

This is an R Markdown (<http://rmarkdown.rstudio.com>) Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Cmd+Shift+Enter*.

— Correlations Between Variables —

To see why we get very low accuracies accross the board for this Wines dataset, let's look at the correlation relationships between the predictors. Let's also take a look at the class label distributions of the dataset (how balanced is it?).

Red Wines Dataset:

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```
red <- read.csv('winequality-red.csv', header = TRUE, sep=";")
red <- na.omit(red)
red.quality <- red$quality
red[, -12] <- scale(red[, -12])

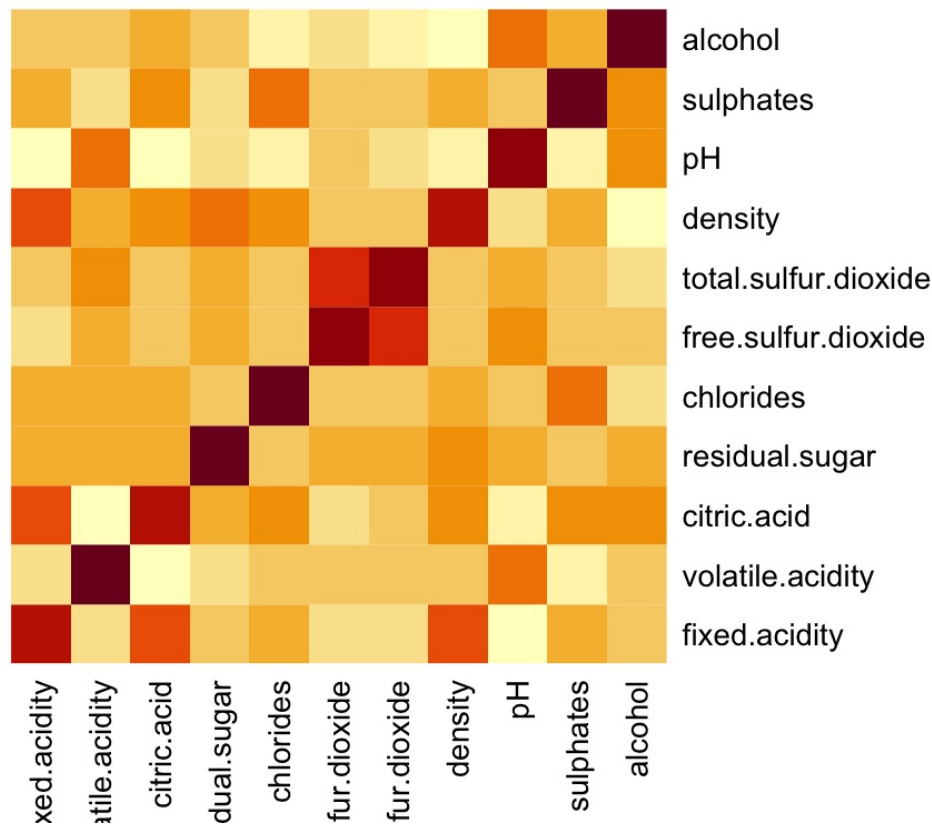
# Correlation matrix between variables
corr <- cor(red[, -12])
corr
```

	fixed.acidity	volatile.acidity	citric.acid	residual.sugar	chlorides	free.sulfur.dioxide	t
otal.sulfur.dioxide	density	pH					
fixed.acidity	1.00000000	-0.256130895	0.67170343	0.114776724	0.093705186	-0.153794193	
-0.11318144	0.66804729	-0.68297819					
volatile.acidity	-0.25613089	1.000000000	-0.55249568	0.001917882	0.061297772	-0.010503827	
0.07647000	0.02202623	0.23493729					
citric.acid	0.67170343	-0.552495685	1.00000000	0.143577162	0.203822914	-0.060978129	
0.03553302	0.36494718	-0.54190414					
residual.sugar	0.11477672	0.001917882	0.14357716	1.000000000	0.055609535	0.187048995	
0.20302788	0.35528337	-0.08565242					
chlorides	0.09370519	0.061297772	0.20382291	0.055609535	1.000000000	0.005562147	
0.04740047	0.20063233	-0.26502613					
free.sulfur.dioxide	-0.15379419	-0.010503827	-0.06097813	0.187048995	0.005562147	1.000000000	
0.66766645	-0.02194583	0.07037750					
total.sulfur.dioxide	-0.11318144	0.076470005	0.03553302	0.203027882	0.047400468	0.667666450	
1.00000000	0.07126948	-0.06649456					
density	0.66804729	0.022026232	0.36494718	0.355283371	0.200632327	-0.021945831	
0.07126948	1.00000000	-0.34169933					
pH	-0.68297819	0.234937294	-0.54190414	-0.085652422	-0.265026131	0.070377499	
-0.06649456	-0.34169933	1.00000000					
sulphates	0.18300566	-0.260986685	0.31277004	0.005527121	0.371260481	0.051657572	
0.04294684	0.14850641	-0.19664760					
alcohol	-0.06166827	-0.202288027	0.10990325	0.042075437	-0.221140545	-0.069408354	
-0.20565394	-0.49617977	0.20563251					
	sulphates	alcohol					
fixed.acidity	0.183005664	-0.06166827					
volatile.acidity	-0.260986685	-0.20228803					
citric.acid	0.312770044	0.10990325					
residual.sugar	0.005527121	0.04207544					
chlorides	0.371260481	-0.22114054					
free.sulfur.dioxide	0.051657572	-0.06940835					
total.sulfur.dioxide	0.042946836	-0.20565394					
density	0.148506412	-0.49617977					
pH	-0.196647602	0.20563251					
sulphates	1.000000000	0.09359475					
alcohol	0.093594750	1.00000000					

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```
# Plot Heatmap
heatmap(corr, main="Correlations Between Predictors for Red Wines", Colv = NA, Rowv = NA, scale="column")
```

