

Red Wines - upper

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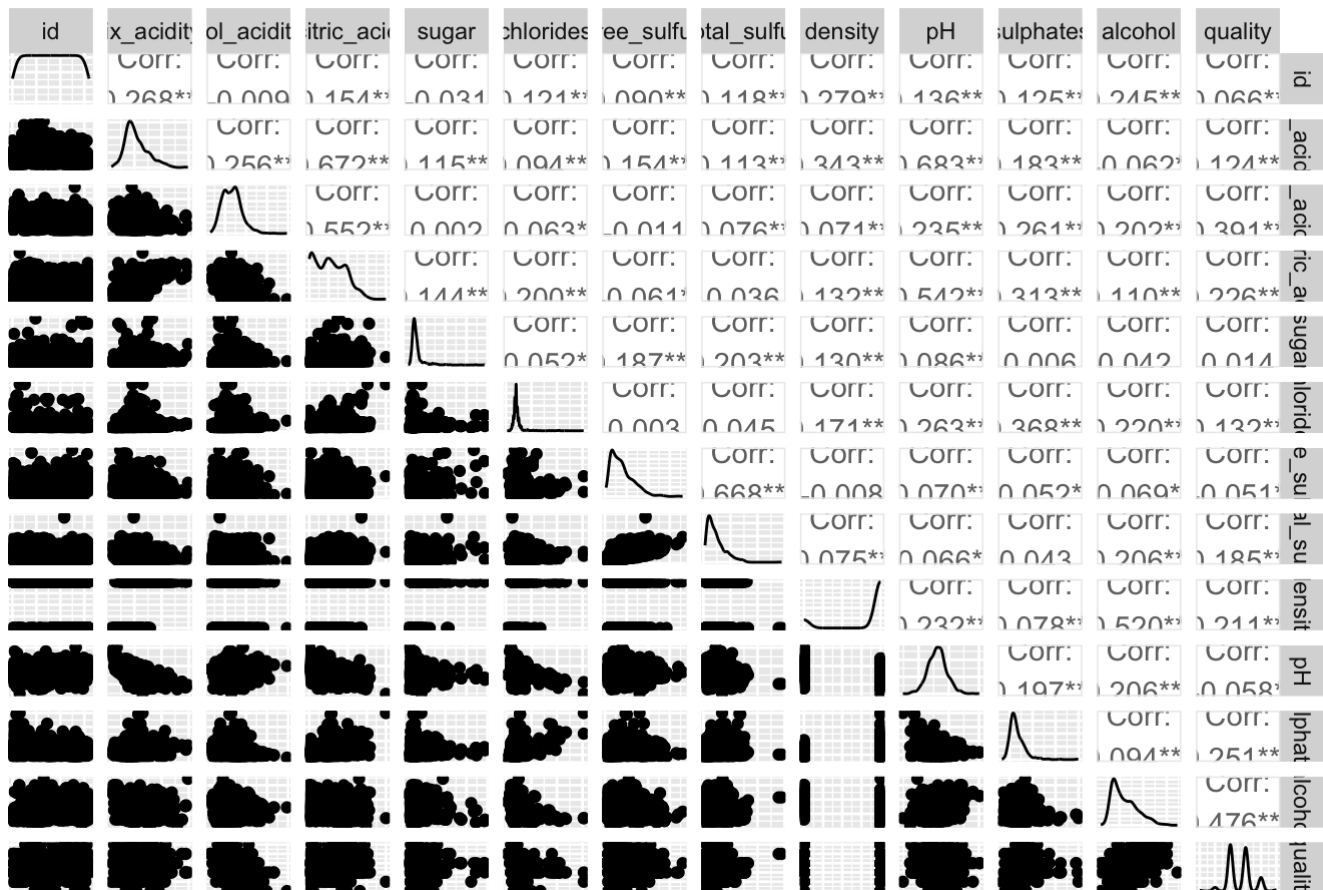
Scatterplot Matrix

```
library("GGally")
ggpairs(red, axisLabels = "none",
        title = "Scatterplot Matrix of Red Wines")
```

```
# corr codes
```

Scatterplot Matrix

Scatterplot Matrix of Red Wines



Create Binary Dependent Variable

```
red$highquality = factor((red$quality >= 6))  
red$highquality <- as.integer(as.logical(red$highquality))
```

Create Test and Training Data

```
library("caTools")  
set.seed = 100  
split = sample.split(red$highquality, SplitRatio = 0.6)  
train = subset(red, split == TRUE)  
test = subset(red, split == FALSE)  
print(dim(train)); print(dim(test))
```

```
## [1] 959 14
```

```
## [1] 640 14
```

Descriptive Statistics

```
library("Rmisc")
```

```
## Loading required package: lattice
```

```
## Loading required package: plyr
```

