

Red Wines - upper

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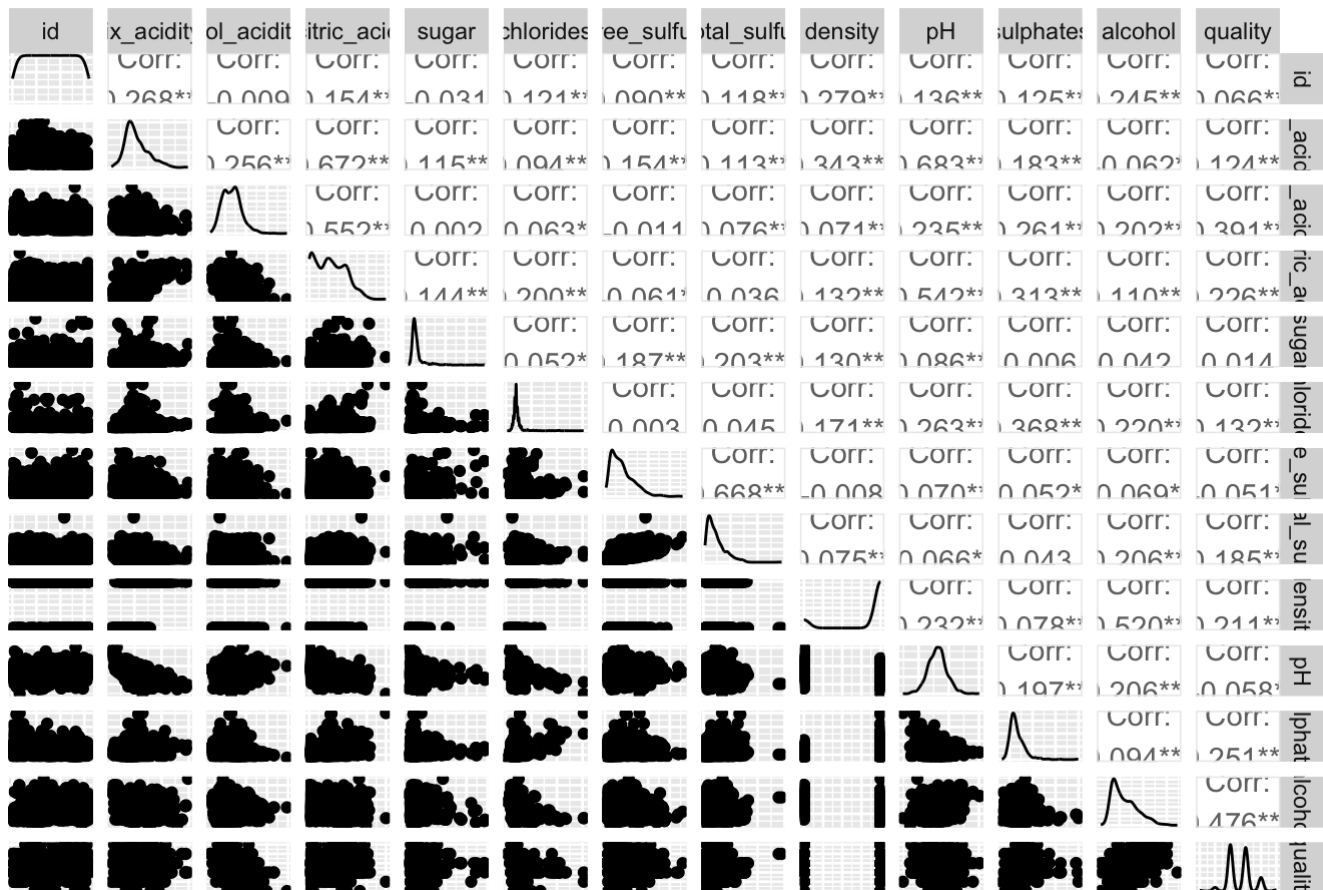
Scatterplot Matrix

```
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
```

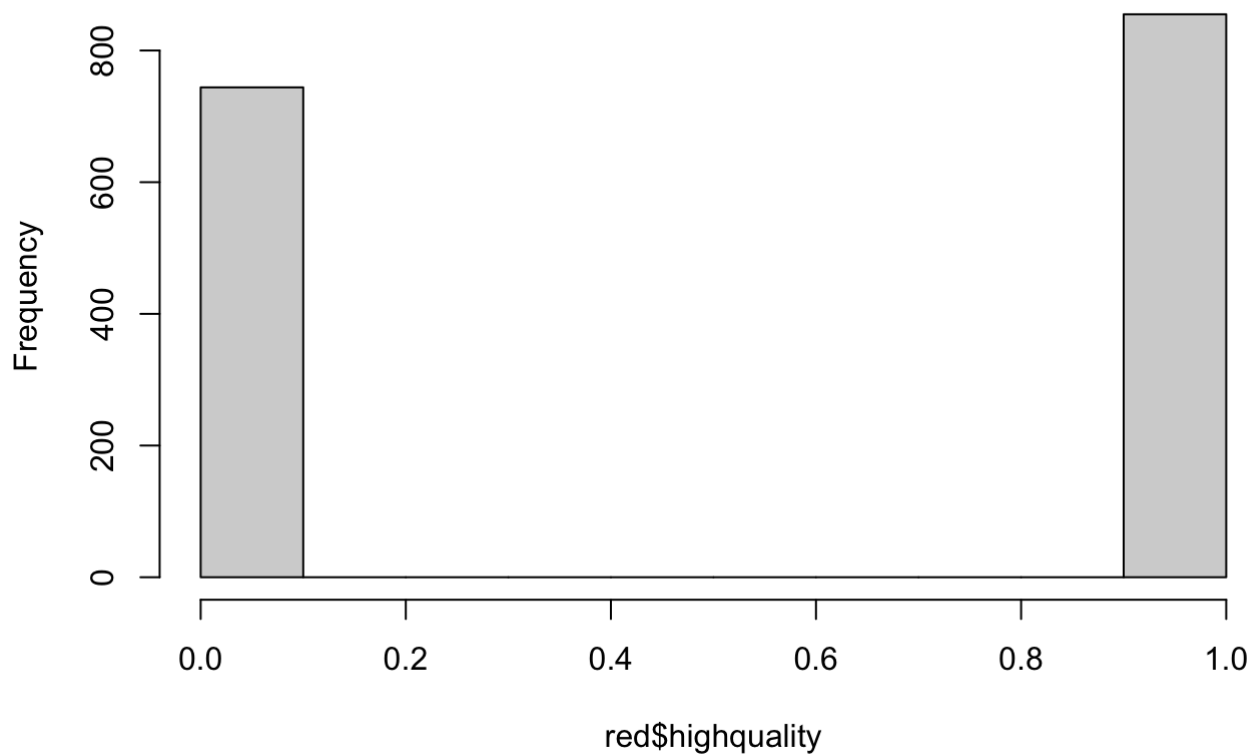
```
sum = summary(red)  
sum
```

```
##          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)
```

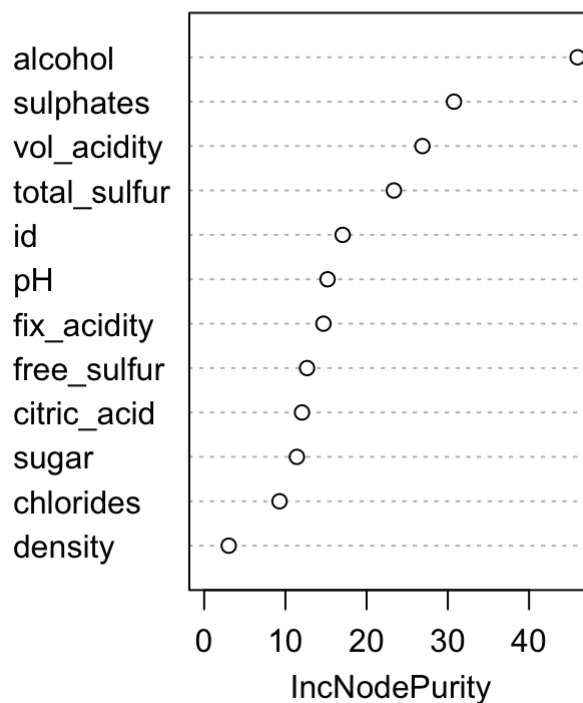
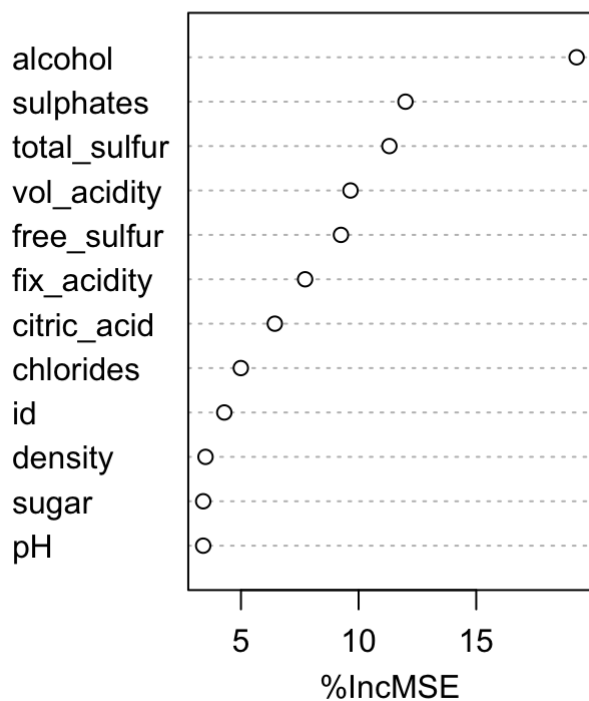
```
## Warning in randomForest.default(m, y, ...): The response has five or fewer  
## unique values. Are you sure you want to do regression?
```

```
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: 0.1482476  
##              % Var explained: 40.41
```

```
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    221   77
##    1     66  276
```

```
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

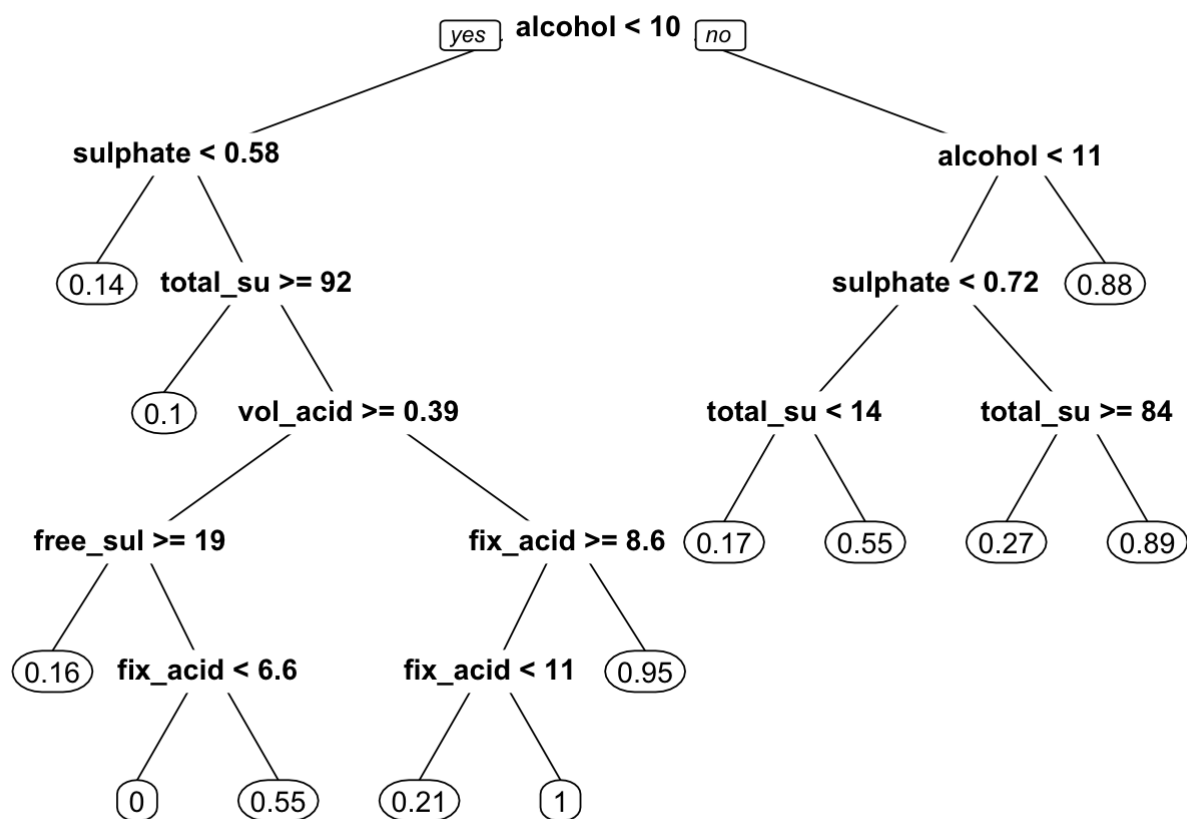
```
library("caret")
library("e1071")
library("rpart")
library("rpart.plot")

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



```
## n= 959
##
## node), split, n, deviance, yval
##      * denotes terminal node
##
## 1) root 959 238.5798000 0.5349322
##    2) alcohol< 9.95 411  84.9635000 0.2919708
##      4) sulphates< 0.575 179  21.5083800 0.1396648 *
##      5) sulphates>=0.575 232  56.0991400 0.4094828
##        10) total_sulfur>=91.5 40  3.6000000 0.1000000 *
##        11) total_sulfur< 91.5 192  47.8697900 0.4739583
##          22) vol_acidity>=0.385 149  35.8389300 0.4026846
##            44) free_sulfur>=18.5 43  5.8604650 0.1627907 *
##            45) free_sulfur< 18.5 106  26.5000000 0.5000000
##              90) fix_acidity< 6.55 9  0.0000000 0.0000000 *
##              91) fix_acidity>=6.55 97  24.0412400 0.5463918 *
##        23) vol_acidity< 0.385 43  8.6511630 0.7209302
##          46) fix_acidity>=8.6 24  5.9583330 0.5416667
##            92) fix_acidity< 11.35 14  2.3571430 0.2142857 *
##            93) fix_acidity>=11.35 