Stat_fp_white.R

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```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.2 --
## v ggplot2 3.4.0      v purrr   0.3.5
## v tibble  3.1.8      v dplyr   1.0.10
## v tidyr   1.2.1      v stringr 1.4.1
## v readr   2.1.3      v forcats 0.5.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(dplyr)
library(GGally)
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```

```
library(corrplot)
```

```
## corrplot 0.92 loaded
```

```
library(rpart)
library(rpart.plot)
library(DMwR2)   # Contains rt.prune
```

```
## Registered S3 method overwritten by 'quantmod':
##   method            from
##   as.zoo.data.frame zoo
```

```
library(ISLR)
library(MASS)
```

```
##
## Attaching package: 'MASS'
##
## The following object is masked from 'package:dplyr':
##
##     select
```

```
library(randomForest)
```

```
## randomForest 4.7-1.1
## Type rfNews() to see new features/changes/bug fixes.
##
## Attaching package: 'randomForest'
##
## The following object is masked from 'package:dplyr':
##
##     combine
##
## The following object is masked from 'package:ggplot2':
##
##     margin
```

```
library(cluster)    # clustering algorithms
library(factoextra) # clustering algorithms & visualization
```

```
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

```
library(maditr)
```

```
##
## To aggregate data: take(mtcars, mean_mpg = mean(mpg), by = am)
##
##
## Attaching package: 'maditr'
##
## The following objects are masked from 'package:dplyr':
##
##     between, coalesce, first, last
##
## The following object is masked from 'package:purrr':
##
##     transpose
##
## The following object is masked from 'package:readr':
##
##     cols
```

```
library(ggpubr)
library(Metrics)
library(glmnet)
```

```
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
##
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
##
## Loaded glmnet 4.1-4
```

```
library(mlbench)
library(caret) # use createDataPartition() function
```

```
## Loading required package: lattice
##
## Attaching package: 'caret'
##
## The following objects are masked from 'package:Metrics':
##
##     precision, recall
##
## The following object is masked from 'package:purrr':
##
##     lift
```

```
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
##
## The following object is masked from 'package:randomForest':
##
##     combine
##
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
#Data reading
white_df <- read.csv(file = "winequality-white.csv", as.is = TRUE,sep = ";", header = TRUE)
head(white_df)
```

```
##   fixed.acidity volatile.acidity citric.acid residual.sugar chlorides
## 1           7.0             0.27        0.36           20.7     0.045
## 2           6.3             0.30        0.34            1.6     0.049
## 3           8.1             0.28        0.40            6.9     0.050
## 4           7.2             0.23        0.32            8.5     0.058
## 5           7.2             0.23        0.32            8.5     0.058
## 6           8.1             0.28        0.40            6.9     0.050
##   free.sulfur.dioxide total.sulfur.dioxide density   pH sulphates alcohol
## 1                  45                  170  1.0010 3.00      0.45     8.8
## 2                  14                  132  0.9940 3.30      0.49     9.5
## 3                  30                   97  0.9951 3.26      0.44    10.1
## 4                  47                  186  0.9956 3.19      0.40     9.9
## 5                  47                  186  0.9956 3.19      0.40     9.9
## 6                  30                   97  0.9951 3.26      0.44    10.1
##   quality
## 1       6
## 2       6
## 3       6
## 4       6
## 5       6
## 6       6
```

```
dim(white_df)
```

```
## [1] 4898   12
```

```
#Data overview
str(white_df)
```

```
## 'data.frame':    4898 obs. of  12 variables:
##  $ fixed.acidity       : num  7 6.3 8.1 7.2 7.2 8.1 6.2 7 6.3 8.1 ...
##  $ volatile.acidity    : num  0.27 0.3 0.28 0.23 0.23 0.28 0.32 0.27 0.3 0.22 ...
##  $ citric.acid         : num  0.36 0.34 0.4 0.32 0.32 0.4 0.16 0.36 0.34 0.43 ...
##  $ residual.sugar      : num  20.7 1.6 6.9 8.5 8.5 6.9 7 20.7 1.6 1.5 ...
##  $ chlorides           : num  0.045 0.049 0.05 0.058 0.058 0.05 0.045 0.045 0.049 0.044 ...
##  $ free.sulfur.dioxide : num  45 14 30 47 47 30 30 45 14 28 ...
##  $ total.sulfur.dioxide: num  170 132 97 186 186 97 136 170 132 129 ...
##  $ density             : num  1.001 0.994 0.995 0.996 0.996 ...
##  $ pH                  : num  3 3.3 3.26 3.19 3.19 3.26 3.18 3 3.3 3.22 ...
##  $ sulphates           : num  0.45 0.49 0.44 0.4 0.4 0.44 0.47 0.45 0.49 0.45 ...
##  $ alcohol             : num  8.8 9.5 10.1 9.9 9.9 10.1 9.6 8.8 9.5 11 ...
##  $ quality             : int  6 6 6 6 6 6 6 6 6 6 ...
```

```
summary(white_df)
```

```
##  fixed.acidity    volatile.acidity  citric.acid     residual.sugar
##  Min.   : 3.800   Min.   :0.0800   Min.   :0.0000   Min.   : 0.600
##  1st Qu.: 6.300   1st Qu.:0.2100   1st Qu.:0.2700   1st Qu.: 1.700
##  Median : 6.800   Median :0.2600   Median :0.3200   Median : 5.200
##  Mean   : 6.855   Mean   :0.2782   Mean   :0.3342   Mean   : 6.391
##  3rd Qu.: 7.300   3rd Qu.:0.3200   3rd Qu.:0.3900   3rd Qu.: 9.900
##  Max.   :14.200   Max.   :1.1000   Max.   :1.6600   Max.   :65.800
##    chlorides       free.sulfur.dioxide total.sulfur.dioxide    density
##  Min.   :0.00900   Min.   :  2.00      Min.   :  9.0        Min.   :0.9871
##  1st Qu.:0.03600   1st Qu.: 23.00      1st Qu.:108.0        1st Qu.:0.9917
##  Median :0.04300   Median : 34.00      Median :134.0        Median :0.9937
##  Mean   :0.04577   Mean   : 35.31      Mean   :138.4        Mean   :0.9940
##  3rd Qu.:0.05000   3rd Qu.: 46.00      3rd Qu.:167.0        3rd Qu.:0.9961
##  Max.   :0.34600   Max.   :289.00      Max.   :440.0        Max.   :1.0390
##        pH          sulphates         alcohol         quality
##  Min.   :2.720   Min.   :0.2200   Min.   : 8.00   Min.   :3.000
##  1st Qu.:3.090   1st Qu.:0.4100   1st Qu.: 9.50   1st Qu.:5.000
##  Median :3.180   Median :0.4700   Median :10.40   Median :6.000
##  Mean   :3.188   Mean   :0.4898   Mean   :10.51   Mean   :5.878
##  3rd Qu.:3.280   3rd Qu.:0.5500   3rd Qu.:11.40   3rd Qu.:6.000
##  Max.   :3.820   Max.   :1.0800   Max.   :14.20   Max.   :9.000
```

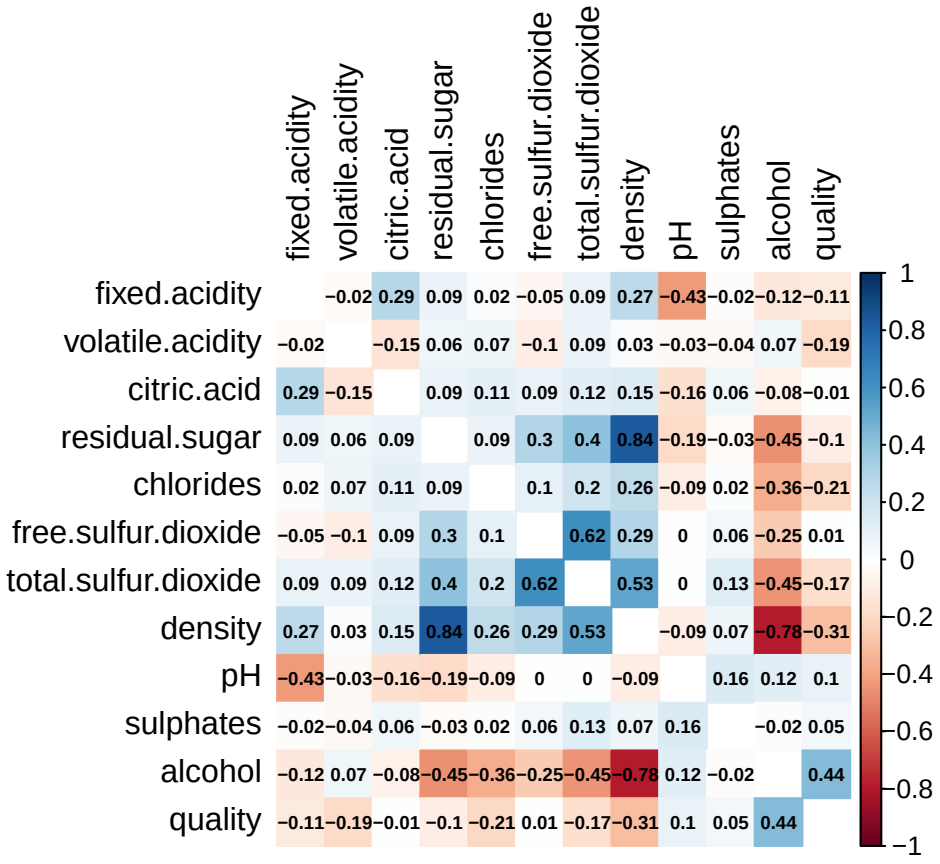
```
#Checking missing values
which(is.na(white_df))
```

```
## integer(0)
```

```
colSums(is.na(white_df))
```

```
##        fixed.acidity     volatile.acidity          citric.acid
##                    0                    0                    0
##       residual.sugar            chlorides  free.sulfur.dioxide
##                    0                    0                    0
## total.sulfur.dioxide              density                   pH
##                    0                    0                    0
##            sulphates              alcohol              quality
##                    0                    0                    0
```

```
#Build correlation and order by decreasing
set.seed(123)

white_dfcor <- cor(white_df)
corrplot(white_dfcor, method = "color", addCoef.col = "black",number.cex = .6,
         tl.col = "black", tl.srt = 90, diag = FALSE)
```




```
#Build correlation atts with Quality variable
dfcor <- cor(white_df)
quality_cor <- dfcor[,12]
absoutcome_cor <- abs(quality_cor)
head(absoutcome_cor[order(absoutcome_cor, decreasing = TRUE)],12)
```

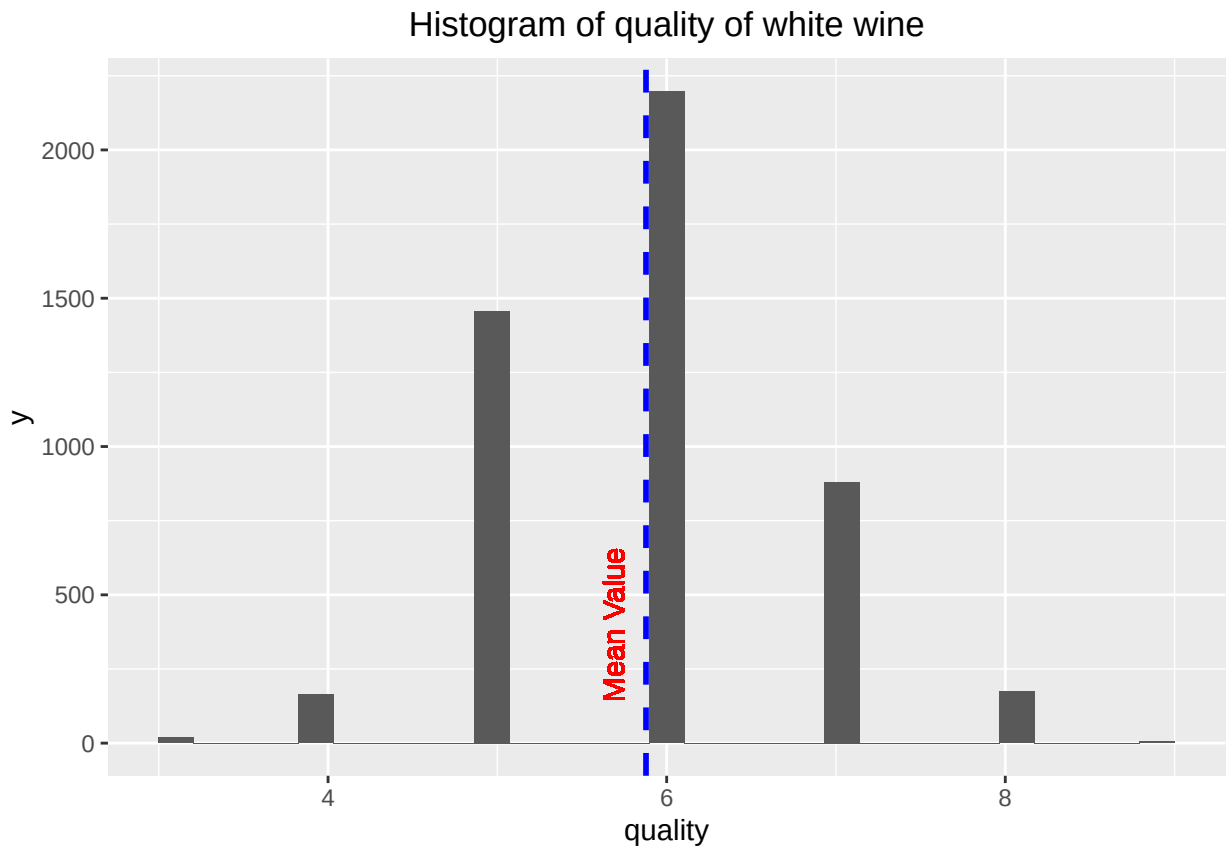
```
##              quality              alcohol              density
```

```
##          1.000000000          0.435574715          0.307123313
##            chlorides     volatile.acidity total.sulfur.dioxide
##          0.209934411          0.194722969          0.174737218
##        fixed.acidity                   pH       residual.sugar
##          0.113662831          0.099427246          0.097576829
##            sulphates          citric.acid  free.sulfur.dioxide
##          0.053677877          0.009209091          0.008158067
```

```
#Analysing the overall quality
ggplot(white_df, aes(quality))+
  geom_histogram() +
  labs(title = "Histogram of quality of white wine") +
  theme(plot.title=element_text(hjust=0.5)) +
  geom_vline(aes(xintercept=mean(quality)), color="blue", linetype="dashed", size=1) +
  geom_text(aes(x=5.6, label="Mean Value", y=400), colour="red", angle=90, vjust = 1.2)
```

```
## Warning: Using 'size' aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use 'linewidth' instead.
```

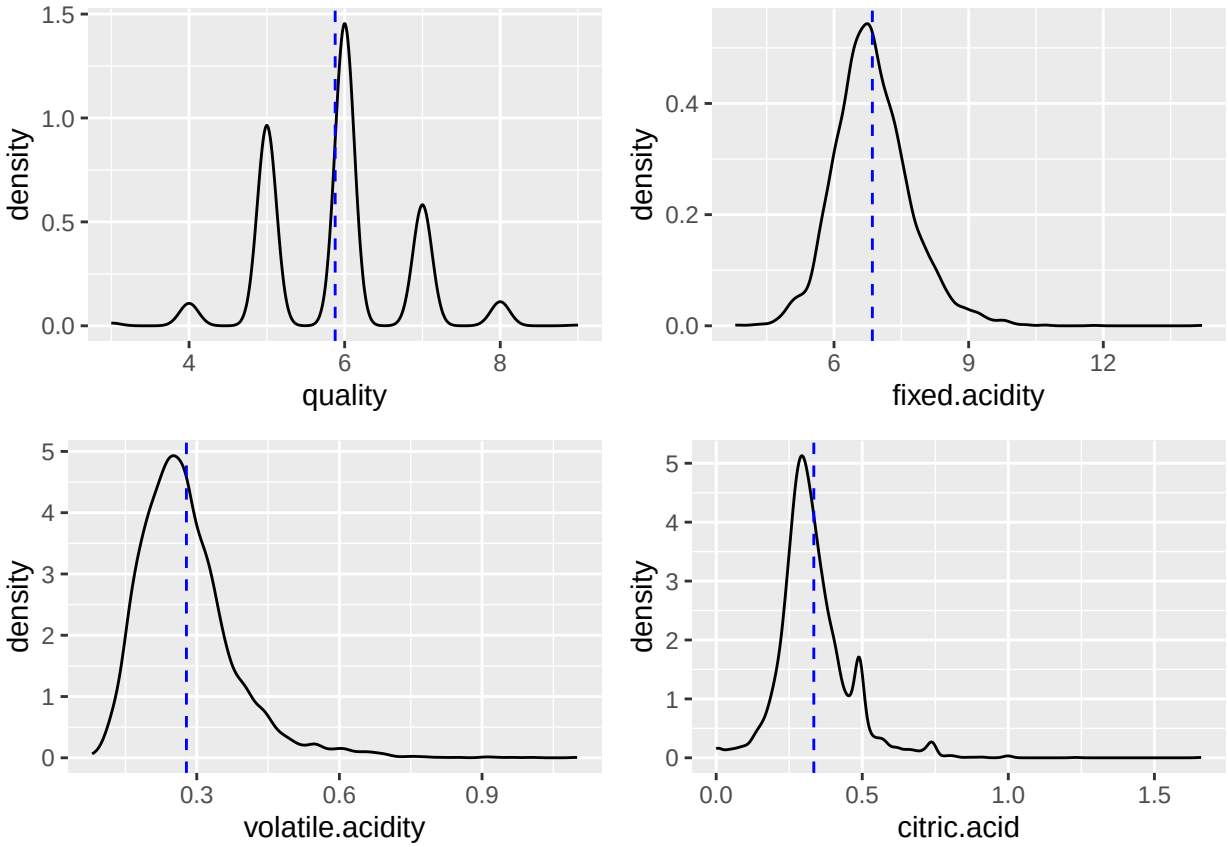
```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```



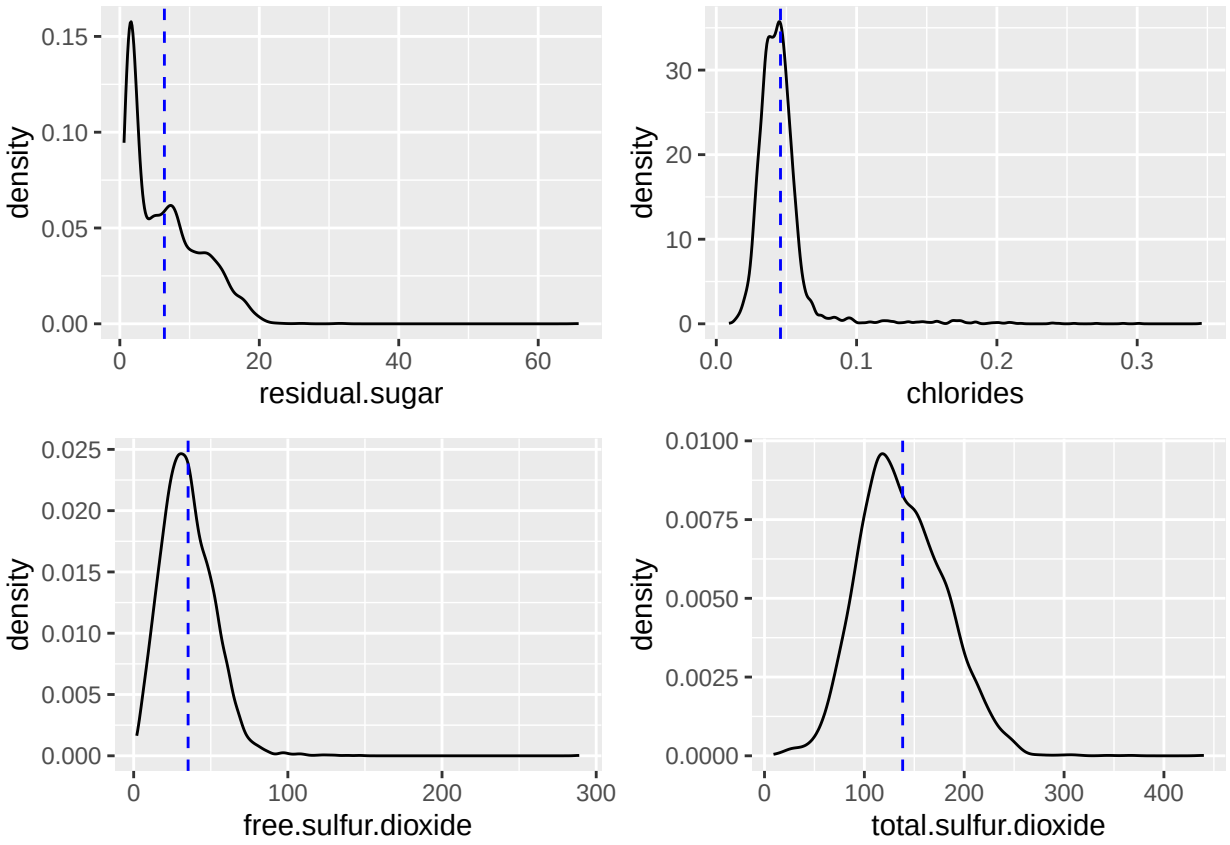

```
mean(white_df$quality)
```

```
## [1] 5.877909
```

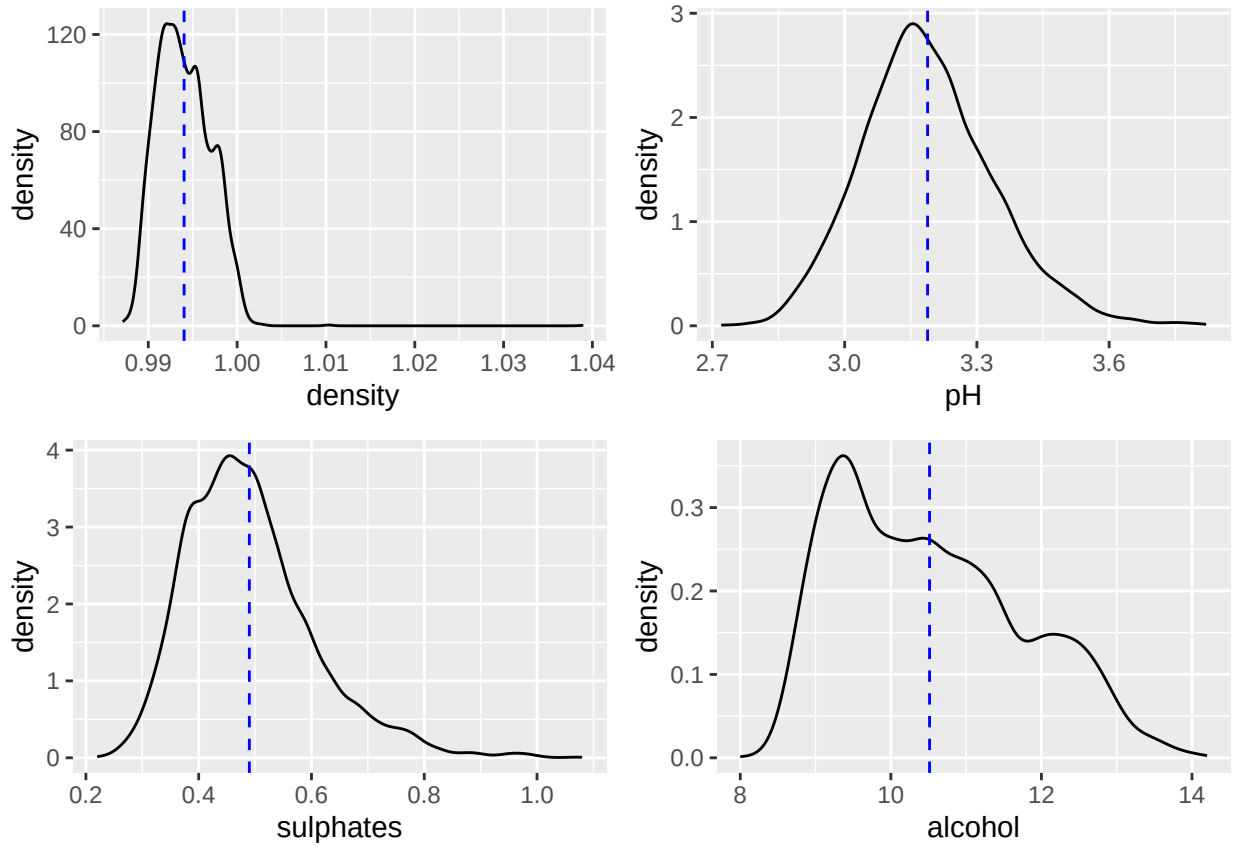
```r
#Plotting the marginal distributions of numerical quantities of interest using density plots

d0 <- ggplot(white_df, aes(x=quality)) +
  geom_density()
d0 <- d0 + geom_vline(aes(xintercept=mean(quality)),
                      color="blue", linetype="dashed")
d1 <- ggplot(white_df, aes(x=fixed.acidity)) +
  geom_density()
d1 <- d1 + geom_vline(aes(xintercept=mean(fixed.acidity)),
                      color="blue", linetype="dashed")
d2 <- ggplot(white_df, aes(x=volatile.acidity)) +
  geom_density()
d2 <- d2 + geom_vline(aes(xintercept=mean(volatile.acidity)),
                      color="blue", linetype="dashed")
d3 <- ggplot(white_df, aes(x=citric.acid)) +
  geom_density()
d3 <- d3 + geom_vline(aes(xintercept=mean(citric.acid)),
                      color="blue", linetype="dashed")
d4 <- ggplot(white_df, aes(x=residual.sugar)) +
  geom_density()
d4 <- d4 + geom_vline(aes(xintercept=mean(residual.sugar)),
                      color="blue", linetype="dashed")
d5 <- ggplot(white_df, aes(x=chlorides)) +
  geom_density()
d5 <- d5 + geom_vline(aes(xintercept=mean(chlorides)),
                      color="blue", linetype="dashed")
d6 <- ggplot(white_df, aes(x=free.sulfur.dioxide)) +
  geom_density()
d6 <- d6 + geom_vline(aes(xintercept=mean(free.sulfur.dioxide)),
                      color="blue", linetype="dashed")
d7 <- ggplot(white_df, aes(x=total.sulfur.dioxide)) +
  geom_density()
d7 <- d7 + geom_vline(aes(xintercept=mean(total.sulfur.dioxide)),
                      color="blue", linetype="dashed")
d8 <- ggplot(white_df, aes(x=density)) +
  geom_density()
d8 <- d8 + geom_vline(aes(xintercept=mean(density)),
                      color="blue", linetype="dashed")
d9 <- ggplot(white_df, aes(x=pH)) +
  geom_density()
d9 <- d9 + geom_vline(aes(xintercept=mean(pH)),
                      color="blue", linetype="dashed")
d10 <- ggplot(white_df, aes(x=sulphates)) +
  geom_density()
d10 <- d10 + geom_vline(aes(xintercept=mean(sulphates)),
                        color="blue", linetype="dashed")
d11 <- ggplot(white_df, aes(x=alcohol)) +
  geom_density()
d11 <- d11 + geom_vline(aes(xintercept=mean(alcohol)),
                        color="blue", linetype="dashed")
ggarrange(d0, d1, d2, d3, nrow = 2, ncol =2)
```



