

# Short Report 2 Code

Anna Ursin and Kunwu Lyu

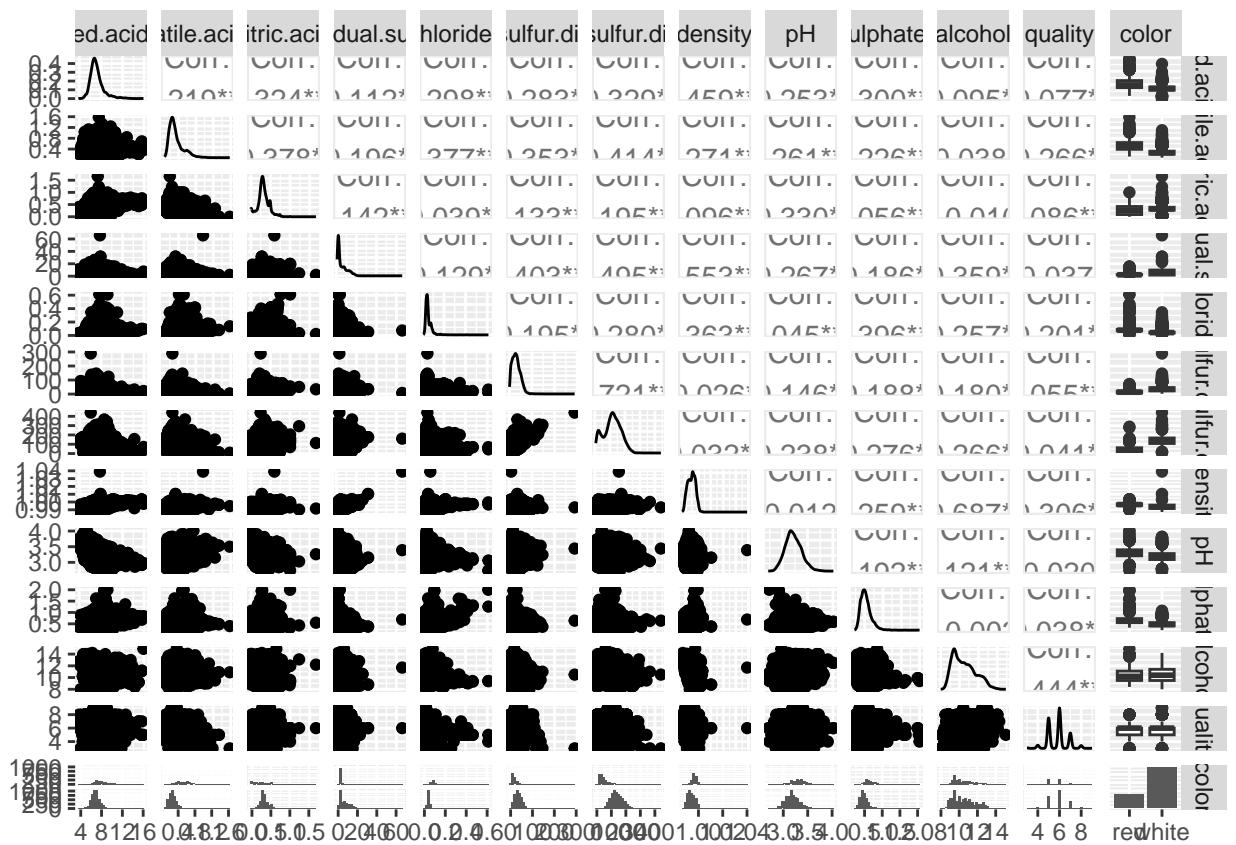
2024-11-04

## Data Wrangling

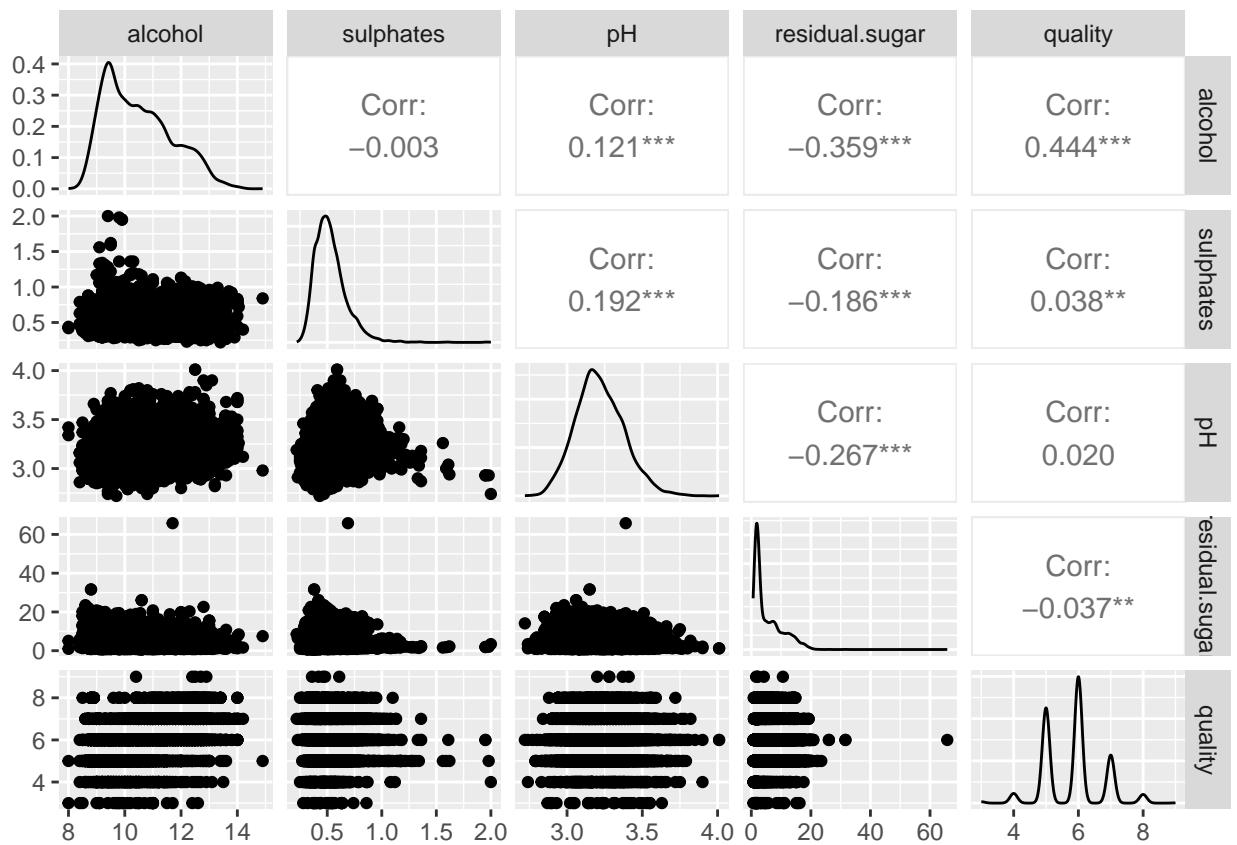
```
## Data Wrangling & Scatterplot Matrix
wine_dat <- read.csv("https://www.math.carleton.edu/ckelling/data/wine_project.csv")
glimpse(wine_dat)

## Rows: 6,497
## Columns: 13
## $ fixed.acidity      <dbl> 7.4, 7.8, 7.8, 11.2, 7.4, 7.4, 7.9, 7.3, 7.8, 7.5~
## $ volatile.acidity    <dbl> 0.700, 0.880, 0.760, 0.280, 0.700, 0.660, 0.600, ~
## $ citric.acid        <dbl> 0.00, 0.00, 0.04, 0.56, 0.00, 0.00, 0.06, 0.00, 0~
## $ residual.sugar     <dbl> 1.9, 2.6, 2.3, 1.9, 1.9, 1.8, 1.6, 1.2, 2.0, 6.1,~
## $ chlorides           <dbl> 0.076, 0.098, 0.092, 0.075, 0.076, 0.075, 0.069, ~
## $ free.sulfur.dioxide <dbl> 11, 25, 15, 17, 11, 13, 15, 15, 9, 17, 15, 17, 16~
## $ total.sulfur.dioxide <dbl> 34, 67, 54, 60, 34, 40, 59, 21, 18, 102, 65, 102,~
## $ density              <dbl> 0.9978, 0.9968, 0.9970, 0.9980, 0.9978, 0.9978, 0~
## $ pH                   <dbl> 3.51, 3.20, 3.26, 3.16, 3.51, 3.51, 3.30, 3.39, 3~
## $ sulphates            <dbl> 0.56, 0.68, 0.65, 0.58, 0.56, 0.56, 0.46, 0.47, 0~
## $ alcohol               <dbl> 9.4, 9.8, 9.8, 9.8, 9.4, 9.4, 9.4, 10.0, 9.5, 10.~
## $ quality               <int> 5, 5, 5, 6, 5, 5, 5, 7, 7, 5, 5, 5, 5, 5, 5, 5, 7~
## $ color                 <chr> "red", "red", "red", "red", "red", "red", "red", ~

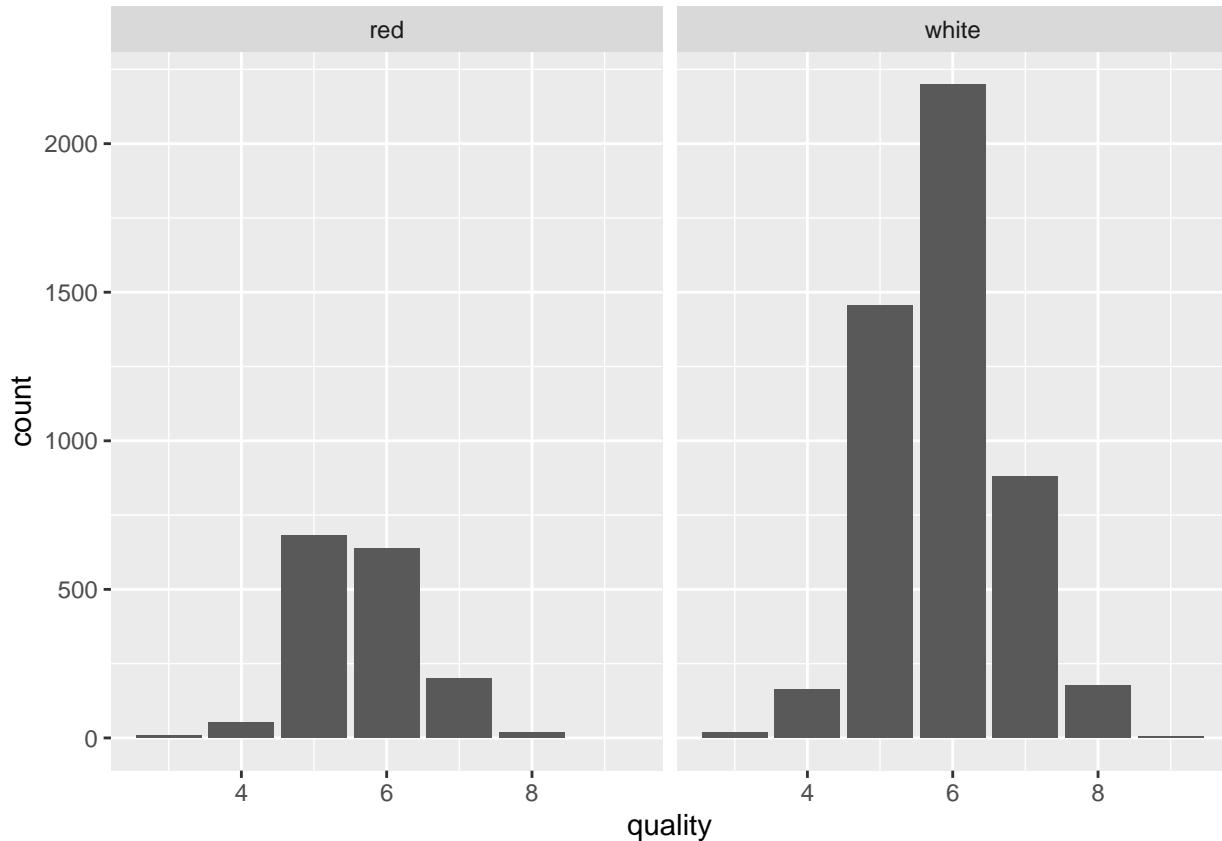
ggpairs(wine_dat) # for all
```



```
ggpairs(data = wine_dat, columns = c("alcohol", "sulphates", "pH", "residual.sugar", "quality")) # for
```



```
## dist of quality scores
ggplot(wine_dat, aes(x = quality)) +
  geom_bar() +
  facet_grid(cols = vars(color))
```



```
  labs(title = "Distribution of Wine Quality Scores")
```

