

# Prediction of Wine Quality

1.

For task 4, we try to predict of red wine qualities. The [data set](#) that we used.

2.

For that step, we'll describe the data set in our task in terms of the dimension, variable type and etc. Firstly;

```
winequality.red <- read.csv("winequality-red.csv")
```

After that;

```
str(winequality.red)
```

```
'data.frame':  1599 obs. of  12 variables:
 $ fixed.acidity      : num  7.4 7.8 7.8 11.2 7.4 7.4 7.9 7.3 7.8 7.5 ...
 $ volatile.acidity   : num  0.7 0.88 0.76 0.28 0.7 0.66 0.6 0.65 0.58 0.5 ...
 $ citric.acid        : num  0 0 0.04 0.56 0 0 0.06 0 0.02 0.36 ...
 $ residual.sugar     : num  1.9 2.6 2.3 1.9 1.9 1.8 1.6 1.2 2 6.1 ...
 $ chlorides          : num  0.076 0.098 0.092 0.075 0.076 0.075 0.069 0.065 0.073 0.071 ..
 $ free.sulfur.dioxide : num  11 25 15 17 11 13 15 15 9 17 ...
 $ total.sulfur.dioxide: num  34 67 54 60 34 40 59 21 18 102 ...
 $ density            : num  0.998 0.997 0.997 0.998 0.998 ...
 $ pH                 : num  3.51 3.2 3.26 3.16 3.51 3.51 3.3 3.39 3.36 3.35 ...
 $ sulphates          : num  0.56 0.68 0.65 0.58 0.56 0.56 0.46 0.47 0.57 0.8 ...
 $ alcohol            : num  9.4 9.8 9.8 9.8 9.4 9.4 9.4 10 9.5 10.5 ...
 $ quality            : int  5 5 5 6 5 5 5 7 7 5 ...
```

The data set has 1599 obs. and 12 variables. **quality** is our *target*. That means our data set have 11 column. In addition to this, all of our *features* seems like they are all **numeric**.

### 3.

We are going to use `sample()` function to *split the data set* as test and train set.

```
set.seed(123)
index <- sample(1 : nrow(winequality.red), round(nrow(winequality.red) * 0.80))
train <- winequality.red[index, ]
test  <- winequality.red[-index, ]
```

Then; we can use the `glm()` function to train a logistic regression model.

```
lr_model <- glm(quality ~ ., data = train)
summary(lr_model)
```

Call:

```
glm(formula = quality ~ ., data = train)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.65018	-0.38387	-0.04515	0.45703	2.01377

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	1.492e+01	2.405e+01	0.620	0.5351
fixed.acidity	1.245e-02	2.998e-02	0.415	0.6780
volatile.acidity	-1.022e+00	1.398e-01	-7.306	4.87e-13 ***
citric.acid	-1.298e-01	1.687e-01	-0.769	0.4419
residual.sugar	6.223e-03	1.749e-02	0.356	0.7220
chlorides	-2.059e+00	4.711e-01	-4.370	1.34e-05 ***
free.sulfur.dioxide	4.125e-03	2.501e-03	1.649	0.0994 .
total.sulfur.dioxide	-3.556e-03	8.348e-04	-4.260	2.20e-05 ***
density	-1.026e+01	2.455e+01	-0.418	0.6760
pH	-5.780e-01	2.193e-01	-2.636	0.0085 **
sulphates	8.652e-01	1.329e-01	6.509	1.09e-10 ***
alcohol	2.907e-01	3.040e-02	9.564	< 2e-16 ***

---

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

(Dispersion parameter for gaussian family taken to be 0.4401224)

Null deviance: 864.63 on 1278 degrees of freedom  
Residual deviance: 557.64 on 1267 degrees of freedom  
AIC: 2593.9

Number of Fisher Scoring iterations: 2

After all of this, the last part of this step is prediction.

```
predicted_quality <- predict(lr_model, test)
head(predicted_quality)
```

```
      3      7     15     22     23     27
5.226765 5.116426 5.096636 5.368662 5.743560 5.542505
```

#### 4.

In that part, We will use the *Root Mean Square Error (RMSE)* metric to measure the performance of the regression model.

```
error <- test$quality - predicted_quality
rmse.model <- sqrt(mean(error^2))
rmse.model
```

```
[1] 0.5859451
```

The performance of the model seems really acceptable because that value is low.

#### 5.

Last but not least, we'll check if there is an *overfitting problem*.

```
rmse.test <- sqrt(mean((lr_model$residuals)^2))
rmse.model - rmse.test
```

```
[1] -0.07435255
```

Because of the difference which is negative, it can be means that we have the overfitting problem of the model.

## 6.

We will create *new observations* for last step of task 4.

```
fixed.acidity <- as.numeric(c(7.1, 8.1, 7.5))
volatile.acidity <- as.numeric(c(0.5, 0.67, 0.89))
citric.acid <- as.numeric(c(0.4, 0.6, 0.58))
residual.sugar <- as.numeric(c(2.1, 2.9, 1.99))
chlorides <- as.numeric(c(0.01, 0.03, 0.055))
free.sulfur.dioxide <- as.numeric(c(18, 17, 26))
total.sulfur.dioxide <- as.numeric(c(37, 41, 51))
density <- as.numeric(c(0.950, 0.917, 0.940))
pH <- as.numeric(c(3.72, 3.81, 3.1))
sulphates <- as.numeric(c(0.91, 0.89, 0.85))
alcohol <- as.numeric(c(9.91, 9.87, 9.83))
```

```
new.observations <- data.frame(fixed.acidity, volatile.acidity, citric.acid , residual.sug
```

```
new.observations
```

	fixed.acidity	volatile.acidity	citric.acid	residual.sugar	chlorides
1	7.1	0.50	0.40	2.10	0.010
2	8.1	0.67	0.60	2.90	0.030
3	7.5	0.89	0.58	1.99	0.055

  

	free.sulfur.dioxide	total.sulfur.dioxide	density	pH	sulphates	alcohol
1	18	37	0.950	3.72	0.91	9.91
2	17	41	0.917	3.81	0.89	9.87
3	26	51	0.940	3.10	0.85	9.83

Now, we can prediction with new ones.

```
predicted_quality_new <- predict(lr_model, new.observations)
predicted_quality_new
```

```
      1      2      3
6.150804 6.166856 6.009734
```