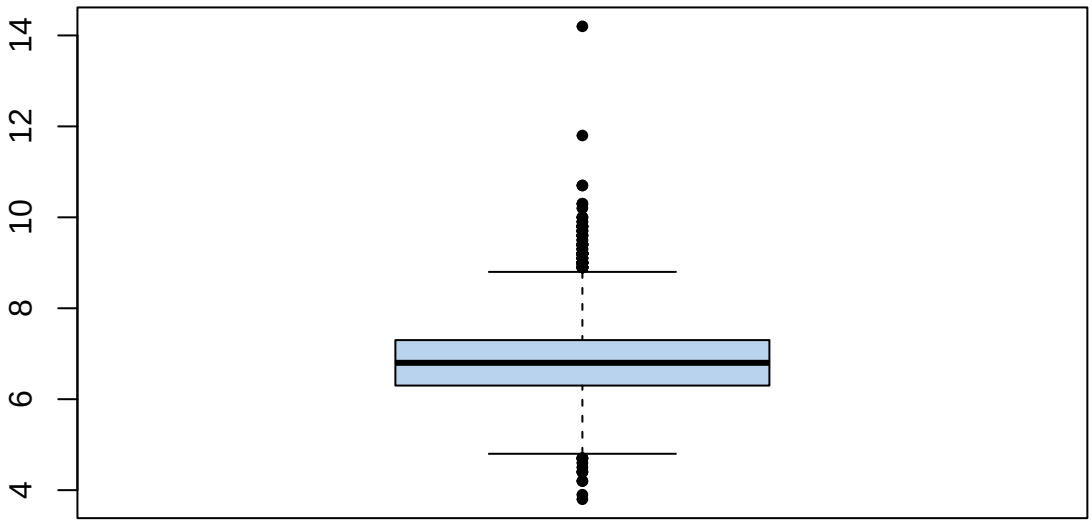

```
ggarrange(d4, d5, d6, d7, nrow = 2, ncol =2)
```



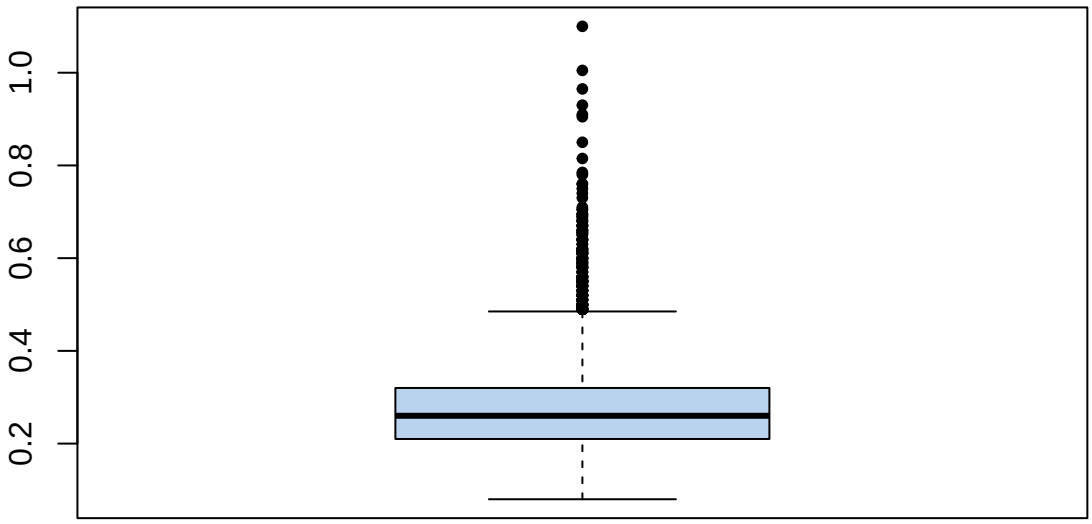

```
ggarrange(d8, d9, d10, d11, nrow = 2, ncol =2)
```



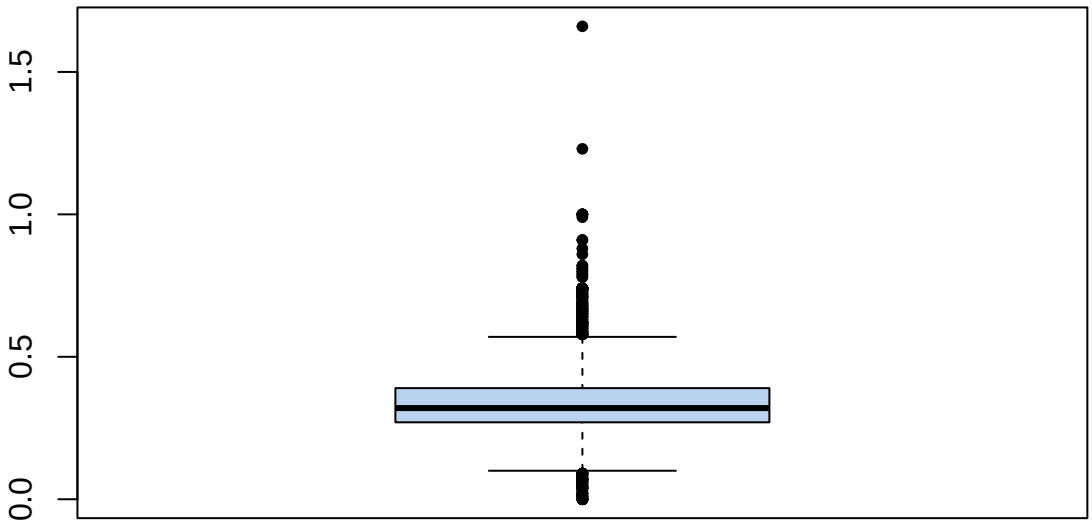

```
#Plotting the marginal distributions of numerical quantities of interest using box plots
b1 <- boxplot(white_df$fixed.acidity, col="slategray2", pch=20)
```



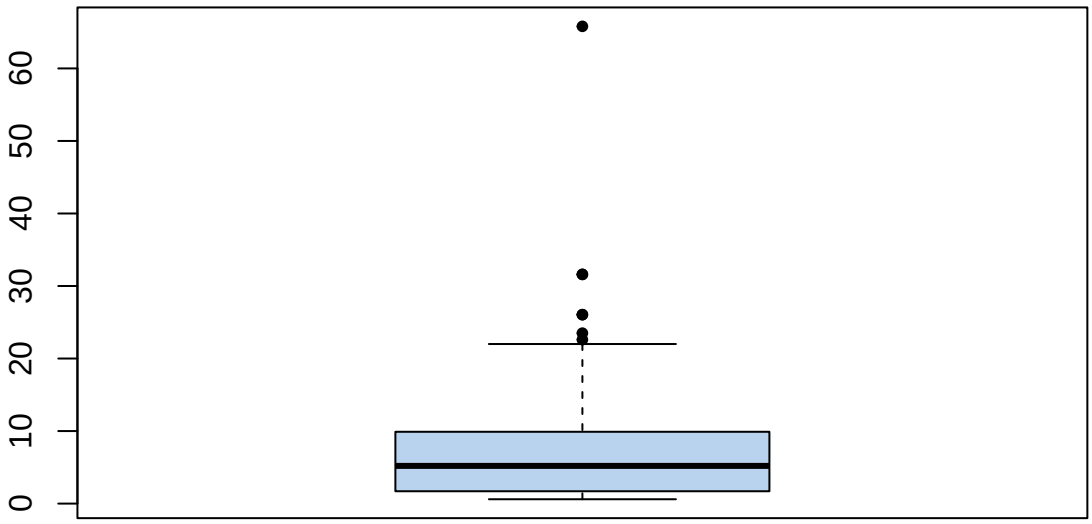

```
b2 <- boxplot(white_df$volatile.acidity, col="slategray2", pch=20)
```



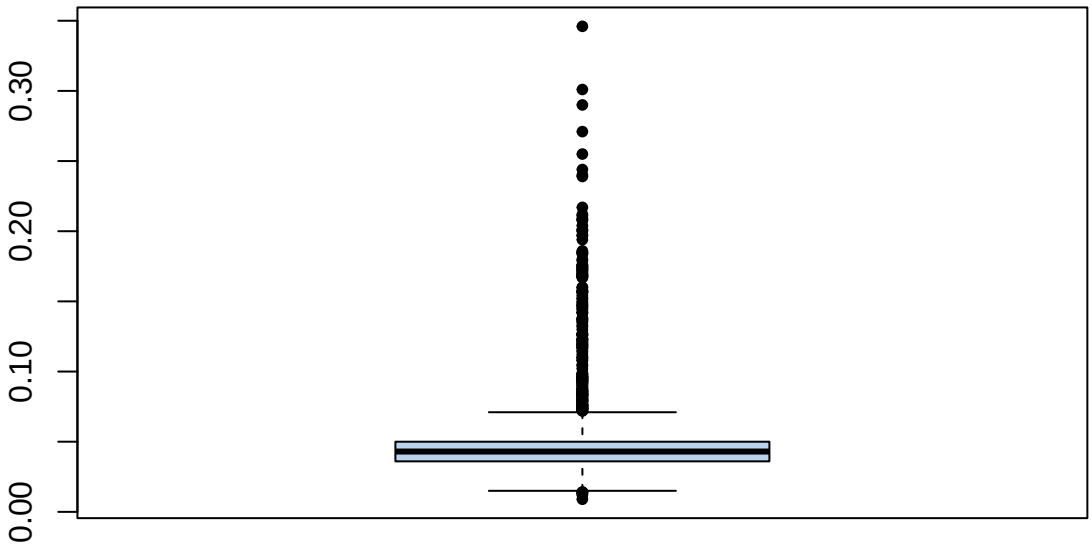

```
b3 <- boxplot(white_df$citric.acid, col="slategray2", pch=20)
```



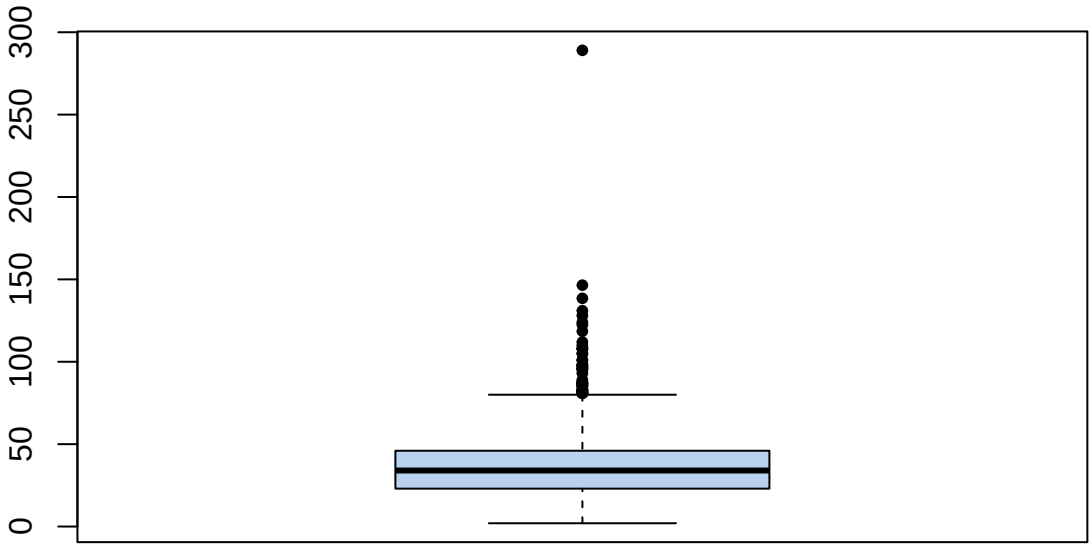

```
b4 <- boxplot(white_df$residual.sugar, col="slategray2", pch=20)
```



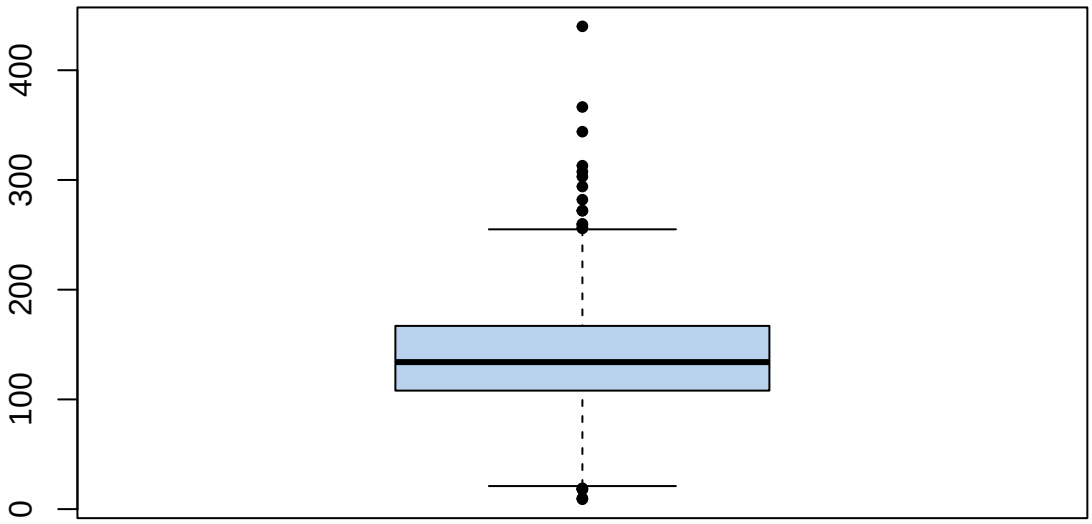

```
b5 <- boxplot(white_df$chlorides, col="slategray2", pch=20)
```



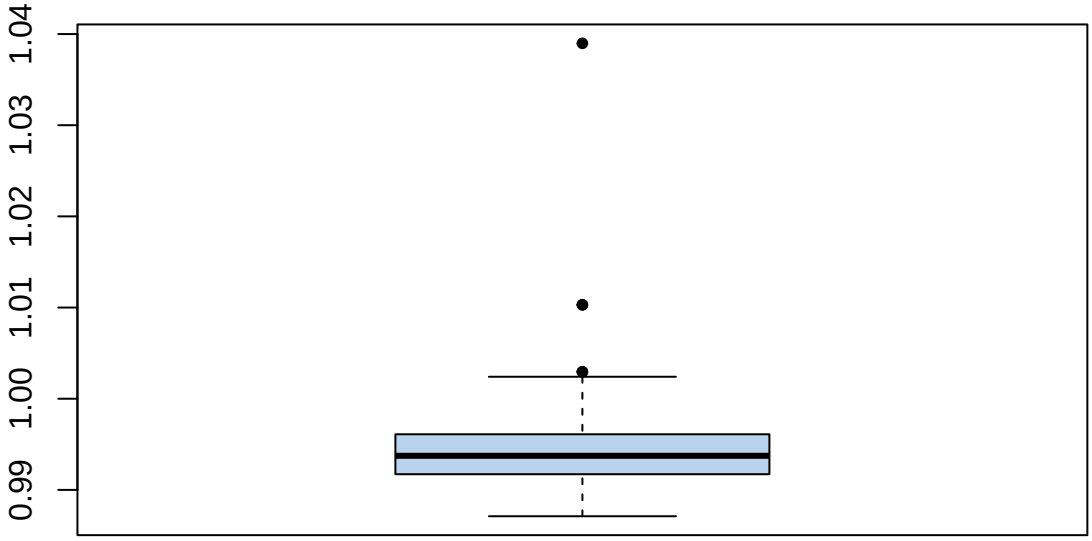

```
b6 <- boxplot(white_df$free.sulfur.dioxide, col="slategray2", pch=20)
```



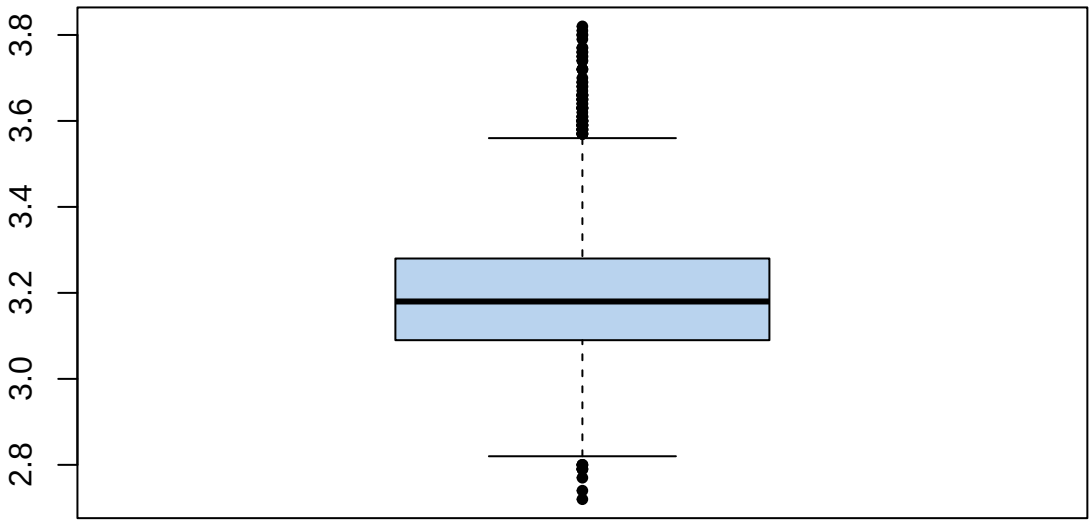

```
b7 <- boxplot(white_df$total.sulfur.dioxide, col="slategray2", pch=20)
```



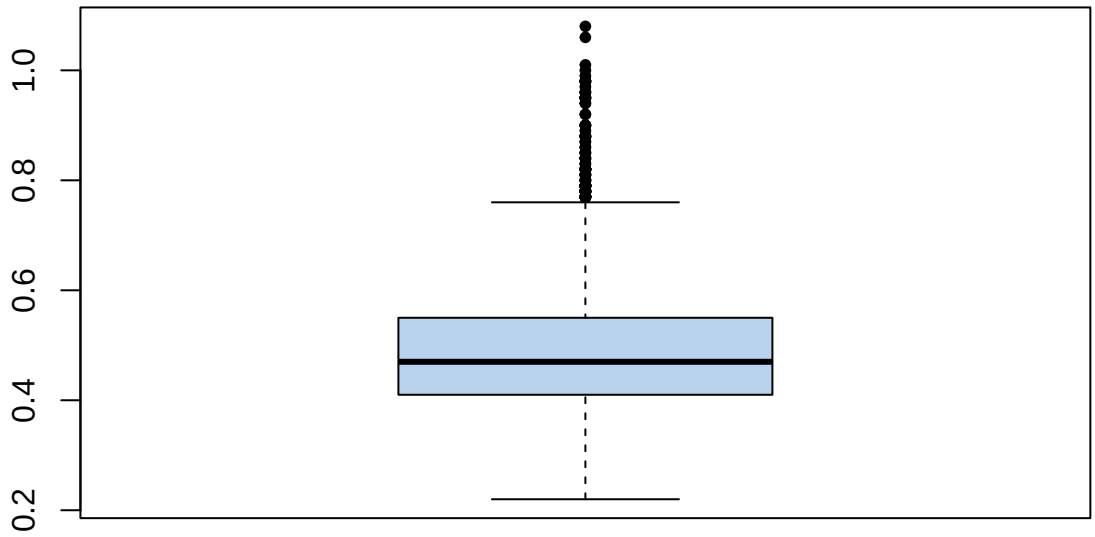

```
b8 <- boxplot(white_df$density, col="slategray2", pch=20)
```



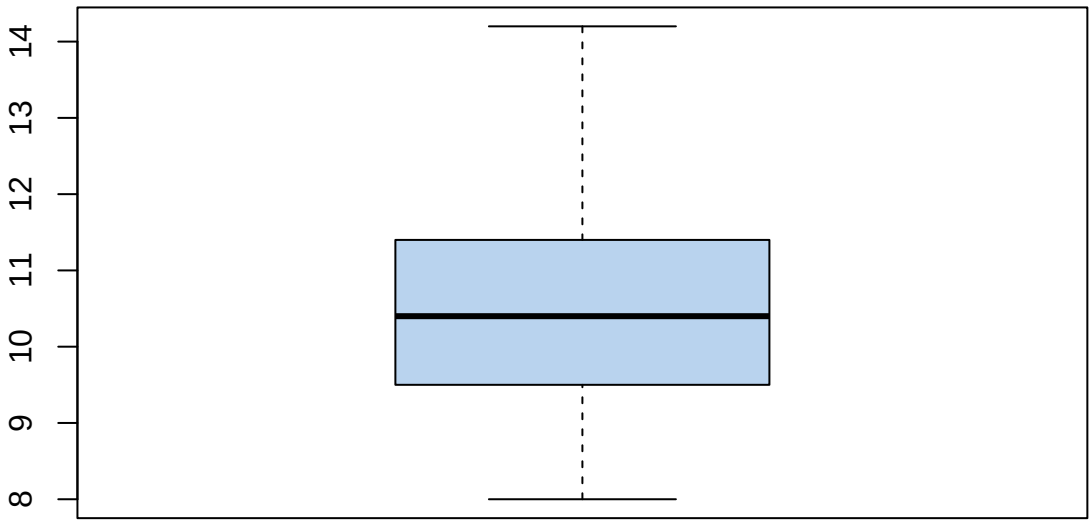

```
b9 <- boxplot(white_df$pH, col="slategray2", pch=20)
```



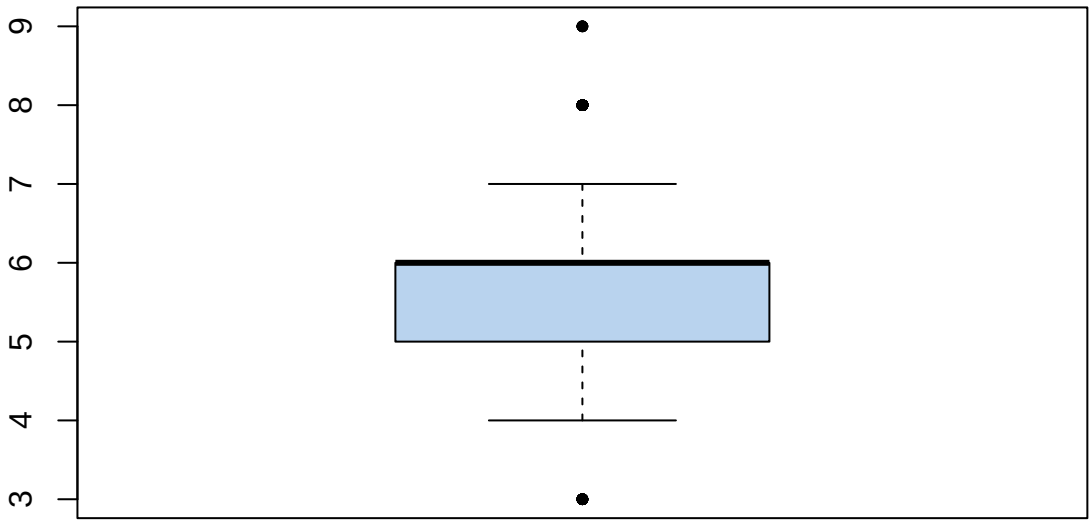

```
b10 <- boxplot(white_df$sulphates, col="slategray2", pch=20)
```



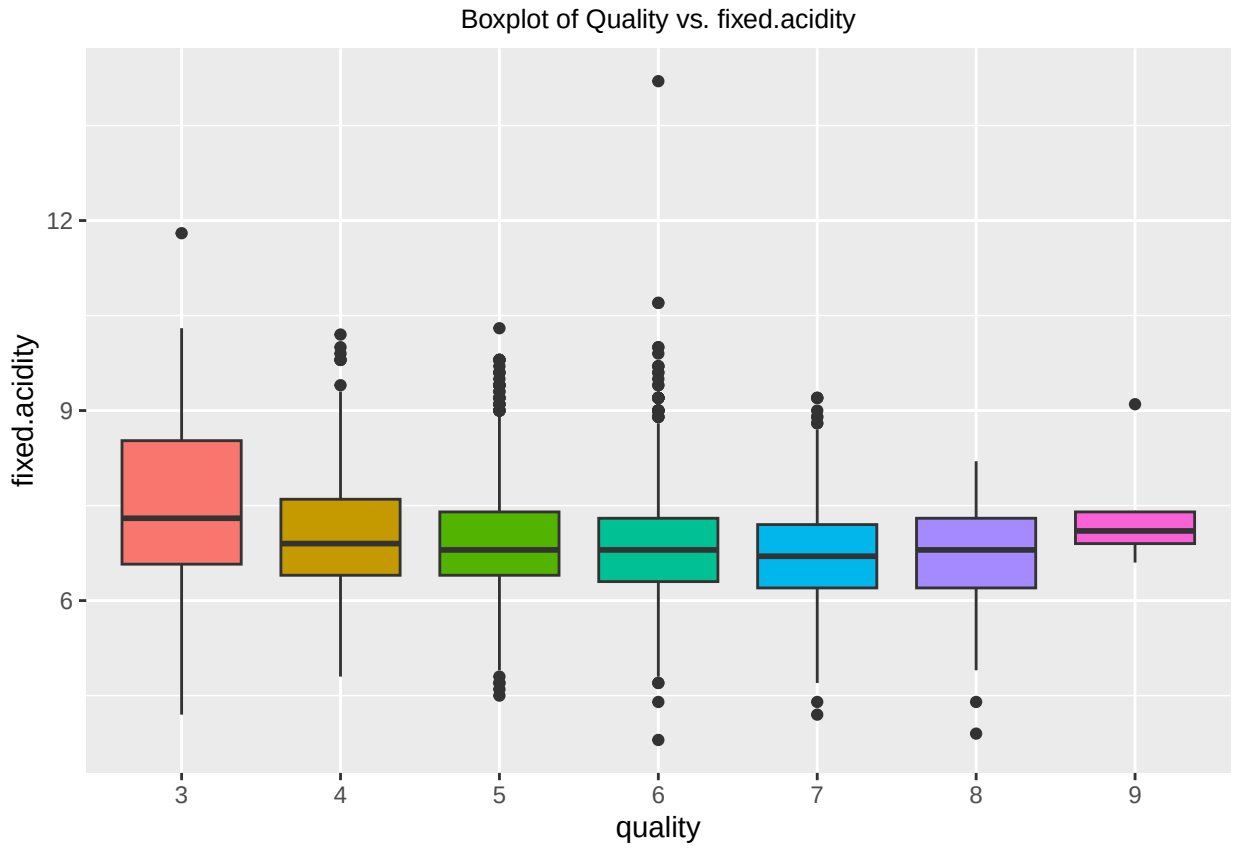

```
b11 <- boxplot(white_df$alcohol, col="slategray2", pch=20)
```



