuracy, but due to the nature of the data, I do not believe it will be the most informative to an audience. This would suggest Decision Tree and Naive Bayes to be the next best options based on accuracy. As, decision trees are much easier to visualize and conceptually understand the flow of the diagram, this will be the preferred method for any further analysis and discussion.

##Preferred Model##

```
rpart.plot::rpart.plot(tree)
```



~Cupper points are the most informative parameter in deciding if a coffee is to be in the 80s or below this.

~If place coffee is <7 cupper points, the next deciding factor is how good is the flavor of the coffee.

~ If coffee is >7 cupper points, the next deciding factor is how clean the coffee leaves the cup.

#Export Data to be used in Interactive Visuals#

```
#write.csv(coffee,"coffee.csv", row.names = FALSE)
```