10  0.0000000 1.0000000 *
##          47) fix_acidity< 8.6 19  0.9473684 0.9473684 *
##    3) alcohol>=9.95 548 111.1588000 0.7171533
##      6) alcohol< 11.15 340  80.5264700 0.6147059
##        12) sulphates< 0.715 227  56.7400900 0.5066079
##          24) total_sulfur< 13.5 24  3.3333330 0.1666667 *
##          25) total_sulfur>=13.5 203  50.3054200 0.5467980 *
##        13) sulphates>=0.715 113  15.8053100 0.8318584
##          26) total_sulfur>=84 11  2.1818180 0.2727273 *
##          27) total_sulfur< 84 102  9.8137250 0.8921569 *
##        7) alcohol>=11.15 208  21.2307700 0.8846154 *
```

```
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     146  152
##    1      45  297

```

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
```

##	6	11	14	16	18	19	25
##	0.22573317	0.18064756	0.69723806	0.13867752	0.56805457	0.20109254	0.49785778
##	26	28	30	33	34	35	36
##	0.42819628	0.58076699	0.38187954	0.17799414	0.15765907	0.37517558	0.31575154
##	40	41	43	44	46	49	50
##	0.60541307	0.60541307	0.78970651	0.75462869	0.91140600	0.43019840	0.27520137
##	51	53	56	60	61	64	67
##	0.30073364	0.43459537	0.24266029	0.37446288	0.35540196	0.22177359	0.36302140
##	72	75	77	79	81	82	83
##	0.11856745	0.50539651	0.67706290	0.19429727	0.38434763	0.65378965	0.19907576
##	84	86	88	89	94	95	100
##	0.44994570	0.45450681	0.43771981	0.50840606	0.43771981	0.11648871	0.24182616
##	101	102	103	106	110	112	113
##	0.41257714	0.59957642	0.24182616	0.17168420	0.05669027	0.20639675	0.21064410
##	115	116	119	123	126	127	128
##	0.46170336	0.61534547	0.59589245	0.21410390	0.19469456	0.15237332	0.14973294
##	132	133	137	138	139	142	143
##	0.88460563	0.88460563	0.26189520	0.36049701	0.16095337	0.26189520	0.98548676
##	146	148	150	152	154	155	158
##	0.08710726	0.29279616	0.65840863	0.86018228	0.24118269	0.44034290	0.43822117
##	159	160	163	164	167	168	169
##	0.21501940	0.15834014	0.45821490	0.10323416	0.22409934	0.18953659	