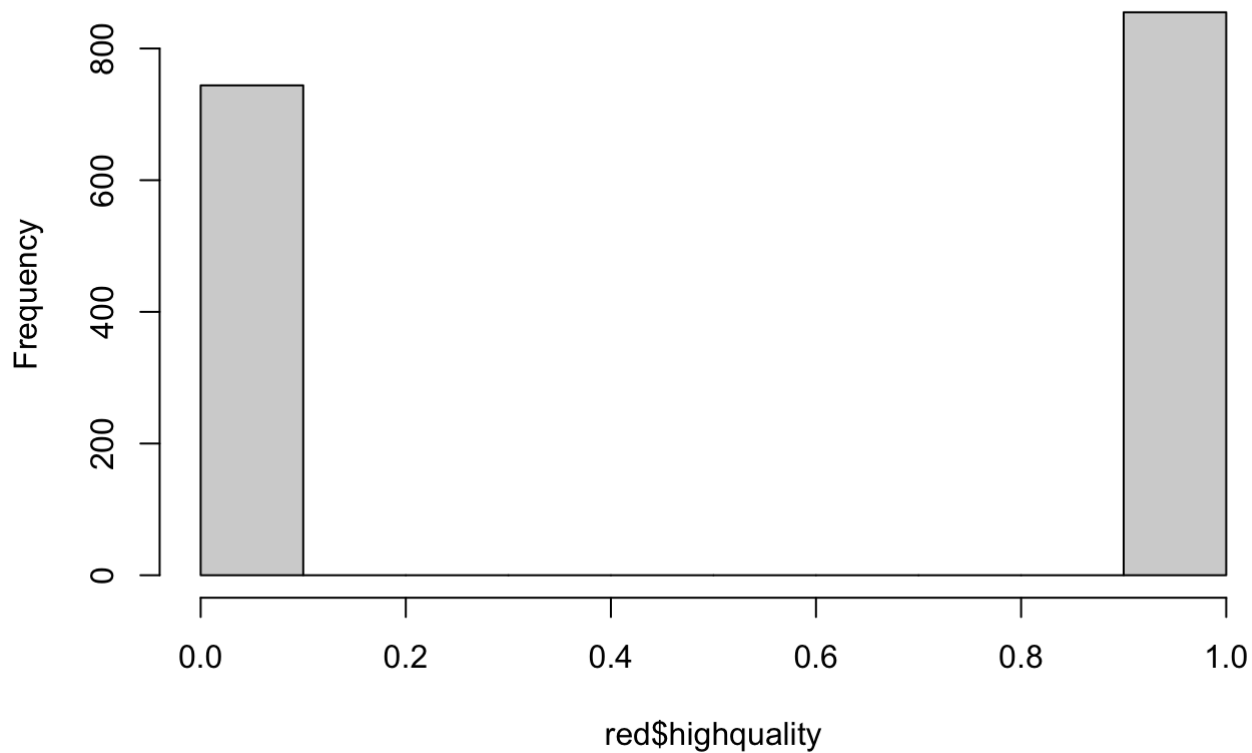
```
sum = summary(red)  
sum
```

```
##          id          fix_acidity    vol_acidity    citric_acid
## Min.      : 1.0    Min.      : 4.60    Min.      :0.1200    Min.      :0.000
## 1st Qu.: 400.5    1st Qu.: 7.10    1st Qu.:0.3900    1st Qu.:0.090
## Median : 800.0    Median : 7.90    Median :0.5200    Median :0.260
## Mean      : 800.0    Mean      : 8.32    Mean      :0.5284    Mean      :0.271
## 3rd Qu.:1199.5    3rd Qu.: 9.20    3rd Qu.:0.6400    3rd Qu.:0.420
## Max.      :1599.0    Max.      :15.90    Max.      :1.5800    Max.      :1.000
##          sugar          chlorides          free_sulfur          total_sulfur
## Min.      : 0.900    Min.      :0.01000    Min.      : 1.00    Min.      : 6.00
## 1st Qu.: 1.900    1st Qu.:0.07000    1st Qu.: 7.00    1st Qu.: 22.00
## Median : 2.200    Median :0.08000    Median :14.00    Median : 38.00
## Mean      : 2.539    Mean      :0.08787    Mean      :15.87    Mean      : 46.47
## 3rd Qu.: 2.600    3rd Qu.:0.09000    3rd Qu.:21.00    3rd Qu.: 62.00
## Max.      :15.500    Max.      :0.61000    Max.      :72.00    Max.      :289.00
##          density          pH          sulphates          alcohol
## Min.      :0.9900    Min.      :2.740    Min.      :0.3300    Min.      : 8.40
## 1st Qu.:1.0000    1st Qu.:3.210    1st Qu.:0.5500    1st Qu.: 9.50
## Median :1.0000    Median :3.310    Median :0.6200    Median :10.20
## Mean      :0.9985    Mean      :3.311    Mean      :0.6581    Mean      :10.42
## 3rd Qu.:1.0000    3rd Qu.:3.400    3rd Qu.:0.7300    3rd Qu.:11.10
## Max.      :1.0000    Max.      :4.010    Max.      :2.0000    Max.      :14.90
##          quality    highquality
## Min.      :3.000    Min.      :0.0000
## 1st Qu.:5.000    1st Qu.:0.0000
## Median :6.000    Median :1.0000
## Mean      :5.636    Mean      :0.5347
## 3rd Qu.:6.000    3rd Qu.:1.0000
## Max.      :8.000    Max.      :1.0000
```

Plot high quality vs low quality distribution

```
hist (red$highquality)
```

Histogram of red\$highquality



Random Forest

```
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:ggplot2':  
##  
## margin
```

```
library("caret")  
library("e1071")  
library("rpart")
```

```
rf <- randomForest(highquality ~ . - quality, data = train, mtry = 4, importance = TRUE,  
ntree = 50, na.action = na.omit)
```

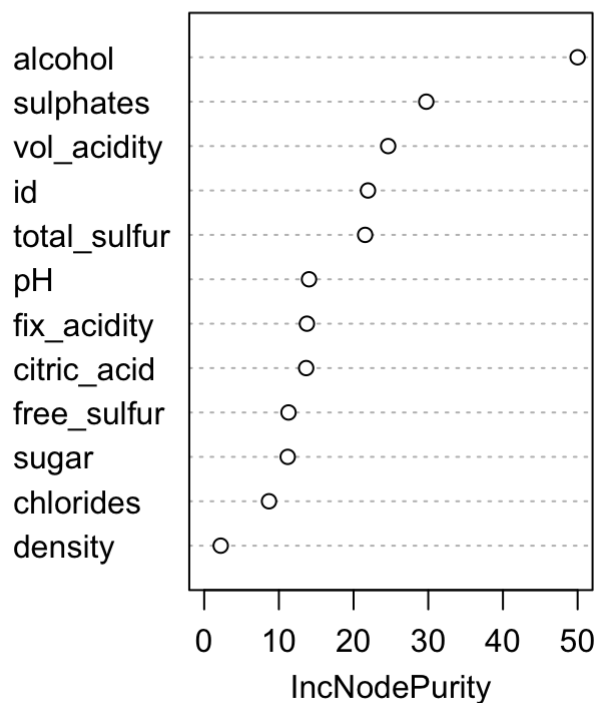
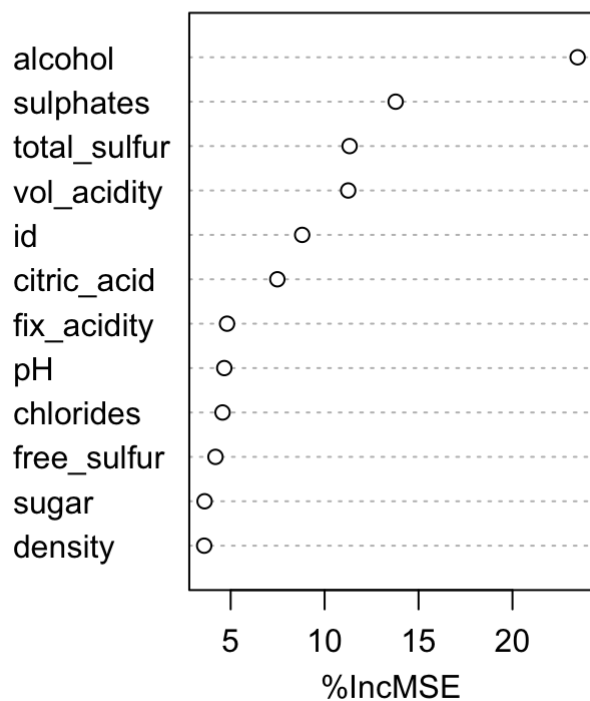
```
## Warning in randomForest.default(m, y, ...): The response has five or fewer  
## unique values. Are you sure you want to do regression?
```

```
print(rf)
```

```
##  
## Call:  
## randomForest(formula = highquality ~ . - quality, data = train,      mtry = 4, impor  
tance = TRUE, ntree = 50, na.action = na.omit)  
##              Type of random forest: regression  
##              Number of trees: 50  
## No. of variables tried at each split: 4  
##  
##              Mean of squared residuals: 0.1566168  
##              % Var explained: 37.05
```

```
varImpPlot(rf)
```