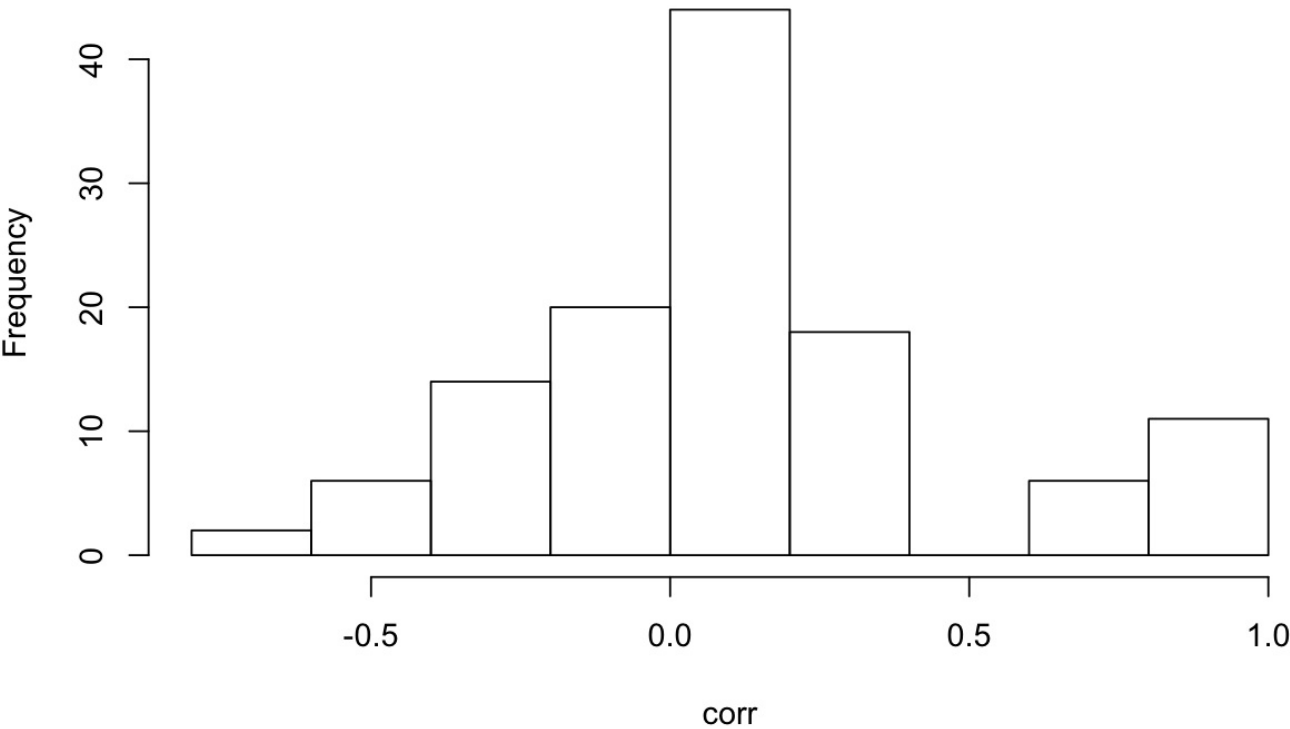
Correlations Between Predictors for Red Wines