0.43015992
##	171	176	177	179	184	188	189
##	0.09027691	0.42523959	0.40084611	0.21924830	0.19319740	0.25256465	0.13003255
##	197	200	202	204	209	212	213
##	0.41050290	0.29660130	0.32718865	0.33477584	0.27161312	0.23949363	0.67118625
##	215	218	219	223	224	232	234
##	0.30759231	0.14689457	0.37301967	0.36725609	0.39670029	0.47608964	0.64457164
##	239	240	241	243	244	248	250
##	0.19063712	0.06682702	0.39273703	0.17002266	0.67646997	0.14653731	0.56422747
##	251	254	258	259	261	269	271
##	0.70288800	0.11931143	0.18145879	0.71498229	0.45452948	0.50344768	0.57130009
##	273	274	276	277	278	290	291
##	0.61403829	0.22637701	0.57130009	0.50344768	0.87483178	0.36131597	0.69463023
##	294	297	299	302	303	304	308
##	0.67070411	0.14998798	0.42029514	0.79587338	0.41165107	0.27204195	0.51647504
##	309	312	313	318	321	322	326
##	0.51219806	0.16092124	0.25470497	0.29176280	0.68916140	0.22451563	0.32170068
##	330	331	334	336	337	339	340
##	0.47496687	0.94054119	0.60570094	0.88542182	0.94917073	0.80821030	0.88983001
##	341	342	343	344	345	346	349
##	0.74512435	0.89763321	0.66228068	0.66228068	0.68982583	0.34930907	0.57482872
##	353	355	356	363	365	367	370
##	0.31982246	0.73846936	0.86315416	0.40286206	0.44355920	0.44355920	0.97850481
##	371	372	374	381	385	387	388
##	0.28282101	0.55754674	0.21115302	0.65714868	0.32025802	0.31578174	0.24745643
##	389	390	395	396	402	405	407
##	0.35745073	0.59089106	0.40524750	0.95715624	0.75725600	0.20675079	0.74518550
##	408	410	411	413	415	421	422
##	0.76171904	0.37340589	0.29774721	0.13582974	0.16976587	0.79052736	0.69125350
##	423	424	430	431	433	435	437
##	0.22216089	0.91967155	0.32784541	0.91967155	0.96051533	0.62568563	0.31324574

##	443	444	445	446	447	448	454
##	0.63537526	0.86779419	0.93413308	0.32689043	0.64968242	0.83321168	0.88497153
##	456	459	462	465	466	468	470
##	0.95768591	0.88497153	0.29995555	0.55427468	0.74550780	0.98771509	0.19630137
##	473	474	475	477	479	480	482
##	0.68760803	