rf



```
# predictions on test set
set.seed(100)
predictTest = predict(rf, newdata = test, type = "response")

# confusion matrix on test set
table(test$highquality, predictTest >= 0.5)
```

```
##
##      FALSE TRUE
##    0    231   67
##    1     65  277
```

```
520/nrow(test)
```

```
## [1] 0.8125
```

```
# the model is accurate 81.3 percent of the time
```

Random Forest Model

```
# Logit
randomforestmodlogit <- glm(highquality ~ alcohol + sulphates + total_sulfur + vol_acidity, data = red, family = "binomial"(link = "logit"))
summary(randomforestmodlogit)
```

```
##
## Call:
## glm(formula = highquality ~ alcohol + sulphates + total_sulfur +
##      vol_acidity, family = binomial(link = "logit"), data = red)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.1638  -0.8675   0.3076   0.8629   2.3262
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -8.588813   0.795118 -10.802  < 2e-16 ***
## alcohol       0.927362   0.069268  13.388  < 2e-16 ***
## sulphates     2.059047   0.365976   5.626 1.84e-08 ***
## total_sulfur -0.011976   0.001924  -6.225 4.83e-10 ***
## vol_acidity  -3.083277   0.364832  -8.451  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 2209.0  on 1598  degrees of freedom
## Residual deviance: 1684.2  on 1594  degrees of freedom
## AIC: 1694.2
##
## Number of Fisher Scoring iterations: 4
```

```
# Cloglog
randomforestmodcloglog <- glm(highquality ~ alcohol + sulphates + total_sulfur + vol_acidity, data = red, family = "binomial"(link = "cloglog"))
summary(randomforestmodcloglog)
```

```
##
## Call:
## glm(formula = highquality ~ alcohol + sulphates + total_sulfur +
##       vol_acidity, family = binomial(link = "cloglog"), data = red)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -4.5006  -0.9020   0.2185   0.9295   2.0506
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -4.958517   0.478252 -10.368 < 2e-16 ***
## alcohol       0.505807   0.038543  13.123 < 2e-16 ***
## sulphates     1.324184   0.221318   5.983 2.19e-09 ***
## total_sulfur -0.009109   0.001364  -6.679 2.41e-11 ***
## vol_acidity  -2.022997   0.238813  -8.471 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 2209  on 1598  degrees of freedom
## Residual deviance: 1701  on 1594  degrees of freedom
## AIC: 1711
##
## Number of Fisher Scoring iterations: 7
```

```
# The logit model performed better with a lower AIC value
```

Cart

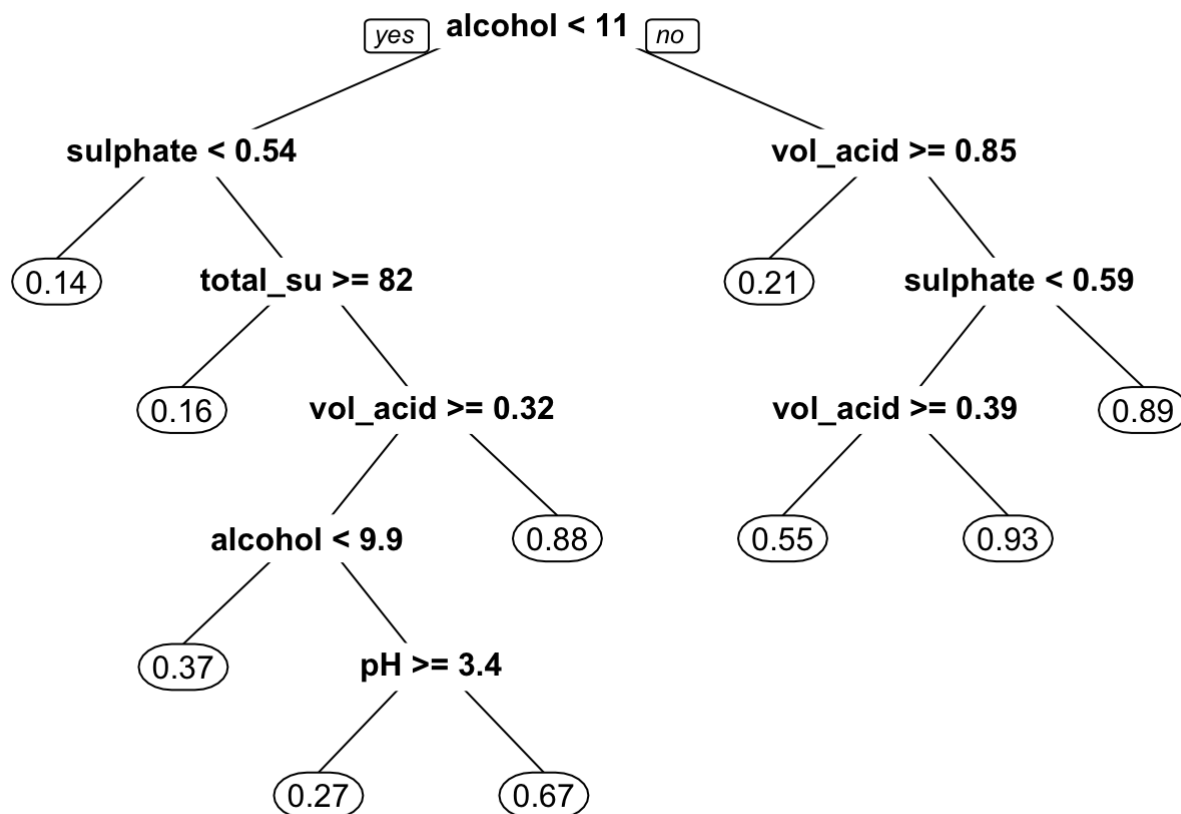
```
library("caret")
library("e1071")
library("rpart")
library("rpart.plot")

cartmodel = rpart(highquality ~ . - quality, data = train)
print(cartmodel)
```



```
## n= 959
##
## node), split, n, deviance, yval
##      * denotes terminal node
##
## 1) root 959 238.579800 0.5349322
##    2) alcohol< 10.525 593 138.381100 0.3709949
##      4) sulphates< 0.535 145 17.958620 0.1448276 *
##      5) sulphates>=0.535 448 110.604900 0.4441964
##        10) total_sulfur>=82 75 10.080000 0.1600000 *
##        11) total_sulfur< 82 373 93.249330 0.5013405
##          22) vol_acidity>=0.315 339 84.289090 0.4631268
##            44) alcohol< 9.85 193 45.139900 0.3730570 *
##            45) alcohol>=9.85 146 35.513700 0.5821918
##              90) pH>=3.425 33 6.545455 0.2727273 *
##              91) pH< 3.425 113 24.884960 0.6725664 *
##                23) vol_acidity< 0.315 34 3.529412 0.8823529 *
##                3) alcohol>=10.525 366 58.439890 0.8005464
##                  6) vol_acidity>=0.845 19 3.157895 0.2105263 *
##                  7) vol_acidity< 0.845 347 48.305480 0.8328530
##                    14) sulphates< 0.585 87 19.333330 0.6666667
##                      28) vol_acidity>=0.385 60 14.850000 0.5500000 *
##                      29) vol_acidity< 0.385 27 1.851852 0.9259259 *
##                        15) sulphates>=0.585 260 25.765380 0.8884615 *
```

```
prp(cartmodel)
```



```

# predictions on test set
set.seed(100)
predictTest = predict(cartmodel, newdata = test, type = "matrix")

# confusion matrix on test set
table(test$highquality, predictTest >= 0.5)