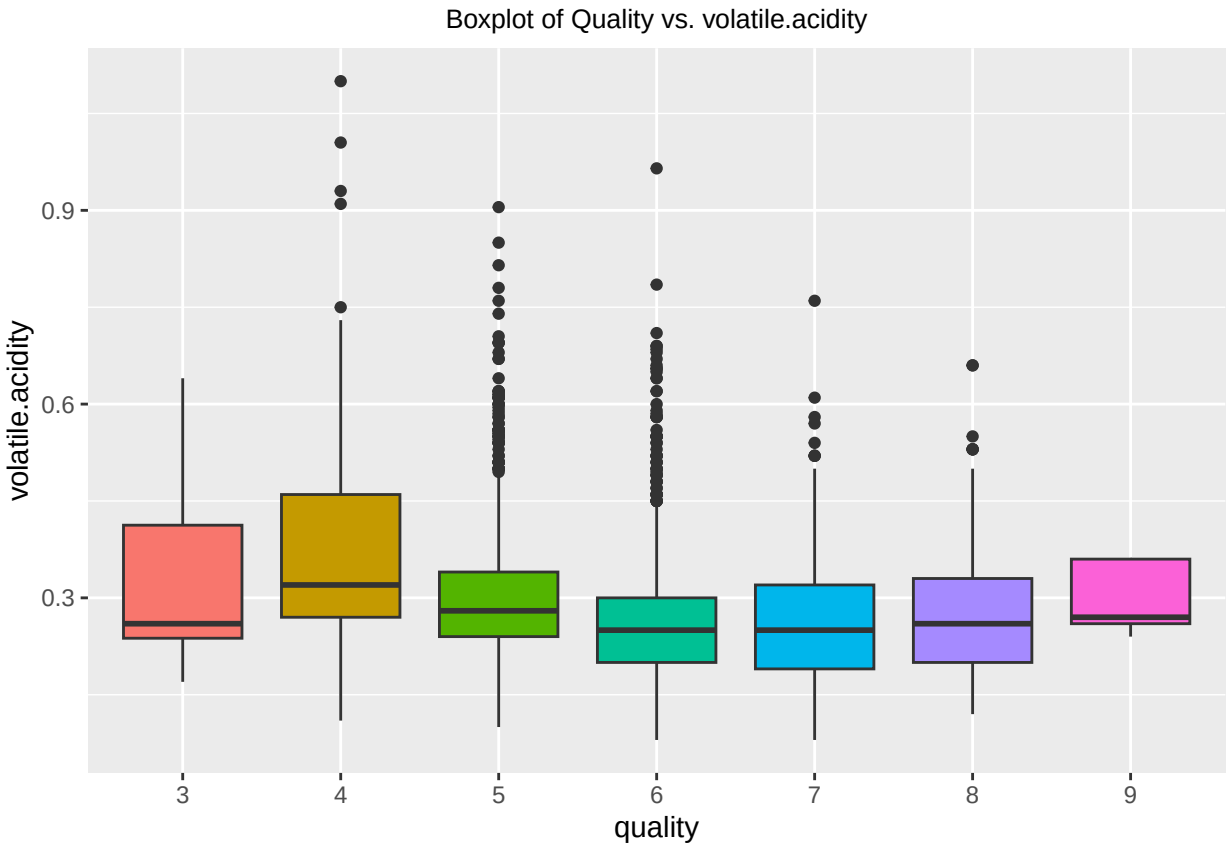

```
b12 <- boxplot(white_df$quality, col="slategray2", pch=20)
```



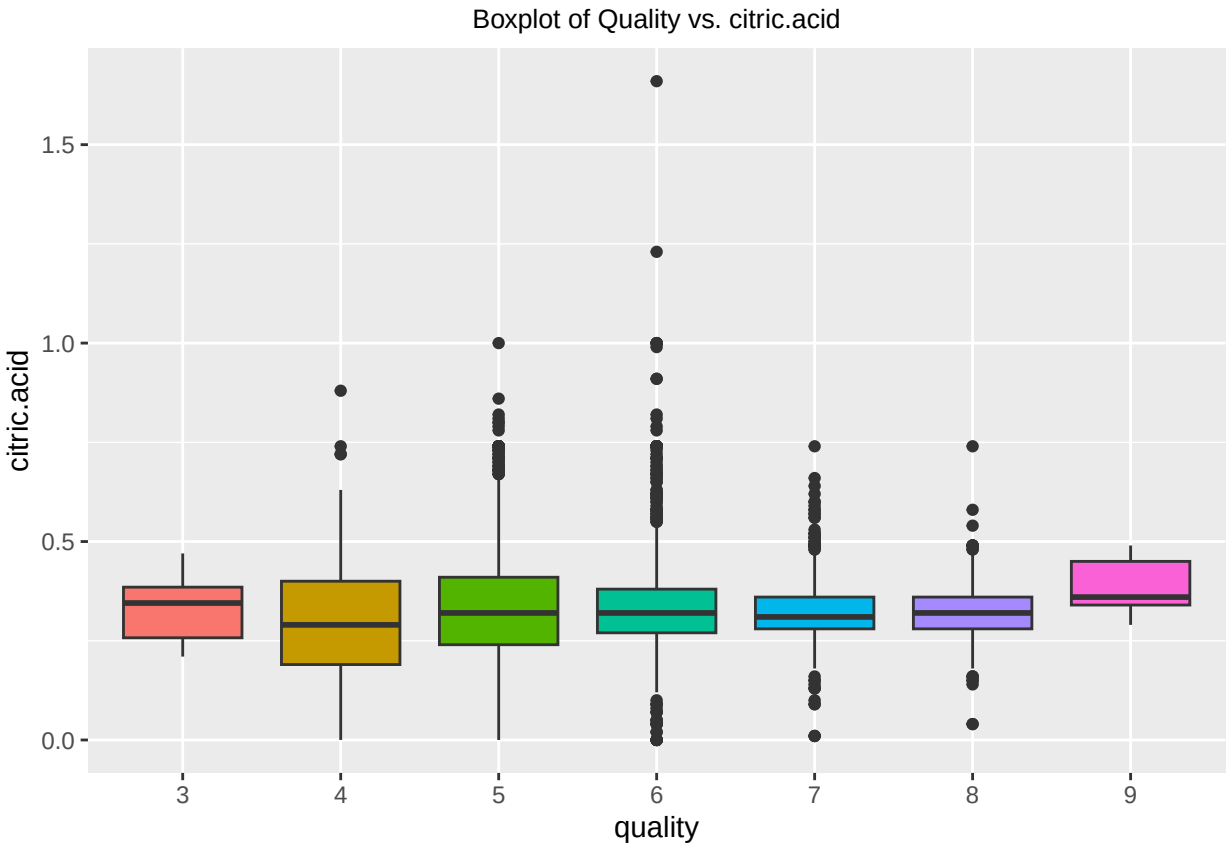

```
#Plotting quality against numerical variables
bp1 <- ggplot(white_df, aes(factor(quality), fixed.acidity, fill=factor(quality))) +
  geom_boxplot() +
  labs(x = "quality", y = "fixed.acidity", title = "Boxplot of Quality vs. fixed.acidity") +
  theme(legend.position = 'none', plot.title = element_text(size = 10, hjust=0.5))
bp1
```



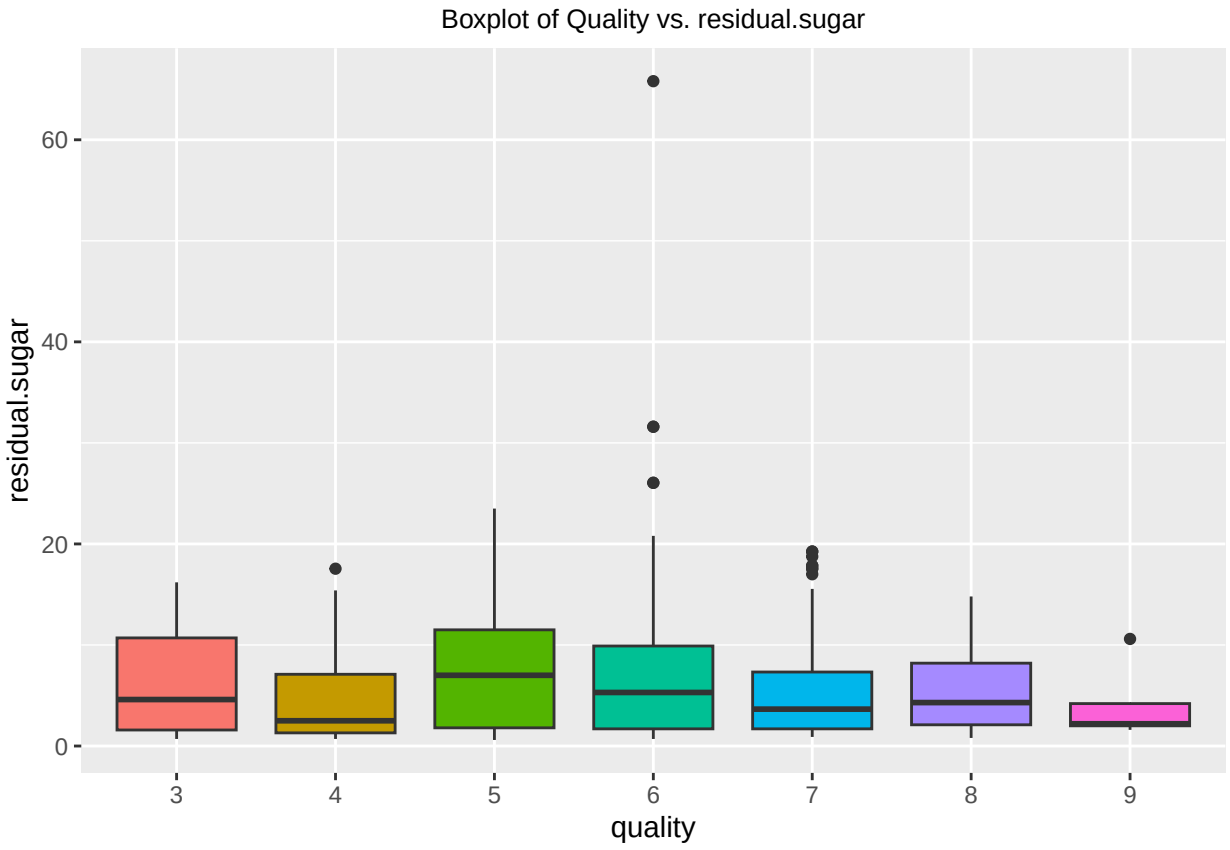

```
bp2 <- ggplot(white_df, aes(factor(quality), volatile.acidity, fill=factor(quality))) +
  geom_boxplot() +
  labs(x = "quality", y = "volatile.acidity", title = "Boxplot of Quality vs. volatile.acidity") +
  theme(legend.position = 'none', plot.title = element_text(size = 10, hjust=0.5))
bp2
```



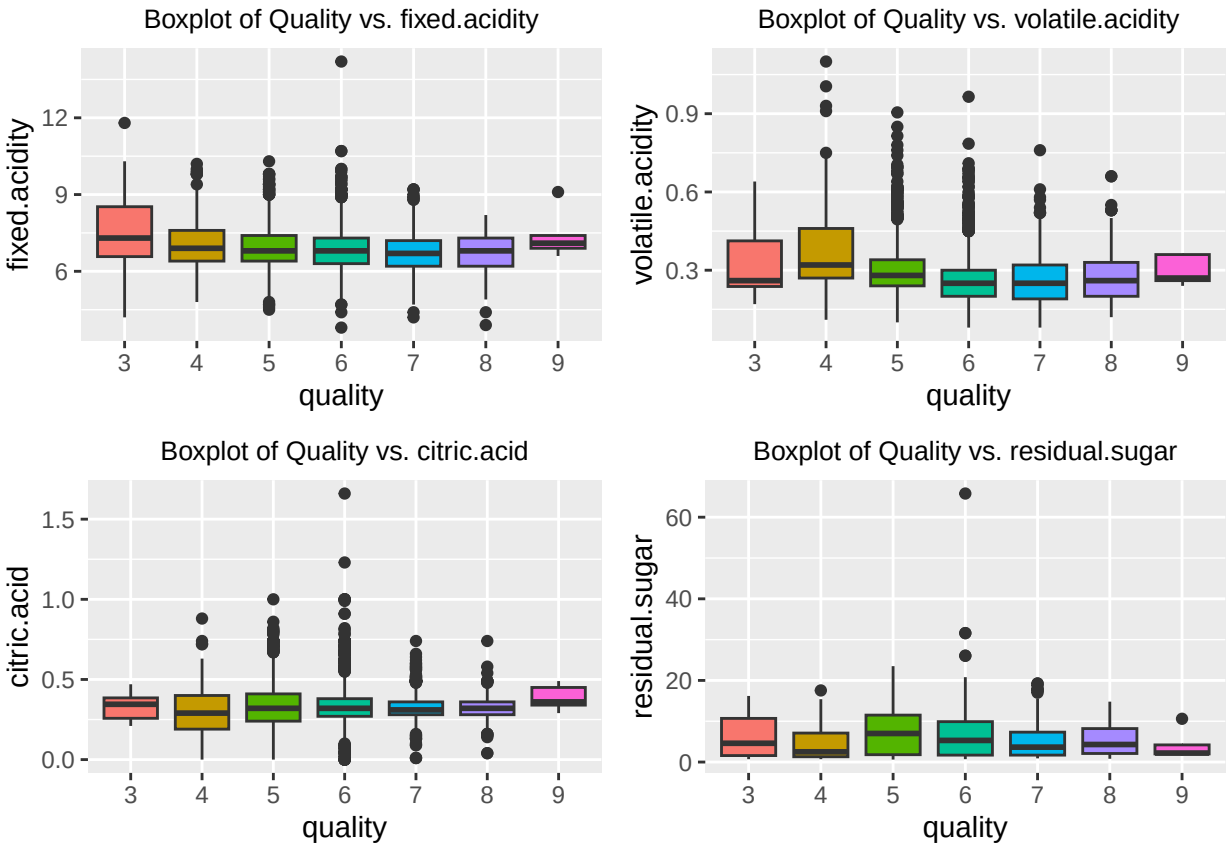

```
bp3 <- ggplot(white_df, aes(factor(quality), citric.acid, fill=factor(quality))) +
  geom_boxplot() +
  labs(x = "quality", y = "citric.acid", title = "Boxplot of Quality vs. citric.acid") +
  theme(legend.position = 'none', plot.title = element_text(size = 10, hjust=0.5))
bp3
```



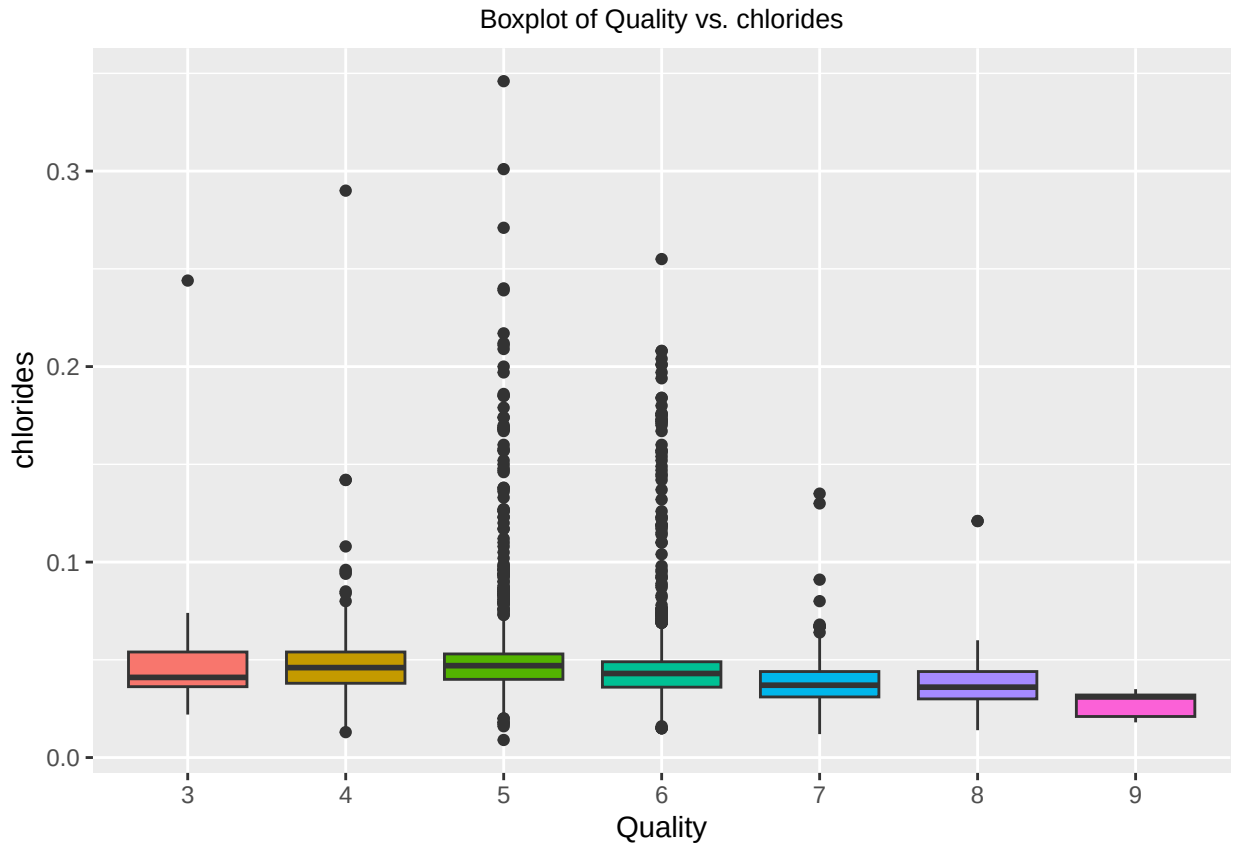

```
bp4 <- ggplot(white_df, aes(factor(quality), residual.sugar, fill=factor(quality))) +
  geom_boxplot() +
  labs(x = "quality", y = "residual.sugar", title = "Boxplot of Quality vs. residual.sugar") +
  theme(legend.position = 'none', plot.title = element_text(size = 10, hjust=0.5))
bp4
```



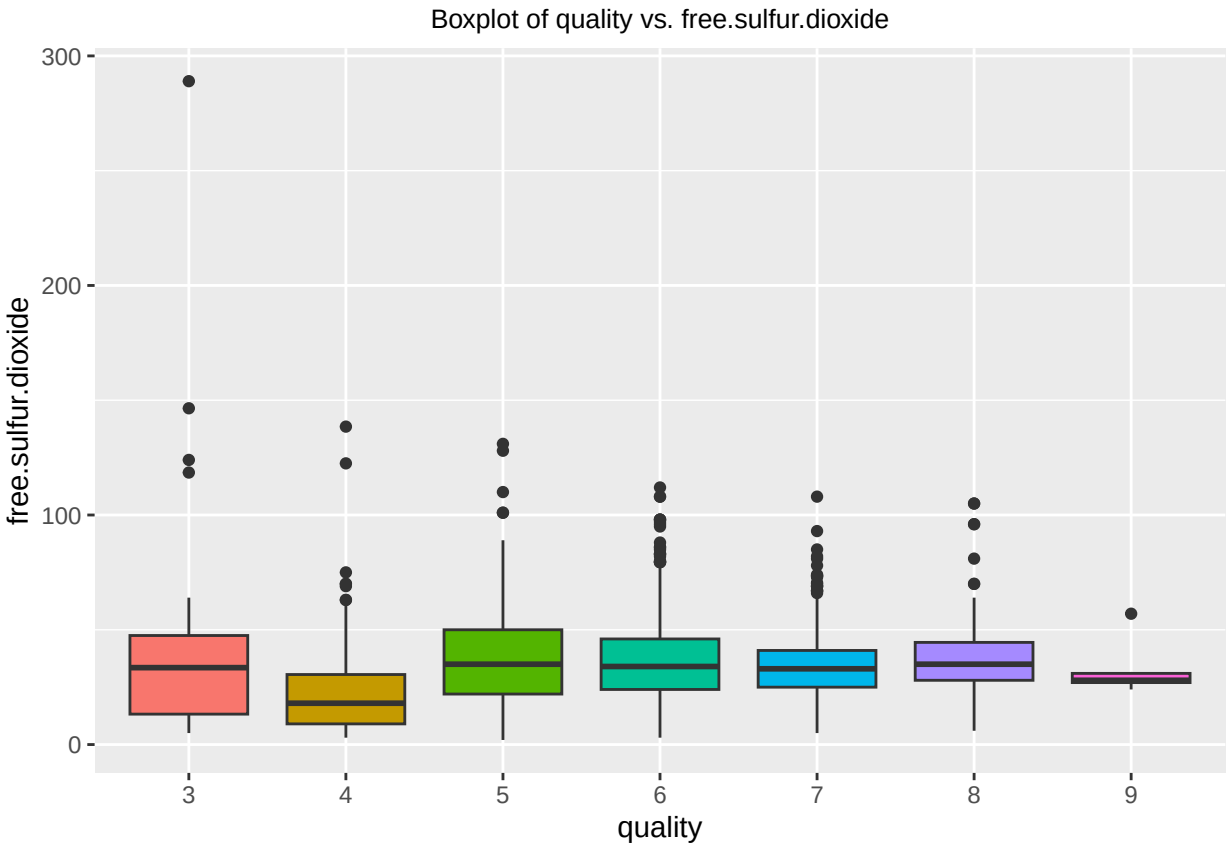

```
ggarrange(bp1, bp2, bp3, bp4, nrow = 2, ncol =2)
```



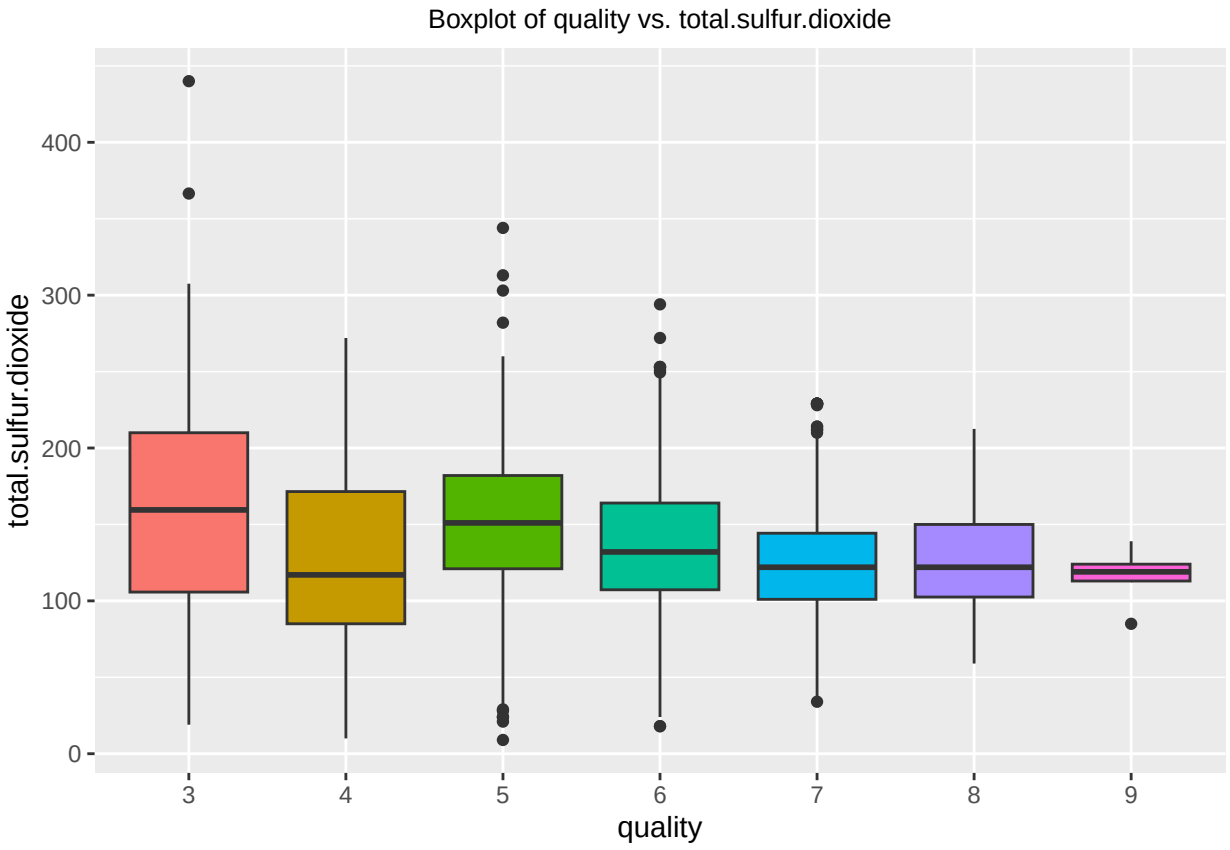

```
bp5 <- ggplot(white_df, aes(factor(quality), chlorides, fill=factor(quality))) +
  geom_boxplot() +
  labs(x = "Quality", y = "chlorides", title = "Boxplot of Quality vs. chlorides") +
  theme(legend.position = 'none', plot.title = element_text(size = 10, hjust=0.5))
bp5
```