0.83494087	0.69215031	0.69504790	0.41915117	0.43048988	0.95378202
##	485	486	487	494	495	496	501
##	0.97215159	0.35050201	0.35050201	0.64444930	0.81342325	0.84287574	0.27636155
##	503	508	509	513	515	516	520
##	0.88317746	0.36855117	0.40270830	0.56322747	0.87663195	0.18839969	0.69166380
##	522	524	527	529	531	534	536
##	0.35179506	0.15801090	0.69166380	0.28289255	0.85077943	0.96809870	0.85077943
##	538	540	542	547	550	554	555
##	0.55097625	0.79067776	0.81658345	0.44918649	0.36606459	0.26817772	0.72091694
##	556	560	565	567	570	571	572
##	0.72091694	0.92935383	0.92935383	0.20667837	0.86080487	0.87692510	0.86080487
##	573	574	578	582	584	585	589
##	0.77494478	0.28595807	0.22627342	0.38002007	0.69766881	0.71570169	0.98243548
##	590	592	593	597	606	608	611
##	0.83511782	0.52956620	0.33060442	0.43790682	0.27296251	0.53420556	0.40906300
##	612	622	623	624	626	629	633
##	0.46929105	0.17261769	0.30620045	0.92396940	0.38478177	0.31752796	0.63251372
##	634	636	638	646	649	650	652
##	0.32737388	0.19060263	0.03693294	0.52329572	0.79606704	0.49913547	0.19901970
##	657	659	661	662	663	666	668
##	0.40958829	0.53465925	0.53465925	0.32678756	0.41930315	0.30272887	0.51847411
##	670	673	676	679	680	686	687
##	0.51847411	0.01313453	0.63951248	0.15831687	0.50931169	0.61274001	0.19820088
##	688	690	695	698	704	706	707
##	0.30853776	0.71405217	0.17339004	0.33118031	0.39592542	0.09514858	0.27290235
##	713	714	716	718	720	721	722
##	0.18728926	0.30467669	0.27155586	0.46339361	0.22428109	0.31642036	0.15248206
##	723	725	726	729	731	733	736
##	0.50744957	0.36264216	0.49939352	0.43341582	0.39042992	0.17713379	0.11882456
##	738	741	745	747	749	752	758
##	0.24236950	0.71932009	0.24216251	0.26780776	0.47090034	0.24423781	0.17874689
##	759	761	762	763	764	765	768
##	0.17874689	0.18944864	0.21832154	0.35211810	0.21832154	0.21925919	0.17859090
##	769	770	771	773	776	778	779
##	0.19045961	0.23550990	0.19045961	0.09786165	0.16206695	0.49724573	