```

```

##
##      FALSE TRUE
##    0     223   75
##    1      93  249

```

Cart Model

```

# Logit
cartmodlogit <- glm(highquality ~ alcohol + sulphates + total_sulfur + fix_acidity, data
= red, family = "binomial"(link = "logit"))
summary(cartmodlogit)

```

```
##
## Call:
## glm(formula = highquality ~ alcohol + sulphates + total_sulfur +
##       fix_acidity, family = binomial(link = "logit"), data = red)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3737  -0.9154   0.3562   0.8762   2.0206
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -12.172146    0.828396  -14.694 < 2e-16 ***
## alcohol        0.989178    0.068276   14.488 < 2e-16 ***
## sulphates     2.587844    0.370028    6.994 2.68e-12 ***
## total_sulfur  -0.011171    0.001895   -5.895 3.75e-09 ***
## fix_acidity   0.109461    0.035511    3.082 0.00205 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 2209.0  on 1598  degrees of freedom
## Residual deviance: 1752.5  on 1594  degrees of freedom
## AIC: 1762.5
##
## Number of Fisher Scoring iterations: 4
```

```
# Cloglog
cartmodcloglog <- glm(highquality ~ alcohol + sulphates + total_sulfur + fix_acidity, data = red, family = "binomial"(link = "cloglog"))
summary(cartmodcloglog)
```

```
##
## Call:
## glm(formula = highquality ~ alcohol + sulphates + total_sulfur +
##       fix_acidity, family = binomial(link = "cloglog"), data = red)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -4.7058  -0.9408   0.3075   0.9490   1.9387
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -6.835907   0.481268 -14.204 < 2e-16 ***
## alcohol       0.542953   0.037720  14.394 < 2e-16 ***
## sulphates     1.639060   0.217233   7.545 4.52e-14 ***
## total_sulfur -0.009315   0.001384  -6.732 1.67e-11 ***
## fix_acidity   0.027351   0.021284   1.285  0.199
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 2209.0  on 1598  degrees of freedom
## Residual deviance: 1777.5  on 1594  degrees of freedom
## AIC: 1787.5
##
## Number of Fisher Scoring iterations: 18
```

```
# The logit model performed better with the lower AIC value
```

Compare best logit model with AIC

```
library("AICcmodavg")
```

```
##
## Attaching package: 'AICcmodavg'
```

```
## The following object is masked from 'package:randomForest':
##
##      importance
```

```
models <- list(randomforestmodlogit, cartmodlogit)
mod.names <- c('RandomForest', 'Cart')
aictab(cand.set = models, modnames = mod.names)
```

```
##
## Model selection based on AICc:
##
##           K      AICc Delta_AICc AICcWt Cum.Wt      LL
## RandomForest 5 1694.21      0.00      1      1 -842.09
## Cart         5 1762.56     68.35      0      1 -876.26
```

```
# The random forest logit model performed the best
```

Compare best model with BIC

```
library("flexmix")
BIC(randomforestmodlogit)
```

```
## [1] 1721.058
```

```
BIC(randomforestmodcloglog)
```

```
## [1] 1737.845
```

```
BIC(cartmodlogit)
```

```
## [1] 1789.404
```

```
BIC(cartmodcloglog)
```

```
## [1] 1814.418
```

```
# The random forest logit model performed the best
```

Confusion matrix for random forest logit model

```
confusionred = predict(randomforestmodlogit, newdata = red, type = "response")

# confusion matrix on test set
table(red$highquality, confusionred >= 0.5)
```

```
##  
##      FALSE TRUE  
##    0    548  196  
##    1    216  639
```

Predictions for random forest logit model

```
pred_test <- predict(randomforestmodlogit, test, type = "response")  
  
pred_test
```