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```
# Plot histogram
hist(corr, main='Histogram of Predictor Pair Correlation Distribution for Red Wines')
```

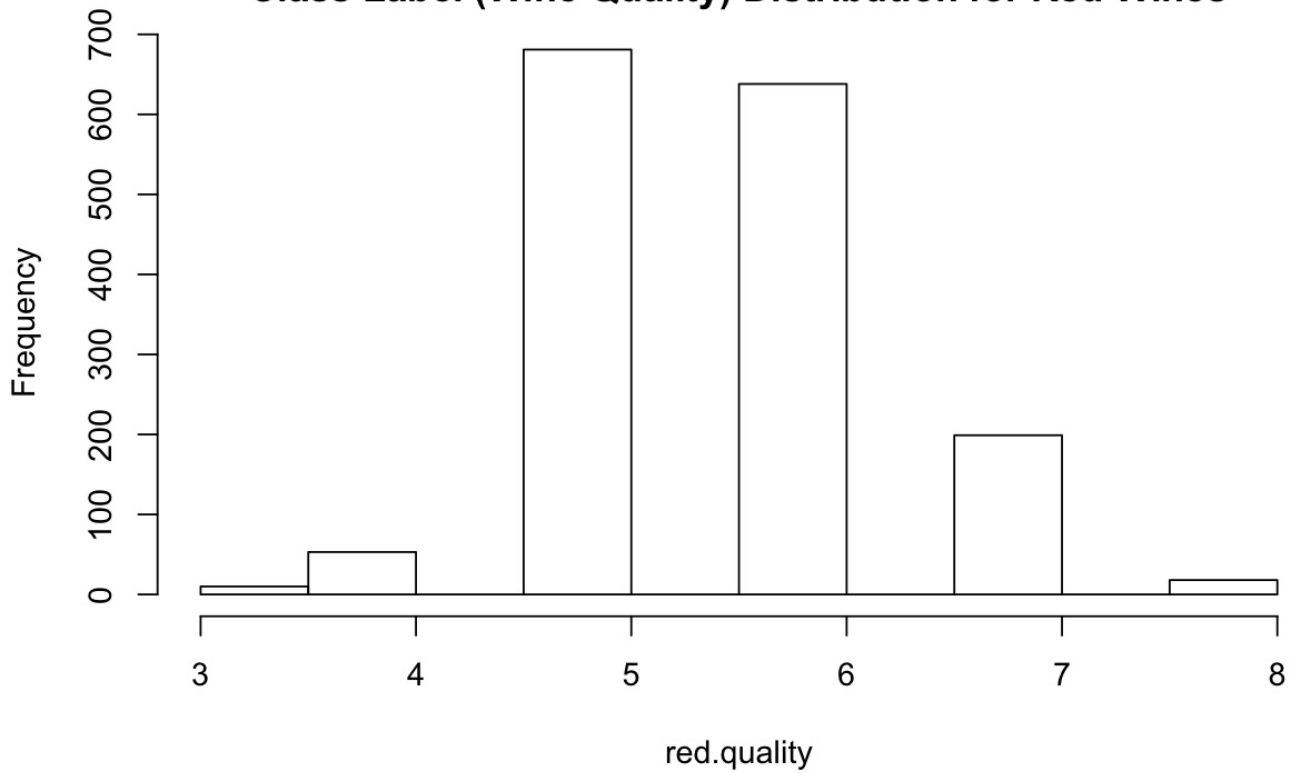
Histogram of Predictor Pair Correlation Distribution for Red Wines



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```
# Plot histogram between class labels
class_dist <- hist(red.quality, main='Class Label (Wine Quality) Distribution for Red Wines')
```