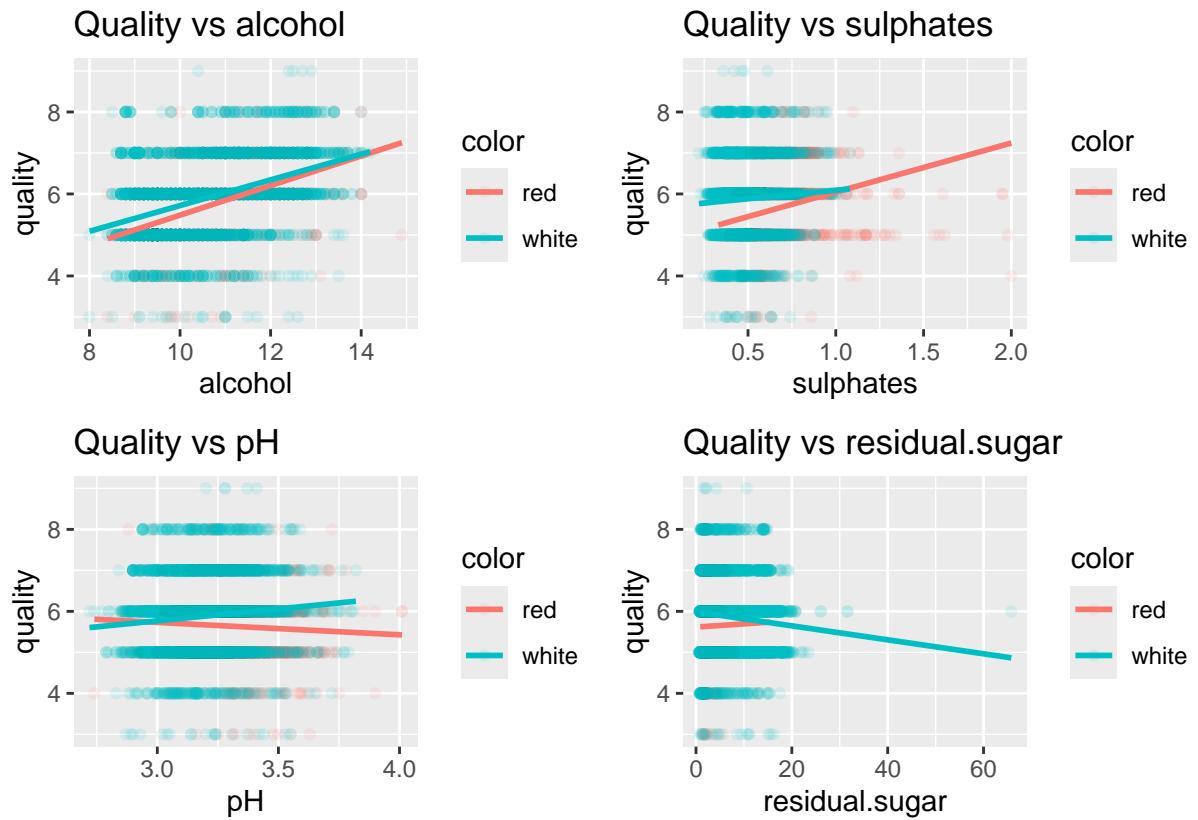
```
## $title
## [1] "Distribution of Wine Quality Scores"
##
## attr(,"class")
## [1] "labels"
```