0.66183909
##	781	784	786	787	792	795	799
##	0.28239984	0.49407054	0.36376503	0.36376503	0.10866121	0.95029362	0.66715805
##	802	803	804	805	809	810	813
##	0.42345371	0.92132982	0.35326525	0.48671568	0.48396705	0.60727563	0.74001422
##	814	815	821	822	823	824	825
##	0.86887538	0.84554487	0.32105800	0.98401461	0.43070016	0.43070016	0.59452832
##	827	829	831	832	835	837	839
##	0.88097191	0.91803729	0.60268443	0.75438553	0.21302698	0.73172430	0.90163251
##	840	841	843	847	852	856	859
##	0.45005102	0.92522550	0.65608836	0.38077515	0.44134957	0.78141884	0.79806178
##	860	864	872	873	874	878	881
##	0.81336010	0.19469921	0.53427892	0.53560900	0.89396556	0.68842602	0.40681831

##	883	891	897	898	907	909	912
##	0.94676764	0.57461423	0.95762419	0.54837049	0.61655717	0.57631602	0.85616038
##	914	915	918	924	925	926	928
##	0.93641743	0.88685399	0.57254719	0.57254719	0.84029182	0.85851776	0.14108907
##	932	933	935	937	943	944	946
##	0.37796683	0.35714165	0.61571145	0.88587548	0.51350024	0.39208642	0.85009985
##	948	950	951	953	954	958	963
##	0.96007673	0.96739607	0.96739607	0.89304382	0.94769354	0.75906185	0.42379344
##	967	970	971	972	975	976	979
##	0.91290529	0.53399341	0.91601469	0.91601469	0.93910091	0.28346202	0.78896295
##	980	982	984	986	988	990	991
##	0.70963694	0.26394962	0.70374096	0.76216515	0.31207909	0.80108051	0.40407434
##	992	994	995	998	1000	1001	1003
##	0.32169795	0.32169795	0.24614218	0.91773179	0.89973442	0.88981382	0.94122194
##	1005	1007	1009	1010	1011	1012	1013
##	0.55234587	0.94122194	0.93177532	0.67244034	0.94994037	0.72592191	0.13893015
##	1014	1016	1017	1018	1019	1020	1022
##	0.33596228	0.89906458	0.95824366	0.90328264	0.90328264	0.62120744	0.91151720
##	1024	1026	1028	1031	1034	1035	1040
##	0.94561683	0.31368976	0.53740392	0.77233191	0.54729817	0.18049828	0.80300719
##	1041	1046	1049	1050	1051	1052	1054
##	0.24523640	0.79667103	0.80953886	0.78021636	0.60752858	0.67804325	0.97117164
##	1063	1065	