Class Label (Wine Quality) Distribution for Red Wines



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```
class_dist$counts
```

```
[1] 10 53 0 681 0 638 0 199 0 18
```

White Wines Dataset:

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```
white <- read.csv('winequality-white.csv', header = TRUE, sep=";")
white <- na.omit(white)
white.quality <- white$quality
white[,-12] <- scale(white[,-12])

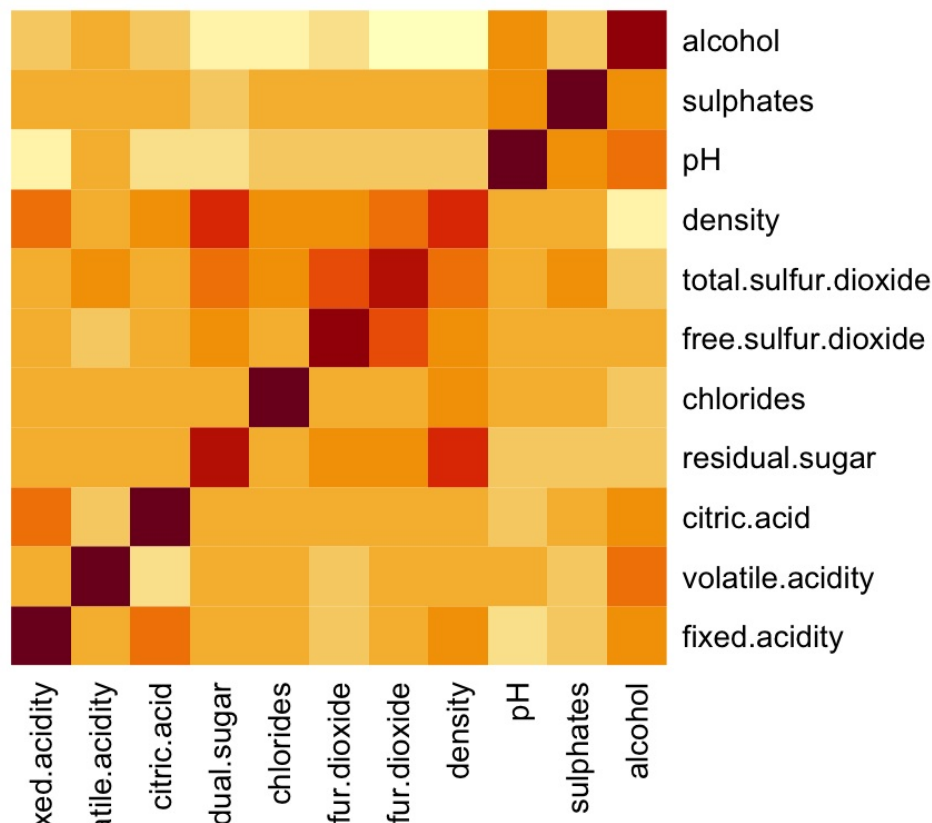
# Correlation matrix between variables
corr <- cor(white[,-12])
corr
```

	fixed.acidity	volatile.acidity	citric.acid	residual.sugar	chlorides	free.sulfur.dioxide	total.sulfur.dioxide
fixed.acidity	1.00000000	-0.02269729	0.28918070	0.08902070	0.02308564	-0.0493958591	0.091069756
volatile.acidity	-0.02269729	1.00000000	-0.14947181	0.06428606	0.07051157	-0.0970119393	0.089260504
citric.acid	0.28918070	-0.14947181	1.00000000	0.09421162	0.11436445	0.0940772210	0.121130798
residual.sugar	0.08902070	0.06428606	0.09421162	1.00000000	0.08868454	0.2990983537	0.401439311
chlorides	0.02308564	0.07051157	0.11436445	0.08868454	1.00000000	0.1013923521	0.198910300
free.sulfur.dioxide	-0.04939586	-0.09701194	0.09407722	0.29909835	0.10139235	1.0000000000	0.615500965
total.sulfur.dioxide	0.09106976	0.08926050	0.12113080	0.40143931	0.19891030	0.6155009650	1.0000000000
density	0.26533101	0.02711385	0.14950257	0.83896645	0.25721132	0.2942104109	0.529881324
pH	-0.42585829	-0.03191537	-0.16374821	-0.19413345	-0.09043946	-0.0006177961	0.002320972
sulphates	-0.01714299	-0.03572815	0.06233094	-0.02666437	0.01676288	0.0592172458	0.134562367
alcohol	-0.12088112	0.06771794	-0.07572873	-0.45063122	-0.36018871	-0.2501039415	-0.448892102
	pH	sulphates	alcohol				
fixed.acidity	-0.4258582910	-0.01714299	-0.12088112				
volatile.acidity	-0.0319153683	-0.03572815	0.06771794				
citric.acid	-0.1637482114	0.06233094	-0.07572873				
residual.sugar	-0.1941334540	-0.02666437	-0.45063122				
chlorides	-0.0904394560	0.01676288	-0.36018871				
free.sulfur.dioxide	-0.0006177961	0.05921725	-0.25010394				
total.sulfur.dioxide	0.0023209718	0.13456237	-0.44889210				
density	-0.0935914935	0.07449315	-0.78013762				
pH	1.0000000000	0.15595150	0.12143210				
sulphates	0.1559514973	1.00000000	-0.01743277				
alcohol	0.1214320987	-0.01743277	1.00000000				