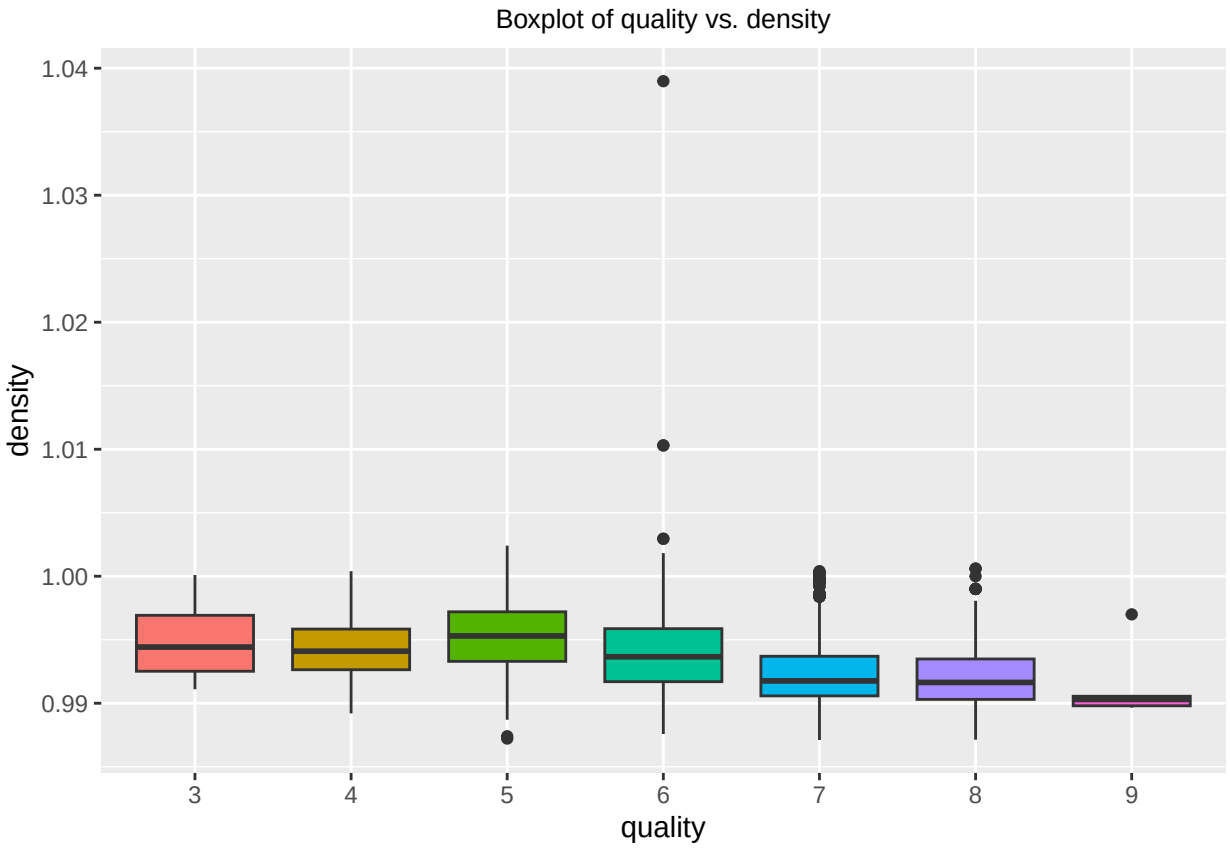

```
bp6 <- ggplot(white_df, aes(factor(quality), free.sulfur.dioxide, fill=factor(quality))) +
  geom_boxplot() +
  labs(x = "quality", y = "free.sulfur.dioxide", title = "Boxplot of quality vs. free.sulfur.dioxide") +
  theme(legend.position = 'none', plot.title = element_text(size = 10, hjust=0.5))
bp6
```



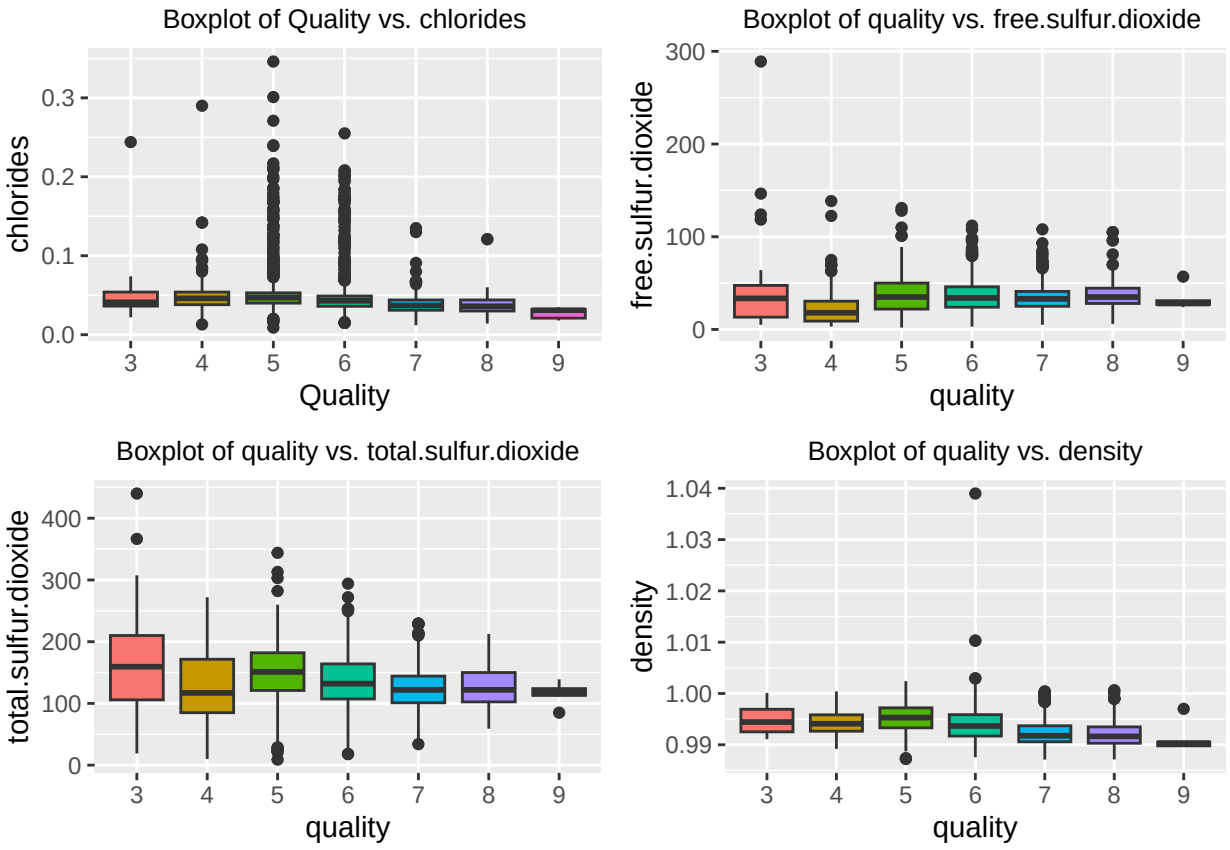

```
bp7 <- ggplot(white_df, aes(factor(quality), total.sulfur.dioxide, fill=factor(quality))) +
  geom_boxplot() +
  labs(x = "quality", y = "total.sulfur.dioxide", title = "Boxplot of quality vs. total.sulfur.dioxide")
  theme(legend.position = 'none', plot.title = element_text(size = 10, hjust=0.5))
bp7
```



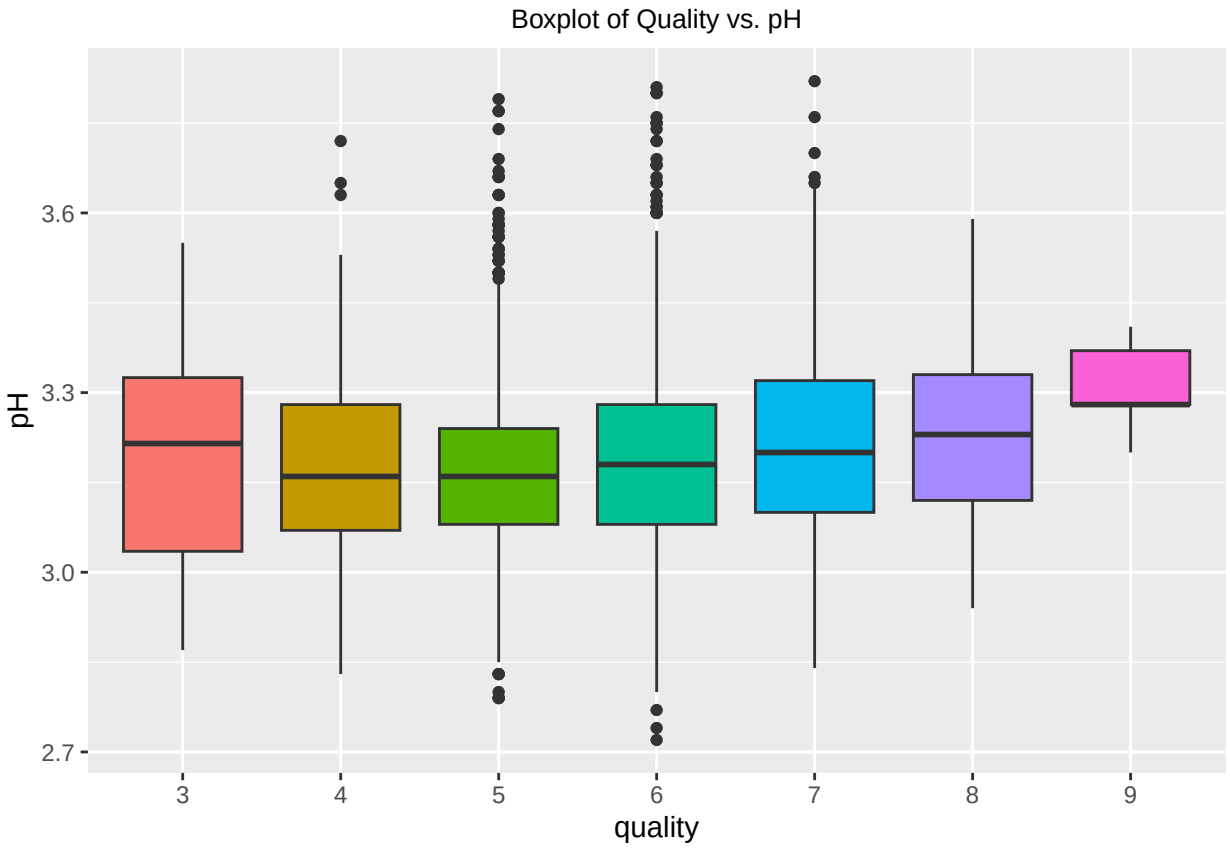

```
bp8 <- ggplot(white_df, aes(factor(quality), density, fill=factor(quality))) +
  geom_boxplot() +
  labs(x = "quality", y = "density", title = "Boxplot of quality vs. density") +
  theme(legend.position = 'none', plot.title = element_text(size = 10, hjust=0.5))
bp8
```



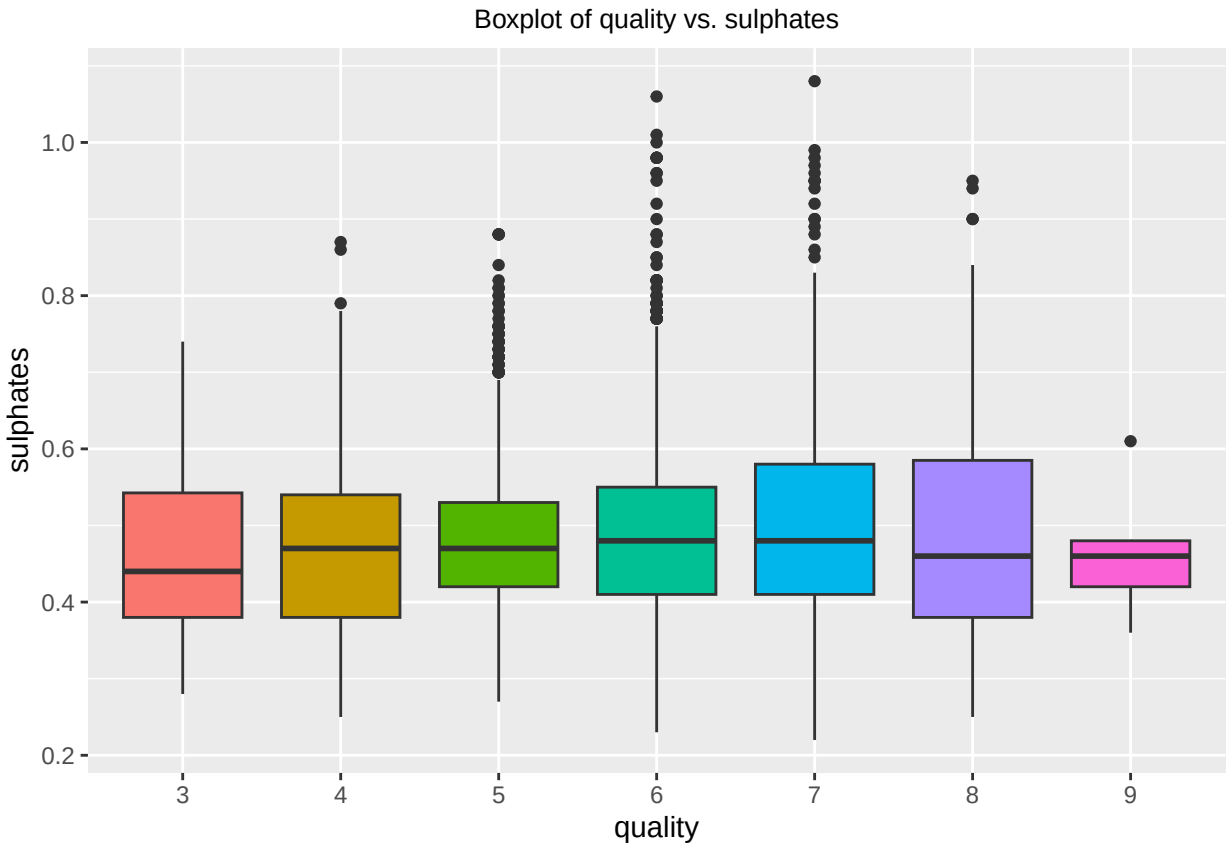

```
ggarrange(bp5, bp6, bp7, bp8, nrow = 2, ncol =2)
```



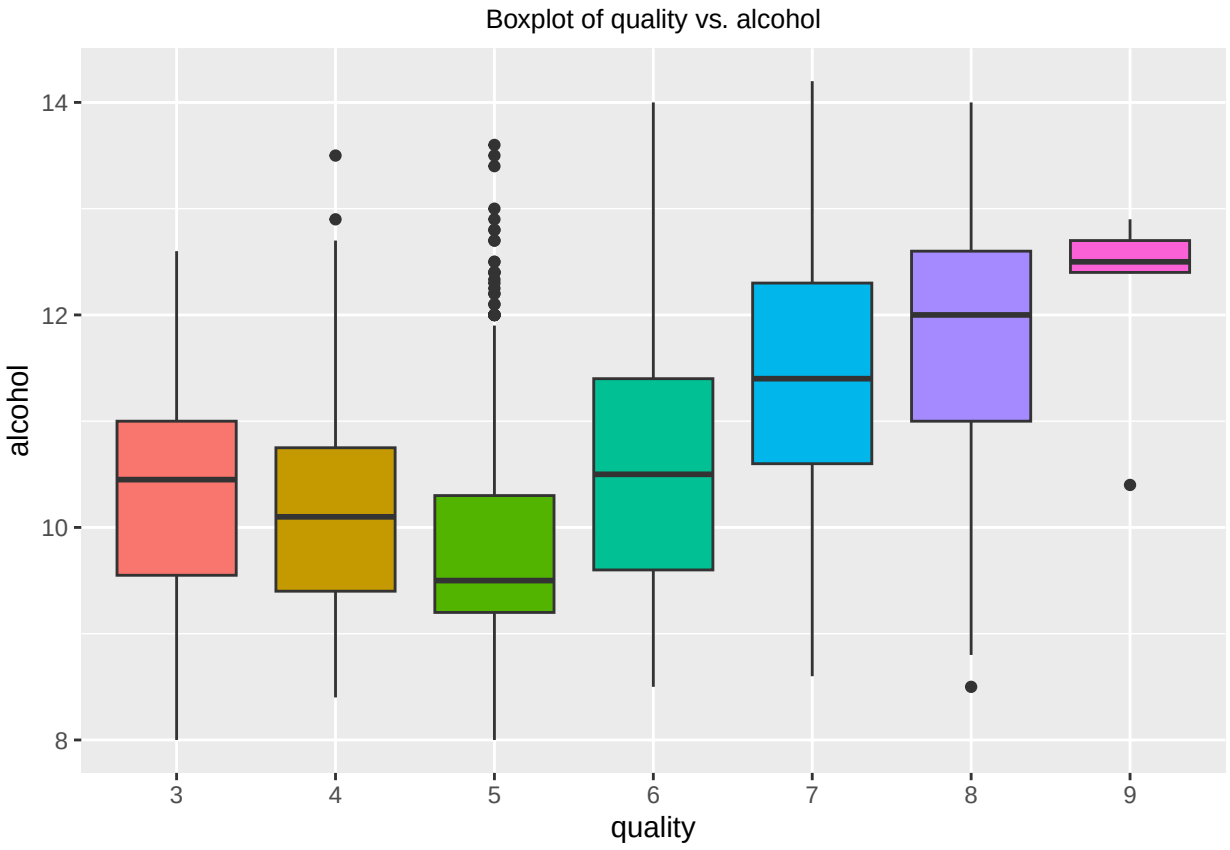

```
bp9 <- ggplot(white_df, aes(factor(quality), pH, fill=factor(quality))) +
  geom_boxplot() +
  labs(x = "quality", y = "pH", title = "Boxplot of Quality vs. pH") +
  theme(legend.position = 'none', plot.title = element_text(size = 10, hjust=0.5))
bp9
```



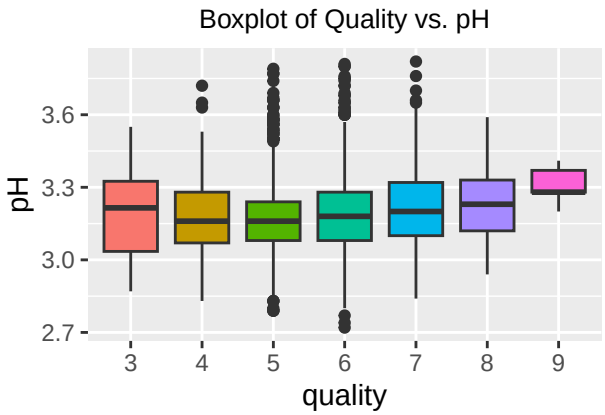

```
bp10 <- ggplot(white_df, aes(factor(quality), sulphates, fill=factor(quality))) +
  geom_boxplot() +
  labs(x = "quality", y = "sulphates", title = "Boxplot of quality vs. sulphates") +
  theme(legend.position = 'none', plot.title = element_text(size = 10, hjust=0.5))
bp10
```

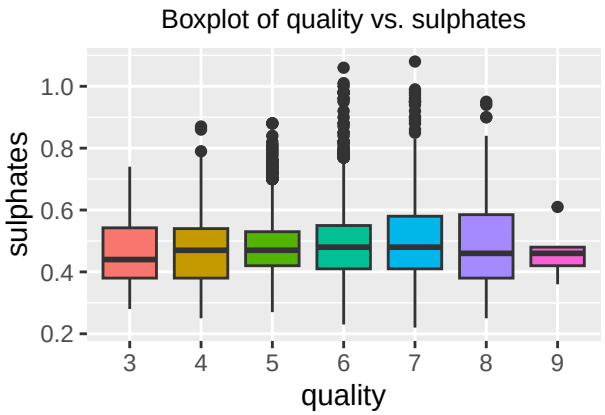


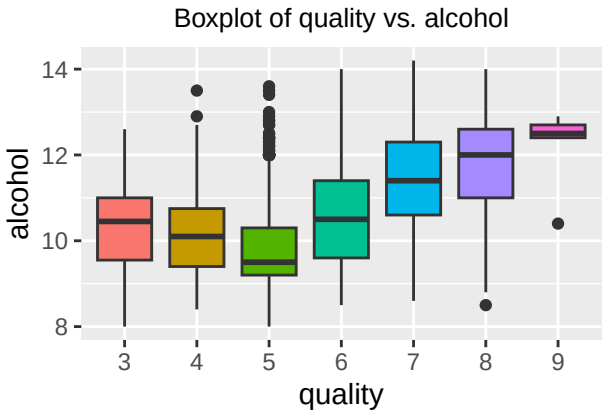

```
bp11 <- ggplot(white_df, aes(factor(quality), alcohol, fill=factor(quality))) +
  geom_boxplot() +
  labs(x = "quality", y = "alcohol", title = "Boxplot of quality vs. alcohol") +
  theme(legend.position = 'none', plot.title = element_text(size = 10, hjust=0.5))
bp11
```



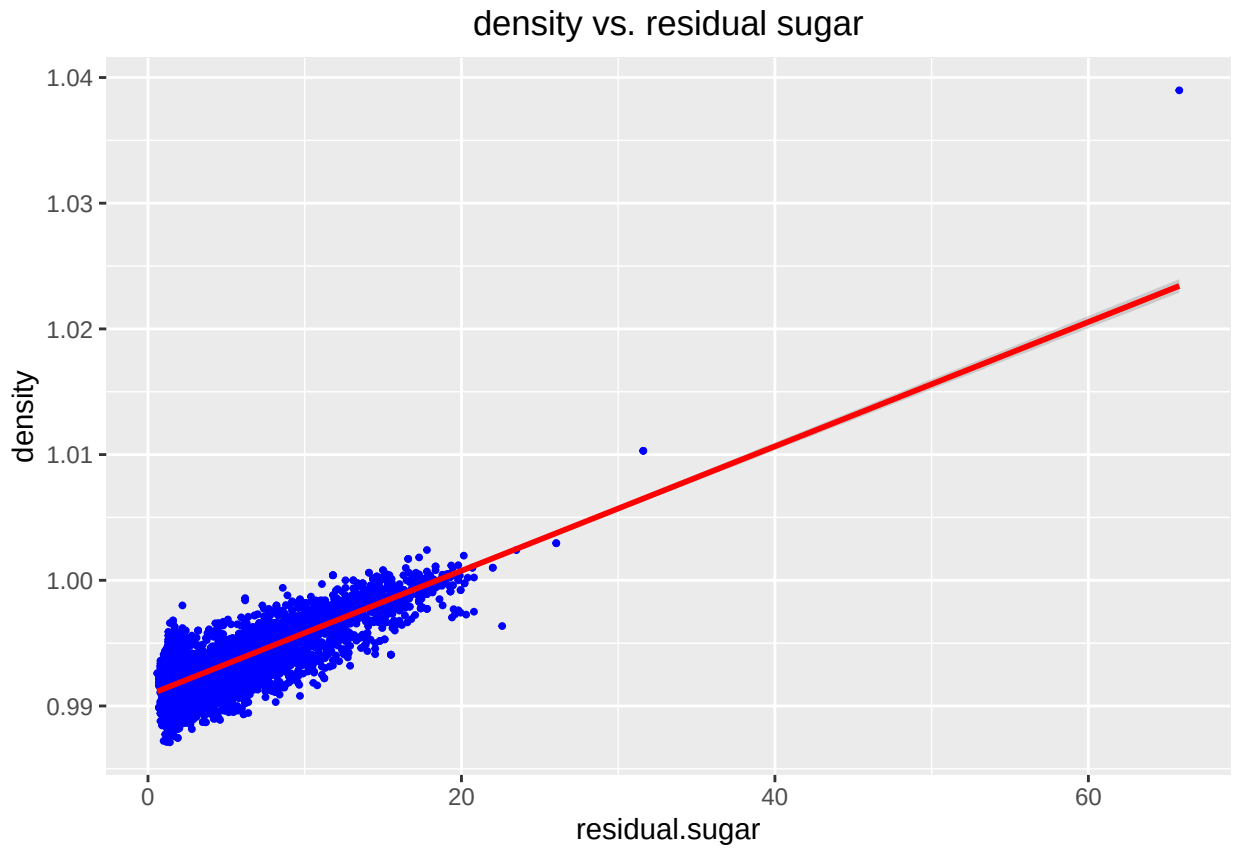

```
ggarrange(bp9, bp10, bp11, nrow = 2, ncol =2)
```