1067	1068	1078	1082	1084
##	0.87540468	0.75516090	0.92897417	0.89593617	0.82775448	0.37324283	0.89315798
##	1090	1092	1093	1102	1103	1105	1107
##	0.59911292	0.87464611	0.80753908	0.88355318	0.74464695	0.92344246	0.95333070
##	1108	1112	1113	1118	1123	1125	1131
##	0.94262703	0.89860782	0.83718598	0.67849027	0.87671921	0.80352421	0.59465043
##	1133	1136	1145	1146	1149	1153	1154
##	0.98621359	0.90991385	0.55703889	0.81699614	0.88830835	0.32861855	0.78814787
##	1162	1163	1164	1168	1169	1173	1177
##	0.68472828	0.93097631	0.34911691	0.95811695	0.89257541	0.94556825	0.38959620
##	1180	1184	1186	1188	1191	1193	1195
##	0.83725702	0.18325571	0.83216767	0.83216767	0.93726418	0.96428659	0.16205917
##	1196	1197	1200	1201	1203	1207	1208
##	0.36820273	0.18261742	0.18261742	0.43683111	0.90407751	0.84882533	0.44462253
##	1210	1212	1216	1219	1220	1223	1225
##	0.89081590	0.33645556	0.86572123	0.75790425	0.80645578	0.19169762	0.77019805
##	1228	1229	1233	1236	1237	1240	1241
##	0.43944184	0.95997919	0.35954537	0.70226268	0.38859556	0.76884549	0.14929864
##	1244	1251	1253	1256	1259	1261	1262
##	0.22116768	0.61830476	0.33313384	0.50363201	0.69403671	0.44018286	0.37701038
##	1263	1264	1268	1269	1273	1277	1278
##	0.38122840	0.18918454	0.90213067	0.37253912	0.71983985	0.91209807	0.35315581
##	1279	1281	1282	1285	1286	1287	1288
##	0.13504841	0.57652097	0.57652097	0.72038518	0.64986391	0.95921380	0.90845738
##	1293	1295	1298	1301	1304	1305	1307
##	0.93827703	0.59190236	0.87066317	0.87211203	0.81440601	0.08307448	0.23809254
##	1308	1314	1317	1321	1322	1324	1330
##	0.58216493	0.50024518	0.79987457	0.27840724	0.79987457	0.82228483	0.21628945
##	1333	1336	1338	1339	1344	1345	1349
##	0.44771727	0.89912713	0.33063230	0.33063230	0.57850387	0.76295728	0.23966391

```