##	1	4	6	8	9	13	14
##	0.21686414	0.52789064	0.22573317	0.35364079	0.35226650	0.27778694	0.69723806
##	16	21	24	31	37	38	40
##	0.13867752	0.45581006	0.25095181	0.23338984	0.65305951	0.59357547	0.60541307
##	43	44	48	49	50	60	61
##	0.78970651	0.75462869	0.51951414	0.43019840	0.27520137	0.37446288	0.35540196
##	64	65	66	69	72	76	78
##	0.22177359	0.48498736	0.48498736	0.76772166	0.11856745	0.67706290	0.41857071
##	81	87	91	92	94	96	98
##	0.38434763	0.81269343	0.12488112	0.81269343	0.43771981	0.81609562	0.36239110
##	99	100	103	106	109	114	116
##	0.22403417	0.24182616	0.24182616	0.17168420	0.49637573	0.56940622	0.61534547
##	121	125	126	127	129	130	132
##	0.03125237	0.17454268	0.19469456	0.15237332	0.73731458	0.47573192	0.88460563
##	134	135	137	138	142	147	152
##	0.46022375	0.13831261	0.26189520	0.36049701	0.26189520	0.18741376	0.86018228
##	155	156	158	160	161	166	167
##	0.44034290	0.43822117	0.43822117	0.15834014	0.15424192	0.16875609	0.22409934
##	173	174	179	181	183	185	189
##	0.42272086	0.69738295	0.21924830	0.27931853	0.16145478	0.19399307	0.13003255
##	190	196	202	207	213	214	215
##	0.13218057	0.11752977	0.32718865	0.85218494	0.67118625	0.29462991	0.30759231
##	217	220	221	223	226	228	230
##	0.56377995	0.12986042	0.40137970	0.36725609	0.56522890	0.26752645	0.64457164
##	231	233	234	237	238	241	247
##	0.77766942	0.47994817	0.64457164	0.19063712	0.20849103	0.39273703	0.19535300
##	252	254	255	257	258	260	267
##	0.44429231	0.11931143	0.44429231	0.50388022	0.18145879	0.80917975	0.19291723
##	268	272	274	278	282	284	288
##	0.97152743	0.87483178	0.22637701	0.87483178	0.86571544	0.71864536	0.63094835
##	289	292	293	294	297	299	300
##	0.69463023	0.85547233	0.50253385	0.67070411	0.14998798	0.42029514	0.33509483
##	301	303	307	310	312	314	319
##	0.59572880	0.41165107	0.20435986	0.51474055	0.16092124	0.13631050	0.68916140
##	322	325	326	327	329	331	332
##	0.22451563	0.32170068	0.32170068	0.85787373	0.66866920	0.94054119	0.94054119
##	338	340	341	342	344	345	346
##	0.56472573	0.88983001	0.74512435	0.89763321	0.66228068	0.68982583	0.34930907
##	347	348	351	352	354	357	359
##	0.84745884	0.94069892	0.53418258	0.28077747	0.92386355	0.81776585	0.76935573
##	361	364	369	372	373	377	387
##	0.17383851	0.74339678	0.37745429	0.55754674	0.87743922	0.87515687	0.31578174
##	390	391	392	394	400	401	404
##	0.59089106	0.80025092	0.62763464	0.09608587	0.16572036	0.11072664	0.52614838
##	411	413	415	417	419	421	424
##	0.29774721	0.13582974	0.16976587	0.86998145	0.77020269	0.79052736	0.91967155
##	426	430	431	433	434	435	437
##	0.69125350	0.32784541	0.91967155	0.96051533	0.45313982	0.62568563	0.31324574
##	439	444	445	450	451	453	454
##	0.62568563	0.86779419	0.93413308	0.74289381	0.74289381	0.45914078	0.88497153
##	458	461	462	465	466	472	473
##	0.22920186	0.82420951	0.29995555	0.55427468	0.74550780	0.76084070	0.68760803

##	475	480	485	486	492	494	496
##	0.69215031	0.43048988	0.97215159	0.35050201	0.97829349	0.64444930	0.84287574
##	499	504	505	509	510	512	514
##	0.84287574	0.92902168	0.92990496	0.40270830	0.87805407	0.40270830	0.87663195
##	515	518	519	520	522	524	525
##	0.87663195	0.17161954	0.93281411	0.69166380	0.35179506	0.15801090	0.23574293
##	527	529	531	540	541	542	543
##	0.69166380	0.28289255	0.85077943	0.79067776	0.33434428	0.81658345	0.34240899
##	544	546	547	550	551	554	557
##	0.60467189	0.16061952	0.44918649	0.36606459	0.37808419	0.26817772	0.82873036
##	561	565	566	567	568	569	570
##	0.74635299	0.92935383	0.74635299	0.20667837	0.20667837	0.76484762	0.86080487
##	571	572	573	574	579	586	588
##	0.87692510	0.86080487	0.77494478	0.28595807	0.26273769	0.41223315	0.09780108
##	590	594	596	601	602	614	615
##	0.83511782	0.25462429	0.12498036	0.18854205	0.28353983	0.61614952	0.52341231
##	619	621	623	624	629	631	632
##	0.66590198	0.16493964	0.30620045	0.92396940	0.31752796	0.31752796	0.60526652
##	634	642	644	645	649	653	656
##	0.32737388	0.24690166	0.24690166	0.32321697	0.79606704	0.99329501	0.27966086
##	657	659	660	666	668	670	677
##	0.40958829	0.53465925	0.51004428	0.30272887	0.51847411	0.51847411	0.49457701
##	678	680	681	682	683	684	690
##	0.22140871	0.50931169	0.26144196	0.53604318	0.37713648	0.61274001	0.71405217
##	692	694	696	697	700	701	707
##	0.08792767	0.17710261	0.92968944	0.33118031	0.78652604	0.09555064	0.27290235
##	710	711	712	716	717	721	726
##	0.66657651	0.09703634	0.16497241	0.27155586	0.30467669	0.31642036	0.49939352
##	729	734	735	736	737	742	746
##	0.43341582	0.31147678	0.29287694	0.11882456	0.11882456	0.12964712	0.45423361
##	750	751	754	755	756	757	761
##	0.45423361	0.24423781	0.24423781	0.54228709	0.24061283	0.33804274	0.18944864
##	762	763	767	769	770	773	774
##	0.21832154	0.35211810	0.18768624	0.19045961	0.23550990	0.09786165	0.58787221
##	776	777	782	784	787	789	790
##	0.16206695	0.32070205	0.49407054	0.49407054	0.36376503	0.37973849	0.09437875
##	791	794	795	796	797	799	802
##	0.42161900	0.63971010	0.95029362	0.45940264	0.41405130	0.66715805	0.42345371
##	807	808	809	815	818	820	821
##	0.97273626	0.97678970	0.48396705	0.84554487	0.93891093	0.21151380	0.32105800
##	822	831	833	836	838	839	842
##	0.98401461	0.60268443	0.60619390	0.16263773	0.73172430	0.90163251	0.46356092
##	843	849	861	864	866	867	869
##	0.65608836	0.38077515	0.16845476	0.19469921	0.18470531	0.85828874	0.81336010
##	870	874	875	877	879	882	883
##	0.59381839	0.89396556	0.91690605	0.74967371	0.27035098	0.66426561	0.94676764
##	884	886	887	888	889	890	894
##	0.17504411	0.44881228	0.39943319	0.87920584	0.60509698	0.07413691	0.18472125
##	906	907	913	917	918	919	920
##	0.15063496	0.61655717	0.92326068	0.47643991	0.57254719	0.73857291	0.84865159
##	922	926	934	935	939	941	944
##	0.73857291	0.85851776	0.37796683	0.61571145	0.96015192	0.95924086	0.39208642