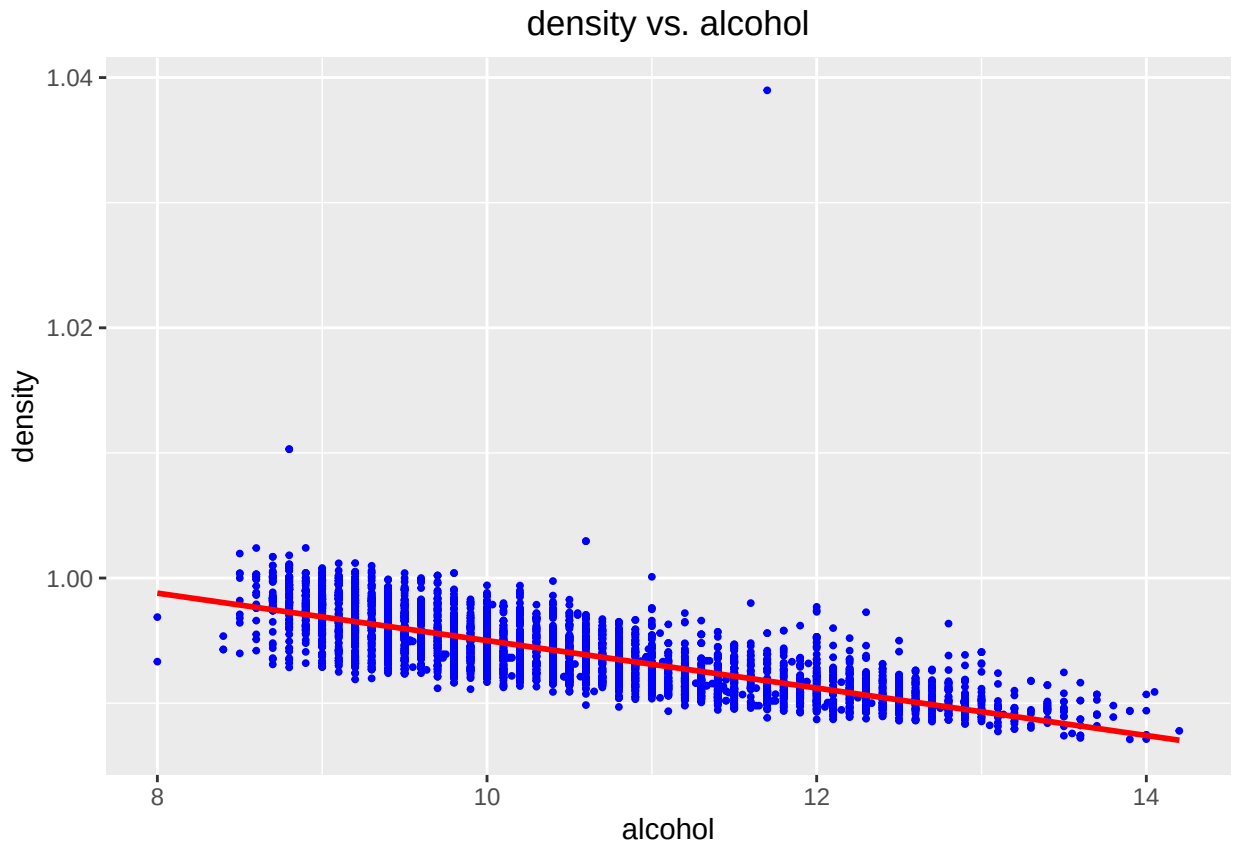




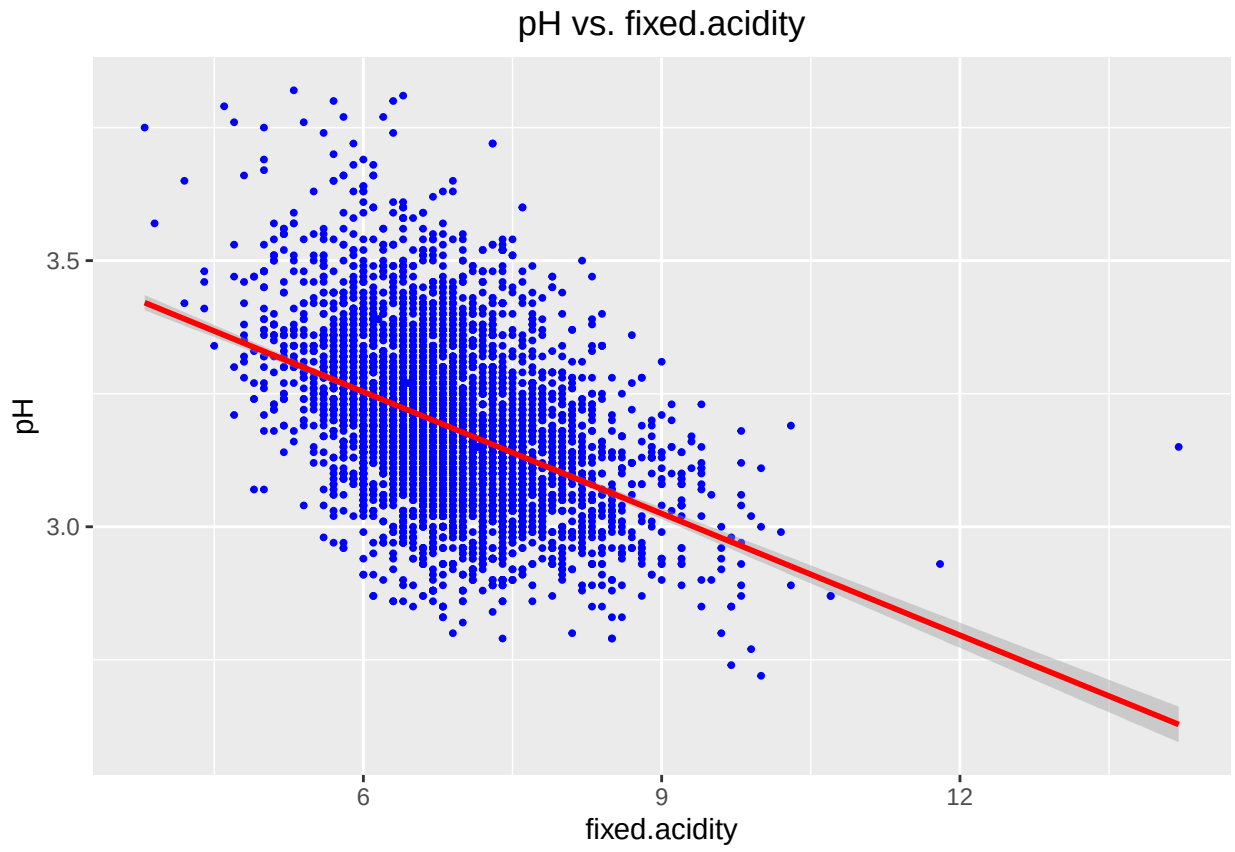

```
#Analysing relationship among numerical variables
gg1 <- ggplot(white_df, aes(x=residual.sugar, y=density)) +
  geom_point(color="blue",size=0.7) +
  labs(title="density vs. residual sugar") +
  geom_smooth(formula=y~x,method=lm, color="red") +
  theme(plot.title=element_text(hjust=0.5))
gg1
```



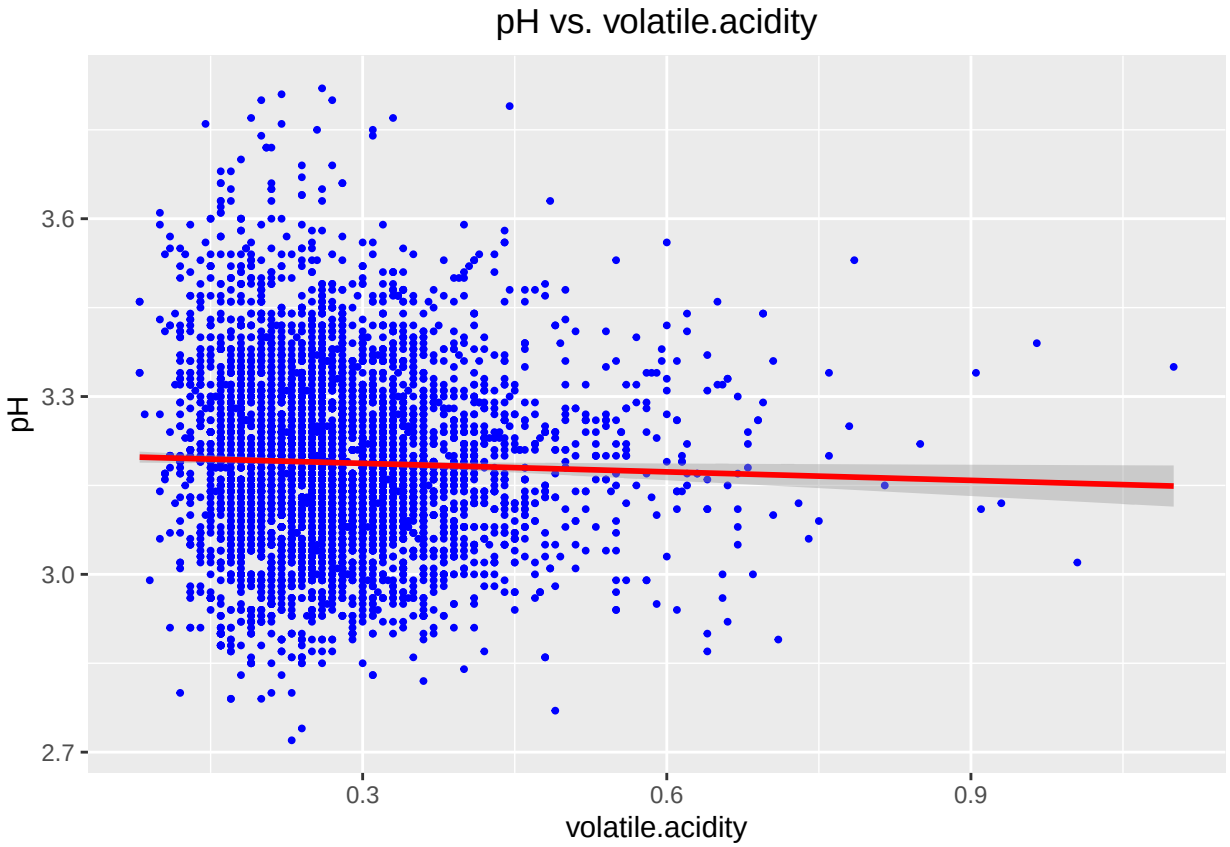

```
gg2 <- ggplot(white_df, aes(x=alcohol, y=density)) +
  geom_point(color="blue",size=0.7) +
  labs(title="density vs. alcohol") +
  geom_smooth(formula=y~x,method=lm, color="red") +
  theme(plot.title=element_text(hjust=0.5))
gg2
```



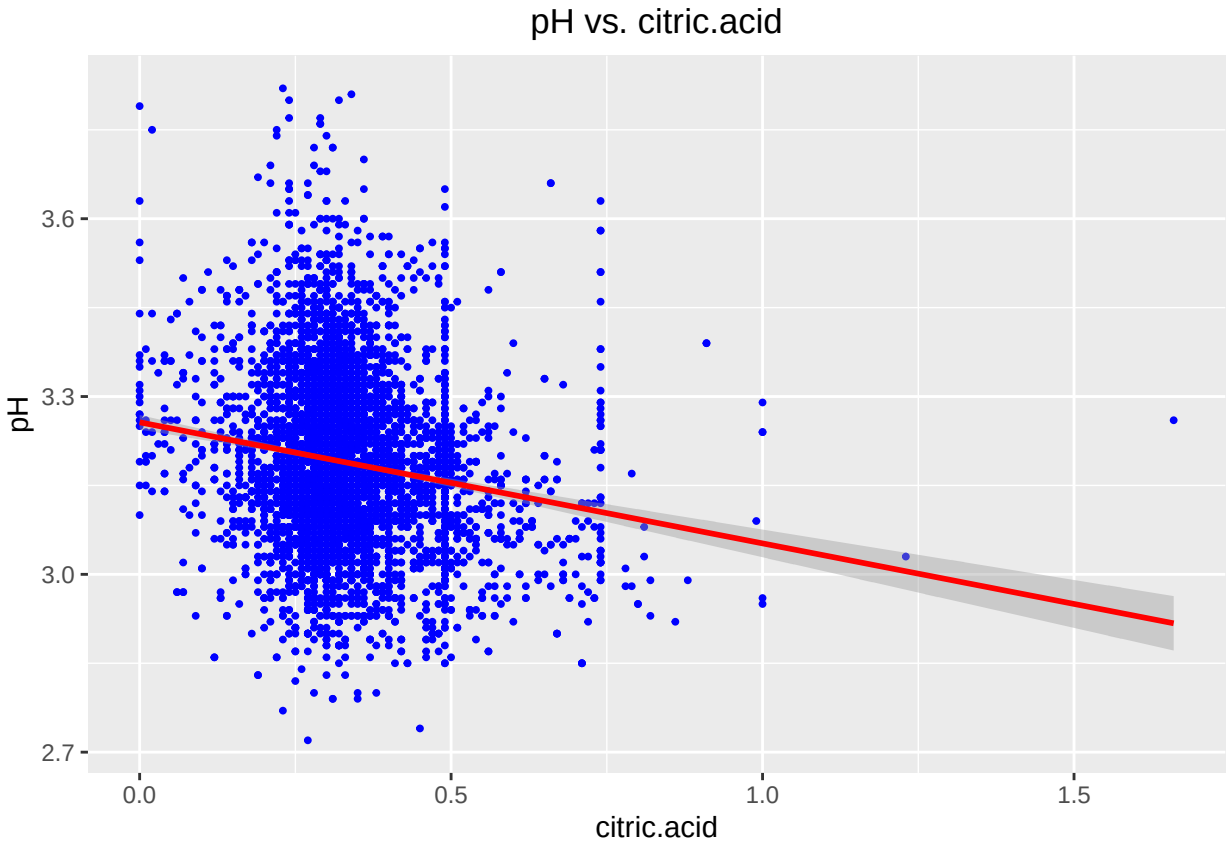

```
gg3 <- ggplot(white_df, aes(x=fixed.acidity, y=pH)) +
  geom_point(color="blue",size=0.7) +
  labs(title="pH vs. fixed.acidity") +
  geom_smooth(formula=y~x,method=lm, color="red") +
  theme(plot.title=element_text(hjust=0.5))
gg3
```



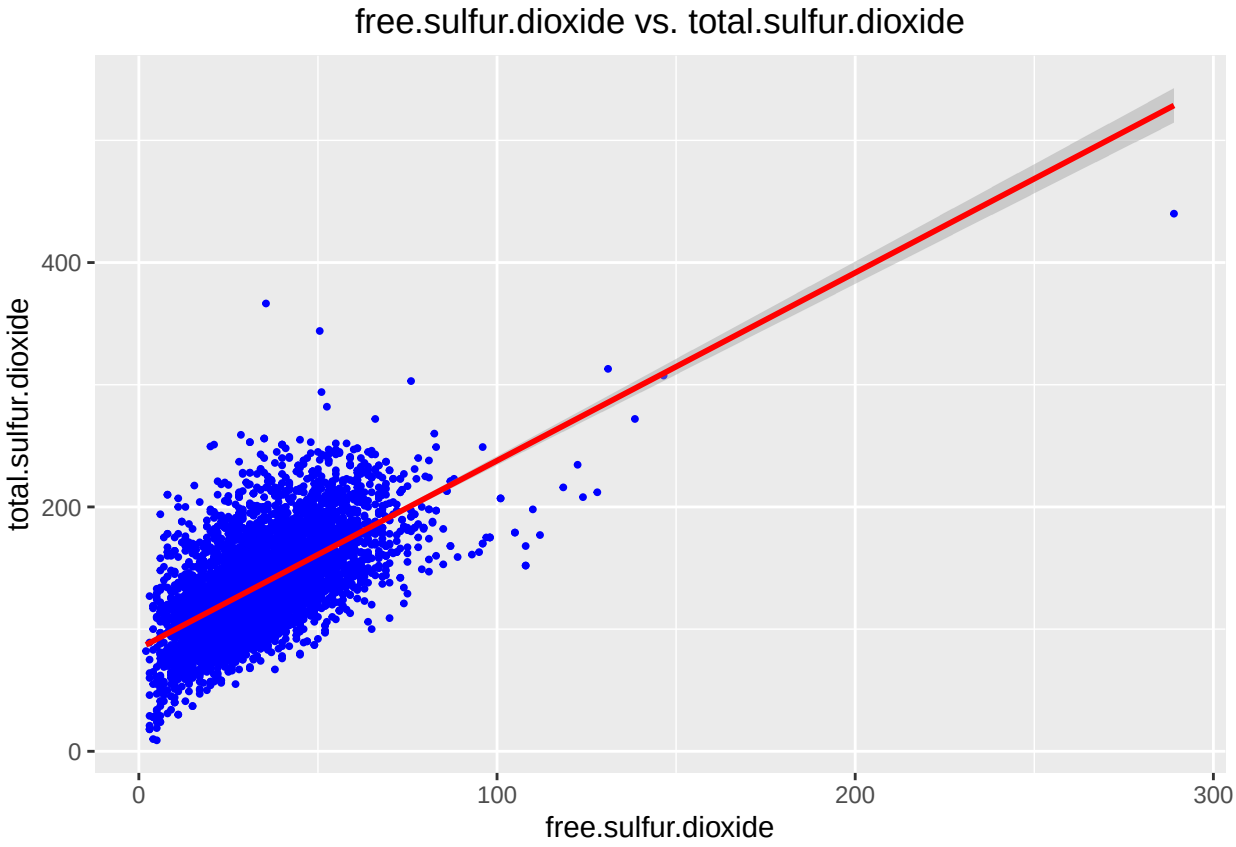

```
gg4 <- ggplot(white_df, aes(x=volatile.acidity, y=pH)) +
  geom_point(color="blue",size=0.7) +
  labs(title="pH vs. volatile.acidity") +
  geom_smooth(formula=y~x,method=lm, color="red") +
  theme(plot.title=element_text(hjust=0.5))
gg4
```



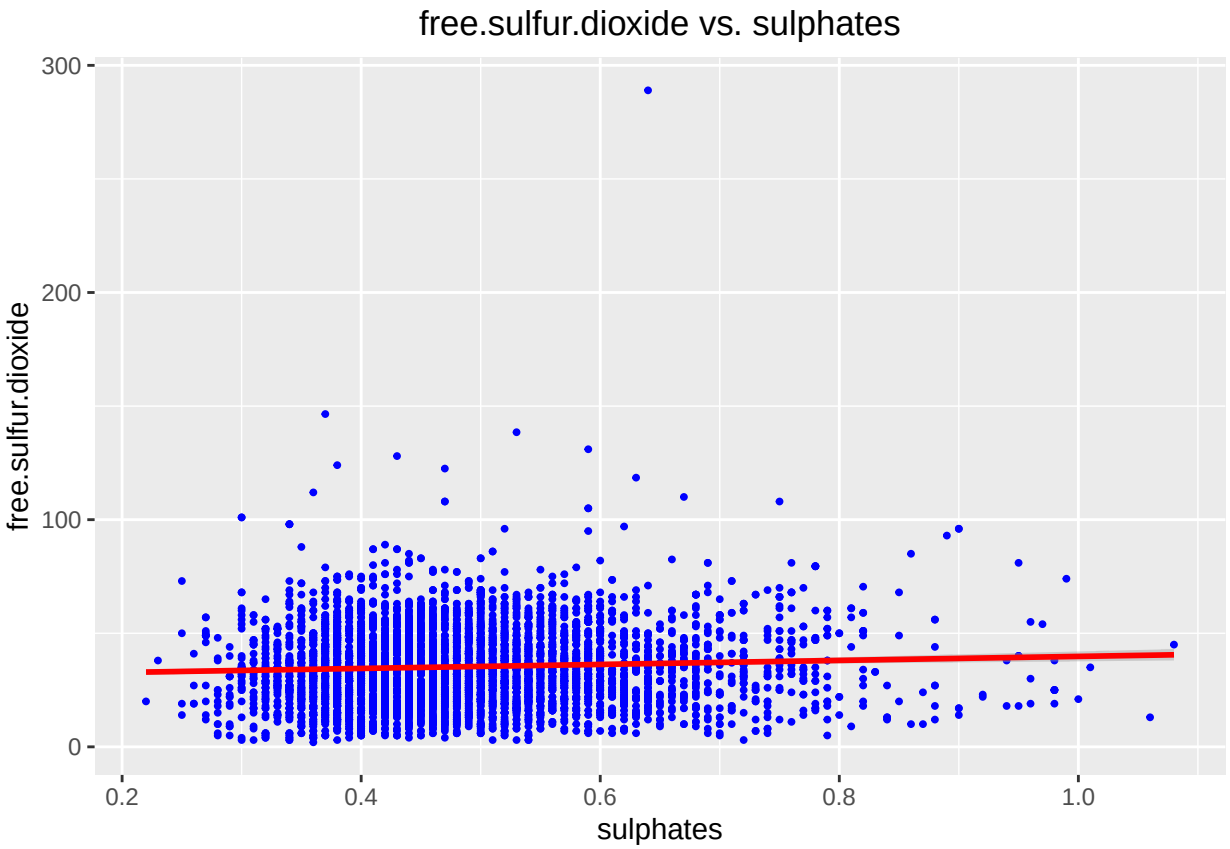

```
gg5 <- ggplot(white_df, aes(x=citric.acid, y=pH)) +
  geom_point(color="blue",size=0.7) +
  labs(title="pH vs. citric.acid") +
  geom_smooth(formula=y~x,method=lm, color="red") +
  theme(plot.title=element_text(hjust=0.5))
gg5
```



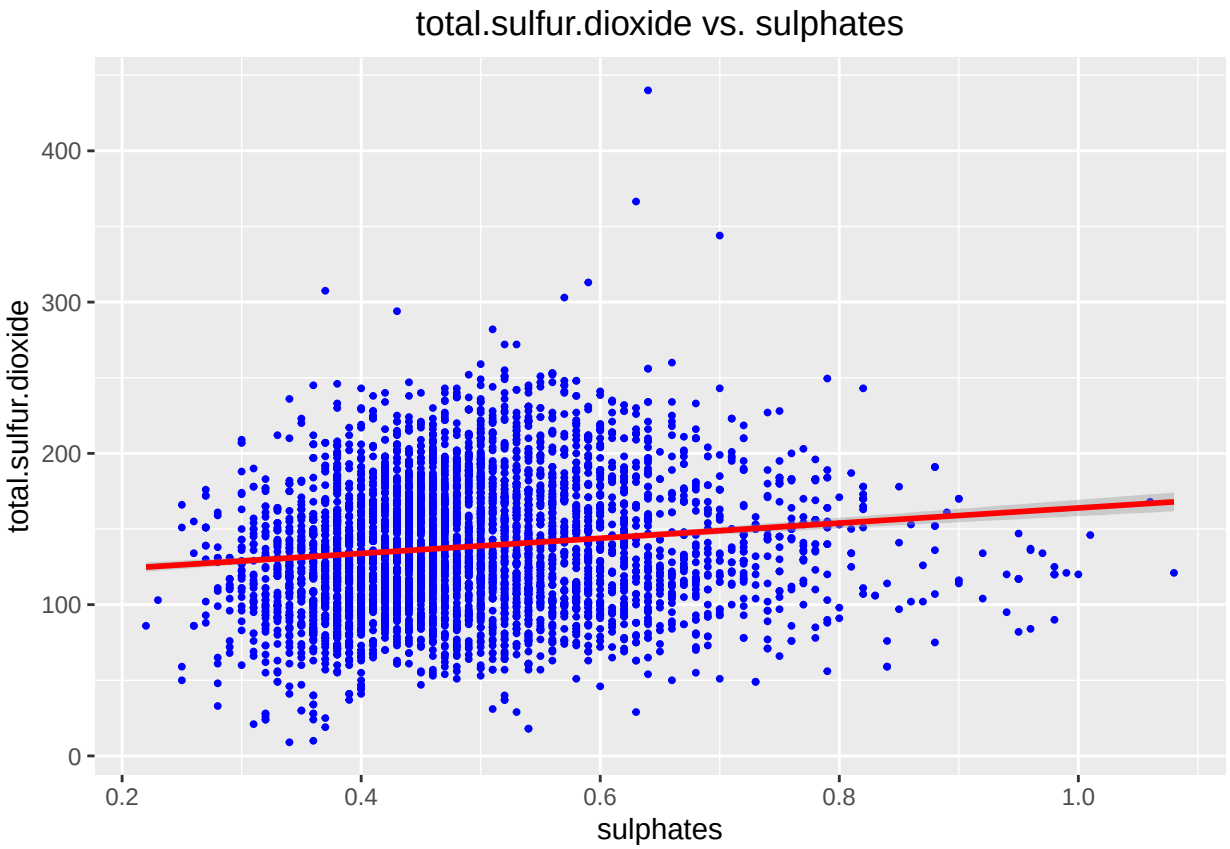

```
gg6 <- ggplot(white_df, aes(x=free.sulfur.dioxide, y=total.sulfur.dioxide)) +
  geom_point(color="blue",size=0.7) +
  labs(title="free.sulfur.dioxide vs. total.sulfur.dioxide") +
  geom_smooth(formula=y~x,method=lm, color="red") +
  theme(plot.title=element_text(hjust=0.5))
gg6
```



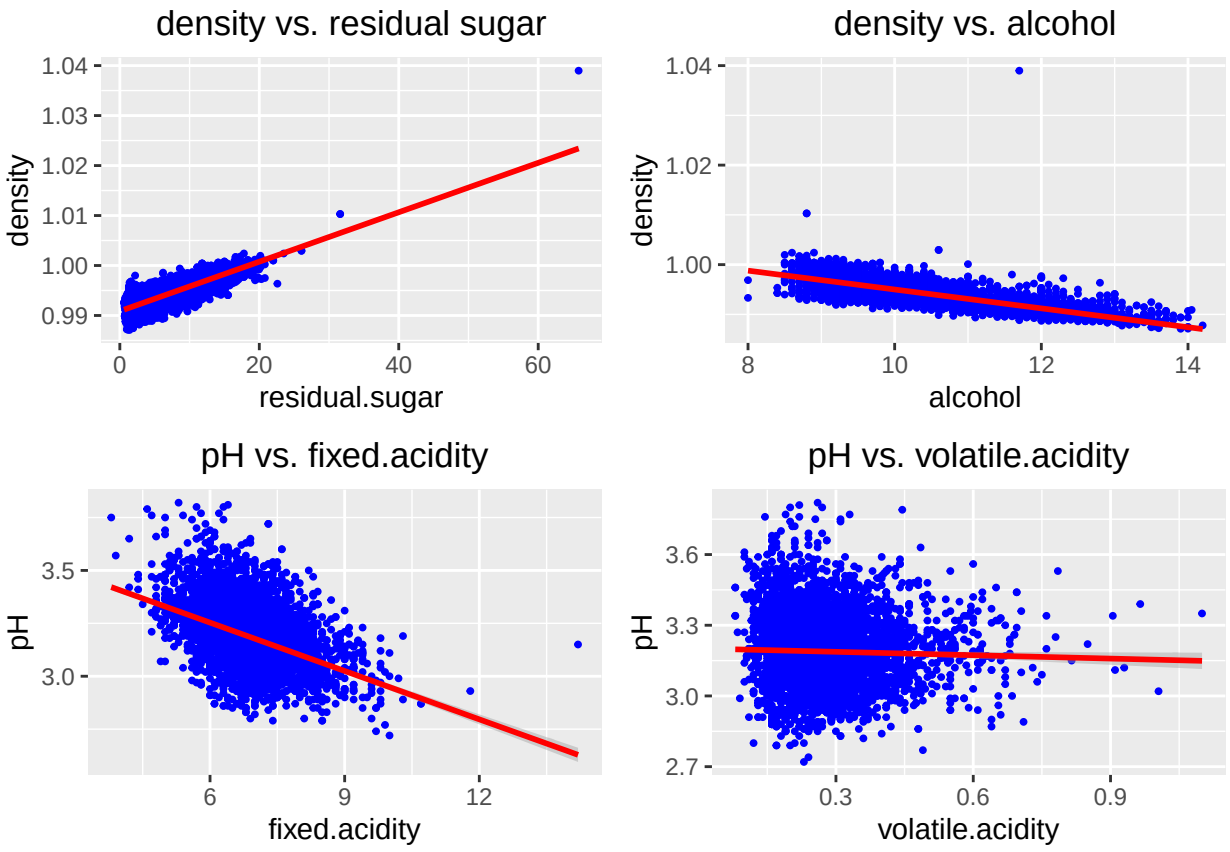

```
gg7 <-ggplot(white_df, aes(x=sulphates, y=free.sulfur.dioxide)) +
  geom_point(color="blue",size=0.7) +
  labs(title="free.sulfur.dioxide vs. sulphates") +
  geom_smooth(formula=y~x,method=lm, color="red") +
  theme(plot.title=element_text(hjust=0.5))
gg7
```