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```
# Plot Heatmap
heatmap(corr, main="Correlations Between Predictors for White Wines", Colv = NA, Rowv = NA, scale="column")
```

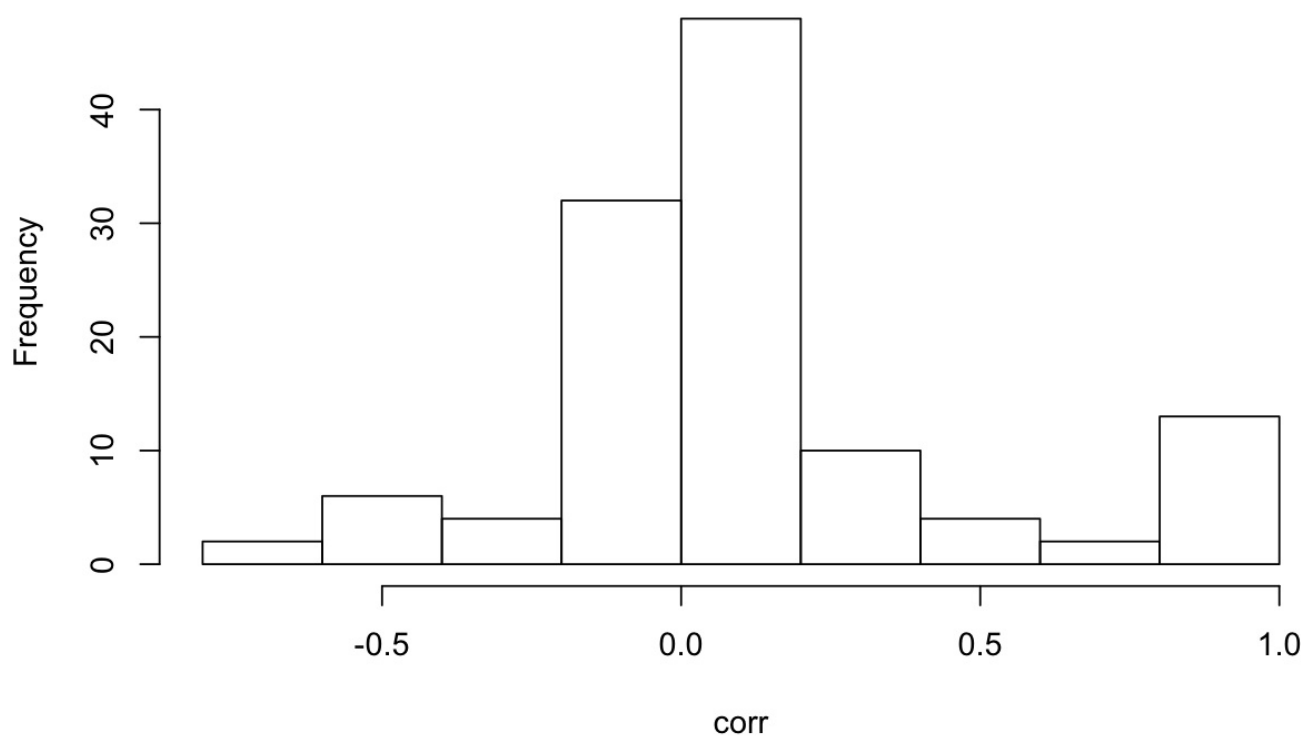
Correlations Between Predictors for White Wines



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```
# Plot histogram
hist(corr, main='Histogram of Predictor Pair Correlation Distribution for White Wines')
```