## EDA Plot

```
## scatterplots for predictors vs wine quality
create_plot <- function(var_name) {
  ggplot(data = wine_dat,
         aes_string(x = var_name, y = "quality", color = "color")) +
    geom_point(alpha = 0.1) +
    geom_smooth(method = "lm", se = FALSE) +
    labs(title = paste("Quality vs", var_name))
}

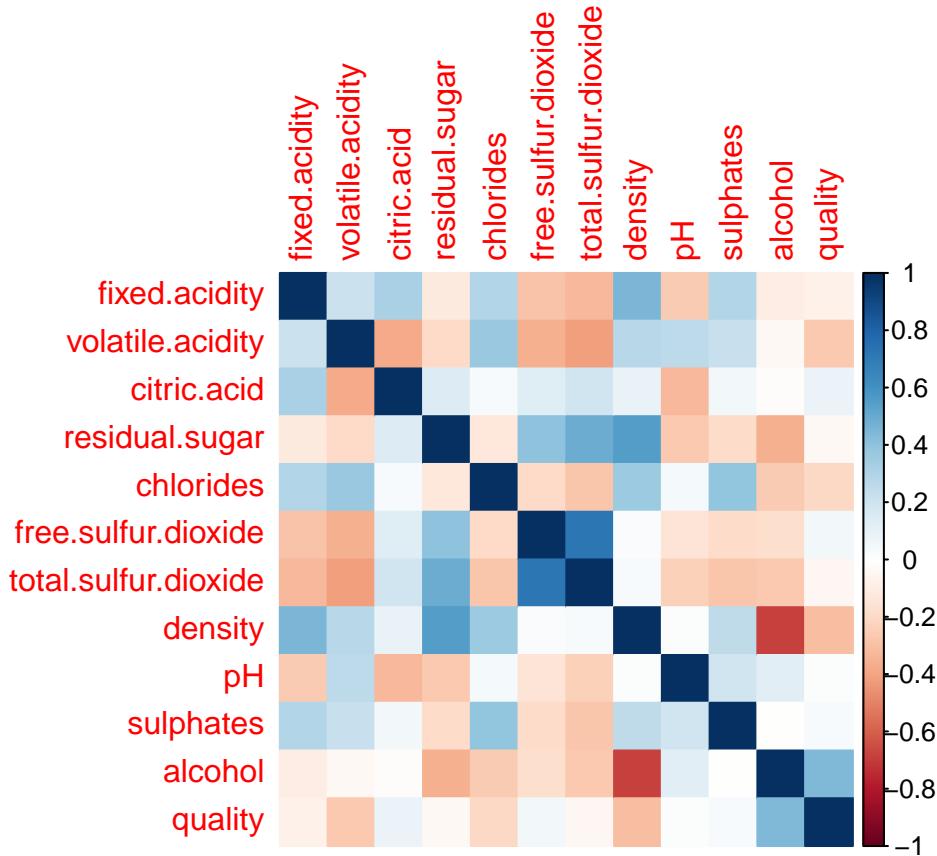
variable_names <- c("alcohol", "sulphates", "pH", "residual.sugar")
plot_list <- map(variable_names, create_plot)

plot_grid <- wrap_plots(plot_list, ncol = 2)
plot_grid
```



```
## correlation matrix
wine_numeric <- wine_dat %>% dplyr::select(-color)

corr_matrix <- cor(wine_numeric, use = "complete.obs")
corrplot(corr_matrix, method = "color")
```



## Regression Model

```

## Main Effects Model
wine_lm_base <- lm(quality ~ alcohol + sulphates + residual.sugar + pH, data = wine_dat)
summary(wine_lm_base)

##
## Call:
## lm(formula = quality ~ alcohol + sulphates + residual.sugar +
##     pH, data = wine_dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -3.4939 -0.5010 -0.0346  0.4919  3.0992 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 1.842152  0.221545  8.315 < 2e-16 ***
## alcohol      0.366868  0.008635 42.486 < 2e-16 ***
## sulphates    0.417133  0.066463  6.276 3.69e-10 ***
## residual.sugar 0.028000  0.002252 12.434 < 2e-16 ***
## pH          -0.076713  0.062563 -1.226     0.22  
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.7717 on 6492 degrees of freedom

```

```

## Multiple R-squared:  0.2195, Adjusted R-squared:  0.219
## F-statistic: 456.3 on 4 and 6492 DF,  p-value: < 2.2e-16
## Interaction Model
wine_lm_interaction <- lm(quality ~ alcohol + sulphates + residual.sugar + pH*color, data = wine_dat)
summary(wine_lm_interaction)

##
## Call:
## lm(formula = quality ~ alcohol + sulphates + residual.sugar +
##     pH * color, data = wine_dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.5422 -0.4971 -0.0404  0.4843  3.0800
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.620360  0.426412  8.490 < 2e-16 ***
## alcohol      0.356333  0.008710 40.913 < 2e-16 ***
## sulphates    0.624165  0.074126  8.420 < 2e-16 ***
## residual.sugar 0.023240  0.002348  9.896 < 2e-16 ***
## pH          -0.654821  0.125466 -5.219 1.85e-07 ***
## colorwhite   -2.926864  0.483888 -6.049 1.54e-09 ***
## pH:colorwhite 0.963311  0.146385  6.581 5.05e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7644 on 6490 degrees of freedom
## Multiple R-squared:  0.2345, Adjusted R-squared:  0.2338
## F-statistic: 331.3 on 6 and 6490 DF,  p-value: < 2.2e-16

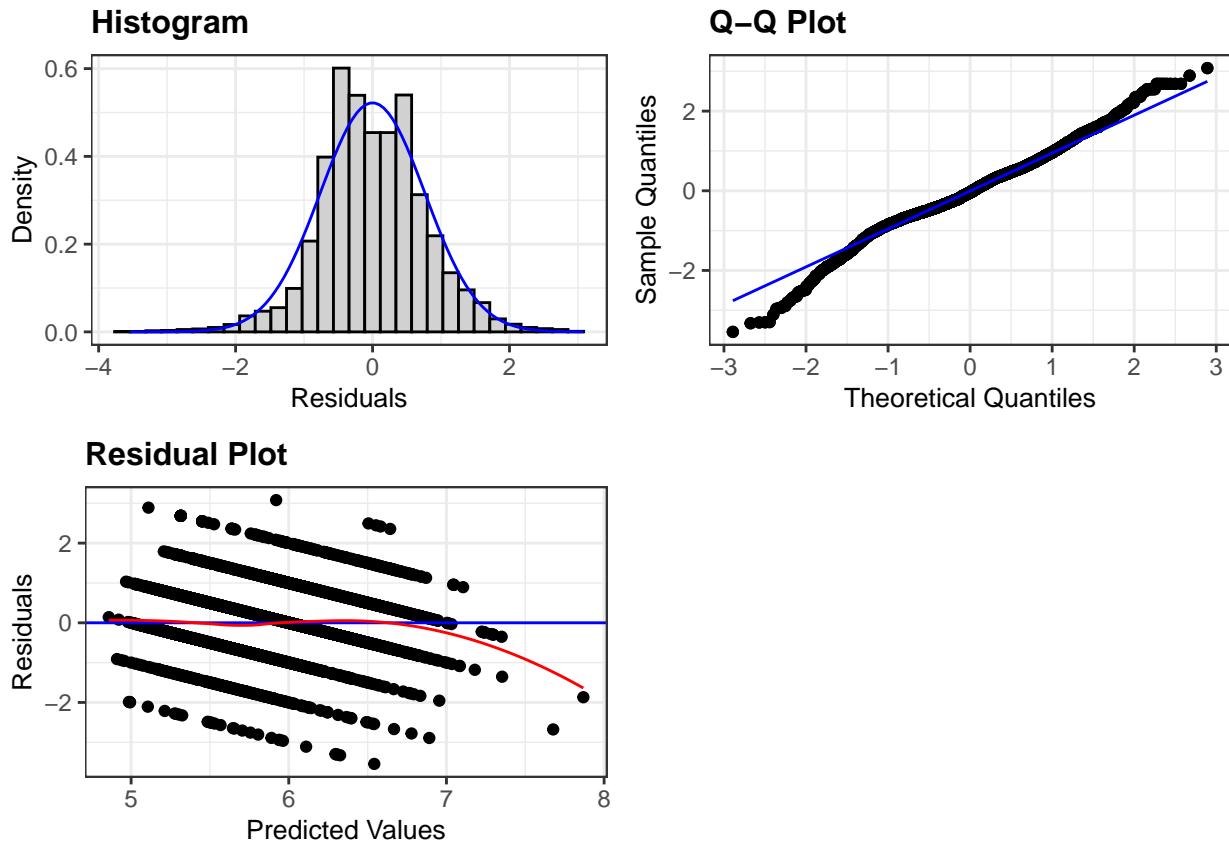
```