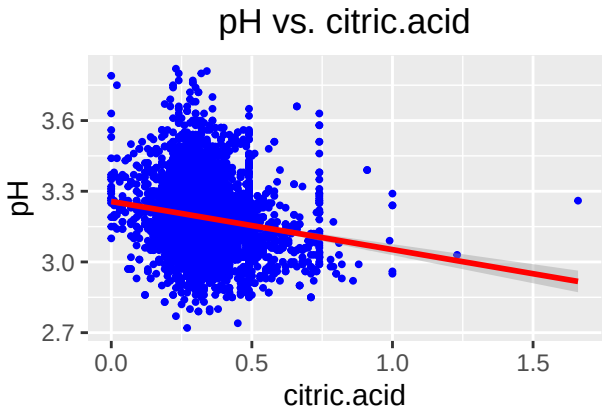

```
gg8 <-ggplot(white_df, aes(x=sulphates, y=total.sulfur.dioxide)) +
  geom_point(color="blue",size=0.7) +
  labs(title="total.sulfur.dioxide vs. sulphates") +
  geom_smooth(formula=y~x,method=lm, color="red") +
  theme(plot.title=element_text(hjust=0.5))
gg8
```

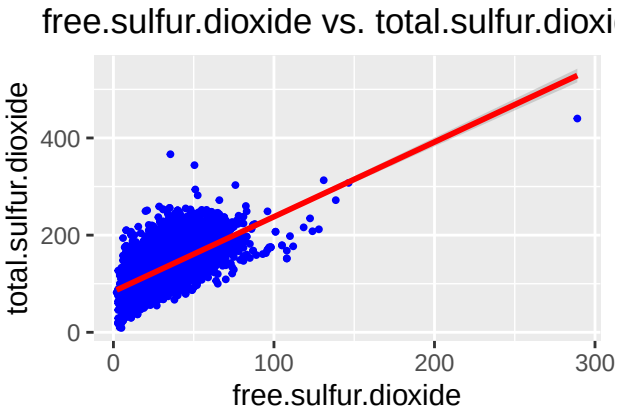


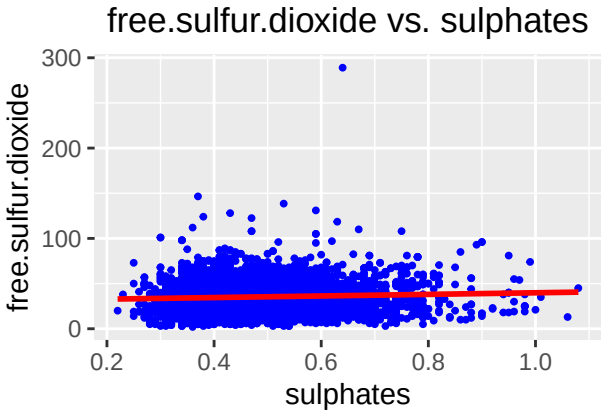

```
ggarrange(gg1, gg2, gg3, gg4, nrow = 2, ncol =2)
```

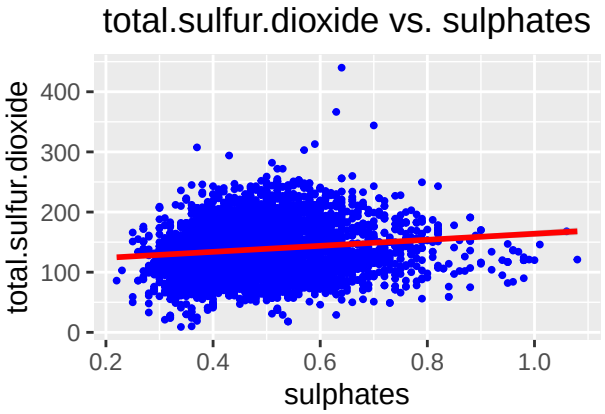



```
ggarrange(gg5, gg6, gg7, gg8, nrow = 2, ncol =2)
```










```
#Baseline Random Forest Model
whitewineRF<-randomForest(quality ~ .,white_df,ntree=150)

whitewineRF
```

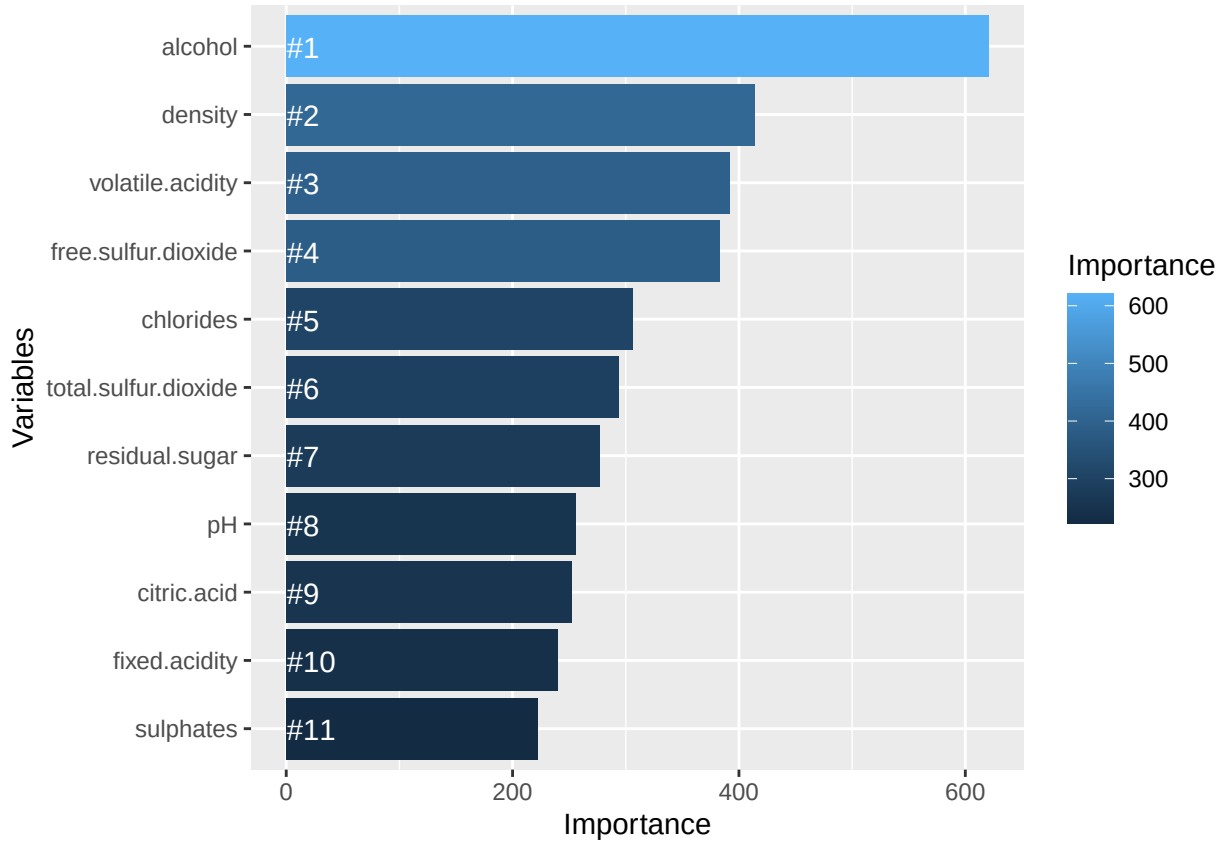
```
##
## Call:
##  randomForest(formula = quality ~ ., data = white_df, ntree = 150)
##                Type of random forest: regression
##                      Number of trees: 150
## No. of variables tried at each split: 3
##
##           Mean of squared residuals: 0.3470637
##                     % Var explained: 55.74
```

```
# Get importance
Importance    <- importance(whitewineRF)
varImportance <- data.frame(Variables = row.names(Importance),
                            Importance = (Importance))

# Create a rank variable based on importance
rankImportance <- varImportance %>%
  mutate(Rank = paste0('#',dense_rank(desc(Importance))))
importance(whitewineRF)
```

```
##                      IncNodePurity
```

```
## fixed.acidity             239.9680
## volatile.acidity          392.2521
## citric.acid               252.4018
## residual.sugar            277.1518
## chlorides                 305.7604
## free.sulfur.dioxide       383.3018
## total.sulfur.dioxide      293.4699
## density                   414.0035
## pH                        255.4234
## sulphates                 222.4904
## alcohol                   620.8299
```

```
# Use ggplot2 to visualize the relative importance of variables
ggplot(rankImportance, aes(x = reorder(Variables, Importance),
                           y = Importance, fill = Importance)) +
  geom_bar(stat='identity') +
  geom_text(aes(x = Variables, y = 0.5, label = Rank),
            hjust=0, vjust=0.55, size = 4, colour = 'white') +
  labs(x = 'Variables') +
  coord_flip()
```

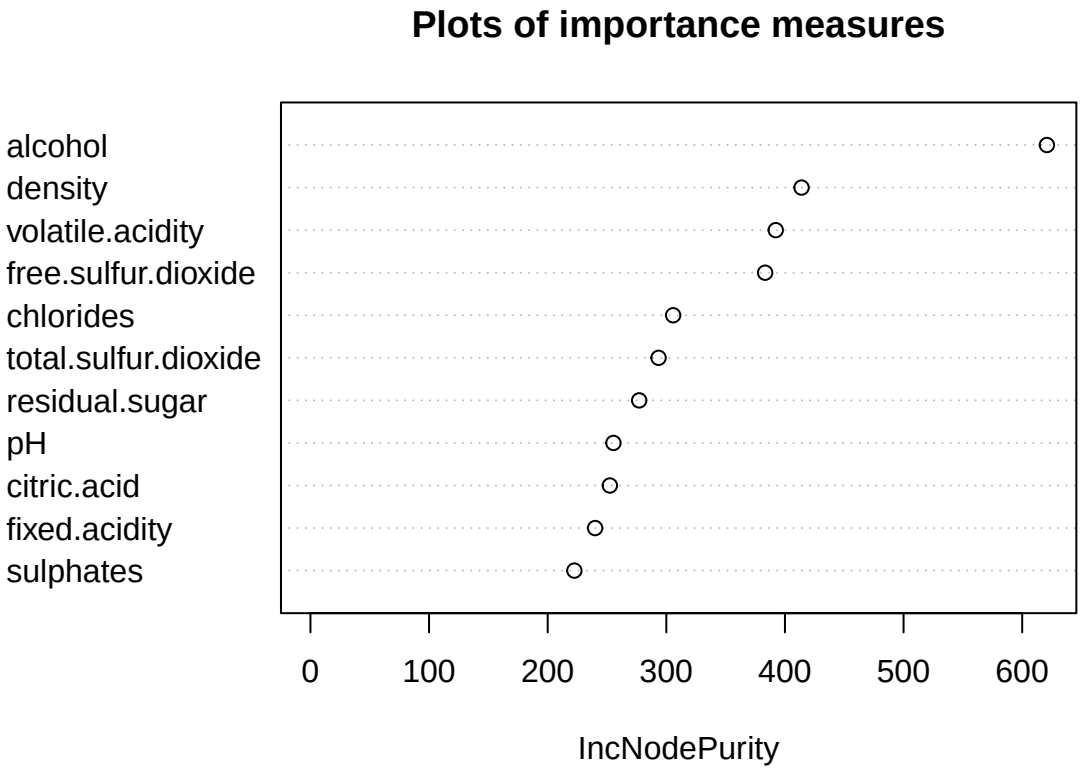



```
#importance plot
importance(whitewineRF)
```

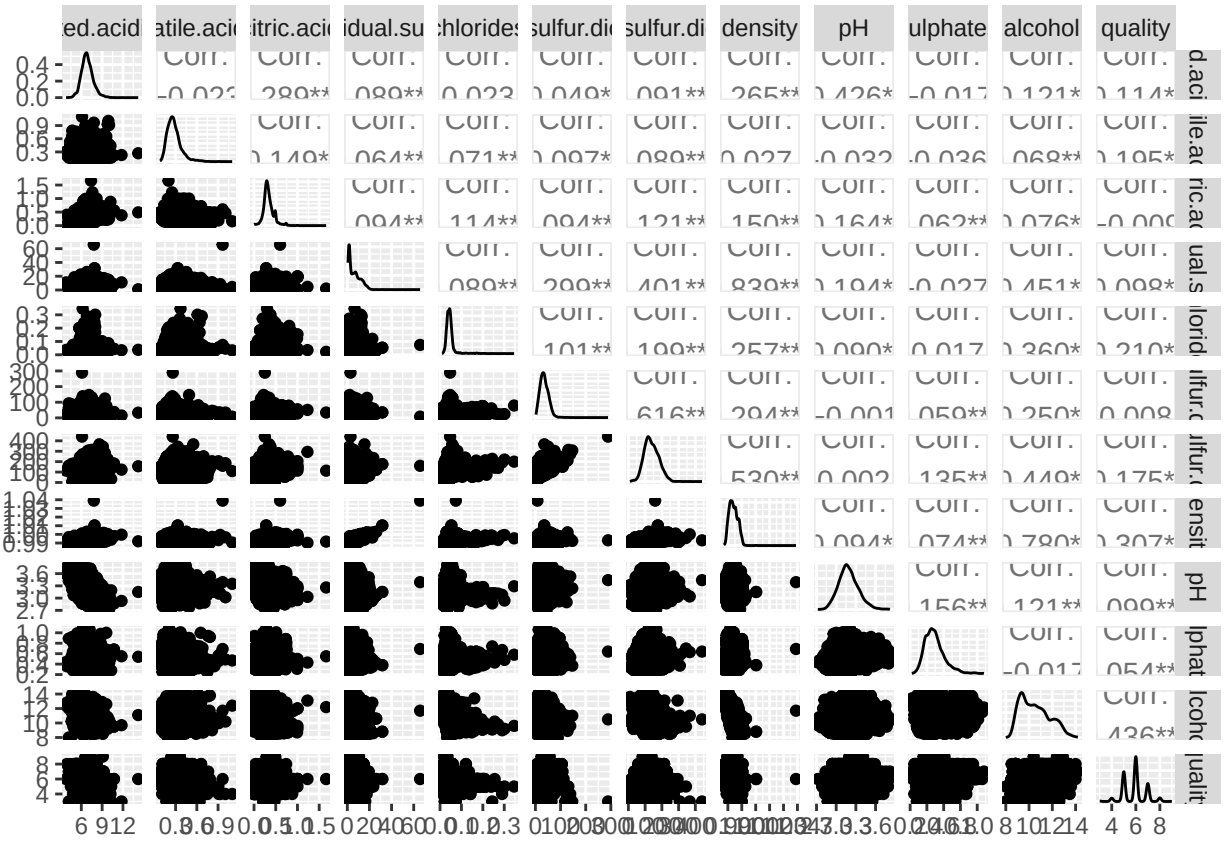
```
##                       IncNodePurity
```

```
## fixed.acidity             239.9680
## volatile.acidity          392.2521
## citric.acid               252.4018
## residual.sugar            277.1518
## chlorides                 305.7604
## free.sulfur.dioxide       383.3018
## total.sulfur.dioxide      293.4699
## density                   414.0035
## pH                        255.4234
## sulphates                 222.4904
## alcohol                   620.8299
```

```
varImpPlot(whitewineRF, main="Plots of importance measures")
```




```
ggpairs(white_df)
```




```
#Linear regression model with top 4 highest correlation with Total Incidents
white_lm <- lm(quality ~ alcohol + volatile.acidity +  sulphates + total.sulfur.dioxide, data = white_d
summary(white_lm)
```

```
##
## Call:
## lm(formula = quality ~ alcohol + volatile.acidity + sulphates +
##     total.sulfur.dioxide, data = white_df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.3107 -0.4984 -0.0413  0.4897  3.1713
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)           2.5096598  0.1346811  18.634  < 2e-16 ***
## alcohol               0.3424202  0.0100918  33.930  < 2e-16 ***
## volatile.acidity     -2.0210739  0.1105420 -18.283  < 2e-16 ***
## sulphates             0.3616881  0.0975247   3.709 0.000211 ***
## total.sulfur.dioxide  0.0011067  0.0002955   3.745 0.000183 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7697 on 4893 degrees of freedom
## Multiple R-squared:  0.2453, Adjusted R-squared:  0.2446
## F-statistic: 397.5 on 4 and 4893 DF,  p-value: < 2.2e-16
```

```r
# Define training control
set.seed(555)
train <- white_df[1:800, ]
test <- white_df[801:nrow(white_df), ]
# Train the model
white_model <- lm(quality ~ alcohol + volatile.acidity +  sulphates + total.sulfur.dioxide, data=train)
summary(white_model)
```

```
##
## Call:
## lm(formula = quality ~ alcohol + volatile.acidity + sulphates +
##     total.sulfur.dioxide, data = train)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.3798 -0.5022  0.0072  0.5062  3.0868
##
## Coefficients:
##                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)           2.5810459  0.3697099   6.981 6.18e-12 ***
## alcohol               0.3310033  0.0288349  11.479  < 2e-16 ***
## volatile.acidity     -2.1264214  0.2772213  -7.670 5.01e-14 ***
## sulphates             1.1123045  0.2597845   4.282 2.08e-05 ***
## total.sulfur.dioxide -0.0003852  0.0007323  -0.526    0.599
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7743 on 795 degrees of freedom
## Multiple R-squared:  0.2507, Adjusted R-squared:  0.2469
## F-statistic: 66.48 on 4 and 795 DF,  p-value: < 2.2e-16
```

```r
#calculate MSE
mean(white_model$residuals^2)
```

```
## [1] 0.5958007
```

```r
#calculate RMSE
sqrt(mean(white_model$residuals^2))
```

```
## [1] 0.7718813
```

```r
#calculate MAE
predValues <- predict(white_model,test)
#MAE for the model
mean(abs(test$quality -predValues))
```

```
## [1] 0.6127622
```

```r
#Lasso regression
x <- model.matrix(quality~., white_df)[,-1]
y <- white_df$quality
```

```
mod <- cv.glmnet(as.matrix(x), y, alpha=1)

#coefficients with the minimum cross-validation error
as.matrix(coef(mod, mod$lambda.min))
```

```
##                                s1
## (Intercept)           1.218573e+02
## fixed.acidity         3.847004e-02
## volatile.acidity     -1.874168e+00
## citric.acid           1.373124e-03
## residual.sugar        6.983052e-02
## chlorides            -3.572286e-01
## free.sulfur.dioxide   3.630384e-03
## total.sulfur.dioxide -2.448370e-04
## density              -1.213902e+02
## pH                    5.588171e-01
## sulphates             5.733381e-01
## alcohol               2.241061e-01
```

```
#coefficients with the "largest value of lambda such that error is
#within 1 standard error of the minimum
as.matrix(coef(mod, mod$lambda.1se))
```

```
##                               s1
## (Intercept)           2.672428715
## fixed.acidity        -0.040800606
## volatile.acidity     -1.773726362
## citric.acid           0.000000000
## residual.sugar        0.016479681
## chlorides            -0.591302671
## free.sulfur.dioxide   0.002676398
## total.sulfur.dioxide  0.000000000
## density               0.000000000
## pH                    0.044969055
## sulphates             0.218520816
## alcohol               0.338160233
```

```
#Lasso regression model using above independent variables
white_lm1 <- lm(quality ~ fixed.acidity + volatile.acidity + chlorides + total.sulfur.dioxide
              + sulphates + alcohol, data=white_df)
summary(white_lm1)
```

```
##
## Call:
## lm(formula = quality ~ fixed.acidity + volatile.acidity + chlorides +
##     total.sulfur.dioxide + sulphates + alcohol, data = white_df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.3885 -0.4967 -0.0518  0.4807  3.3119
##
## Coefficients:
```

```
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)           3.2132033  0.1764150  18.214  < 2e-16 ***
## fixed.acidity        -0.0707338  0.0131049  -5.398 7.08e-08 ***
## volatile.acidity     -2.0011868  0.1106875 -18.080  < 2e-16 ***
## chlorides            -1.6508700  0.5409552  -3.052 0.002287 **
## total.sulfur.dioxide  0.0012086  0.0002949   4.098 4.24e-05 ***
## sulphates             0.3507270  0.0972098   3.608 0.000312 ***
## alcohol               0.3274520  0.0106497  30.748  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7669 on 4891 degrees of freedom
## Multiple R-squared:  0.251,  Adjusted R-squared:  0.2501
## F-statistic: 273.2 on 6 and 4891 DF,  p-value: < 2.2e-16
```

```
# Define training control
set.seed(555)
train <- white_df[1:800, ]
test <- white_df[801:nrow(white_df), ]
# Train the model
white_model1 <- lm(quality ~ fixed.acidity + volatile.acidity + chlorides + total.sulfur.dioxide
                + sulphates + alcohol, data=train)
summary(white_model1)
```

```
##
## Call:
## lm(formula = quality ~ fixed.acidity + volatile.acidity + chlorides +
##     total.sulfur.dioxide + sulphates + alcohol, data = train)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.4447 -0.4958  0.0039  0.4992  3.2031
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)           3.2088704  0.5013010   6.401 2.64e-10 ***
## fixed.acidity        -0.0578413  0.0378383  -1.529    0.127
## volatile.acidity     -2.1456664  0.2791806  -7.686 4.50e-14 ***
## chlorides            -1.4501201  1.1781069  -1.231    0.219
## total.sulfur.dioxide -0.0003389  0.0007329  -0.462    0.644
## sulphates             1.0800241  0.2602024   4.151 3.67e-05 ***
## alcohol               0.3163131  0.0301153  10.503  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7735 on 793 degrees of freedom
## Multiple R-squared:  0.2541, Adjusted R-squared:  0.2485
## F-statistic: 45.03 on 6 and 793 DF,  p-value: < 2.2e-16
```

```
#calculate MSE
mean(white_model1$residuals^2)
```

```
## [1] 0.5930486
```

```r
#calculate RMSE
sqrt(mean(white_model1$residuals^2))
```

```
## [1] 0.7700965
```

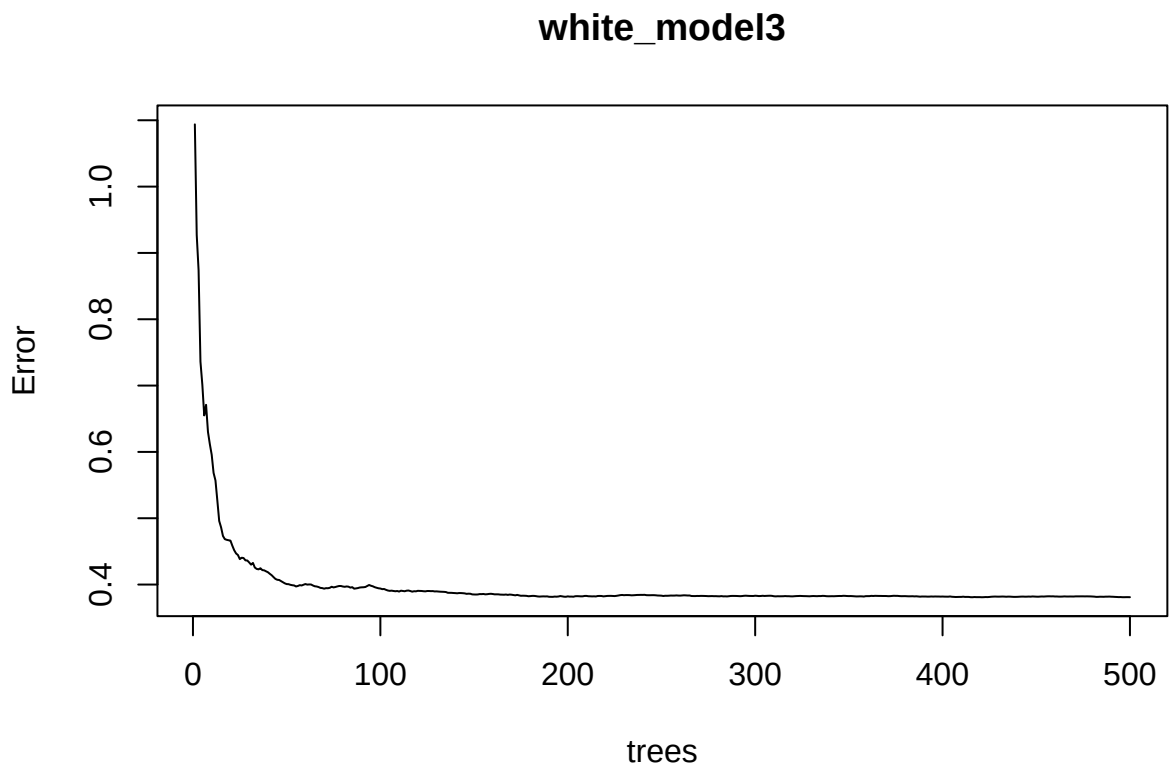
```r
#calculate MAE
predValues <- predict(white_model1,test)
#MAE for the model
mean(abs(test$quality -predValues))
```

```
## [1] 0.6097995
```

```r
#Random forest
set.seed(555)
train <- white_df[1:800, ]
test <- white_df[801:nrow(white_df), ]
white_model3 <- randomForest(quality ~ ., train, mtry = 3,
                             importance = TRUE, na.action = na.omit)
print(white_model3)
```

```
##
## Call:
##  randomForest(formula = quality ~ ., data = train, mtry = 3, importance = TRUE,      na.action = na.
##                Type of random forest: regression
##                      Number of trees: 500
## No. of variables tried at each split: 3
##
##           Mean of squared residuals: 0.3809709
##                     % Var explained: 52.09
```