##	949	952	956	960	962	964	965
##	0.96739607	0.96007673	0.81941210	0.43498225	0.34752279	0.88720837	0.82503678
##	972	973	974	975	976	977	979
##	0.91601469	0.89840541	0.80832015	0.93910091	0.28346202	0.28346202	0.78896295
##	982	983	988	990	991	994	997
##	0.26394962	0.93219598	0.31207909	0.80108051	0.40407434	0.32169795	0.91773179
##	1002	1004	1006	1016	1017	1022	1024
##	0.78374144	0.96113831	0.96113831	0.89906458	0.95824366	0.91151720	0.94561683
##	1025	1026	1030	1031	1034	1036	1037
##	0.57387540	0.31368976	0.57387540	0.77233191	0.54729817	0.77472663	0.94495889
##	1038	1043	1044	1049	1050	1052	1053
##	0.08467347	0.80300719	0.82020006	0.80953886	0.78021636	0.67804325	0.91104211
##	1055	1058	1059	1062	1063	1065	1070
##	0.14570490	0.20603080	0.81405117	0.95253002	0.87540468	0.75516090	0.54212500
##	1071	1072	1073	1074	1079	1080	1083
##	0.88863261	0.08796075	0.36308322	0.54325401	0.82775448	0.40453879	0.36030691
##	1084	1085	1086	1092	1094	1095	1098
##	0.89315798	0.36030691	0.28421079	0.87464611	0.95181067	0.49531036	0.34983074
##	1100	1103	1106	1108	1109	1110	1113
##	0.34983074	0.74464695	0.89775611	0.94262703	0.20906211	0.67961164	0.83718598
##	1114	1115	1117	1118	1119	1122	1125
##	0.64019617	0.96048872	0.67849027	0.67849027	0.96598962	0.88827487	0.80352421
##	1127	1129	1136	1138	1139	1142	1150
##	0.98230418	0.42390723	0.90991385	0.85680402	0.20660676	0.79255354	0.91677782
##	1154	1156	1158	1160	1164	1165	1169
##	0.78814787	0.32861855	0.91555543	0.75007048	0.34911691	0.34911691	0.89257541
##	1174	1176	1180	1183	1184	1186	1187
##	0.40354568	0.71702966	0.83725702	0.73870157	0.18325571	0.83216767	0.75844840
##	1189	1190	1193	1194	1204	1211	1213
##	0.39228204	0.12264121	0.96428659	0.39866755	0.12664335	0.53707859	0.53707859
##	1217	1220	1221	1224	1226	1228	1230
##	0.25697732	0.80645578	0.89545422	0.93813689	0.23830590	0.43944184	0.35954537
##	1231	1239	1242	1247	1250	1251	1260
##	0.93764299	0.21802710	0.44890191	0.23445159	0.61830476	0.61830476	0.69403671
##	1261	1264	1269	1272	1273	1274	1275
##	0.44018286	0.18918454	0.37253912	0.78782193	0.71983985	0.19873507	0.66138806
##	1278	1284	1286	1290	1292	1293	1297
##	0.35315581	0.35403270	0.64986391	0.52796774	0.59190236	0.93827703	0.15149263
##	1298	1300	1302	1304	1306	1308	1311
##	0.87066317	0.06683777	0.61081590	0.81440601	0.20683713	0.58216493	0.20683713
##	1312	1313	1316	1317	1319	1320	1321
##	0.93088901	0.11783860	0.20771741	0.79987457	0.20771741	0.37260225	0.27840724
##	1323	1326	1328	1329	1331	1332	1333
##	0.86432689	0.65726913	0.65726913	0.27847288	0.21628945	0.06947426	0.44771727
##	1336	1337	1339	1340	1342	1346	1349
##	0.89912713	0.33063230	0.33063230	0.57850387	0.57850387	0.56699331	0.23966391
##	1351	1357	1358	1360	1361	1362	1369
##	0.29613263	0.57441114	0.68815611	0.55865303	0.63469844	0.20131694	0.15039302
##	1371	1372	1376	1379	1380	1381	1386
##	0.30081941	0.91160867	0.22071490	0.47985390	0.62870483	0.62870483	0.06251845
##	1388	1389	1390	1392	1394	1395	1396
##	0.32286340	0.45091508	0.21224158	0.60775822	0.38905380	0.15440151	0.33954980

```
##      1397      1400      1401      1402      1404      1406      1407
## 0.34921494 0.69724047 0.10211360 0.10211360 0.85527482 0.92222761 0.92066898
##      1409      1410      1414      1415      1418      1420      1423
## 0.96956379 0.73685309 0.45197689 0.67996830 0.93856044 0.11430274 0.80043906
##      1424      1426      1427      1430      1432      1435      1436
## 0.72836169 0.66331164 0.93501778 0.92040632 0.37563680 0.18849461 0.18849461
##      1437      1440      1442      1443      1447      1449      1450
## 0.16556629 0.47741729 0.09511377 0.43582198 0.43582198 0.37160792 0.87394441
##      1454      1456      1457      1461      1466      1468      1474
## 0.17120492 0.45960983 0.37601586 0.59735007 0.33900665 0.30916495 0.58301194
##      1475      1477      1478      1479      1481      1483      1485
## 0.19663663 0.19663663 0.96511629 0.28090696 0.49670748 0.55985828 0.47494678
##      1488      1493      1494      1495      1497      1498      1503
## 0.66158978 0.79984815 0.14135590 0.69740812 0.14135590 0.71090938 0.28363547
##      1504      1508      1509      1510      1511      1512      1514
## 0.81885400 0.85817699 0.83087548 0.91307103 0.57620576 0.36079233 0.46974028
##      1515      1516      1517      1522      1523      1525      1533
## 0.12840124 0.13049129 0.82595385 0.25612152 0.82595385 0.60658881 0.52363402
##      1534      1538      1540      1543      1546      1547      1548
## 0.23235943 0.50712482 0.56882617 0.36046967 0.45450879 0.51435731 0.82069018
##      1549      1552      1555      1557      1558      1559      1560
## 0.60297285 0.24069329 0.48014133 0.23011305 0.48014133 0.12503776 0.14727854
##      1562      1566      1571      1572      1573      1574      1575
## 0.14727854 0.65453799 0.96429949 0.82810158 0.10892466 0.88033989 0.51978506
##      1577      1579      1580      1581      1583      1587      1588
## 0.85326672 0.72404537 0.73417847 0.90818659 0.71768308 0.88684408 0.65976944
##      1593      1596      1599
## 0.75118218 0.74190964 0.81940411
```