## Residual Plots

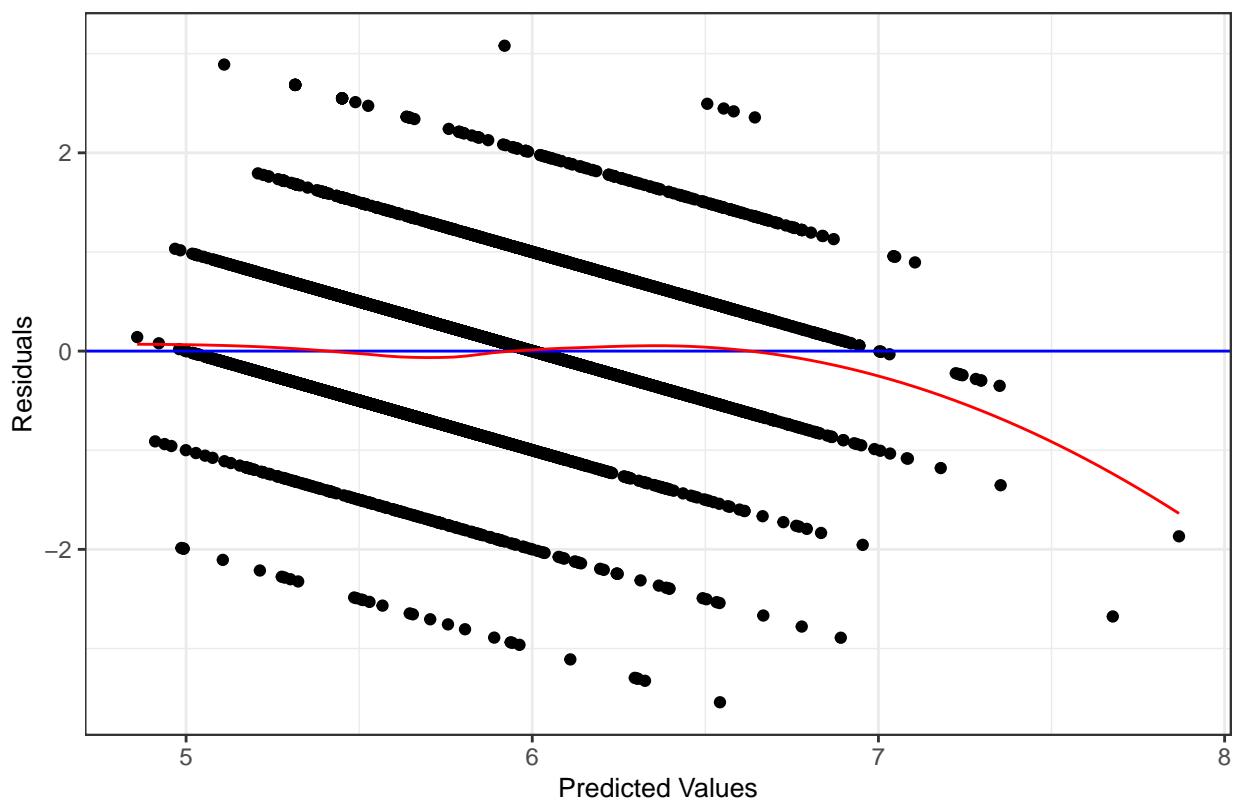
```

## Residual Plots with ggResidPanel
resid_panel(wine_lm_interaction, plots = c("hist", "qq", "resid"), smoother = T)

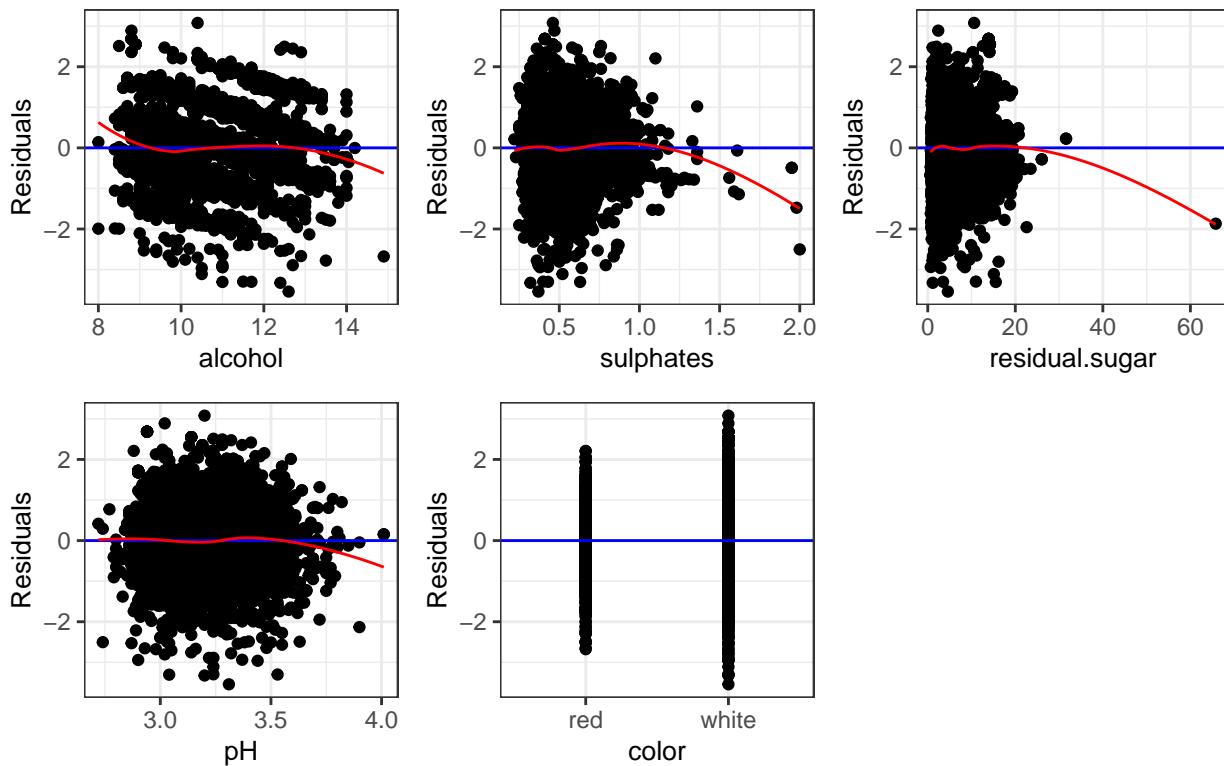
```



## Residual Plot



## Plots of Residuals vs Predictor Variables



```

## Function to create residual plots
create_res_plot <- function(data) {
  # augment data for plotting
  wine_lm_aug <- augment(data, newdata = wine_dat)

  #determine if it's transformed model
  if (identical(data, wine_lm_interaction)) {
    wine_lm_aug$var_sul <- wine_lm_aug$sulphates
    wine_lm_aug$var_sug <- wine_lm_aug$residual.sugar
    sul_name <- "Sulphates"
    sug_name <- "Residual Sugar"
  } else {
    wine_lm_aug$var_sul <- log(wine_lm_aug$sulphates)
    wine_lm_aug$var_sug <- log(wine_lm_aug$residual.sugar)
    sul_name <- "Log(Sulphates)"
    sug_name <- "Log(Residual Sugar)"
  }
  # residual plot
  wine_lm_res1 <- ggplot(wine_lm_aug, aes(x = alcohol, y = .resid)) +
    geom_point(alpha = 0.3) +
    geom_hline(yintercept = 0, linetype = "dashed", color = "blue") +
    geom_smooth(method = "loess", color = "red") +
    labs(x = "Alcohol Content", y = "residuals")

  wine_lm_res2 <- ggplot(wine_lm_aug, aes(x = var_sul, y = .resid)) +
    geom_point(alpha = 0.3) +
    geom_hline(yintercept = 0, linetype = "dashed", color = "blue") +