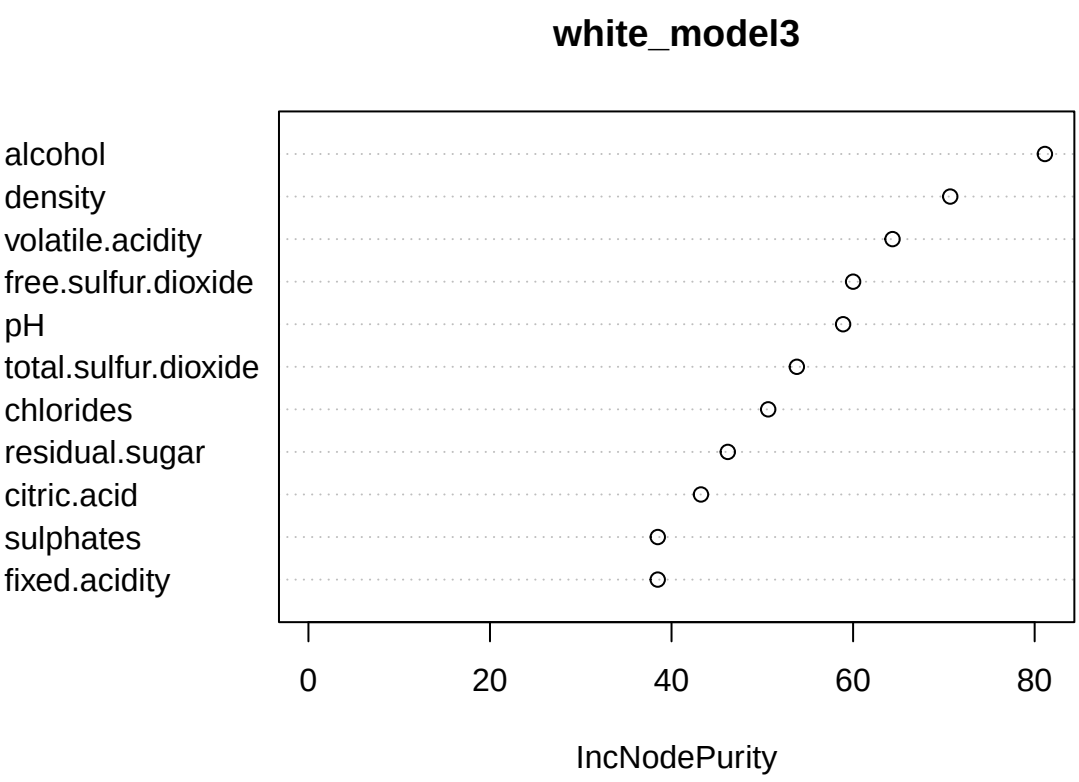
```r
#Plot the error vs the number of trees graph
plot(white_model3)
```




```
importance(white_model3)
```

```
##                       %IncMSE IncNodePurity
## fixed.acidity        19.00341      38.47732
## volatile.acidity     37.85046      64.34346
## citric.acid          29.22456      43.24203
## residual.sugar       23.68386      46.19656
## chlorides            25.12812      50.64720
## free.sulfur.dioxide  29.94043      60.00146
## total.sulfur.dioxide 23.71018      53.80431
## density              27.98187      70.70141
## pH                   28.44408      58.90013
## sulphates            26.12448      38.48484
## alcohol              25.15161      81.12908
```

```
varImpPlot(white_model3,type=2)
```




```
# MSE for the model
white_model3$mse[length(white_model3$mse)]
```

```
## [1] 0.3809709
```

```
# RMSE for the model
sqrt(white_model3$mse[length(white_model3$mse)])
```

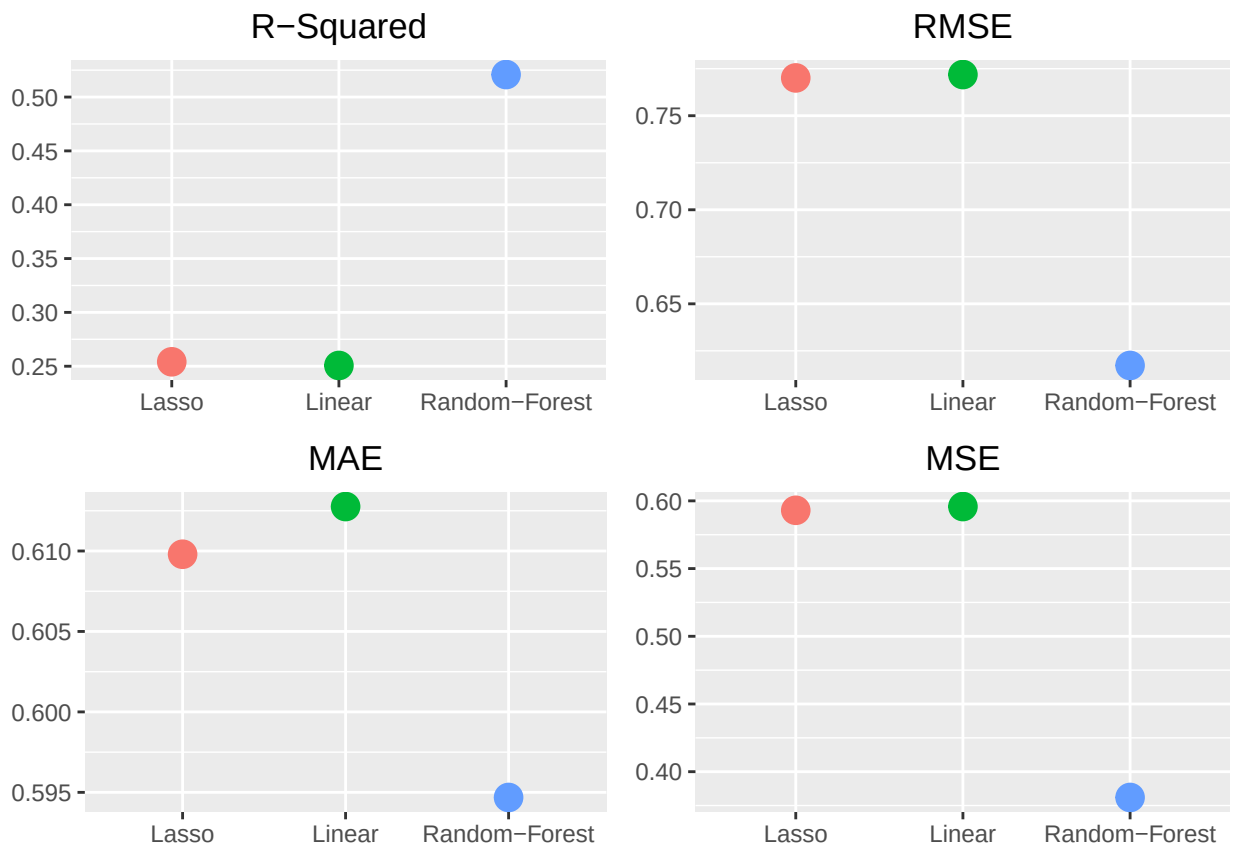
```
## [1] 0.6172284
```

```
predValues <- predict(white_model3,test)
#MAE for the model
mean(abs(test$quality -predValues))
```

```
## [1] 0.5946836
```

```
#Comparing models

Model <- c("Linear", "Lasso", "Random-Forest")
R_squared <- c(0.2507, 0.2541, 0.5209)
RMSE <- c(0.7718813, 0.7700965, 0.6172284)
MAE <- c(0.6127622, 0.6097995, 0.5946836)
MSE <- c(0.5958007, 0.5930486, 0.3809709)
```

```
ml <- data.frame(Model, R_squared, RMSE, MAE, MSE)


p1 <- ggplot(ml, aes(Model, RMSE)) + geom_point(aes(colour = factor(Model), size = 4)) + labs(title="RM
p2 <- ggplot(ml, aes(Model, R_squared)) + geom_point(aes(colour = factor(Model), size = 4)) + labs(titl
p3 <- ggplot(ml, aes(Model, MAE)) + geom_point(aes(colour = factor(Model), size = 4)) + labs(title="MAE
p4 <- ggplot(ml, aes(Model, MSE)) + geom_point(aes(colour = factor(Model), size = 4)) + labs(title="MSE
ggarrange(p2,p1,p3,p4, nrow=2, ncol=2)
```




```
#clustering to find relation between predictors
set.seed(1941)
white_k <- kmeans(white_df, 2, nstart = 25)
names(white_k)
```

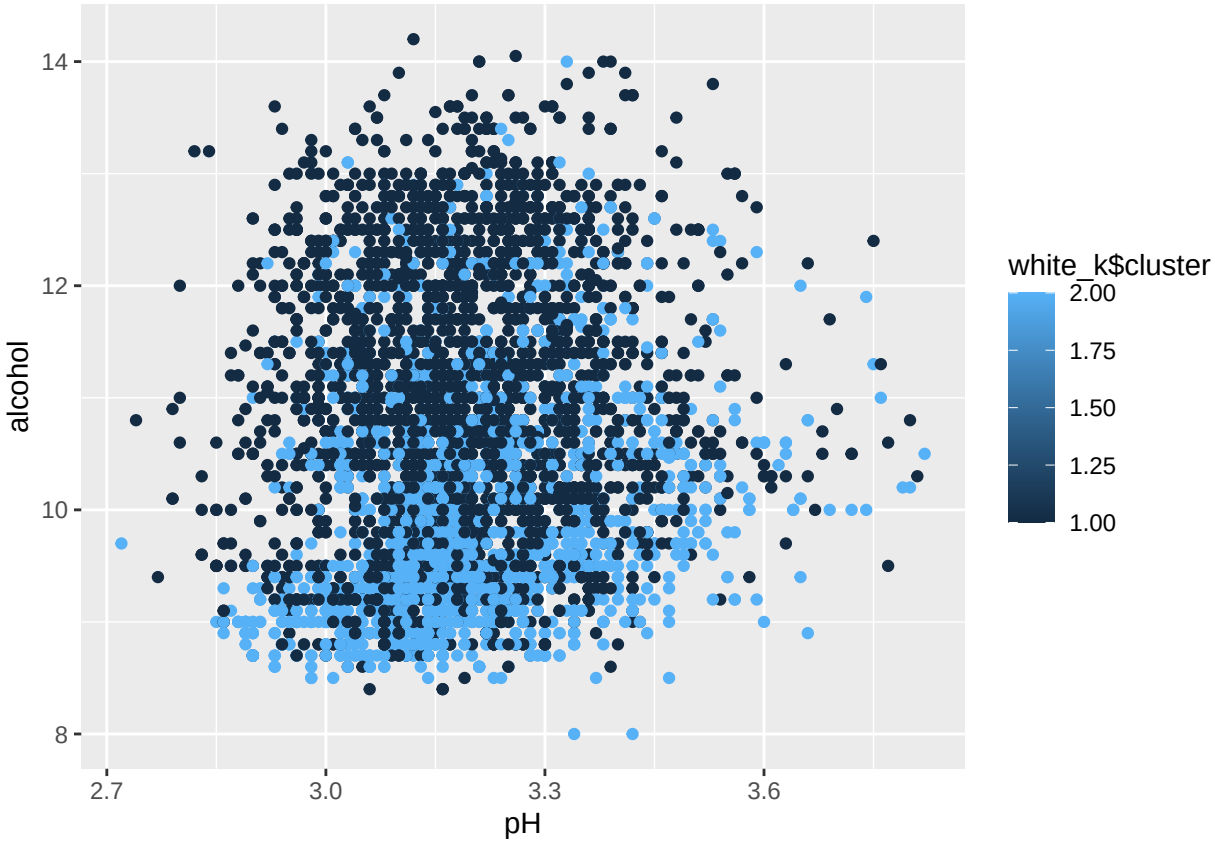
```
## [1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"
```

```
white_k$centers
```

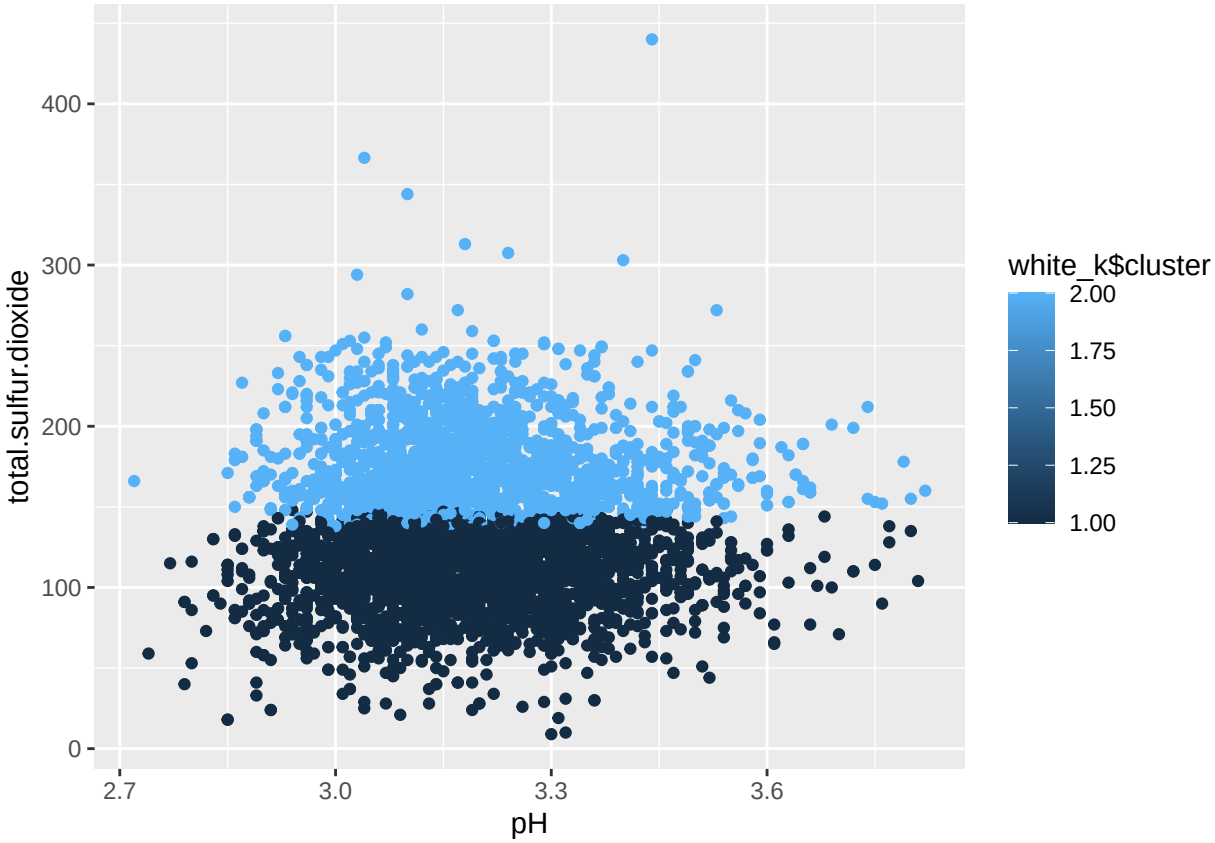
```
##   fixed.acidity volatile.acidity citric.acid residual.sugar  chlorides
## 1      6.785150        0.2728681   0.3218799       4.793352 0.04217691
## 2      6.947571        0.2854000   0.3505952       8.520643 0.05056286
##   free.sulfur.dioxide total.sulfur.dioxide   density       pH sulphates
## 1            27.16976             108.5960 0.9927779 3.188867 0.4793531
```

```
## 2           46.15143             178.0186 0.9956921 3.187467 0.5038286
##     alcohol  quality
## 1 10.962258 6.009650
## 2  9.917373 5.702381
```

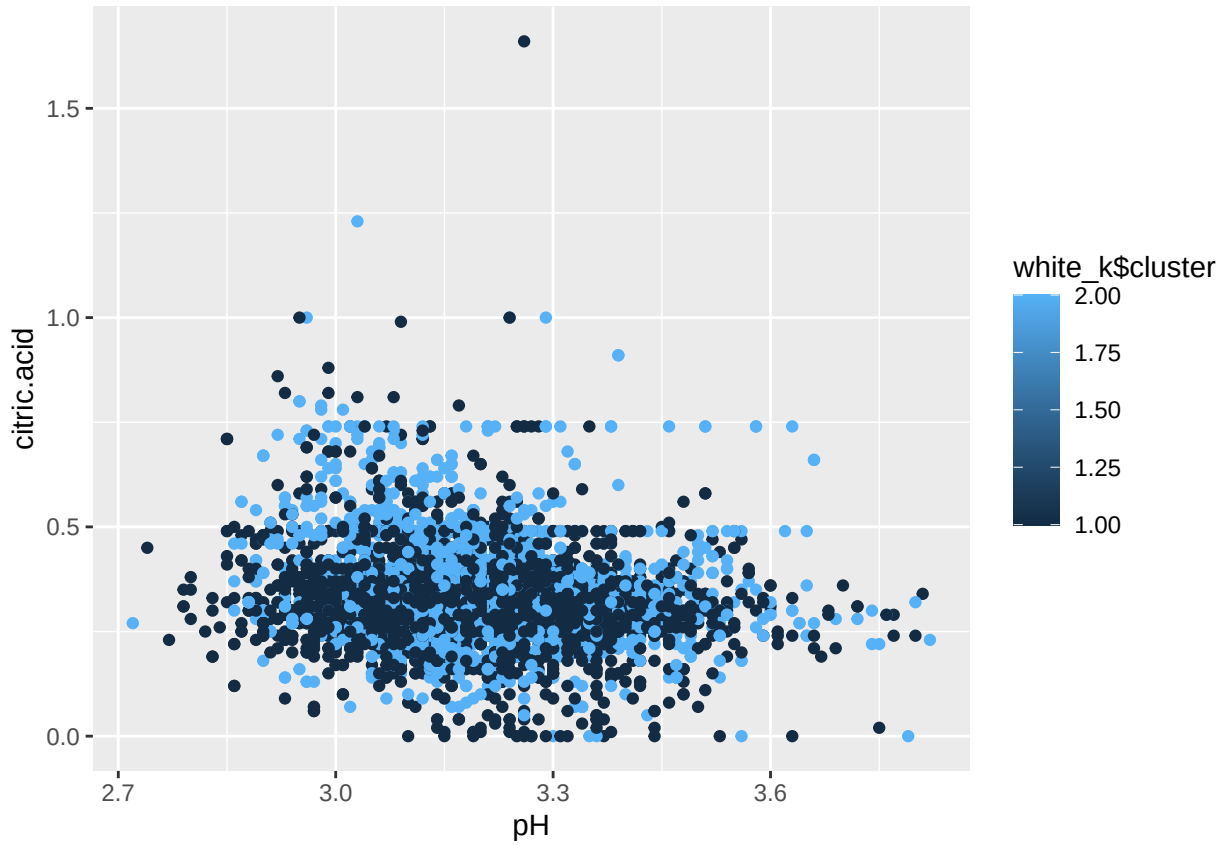
```
c1 <- ggplot(white_df)+geom_point(aes(x=pH,y=alcohol ,color=white_k$cluster))
c1
```



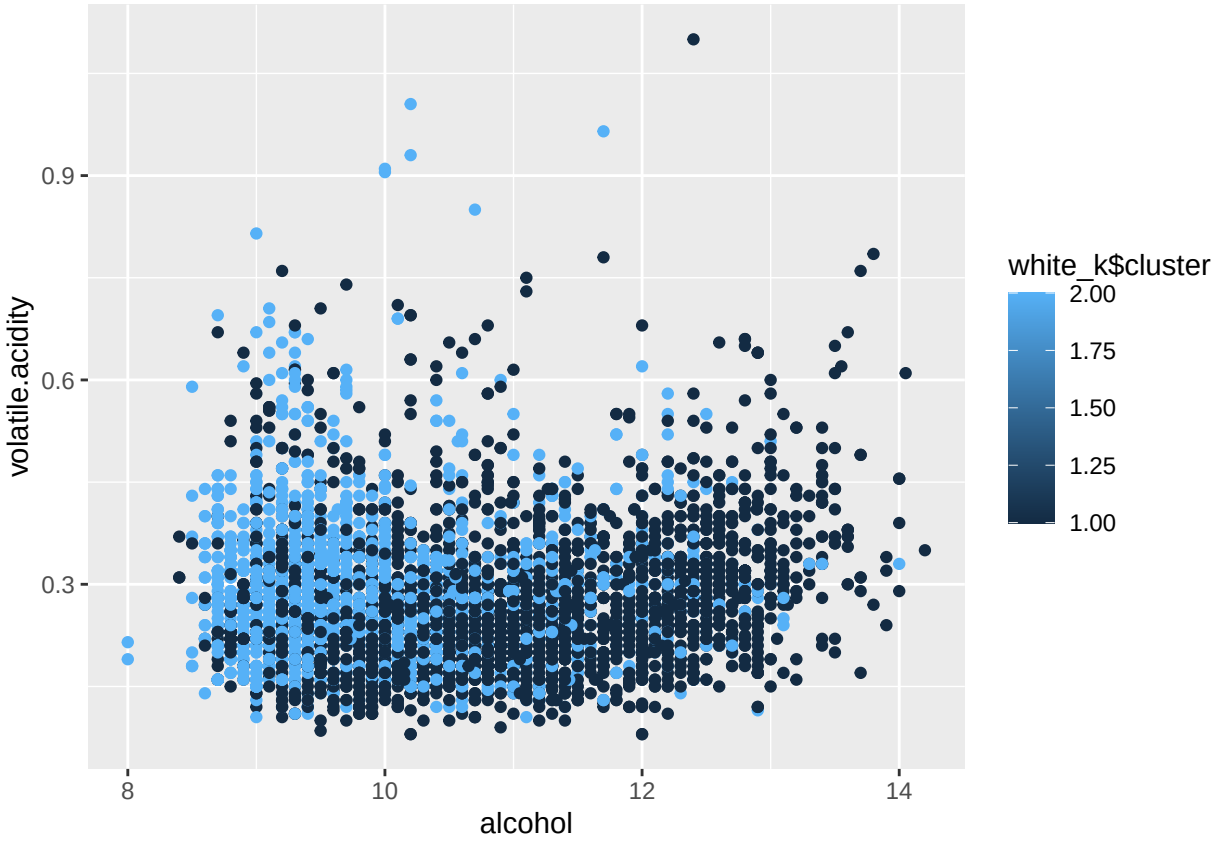

```
c2 <- ggplot(white_df)+geom_point(aes(x=pH,y=total.sulfur.dioxide ,color=white_k$cluster))
c2
```