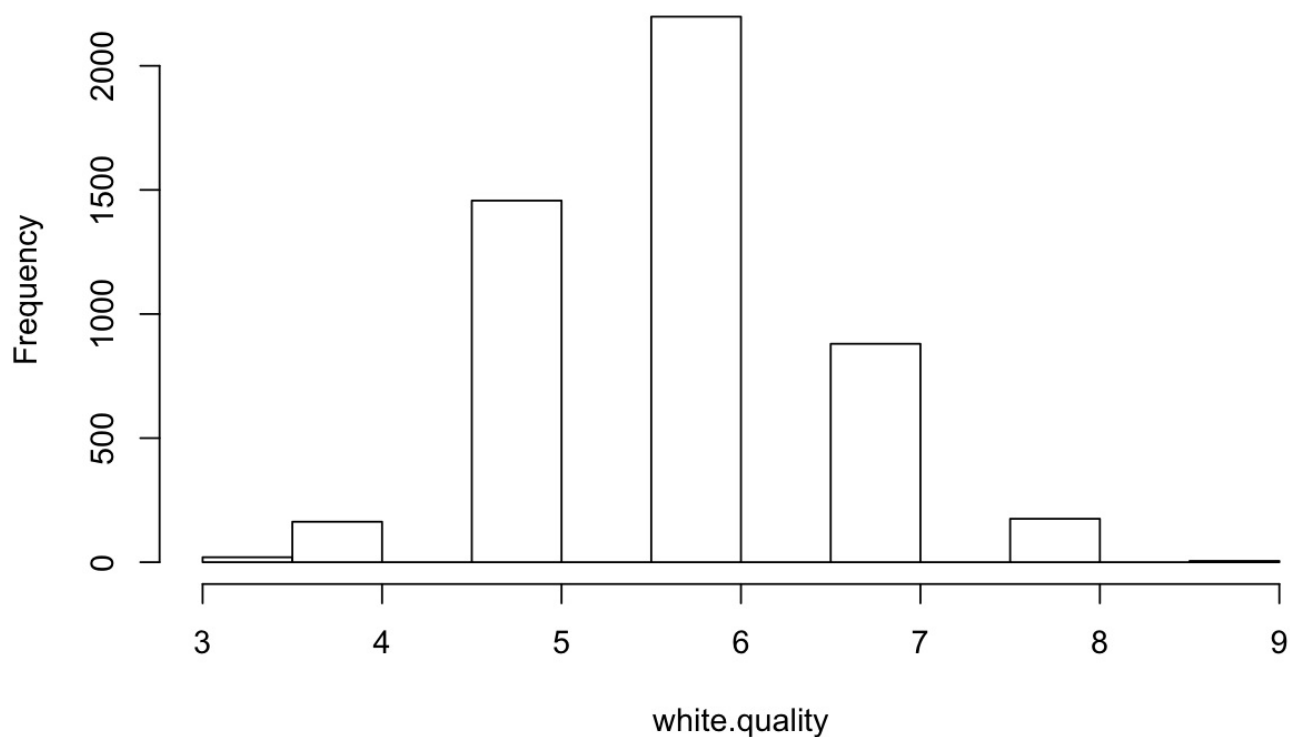
Histogram of Predictor Pair Correlation Distribution for White Wines



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```
# Plot histogram between class labels
class_dist <- hist(white.quality, main='Class Label (Wine Quality) Distribution for White Wines')
```

Class Label (Wine Quality) Distribution for White Wines



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```
class_dist$counts
```

[1]	20	163	0	1457	0	2198	0	880	0	175	0	5
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We can see that in the Wines dataset, there is very little correlation between the different predictors, so it is very difficult to find patterns among the variables, because there is not that many predictors (only 12 of them) and they are not very strong indicators. From the heat maps, we can see that most of the non-diagonal entries have a lighter color, which shows a weak relationship between the variables. Looking at the histograms, most of these predictor pairs have a correlation closer to zero, and very few of them greater than 0.3. This contributes to low accuracies accross different models, since we can't utilize any inter-predictor patterns to better learn about the data.

Moreover, we can also see that the class labels (wine qualities) are extremely unbalanced, as the bulk of the labels are 5, 6, or 7, yet there are very few examples that are 4 or lower or 8 or above. The models, in turn, will also spit out class labels that are equally unbalanced, as the predictors will also predict mostly 5s, 6s, or 7s, while very rarely predicting any other quality value.

Reference: <https://ai.plainenglish.io/estimating-wine-quality-with-machine-learning-ai-72-accuracy-8a5ff0bab3b2>
(<https://ai.plainenglish.io/estimating-wine-quality-with-machine-learning-ai-72-accuracy-8a5ff0bab3b2>)