```

```

geom_smooth(method = "loess", color = "red") +
  labs(x = sul_name, y = "residuals")

wine_lm_res3 <- ggplot(wine_lm_aug, aes(x = var_sug, y = .resid)) +
  geom_point(alpha = 0.3) +
  geom_hline(yintercept = 0, linetype = "dashed", color = "blue") +
  geom_smooth(method = "loess", color = "red") +
  labs(x = sug_name, y = "residuals")

wine_lm_res4 <- ggplot(wine_lm_aug, aes(x = pH, y = .resid)) +
  geom_point(alpha = 0.3) +
  geom_hline(yintercept = 0, linetype = "dashed", color = "blue") +
  geom_smooth(method = "loess", color = "red") +
  labs(x = "pH Levels", y = "residuals")

wine_lm_res5 <- ggplot(wine_lm_aug, aes(x = color, y = .resid)) +
  geom_boxplot() +
  geom_hline(yintercept = 0, linetype = "dashed", color = "blue") +
  labs(x = "Wine Color", y = "residuals")

wine_lm_res6 <- ggplot(wine_lm_aug, aes(x = .fitted, y = .resid)) +
  geom_point(alpha = 0.3) +
  geom_hline(yintercept = 0, linetype = "dashed", color = "blue") +
  geom_smooth(method = "loess", color = "red") +
  labs(x = "Fitted Values", y = "residuals")

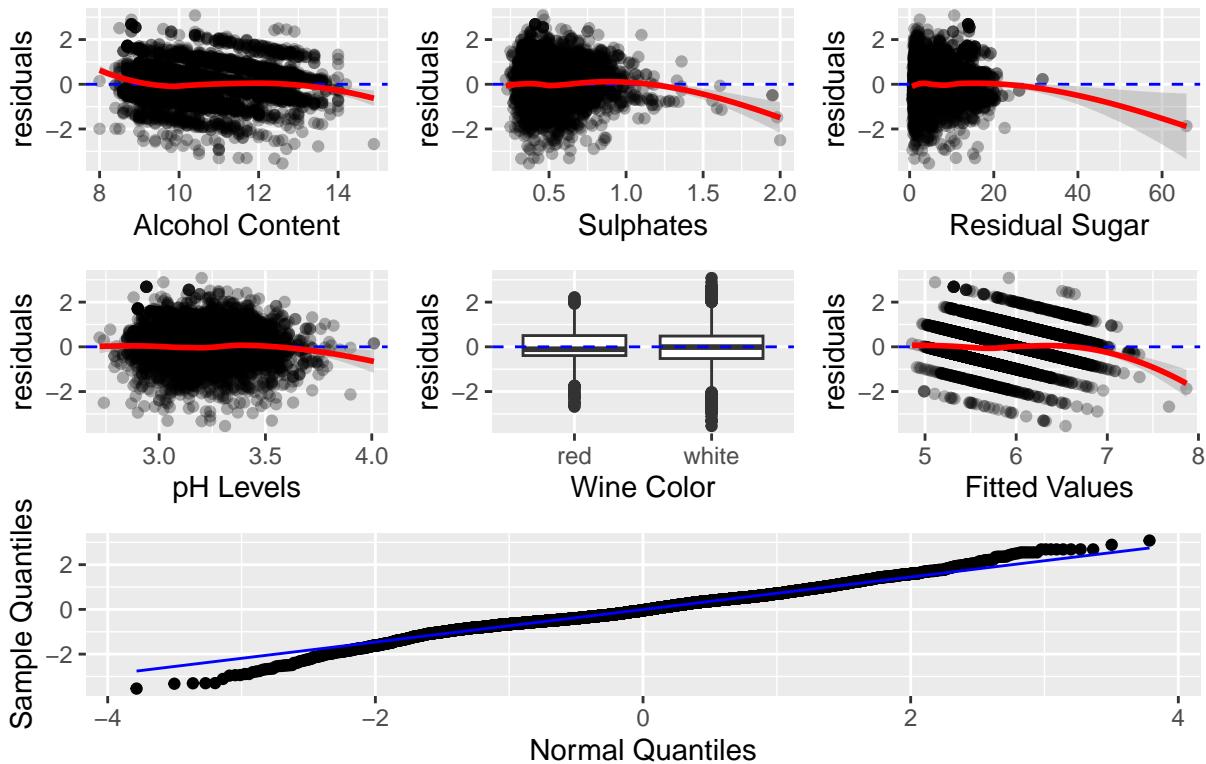
# normal qq plot
wine_lm_qq <- ggplot(wine_lm_aug, aes(sample = .resid)) +
  geom_qq() +
  geom_qq_line(color = "blue") +
  labs(y = "Sample Quantiles", x = "Normal Quantiles")

combined_plot <- (wine_lm_res1 | wine_lm_res2 | wine_lm_res3) /
  (wine_lm_res4 | wine_lm_res5 | wine_lm_res6) / wine_lm_qq
combined_plot +
  plot_layout(guides = 'collect') +
  plot_annotation(title = "Residual Plot and Normal Q-Q Plot of Wine Quality MLR")
}

# Residual Plot for non-transformed model
create_res_plot(wine_lm_interaction)

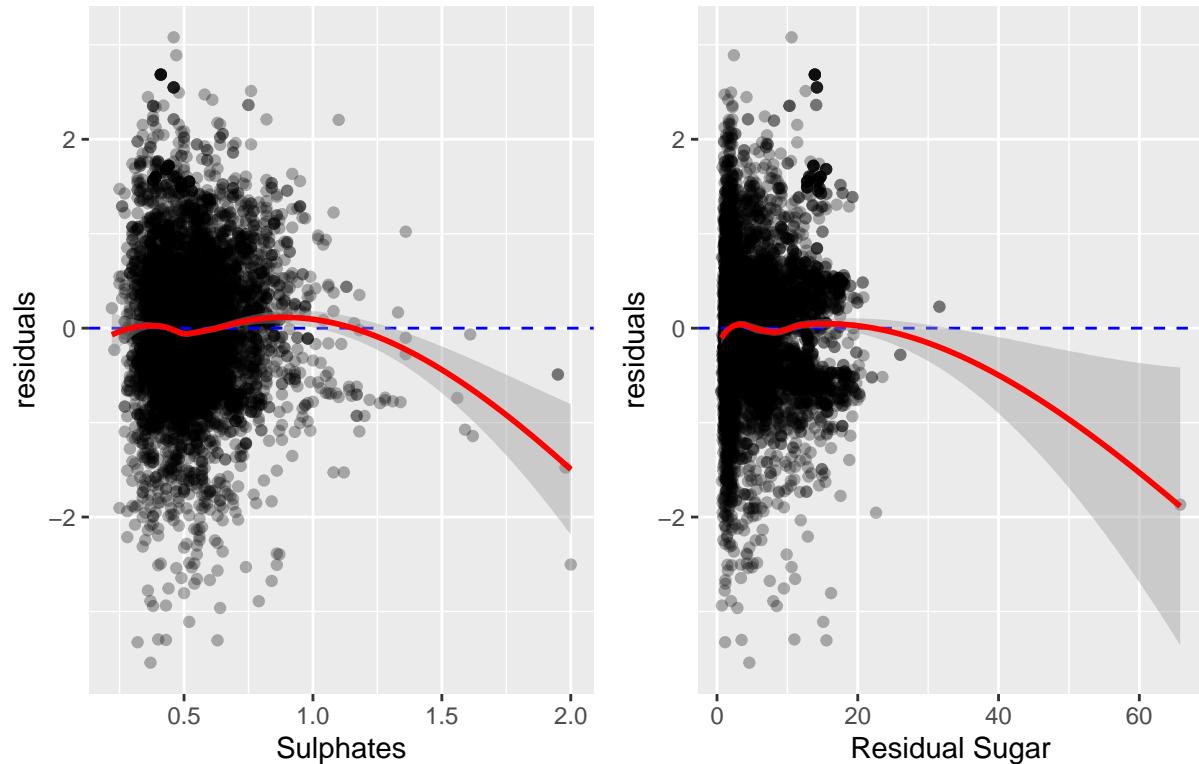
```