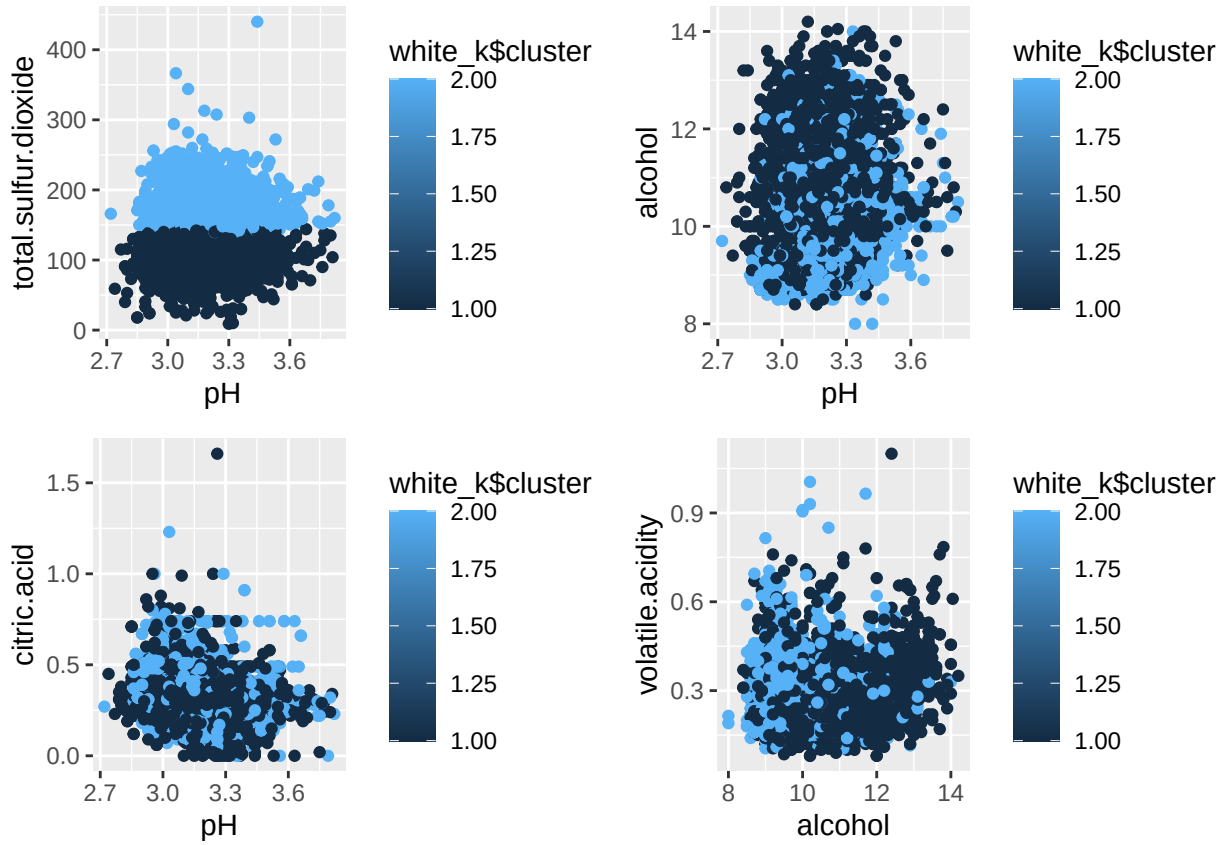

```
c3 <- ggplot(white_df)+geom_point(aes(x=pH,y=citric.acid ,color=white_k$cluster))
c3
```




```
c4 <- ggplot(white_df)+geom_point(aes(x=alcohol,y=volatile.acidity ,color=white_k$cluster))
c4
```




```
ggarrange(c2,c1,c3,c4, nrow=2, ncol=2)
```




```
#clustering
set.seed(1406)
kmeans.re <- kmeans(white_df, centers = 3, nstart = 25)
kmeans.re
```

```
## K-means clustering with 3 clusters of sizes 1125, 1797, 1976
##
## Cluster means:
##   fixed.acidity volatile.acidity citric.acid residual.sugar  chlorides
## 1      6.970133        0.2934800   0.3533956       9.356089 0.05179556
## 2      6.778075        0.2730662   0.3174791       4.170924 0.04090095
## 3      6.858882        0.2742713   0.3384565       6.722874 0.04677328
##   free.sulfur.dioxide total.sulfur.dioxide   density       pH sulphates
## 1            50.69689            196.93911 0.9963027 3.183013 0.5149511
## 2            23.93684             96.05175 0.9923317 3.187863 0.4798164
## 3            36.88790            143.48634 0.9942740 3.191624 0.4846761
##     alcohol  quality
## 1  9.707156 5.555556
## 2 11.109507 6.002226
## 3 10.432463 5.948381
##
## Clustering vector:
##    [1] 1 3 2 1 1 2 3 1 3 3 2 2 2 3 1 2 2 2 3 3 2 2 3 3 3 1 3 3 3 2 3 2 2 3 1 3 3
##   [38] 3 3 3 3 3 3 3 3 3 1 1 3 3 3 3 2 2 3 1 1 3 2 2 3 3 3 2 3 2 3 1 2 2 1 1 1 2
##   [75] 2 2 2 2 2 2 2 3 3 1 3 3 3 1 3 3 3 1 3 3 3 1 3 2 2 3 1 3 3 1 1 2 3 1 1 1 3
##  [112] 1 1 3 3 2 3 2 1 1 2 3 3 3 3 3 3 1 1 1 2 1 1 1 1 1 3 3 2 2 2 3 2 2 2 2 3 2
```

```
##  [149] 2 2 3 3 2 2 2 1 1 3 3 3 3 3 2 1 1 1 1 2 3 2 3 2 2 3 1 3 2 1 2 1 1 1 3 1 1
##  [186] 1 3 3 2 1 1 3 3 3 1 1 1 1 1 1 1 1 1 3 2 3 3 3 2 3 2 2 3 3 2 3 3 3 1 3 3 3
##  [223] 2 3 3 3 1 1 1 3 3 1 1 1 1 1 1 1 3 3 1 2 2 1 3 1 3 2 2 2 1 1 3 2 3 3 2 2 2
##  [260] 2 2 3 2 1 3 3 1 3 3 3 1 3 3 3 1 1 3 2 2 2 2 2 1 1 1 1 1 1 1 1 3 1 3 1 1
##  [297] 3 1 3 3 2 2 2 3 3 3 3 3 3 3 2 3 3 3 3 3 3 3 3 2 2 3 3 3 1 1 1 3 1 2 2 3 2
##  [334] 3 2 2 2 1 3 3 3 3 3 3 3 3 2 3 3 3 3 3 3 3 1 1 1 3 3 3 3 2 3 1 2 2 3 3 1 2
##  [371] 3 1 1 3 2 2 2 2 3 2 2 1 3 3 3 2 2 1 3 1 1 2 3 2 3 1 2 2 1 2 2 3 2 1 3 1 2
##  [408] 3 2 2 3 3 2 2 3 3 2 1 2 3 3 1 1 1 3 1 1 1 2 1 1 2 1 3 2 2 1 1 1 2 2 3 3 1
##  [445] 3 2 3 2 2 3 3 3 3 2 3 2 2 2 1 1 2 1 3 2 1 3 3 2 1 1 3 1 2 3 2 1 2 2 3 3 3
##  [482] 2 3 3 1 2 3 2 1 1 2 2 1 3 2 3 1 3 3 1 1 3 1 1 3 3 3 3 3 3 3 3 3 2 2 3 3 3
##  [519] 2 2 3 3 2 2 2 3 2 2 2 2 2 3 1 1 1 1 1 1 2 1 3 1 3 3 3 3 1 2 3 1 3 2 2 3 2
##  [556] 2 3 3 3 3 3 3 1 3 3 2 2 3 3 1 1 2 1 3 3 1 1 3 2 3 1 2 3 2 3 2 3 3 3 3 3 3
##  [593] 3 3 3 3 3 3 2 2 3 2 3 3 3 3 3 3 3 2 2 2 3 3 3 3 2 1 1 3 1 1 3 2 3 3 1 1 1
##  [630] 2 3 3 3 1 3 3 3 3 1 1 3 1 1 3 3 3 3 3 1 1 1 1 1 3 3 2 2 3 1 1 2 3 1 2 1 3
##  [667] 1 1 1 1 1 2 3 3 1 1 1 2 2 2 3 3 3 1 1 1 2 1 1 3 3 1 1 1 1 1 2 1 1 1 1 3 2
##  [704] 2 2 2 1 3 3 2 1 3 3 1 1 3 1 3 3 3 1 1 3 2 3 3 2 2 3 1 3 1 2 1 1 3 1 1 3 3
##  [741] 2 2 3 3 3 2 1 1 1 1 1 1 1 1 3 2 1 1 3 3 1 1 1 3 3 3 1 2 2 2 2 3 3 1 3 2 2
##  [778] 1 1 3 2 1 1 3 1 2 2 2 2 2 2 2 3 2 1 3 1 3 2 2 3 1 1 3 2 3 1 1 1 1 1 2 3 3
##  [815] 1 3 2 3 3 3 2 1 2 2 2 3 3 3 2 2 2 3 2 2 2 2 1 1 1 3 3 3 3 2 2 2 3 2 3 2 2
##  [852] 3 2 3 2 2 3 1 3 3 2 1 3 2 3 2 2 3 1 2 3 3 3 2 2 3 3 2 2 2 3 2 3 3 1 2 1 2
##  [889] 1 2 3 2 2 3 2 2 1 2 2 1 3 2 1 1 3 2 2 3 3 1 3 3 3 2 2 2 3 3 2 2 3 3 3 1 3
##  [926] 2 2 1 1 2 2 1 1 1 1 1 2 2 1 1 1 1 2 3 3 2 1 3 2 2 3 3 2 2 3 3 3 2 2 1 1 2
##  [963] 1 2 3 2 1 3 2 2 2 2 3 2 2 2 3 1 3 2 2 3 2 2 3 3 3 3 3 2 3 2 1 2 1 3 2 3 1
## [1000] 3 2 1 1 3 3 2 3 2 1 3 2 1 2 1 3 2 3 2 3 1 3 3 1 1 1 3 3 2 3 1 3 1 1 1 1 3
## [1037] 2 2 2 2 3 2 2 1 2 2 2 2 2 2 3 3 2 2 2 2 2 1 2 3 3 1 1 1 3 3 1 3 2 3 3 3 2
## [1074] 1 1 3 1 3 1 1 2 3 3 1 3 3 3 3 1 3 1 1 3 3 1 2 3 3 3 2 3 2 3 2 3 1 3 2 2 3
## [1111] 2 2 1 2 2 2 2 1 2 3 2 2 2 2 3 1 1 2 2 2 3 3 3 2 3 3 1 1 3 2 2 3 3 3 3 1 3
## [1148] 1 2 1 1 1 2 2 3 3 3 3 1 3 3 3 3 1 2 3 2 2 2 3 2 2 2 2 1 1 1 1 3 2 2 3 2 3
## [1185] 3 1 1 2 3 2 2 3 2 3 1 3 3 3 2 2 2 2 1 2 2 1 1 1 3 3 2 1 3 2 2 3 2 1 3 2 1
## [1222] 3 2 3 2 2 2 2 2 2 1 2 2 3 3 1 2 2 3 3 1 1 3 3 3 1 3 2 2 1 3 3 3 3 3 2 3 1
## [1259] 1 1 1 3 3 1 2 1 2 3 3 1 3 3 3 3 1 3 3 3 3 3 3 3 3 3 3 3 3 2 2 2 2 1 2 2 2
## [1296] 1 3 3 3 3 3 1 1 3 1 2 2 3 3 2 3 2 3 1 3 3 1 1 2 1 2 2 3 3 1 2 3 3 2 2 2 2
## [1333] 1 1 2 1 3 1 1 2 3 3 2 1 3 2 3 3 3 2 2 3 1 1 1 3 1 3 2 3 3 1 2 2 3 3 2 2 1
## [1370] 1 2 3 1 1 2 3 3 3 3 2 3 2 2 2 3 3 2 2 3 1 3 2 2 2 2 2 3 1 1 2 1 1 3 3 2 2
## [1407] 2 2 1 2 2 2 3 3 3 2 3 1 3 2 3 2 2 1 3 3 3 3 2 2 2 2 2 2 3 2 1 2 1 1 3 2 2
## [1444] 3 3 3 2 3 3 1 3 3 3 3 1 3 2 3 3 3 3 3 3 3 3 3 1 2 2 3 3 3 2 3 2 3 1 2 3 3
## [1481] 3 3 1 2 3 3 2 3 1 1 2 2 1 1 1 1 2 3 2 3 3 3 2 3 3 3 1 3 1 3 3 3 3 3 3 3 3
## [1518] 3 2 3 3 2 3 1 3 3 3 1 3 3 3 3 1 2 1 2 2 3 2 2 1 2 2 2 2 3 3 3 2 2 3 3 3 3
## [1555] 3 3 1 3 2 2 3 2 3 3 2 2 3 2 1 3 3 1 3 2 2 1 2 3 1 1 2 2 2 1 1 3 3 1 3 3 3
## [1592] 3 2 2 3 1 3 1 2 2 3 1 2 2 3 2 2 3 1 1 2 2 2 3 3 3 1 3 1 3 2 3 3 2 3 3 1 3
## [1629] 2 2 2 2 2 2 1 3 3 3 1 2 3 3 3 3 3 3 3 2 2 3 3 1 2 1 1 3 2 3 1 1 1 1 2 1 1
## [1666] 2 2 3 2 2 3 2 3 3 1 1 2 3 3 2 1 1 1 1 1 1 3 1 1 3 3 1 1 1 3 3 1 1 1 1 2 1
## [1703] 2 3 3 3 3 1 3 1 2 3 1 3 2 3 2 3 1 2 1 1 3 3 3 3 2 1 2 3 2 1 2 3 1 1 2 1 2
## [1740] 2 3 3 3 3 3 3 1 2 3 2 3 1 3 1 3 2 3 1 1 2 1 1 3 2 2 1 1 1 1 3 2 1 3 1 1 2 3
## [1777] 3 3 3 3 3 3 1 3 2 3 3 2 3 3 1 1 2 3 1 2 3 3 3 1 3 1 2 1 3 1 2 2 1 2 1 1 2 2
## [1814] 2 2 3 3 2 2 3 3 2 2 1 3 2 3 1 1 3 3 3 3 3 3 1 2 2 1 2 3 2 1 3 2 3 1 3 1 1
## [1851] 1 2 3 2 1 1 1 3 3 1 3 1 2 1 3 3 1 3 3 3 3 3 3 3 3 3 3 3 2 1 2 1 2 1 1 3 2 2
## [1888] 1 1 2 1 1 3 3 3 1 3 3 2 2 3 2 1 2 1 3 2 3 2 3 1 2 2 3 3 2 1 2 1 1 3 3 3 2
## [1925] 2 2 2 3 1 1 1 1 2 1 2 1 1 3 2 3 1 3 1 1 1 3 3 1 3 3 1 1 3 1 1 1 2 2 1 2 2
## [1962] 3 2 1 1 3 2 1 3 3 2 3 3 3 3 1 1 3 2 1 1 1 1 1 1 1 3 1 1 2 2 1 2 1 3 1 3 1
## [1999] 1 1 3 3 3 1 1 3 1 2 3 2 2 3 3 3 2 2 2 2 3 3 3 3 1 3 1 3 2 1 3 1 3 3 2 1 2
## [2036] 2 3 3 2 2 1 2 2 2 2 2 3 3 3 3 2 3 3 2 2 3 3 3 1 3 1 2 3 3 1 3 3 3 2 3 3 3
## [2073] 3 1 1 3 2 1 2 2 2 2 2 2 3 3 2 3 3 3 1 1 2 3 3 3 3 3 1 3 3 2 1 3 3 3 1 3 1
## [2110] 1 3 3 3 2 1 3 2 2 3 2 3 2 1 3 2 3 3 1 3 2 3 3 3 3 3 1 3 1 2 2 2 2 1 2 3 3
```

```
## [2147] 2 3 2 2 2 2 2 2 1 1 2 2 2 2 3 2 2 2 3 3 3 1 1 1 1 1 2 3 1 1 2 3 3 2 3 2 3
## [2184] 3 2 2 2 3 2 3 2 3 3 3 2 3 2 2 1 1 3 3 1 3 3 1 3 3 3 3 3 3 3 2 3 3 2 3 3 3
## [2221] 3 3 3 3 3 3 1 1 3 3 3 3 2 3 2 3 1 3 3 3 1 1 1 1 1 3 3 3 2 1 1 2 1 1 1 3 3
## [2258] 3 1 3 1 3 2 3 3 3 3 3 3 1 2 3 2 2 2 1 1 2 1 3 2 2 1 1 1 1 3 3 1 2 2 3 1 2
## [2295] 2 3 3 1 2 2 3 3 1 3 3 3 3 3 3 3 3 3 3 2 3 3 2 3 3 2 3 3 2 3 1 2 2 2 2 1 1
## [2332] 3 1 2 1 3 1 1 3 2 3 3 2 3 2 1 1 2 3 1 1 1 3 2 2 3 3 2 1 3 3 2 3 1 1 3 1 1
## [2369] 1 3 2 1 2 2 1 3 1 2 1 1 1 3 2 2 2 3 1 1 2 2 3 3 3 3 1 1 1 2 2 2 2 2 1 3 3
## [2406] 1 2 2 1 2 1 1 1 2 1 2 1 1 2 1 2 1 1 2 1 2 3 1 3 1 1 1 1 1 1 3 1 3 1 3 3 3
## [2443] 1 1 1 1 1 3 2 1 3 3 3 3 1 1 3 3 1 3 3 2 2 1 3 3 3 3 2 2 1 3 2 3 2 2 3 2 1
## [2480] 3 2 1 1 1 1 1 3 3 3 1 2 1 1 3 3 3 2 3 3 1 3 1 2 2 1 1 1 3 1 3 1 1 2 3 3 2
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## [2813] 2 3 2 2 3 2 3 3 3 1 3 2 1 3 1 3 3 3 3 1 2 2 3 3 1 3 2 2 2 2 2 2 2 2 2 2 3
## [2850] 1 3 2 3 2 2 3 3 2 3 2 3 2 2 2 2 2 3 2 3 2 2 2 1 2 3 2 3 3 3 2 2 2 3 2 2 2
## [2887] 2 2 2 3 3 3 1 3 2 1 1 1 2 3 2 2 3 2 2 3 1 2 2 2 1 3 2 1 2 2 3 2 2 3 2 1 3
## [2924] 3 3 1 2 3 3 3 3 2 1 3 2 2 2 1 2 2 3 2 1 2 3 3 2 2 1 3 2 2 2 2 2 3 2 2 2 2
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## [2998] 3 2 2 2 3 3 2 2 3 1 1 1 1 1 2 2 2 2 2 2 3 3 2 2 2 3 2 2 3 2 3 3 3 3 3 2 1
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## [3072] 2 1 3 3 2 2 1 2 2 2 1 2 2 2 2 2 2 1 2 2 2 1 3 3 2 2 2 3 3 2 3 2 2 3 3 3 3
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## [3146] 3 3 3 3 3 2 3 1 2 2 3 3 3 2 3 2 3 3 2 1 3 3 2 2 2 3 2 2 3 3 3 2 3 2 2 2 2
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## [3664] 3 3 3 3 2 2 2 3 2 2 2 2 3 2 3 2 2 1 3 3 1 3 1 1 2 1 3 3 2 2 3 2 3 3 1 2 1
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## [3886] 2 3 2 2 3 2 3 3 2 3 2 1 1 2 3 2 2 2 2 2 2 2 2 3 3 3 2 2 2 3 2 3 1 2 2 3 1
## [3923] 2 2 2 2 2 2 3 3 2 2 2 2 2 1 2 3 2 3 3 3 2 2 3 3 3 3 2 3 3 3 2 3 3 2 3 2 2
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## [3997] 2 3 2 2 2 2 2 2 2 2 2 2 2 2 3 3 3 2 1 1 2 3 2 1 2 2 2 3 3 3 2 3 3 2 3 2 2 2
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## [4071] 3 2 3 2 2 3 3 2 2 2 3 2 3 1 2 2 2 2 2 3 1 2 2 2 2 2 3 2 3 2 2 3 3 2 2 3 3
## [4108] 3 2 3 1 2 2 2 2 2 3 3 3 3 3 3 3 2 2 3 3 1 1 2 3 1 1 2 2 3 3 1 2 3 3 3 3 3
```

```
## [4145] 3 3 3 3 2 2 1 1 2 1 1 1 1 3 3 3 3 3 3 2 2 2 3 3 2 3 3 2 3 2 1 3 3 2 3 1 3
## [4182] 2 3 2 2 1 2 2 2 2 2 3 2 2 2 2 2 2 3 3 2 2 2 2 1 3 2 3 2 2 2 3 1 3 2 1 1 1 2
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## [4256] 2 2 3 3 2 3 2 3 3 2 3 2 2 3 1 1 1 2 2 2 2 2 1 2 3 2 3 3 2 2 2 2 2 2 2 3 1
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## [4552] 2 2 2 2 2 3 1 3 2 2 2 3 2 2 3 1 3 3 3 2 2 2 2 2 3 2 2 2 3 2 3 3 3 2 3 3 2
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## [4811] 3 2 2 1 2 2 3 3 2 2 1 3 3 3 3 3 3 2 3 2 3 3 3 2 2 2 2 1 2 2 3 1 2 1 1 2 3
## [4848] 2 3 3 3 3 2 2 2 3 3 2 1 2 2 2 2 2 3 2 2 2 3 2 3 2 1 3 3 2 2 2 2 2 1 1 2 3 3
## [4885] 1 1 3 2 3 2 2 3 2 2 1 2 2 2
##
## Within cluster sum of squares by cluster:
## [1] 1026873.8  872531.1  849211.8
##  (between_SS / total_SS =  73.6 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"
```
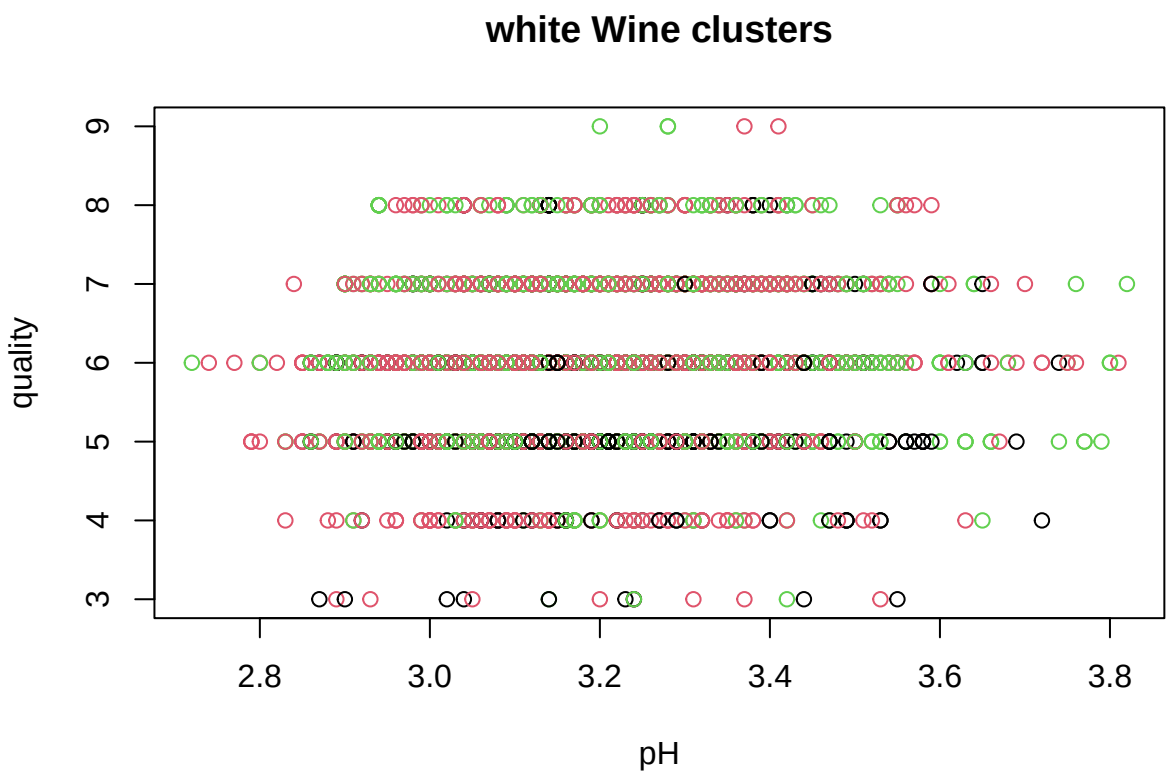

```
plot(white_df[c("pH", "quality")],
     col = kmeans.re$cluster,
     main = "white Wine clusters")
```




```
#Classification trees
library(party)
```

```
## Loading required package: grid
## Loading required package: mvtnorm
## Loading required package: modeltools
## Loading required package: stats4
## Loading required package: strucchange
## Loading required package: zoo
##
## Attaching package: 'zoo'
##
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
##
## Loading required package: sandwich
##
## Attaching package: 'strucchange'
##
## The following object is masked from 'package:stringr':
##
##     boundary
```

```
tree1=ctree(quality~alcohol+volatile.acidity,data=white_df) #~target variable,predicting
tree1
```

```
##
##   Conditional inference tree with 17 terminal nodes
##
## Response:  quality
## Inputs:  alcohol, volatile.acidity
## Number of observations:  4898
##
## 1) alcohol <= 10.8; criterion = 1, statistic = 929.085
##   2) volatile.acidity <= 0.25; criterion = 1, statistic = 412.098
##     3) volatile.acidity <= 0.205; criterion = 1, statistic = 52.154
##       4) alcohol <= 9; criterion = 0.99, statistic = 7.887
##         5)*  weights = 92
##       4) alcohol > 9
##         6) alcohol <= 10.1; criterion = 0.952, statistic = 5.057
##           7) alcohol <= 9.9; criterion = 0.964, statistic = 5.582
##             8)*  weights = 277
##           7) alcohol > 9.9
##             9)*  weights = 85
##         6) alcohol > 10.1
##           10)*  weights = 277
##     3) volatile.acidity > 0.205
##       11) alcohol <= 9.8; criterion = 1, statistic = 28.599
##         12)*  weights = 438
##       11) alcohol > 9.8
##         13)*  weights = 306
##   2) volatile.acidity > 0.25
##     14) volatile.acidity <= 0.3; criterion = 1, statistic = 88.408
##       15) alcohol <= 10.3; criterion = 1, statistic = 25.5
##         16) alcohol <= 9; criterion = 0.97, statistic = 5.915
##           17)*  weights = 115
##         16) alcohol > 9
##           18)*  weights = 435
##       15) alcohol > 10.3
##         19)*  weights = 152
##     14) volatile.acidity > 0.3
##       20) volatile.acidity <= 0.46; criterion = 1, statistic = 39.963
##         21) alcohol <= 9.7; criterion = 1, statistic = 29.619
##           22)*  weights = 482
##         21) alcohol > 9.7
##           23)*  weights = 283
##       20) volatile.acidity > 0.46
##         24)*  weights = 143
## 1) alcohol > 10.8
##   25) alcohol <= 11.73333; criterion = 1, statistic = 115.528
##     26) volatile.acidity <= 0.46; criterion = 1, statistic = 35.936
##       27) volatile.acidity <= 0.18; criterion = 0.995, statistic = 9.253
##         28)*  weights = 168
##       27) volatile.acidity > 0.18
##         29)*  weights = 697
##     26) volatile.acidity > 0.46
```

```
##       30)*  weights = 16
##   25) alcohol > 11.73333
##     31) alcohol <= 12.75; criterion = 1, statistic = 18.802
##       32)*  weights = 699
##     31) alcohol > 12.75
##       33)*  weights = 233
```

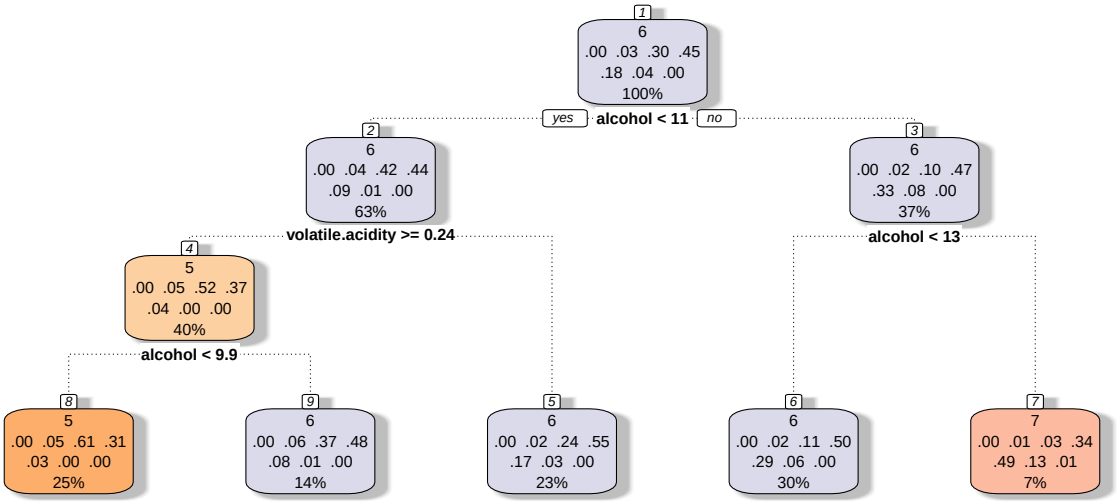
```
library(rpart)
mytree=rpart(quality~alcohol+volatile.acidity,data=white_df,method="class")
mytree
```

```
## n= 4898
##
## node), split, n, loss, yval, (yprob)
##       * denotes terminal node
##
## 1) root 4898 2700 6 (0.0041 0.033 0.3 0.45 0.18 0.036 0.001)
##   2) alcohol< 10.85 3085 1732 6 (0.0039 0.041 0.42 0.44 0.089 0.012 0.00032)
##     4) volatile.acidity>=0.2375 1936  926 5 (0.0041 0.055 0.52 0.37 0.044 0.0036 0.00052)
##       8) alcohol< 9.85 1230  482 5 (0.0041 0.05 0.61 0.31 0.025 0.00081 0) *
##       9) alcohol>=9.85 706  370 6 (0.0042 0.062 0.37 0.48 0.076 0.0085 0.0014) *
##     5) volatile.acidity< 0.2375 1149  515 6 (0.0035 0.017 0.24 0.55 0.17 0.026 0) *
##   3) alcohol>=10.85 1813  968 6 (0.0044 0.02 0.097 0.47 0.33 0.076 0.0022)
##     6) alcohol< 12.55 1458  732 6 (0.0048 0.023 0.11 0.5 0.29 0.064 0.0014) *
##     7) alcohol>=12.55 355  180 7 (0.0028 0.011 0.025 0.34 0.49 0.13 0.0056) *
```

```
library(rattle)
```

```
## Loading required package: bitops
##
## Attaching package: 'bitops'
##
## The following object is masked from 'package:Matrix':
##
##     %&%
##
## Rattle: A free graphical interface for data science with R.
## Version 5.5.1 Copyright (c) 2006-2021 Togaware Pty Ltd.
## Type 'rattle()' to shake, rattle, and roll your data.
##
## Attaching package: 'rattle'
##
## The following object is masked from 'package:randomForest':
##
##     importance
```

```
library(RColorBrewer)
fancyRpartPlot(mytree,caption="white wine Classification")
```



white wine Classification