Model Diagnostics

```
accuracy = (548+639)/(548+196+216+639)
accuracy
```

```
## [1] 0.742339
```

```
sensitivity = 639/(639+196)
sensitivity
```

```
## [1] 0.7652695
```

```
specificity = 548/(548+216)
specificity
```

```
## [1] 0.7172775
```

AUC and ROC

```
library("pROC")
```

```
## Type 'citation("pROC")' for a citation.
```

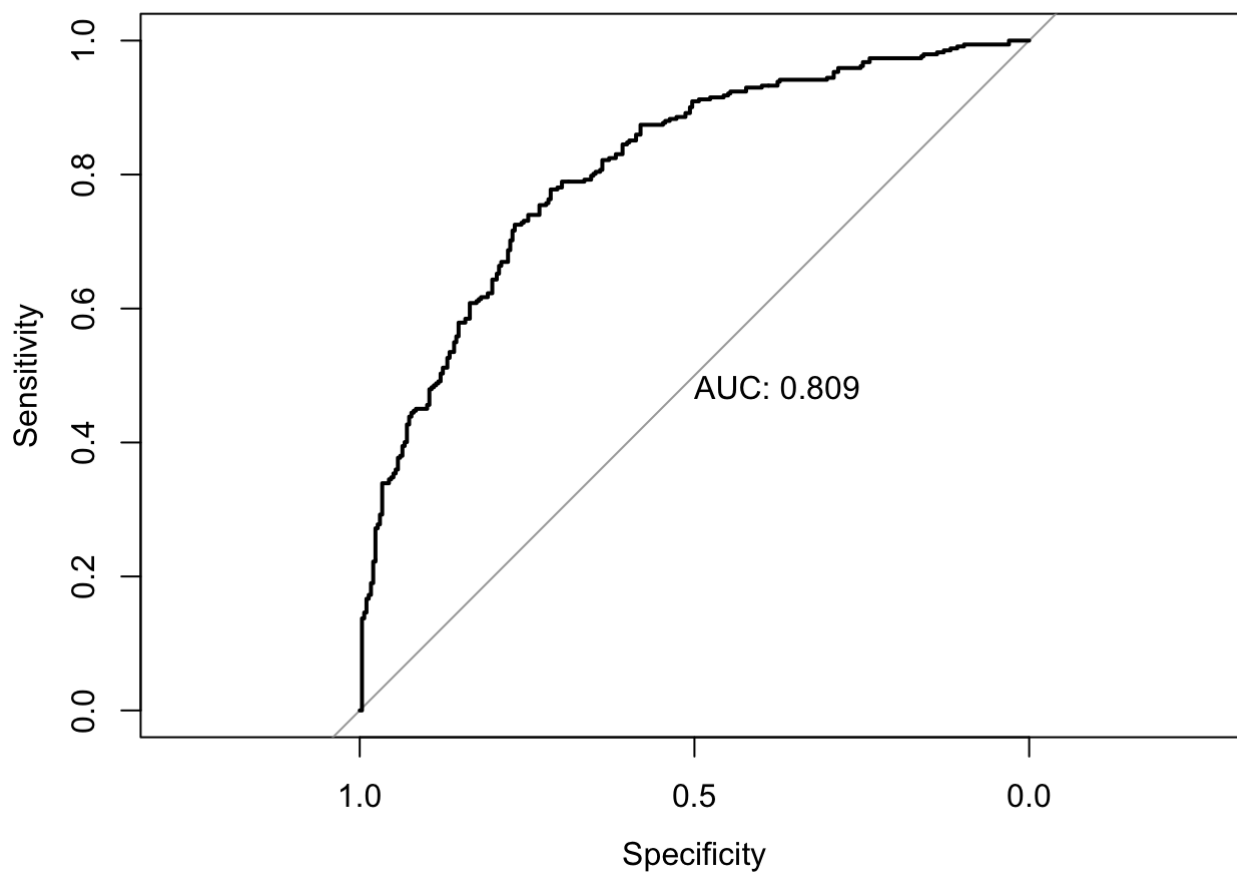
```
##  
## Attaching package: 'pROC'
```

```
## The following objects are masked from 'package:stats':  
##  
## cov, smooth, var
```

```
test_prob = predict(randomforestmodlogit, test, type = "response")  
  
test_roc = roc(test$highquality ~ test_prob, plot = TRUE, print.auc = TRUE)
```

```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```



```
as.numeric(test_roc$auc)
```

```
## [1] 0.8093822
```

AUC and ROC with just one variable

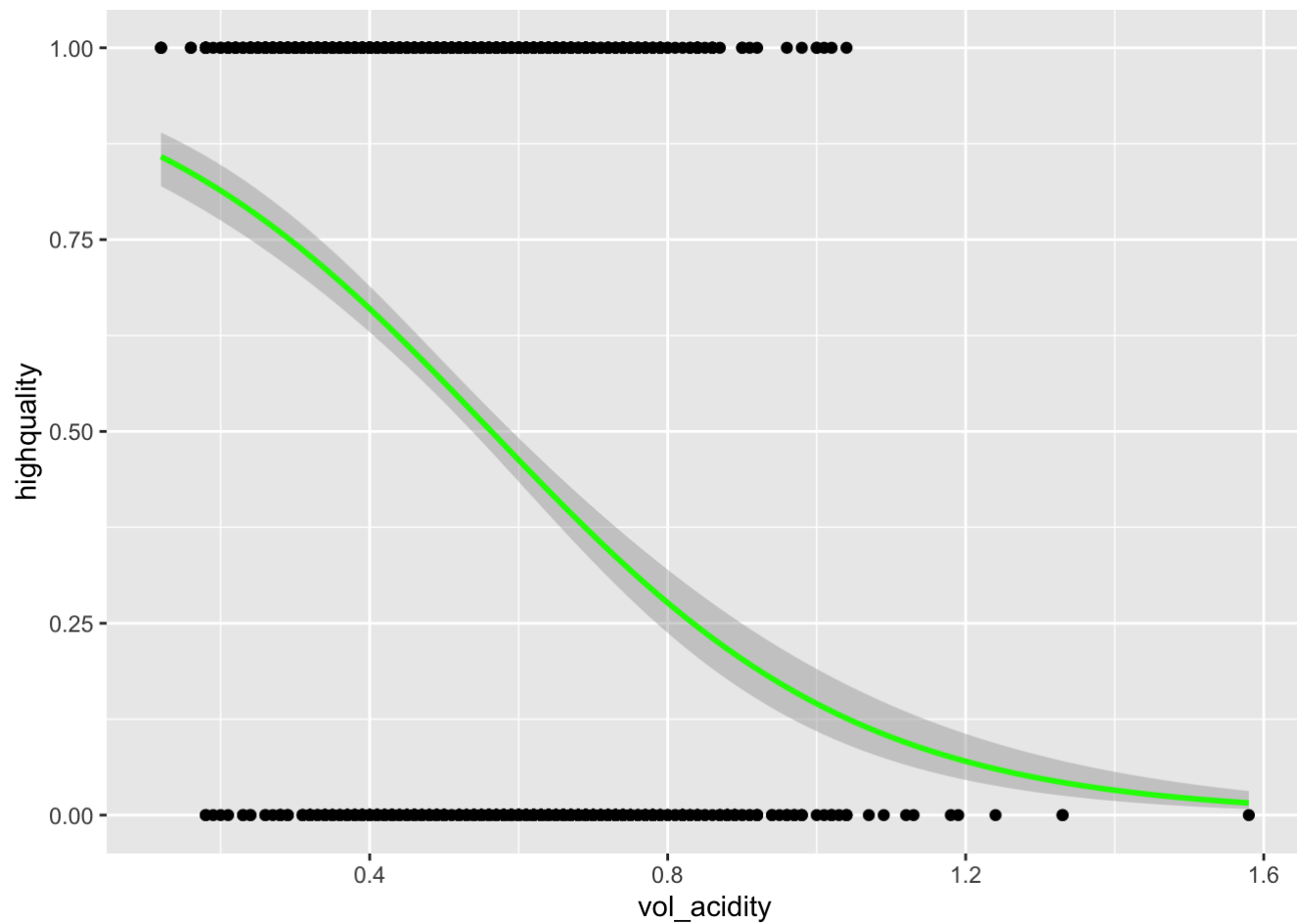
```
library("ggplot2")
```