## Residual Plot and Normal Q–Q Plot of Wine Quality MLR

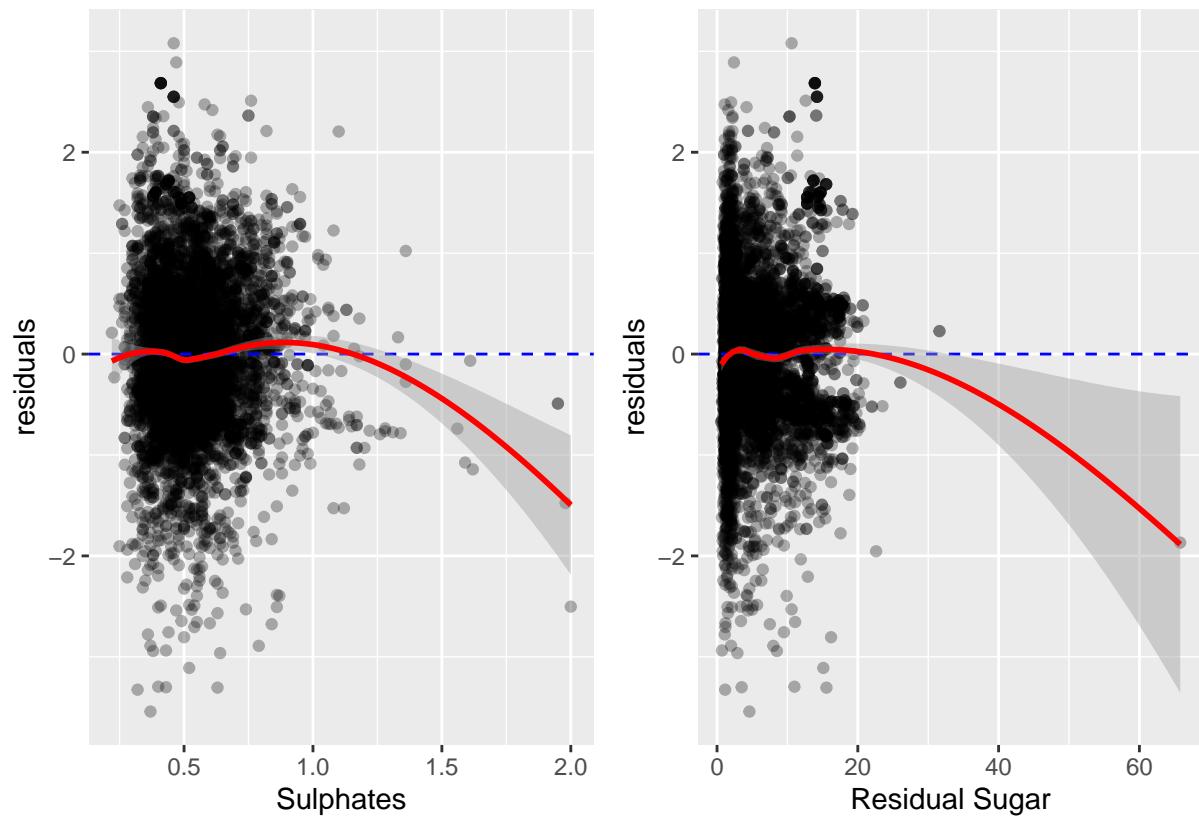


```
# Selected Residual Plots for report
wine_lm_aug <- augment(wine_lm_interaction, newdata = wine_dat)
wine_lm_res2 <- ggplot(wine_lm_aug, aes(x = sulphates, y = .resid)) +
  geom_point(alpha = 0.3) +
  geom_hline(yintercept = 0, linetype = "dashed", color = "blue") +
  geom_smooth(method = "loess", color = "red") +
  labs(x = "Sulphates", y = "residuals")
wine_lm_res3 <- ggplot(wine_lm_aug, aes(x = residual.sugar, y = .resid)) +
  geom_point(alpha = 0.3) +
  geom_hline(yintercept = 0, linetype = "dashed", color = "blue") +
  geom_smooth(method = "loess", color = "red") +
  labs(x = "Residual Sugar", y = "residuals")
combined_plot <- (wine_lm_res2 | wine_lm_res3)
combined_plot +
  plot_layout(guides = 'collect') +
  plot_annotation(title = "Selected Residual Plot of Wine Quality MLR")
```

## Selected Residual Plot of Wine Quality MLR



combined\_plot



```

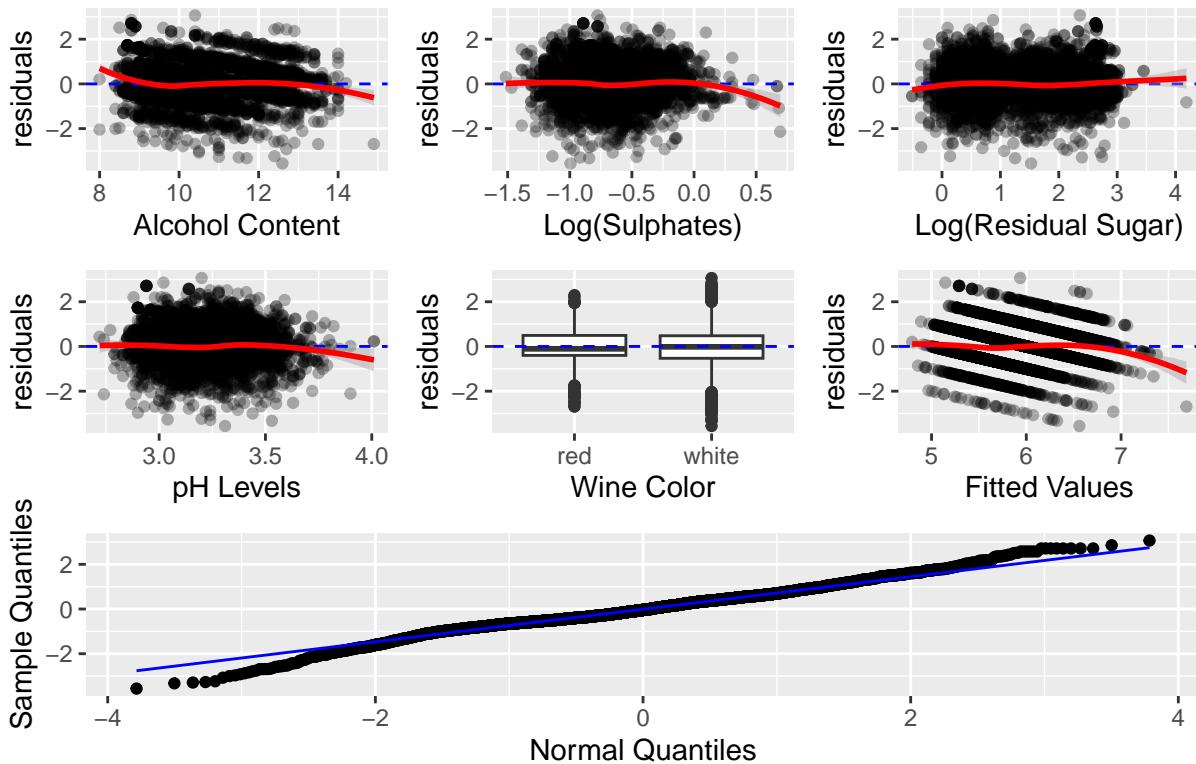
## transformed model
wine_lm_interaction_tran <- lm(quality ~ alcohol + log(sulphates) + log(residual.sugar) + pH*color, data = wine_dat)
summary(wine_lm_interaction_tran)

##
## Call:
## lm(formula = quality ~ alcohol + log(sulphates) + log(residual.sugar) +
##     pH * color, data = wine_dat)
##
## Residuals:
##       Min     1Q     Median      3Q     Max 
## -3.5592 -0.4992 -0.0395  0.4820  3.0638 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 4.315962  0.414703 10.407 < 2e-16 ***
## alcohol      0.352826  0.008495 41.533 < 2e-16 ***
## log(sulphates) 0.369156  0.042944  8.596 < 2e-16 ***
## log(residual.sugar) 0.124058  0.012416  9.992 < 2e-16 ***
## pH          -0.694190  0.124708 -5.567 2.70e-08 ***
## colorwhite   -2.947484  0.479598 -6.146 8.43e-10 ***
## pH:colorwhite 0.972984  0.145300  6.696 2.32e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7642 on 6490 degrees of freedom
## Multiple R-squared:  0.2349, Adjusted R-squared:  0.2342 
## F-statistic: 332.1 on 6 and 6490 DF,  p-value: < 2.2e-16

## residual plots
create_res_plot(wine_lm_interaction_tran)

```

## Residual Plot and Normal Q–Q Plot of Wine Quality MLR



```
## confidence interval for coefficients
confint(wine_lm_interaction_tran)
```

```
##                                     2.5 %    97.5 %
## (Intercept)            3.5030078  5.1289159
## alcohol                 0.3361723  0.3694787
## log(sulphates)          0.2849707  0.4533413
## log(residual.sugar)    0.0997192  0.1483972
## pH                     -0.9386585 -0.4497216
## colorwhite              -3.8876554 -2.0073132
## pH:colorwhite           0.6881475  1.2578207
```

```
confint(wine_lm_interaction_tran)*log(2) # un-transforming logged
```

```
##                                     2.5 %    97.5 %
## (Intercept)            2.42809997  3.5550936
## alcohol                 0.23301691  0.2561032
## log(sulphates)          0.19752662  0.3142323
## log(residual.sugar)    0.06912008  0.1028611
## pH                     -0.65062853 -0.3117233
## colorwhite              -2.69471735 -1.3913635
## pH:colorwhite           0.47698750  0.8718549
```

```
# predictors to the original scale
```

## Model Comparison

```
# nested transformation model
wine_lm_base_tran <- lm(quality ~ alcohol + log(sulphates) +
```

```

            log(residual.sugar) + pH, data = wine_dat)

## interaction vs base, untransformed
anova(wine_lm_base, wine_lm_interaction)

## Analysis of Variance Table
##
## Model 1: quality ~ alcohol + sulphates + residual.sugar + pH
## Model 2: quality ~ alcohol + sulphates + residual.sugar + pH * color
##   Res.Df   RSS Df Sum of Sq      F    Pr(>F)
## 1     6492 3866.6
## 2     6490 3792.2  2     74.358 63.628 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## interaction vs base, transformed
anova(wine_lm_base, wine_lm_interaction_tran)

## Analysis of Variance Table
##
## Model 1: quality ~ alcohol + sulphates + residual.sugar + pH
## Model 2: quality ~ alcohol + log(sulphates) + log(residual.sugar) + pH *
##   color
##   Res.Df   RSS Df Sum of Sq      F    Pr(>F)
## 1     6492 3866.6
## 2     6490 3790.0  2     76.52 65.516 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#model comparison with transformed model
anova(wine_lm_base_tran, wine_lm_interaction_tran)

## Analysis of Variance Table
##
## Model 1: quality ~ alcohol + log(sulphates) + log(residual.sugar) + pH
## Model 2: quality ~ alcohol + log(sulphates) + log(residual.sugar) + pH *
##   color
##   Res.Df   RSS Df Sum of Sq      F    Pr(>F)
## 1     6492 3869.5
## 2     6490 3790.0  2     79.44 68.016 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## AIC's
AIC(wine_lm_base)

## [1] 15077.92
AIC(wine_lm_interaction)

## [1] 14955.76
AIC(wine_lm_interaction_tran)

## [1] 14952.05

```

## Confidence Intervals

```
# linear comb for white wine ph
wine_lm_interaction_tran$coefficients[5] -> redPH
wine_lm_interaction_tran$coefficients[7] -> whtPH_int

whtPH <- (redPH + whtPH_int)[[1]]

vcov(wine_lm_interaction_tran)[c(5, 7), c(5, 7)] -> ph_cov

# point estimate
ph_se <- sqrt(ph_cov[[1, 1]] + ph_cov[[2, 2]] + 2 * ph_cov[[1, 2]])

test_stat <- whtPH/ph_se # t-stat
2*pt(test_stat, df = 6497 - 7, lower.tail = F) # p-val

## [1] 0.0001759616

# confidence interval
wht_ci <- whtPH + c(-1, 1)*qt(0.975, df = 6497 - 7)*ph_se

# untransformed predictor
wine_lm_interaction_tran$coefficients[3] * log(2)

## log(sulphates)
## 0.2558794

wine_lm_interaction_tran$coefficients[4] * log(2)

## log(residual.sugar)
## 0.08599059
```

## Multicollinearity

```
#checking for VIF - must use base model, not interaction model
vif(wine_lm_base)

##          alcohol      sulphates residual.sugar          pH
## 1.156899     1.066847     1.252074    1.103660

vif(lm(quality ~ alcohol + sulphates + residual.sugar + pH + color, data = wine_dat)) # Might be this one

##          alcohol      sulphates residual.sugar          pH          color
## 1.194803     1.313478     1.373106    1.164569    1.563968

vif(lm(quality ~ alcohol + log(sulphates) + log(residual.sugar) + pH + color, data = wine_dat)) # or this one

##          alcohol      log(sulphates) log(residual.sugar)          pH
## 1.139456     1.330182     1.270040    1.168728

##          color
## 1.517815
```

## Influential Statistics

```
#figuring out outliers based on scatterplot matrix
mean_values <- wine_dat %>%
```

```

  summarize(across(c(alcohol, sulphates, pH, residual.sugar, citric.acid, fixed.acidity), mean, na.rm = TRUE)
mean_values

##   alcohol sulphates      pH residual.sugar citric.acid fixed.acidity
## 1 10.4918 0.5312683 3.218501      5.443235  0.3186332    7.215307
row_num <- 4381
case_values <- wine_dat[row_num, c("alcohol", "sulphates", "pH", "residual.sugar", "citric.acid", "fixed.acidity")]
case_values

##   alcohol sulphates      pH residual.sugar citric.acid fixed.acidity
## 4381 11.7      0.69 3.39       65.8        0.6       7.8
#This case has a very large residual sugar

# checking for influential observations
wine_dat$row <- wine_dat %>% mutate(case = row_number())
AUGwine_lm_interaction_tran <- augment(wine_lm_interaction_tran,
                                         data = wine_dat$row)

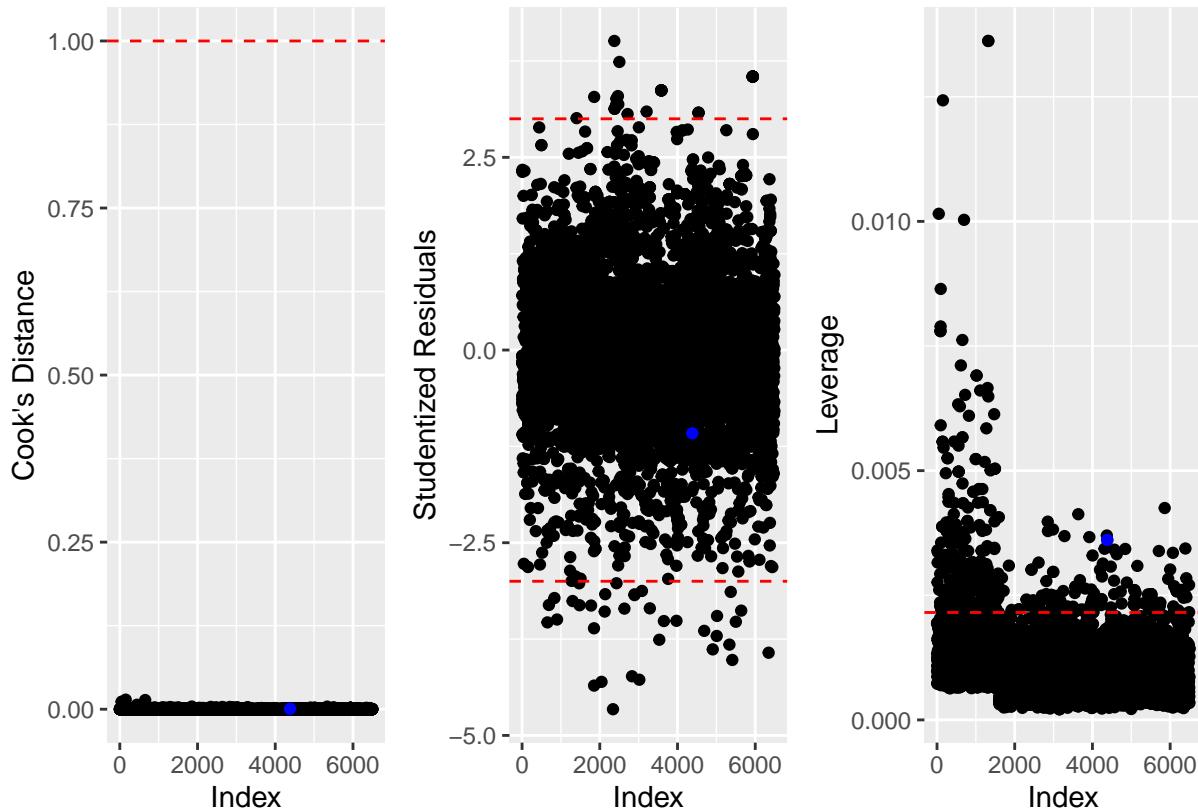
# Cook's Distance
ggplot(data = AUGwine_lm_interaction_tran, aes(x = case, y = .cooksdf)) +
  geom_point() +
  geom_point(data = AUGwine_lm_interaction_tran %>%
              filter(case == 4381), color = "blue") +
  geom_hline(yintercept=1, linetype="dashed", color = "red") +
  labs(y = "Cook's Distance", x = "Index") -> cookDistancePlot

# Studentized Residuals
ggplot(AUGwine_lm_interaction_tran, aes(x = case, y = .std.resid)) + geom_point() +
  geom_point(data = AUGwine_lm_interaction_tran %>%
              filter(case == 4381), color = "blue") +
  geom_hline(yintercept=3, linetype="dashed", color = "red") +
  geom_hline(yintercept=-3, linetype="dashed", color = "red") +
  labs(y = "Studentized Residuals", x = "Index") -> studResiPlot

# Leverages
ggplot(AUGwine_lm_interaction_tran, aes(x = case, y = .hat)) +
  geom_point() +
  geom_point(data = AUGwine_lm_interaction_tran %>%
              filter(case == 4381), color = "blue") +
  geom_hline(yintercept=2*7/6497, linetype="dashed", color = "red") +
  labs(y = "Leverage", x = "Index") -> leveragePlot

cookDistancePlot|studResiPlot|leveragePlot # for report