```
simple <- glm(highquality ~ vol_acidity, data = red, family = "binomial"(link = "logit"))
summary(simple)
```

```
##
## Call:
## glm(formula = highquality ~ vol_acidity, family = binomial(link = "logit"),
##      data = red)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8697  -1.1148   0.7156   1.0375   2.0349
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    2.2874     0.1838  12.45  <2e-16 ***
## vol_acidity   -4.0607     0.3334  -12.18  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 2209.0  on 1598  degrees of freedom
## Residual deviance: 2033.4  on 1597  degrees of freedom
## AIC: 2037.4
##
## Number of Fisher Scoring iterations: 4
```

```
ggplot(red, aes(x = vol_acidity, y = highquality)) +geom_point()+stat_smooth(method="glm", color="green", se=TRUE, method.args = list(family=binomial))
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

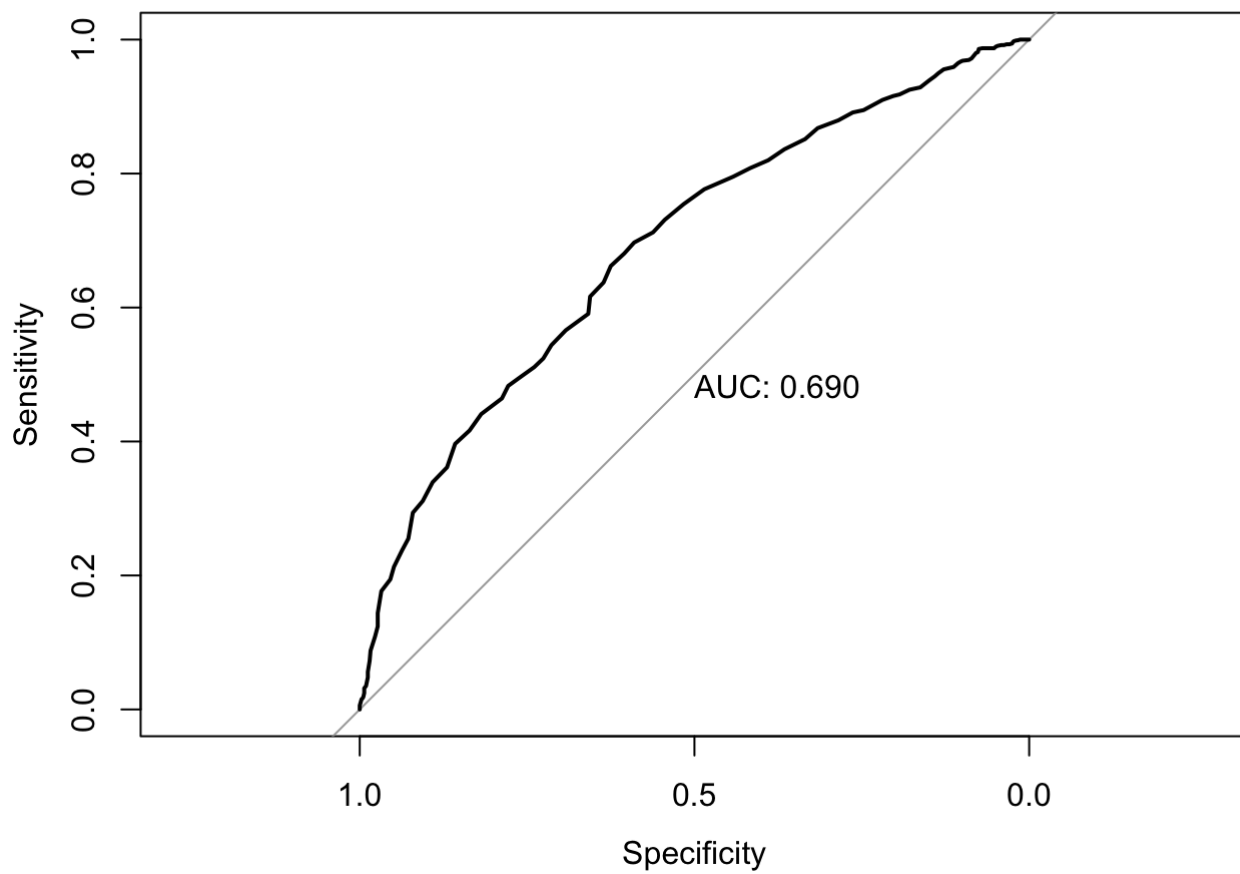


```
test_prop1 = predict(simple, red, type = "response")
```

```
test_roc1 = roc(red$highquality ~ test_prop1, plot = TRUE, print.auc = TRUE)
```

```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```



```
as.numeric(test_roc1$auc)
```

```
## [1] 0.6900011
```