```



```
# Selection of influential stats
high_L <- AUGwine_lm_interaction_tran %>% dplyr::select(case, .hat) %>%
  arrange(desc(.hat)) %>%
  filter(.hat > 2*7/6497) # greater than twice the average
high_SR <- AUGwine_lm_interaction_tran %>% dplyr::select(case, .std.resid) %>%
  arrange(desc(.std.resid)) %>%
  filter(.std.resid > 3) # greater than 3 se's
high_CD <- AUGwine_lm_interaction_tran %>% dplyr::select(case, .cooksdi) %>%
  arrange(desc(.cooksdi)) %>%
  filter(.cooksdi > 1) # greater than 1

# List of influential stats
high_L
```

```
## # A tibble: 380 x 2
##       case     .hat
##   <int>    <dbl>
## 1 1317 0.0136
## 2 1322 0.0136
## 3 152  0.0124
## 4 46   0.0102
## 5 696  0.0100
## 6 96   0.00865
## 7 93   0.00789
## 8 87   0.00780
## 9 92   0.00780
## 10 653  0.00762
## # i 370 more rows
```

```
high_SR
```

```
## # A tibble: 29 x 2
##   case .std.resid
##   <int>     <dbl>
## 1 2374      4.01
## 2 2504      3.74
## 3 5932      3.55
## 4 5933      3.55
## 5 5934      3.55
## 6 5935      3.55
## 7 5936      3.55
## 8 5937      3.55
## 9 5938      3.55
## 10 5940     3.55
## # i 19 more rows
```

```
high_CD
```

```
## # A tibble: 0 x 2
## # i 2 variables: case <int>, .cooksdi <dbl>
```

```
## Reg on no outlier
```

```
wine_dat_no_outliers <- wine_dat %>%
  filter(residual.sugar != 65.8)
```

```
winenooutlierslm <- lm(quality ~ alcohol + sulphates + residual.sugar + pH * color, data = wine_dat_no_outliers)
summary(winenooutlierslm) #doesn't change conclusion
```

```
##
```

```
## Call:
```

```
## lm(formula = quality ~ alcohol + sulphates + residual.sugar +
##     pH * color, data = wine_dat_no_outliers)
##
```

```
## Residuals:
```

```
##    Min     1Q Median     3Q    Max
## -3.5451 -0.4979 -0.0397  0.4817  3.0750
##
```

```
##
```

```
## Coefficients:
```

```
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.600042  0.426319  8.444 < 2e-16 ***
## alcohol      0.358163  0.008737 40.994 < 2e-16 ***
## sulphates    0.627085  0.074105  8.462 < 2e-16 ***
## residual.sugar 0.024378  0.002391 10.194 < 2e-16 ***
## pH          -0.655899  0.125416 -5.230 1.75e-07 ***
## colorwhite   -2.962047  0.483900 -6.121 9.83e-10 ***
## pH:colorwhite 0.973157  0.146380  6.648 3.21e-11 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Residual standard error: 0.7641 on 6489 degrees of freedom
```

```
## Multiple R-squared:  0.2352, Adjusted R-squared:  0.2345
```

```
## F-statistic: 332.6 on 6 and 6489 DF, p-value: < 2.2e-16
```

```
# visuals of (not) removing the outlier
```

```
create_inf_plot <- function(var_name) {
```

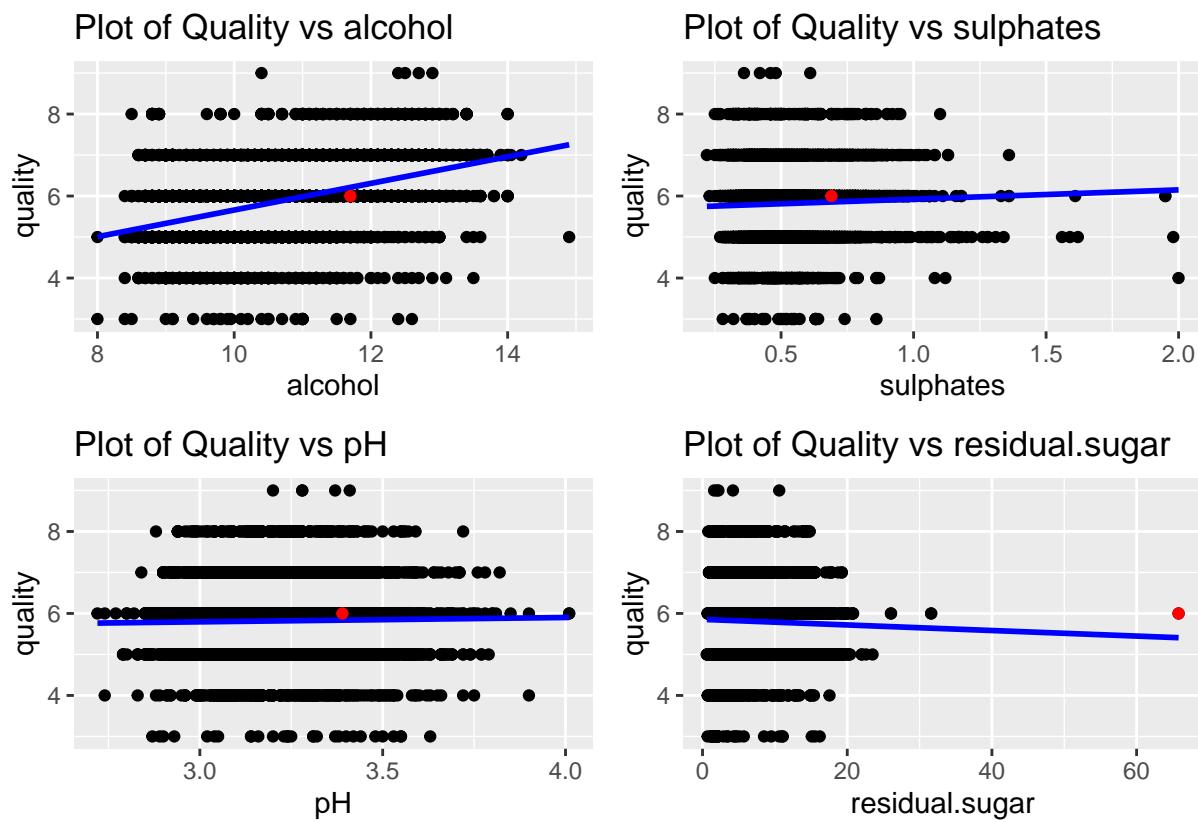
```
  ggplot(data = wine_dat,
```

```

    aes_string(x = var_name, y = "quality")) +
geom_point() +
geom_smooth(method = "lm", se = FALSE, color = "blue") +
geom_point(data = wine_dat %>% filter(residual.sugar == 65.8),
           color = "red") +
geom_smooth(data = wine_dat %>% filter(residual.sugar == 65.8),
            method = "lm", se = FALSE, color = "red") +
labs(title = paste("Plot of Quality vs", var_name))
}

plot_list2 <- map(variable_names, create_inf_plot)
plot_grid2 <- wrap_plots(plot_list2, ncol = 2)
plot_grid2

```



## Sequential Selection

```

set.seed(67393937)

upper_model <- lm(quality ~ (pH + alcohol + log(residual.sugar) + color + log(sulphates) + fixed.acidity,
                             data = wine_dat)
lower_model <- lm(quality ~ 1, data = wine_dat)

#backward selection
backwardSelectModel <- stepAIC(upper_model, scope = list(lower = lower_model,
                                                          upper = upper_model),
                                 direction = "backward")
summary(backwardSelectModel)

```

```
#forward selection
forwardSelectModel <- stepAIC(lower_model, scope = list(lower = lower_model,
                                                       upper = upper_model),
                               direction = "forward")
summary(forwardSelectModel)

anova(wine_lm_interaction_tran, backwardSelectModel)
anova(wine_lm_interaction_tran, forwardSelectModel)
```