##      1352      1357      1358      1359      1361      1363      1364
## 0.71942809 0.57441114 0.68815611 0.13052325 0.63469844 0.55865303 0.13872049
##      1365      1372      1373      1377      1378      1380      1382
## 0.76732852 0.91160867 0.30081941 0.18491208 0.83265348 0.62870483 0.16546771
##      1383      1388      1391      1399      1401      1405      1409
## 0.18145955 0.32286340 0.90986800 0.49039723 0.10211360 0.62668380 0.96956379
##      1417      1420      1421      1425      1428      1441      1442
## 0.67996830 0.11430274 0.39766821 0.66331164 0.81035058 0.87184058 0.09511377
##      1443      1444      1446      1450      1451      1457      1459
## 0.43582198 0.77179526 0.09753535 0.87394441 0.87184058 0.37601586 0.77734136
##      1461      1462      1463      1466      1468      1469      1472
## 0.59735007 0.34284216 0.47637617 0.33900665 0.30916495 0.47414501 0.86017441
##      1473      1474      1476      1479      1482      1489      1492
## 0.84882869 0.58301194 0.96416743 0.28090696 0.81973890 0.79522301 0.79522301
##      1493      1495      1496      1497      1503      1505      1506
## 0.79984815 0.69740812 0.77693701 0.14135590 0.28363547 0.85817699 0.36554744
##      1508      1513      1515      1517      1522      1526      1530
## 0.85817699 0.43899218 0.12840124 0.82595385 0.25612152 0.45939419 0.34422384
##      1531      1532      1536      1537      1542      1543      1545
## 0.85054796 0.42672777 0.37906001 0.54738050 0.84898279 0.36046967 0.89062172
##      1546      1548      1552      1553      1555      1556      1558
## 0.45450879 0.82069018 0.24069329 0.62386686 0.48014133 0.64128386 0.48014133
##      1559      1560      1563      1568      1570      1571      1573
## 0.12503776 0.14727854 0.37557065 0.37557065 0.78071517 0.96429949 0.10892466
##      1574      1575      1576      1581      1586      1589      1591
## 0.88033989 0.51978506 0.86164481 0.90818659 0.88371638 0.83629523 0.85094463
##      1596      1597      1598
## 0.74190964 0.75118218 0.45044094
```

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.
```

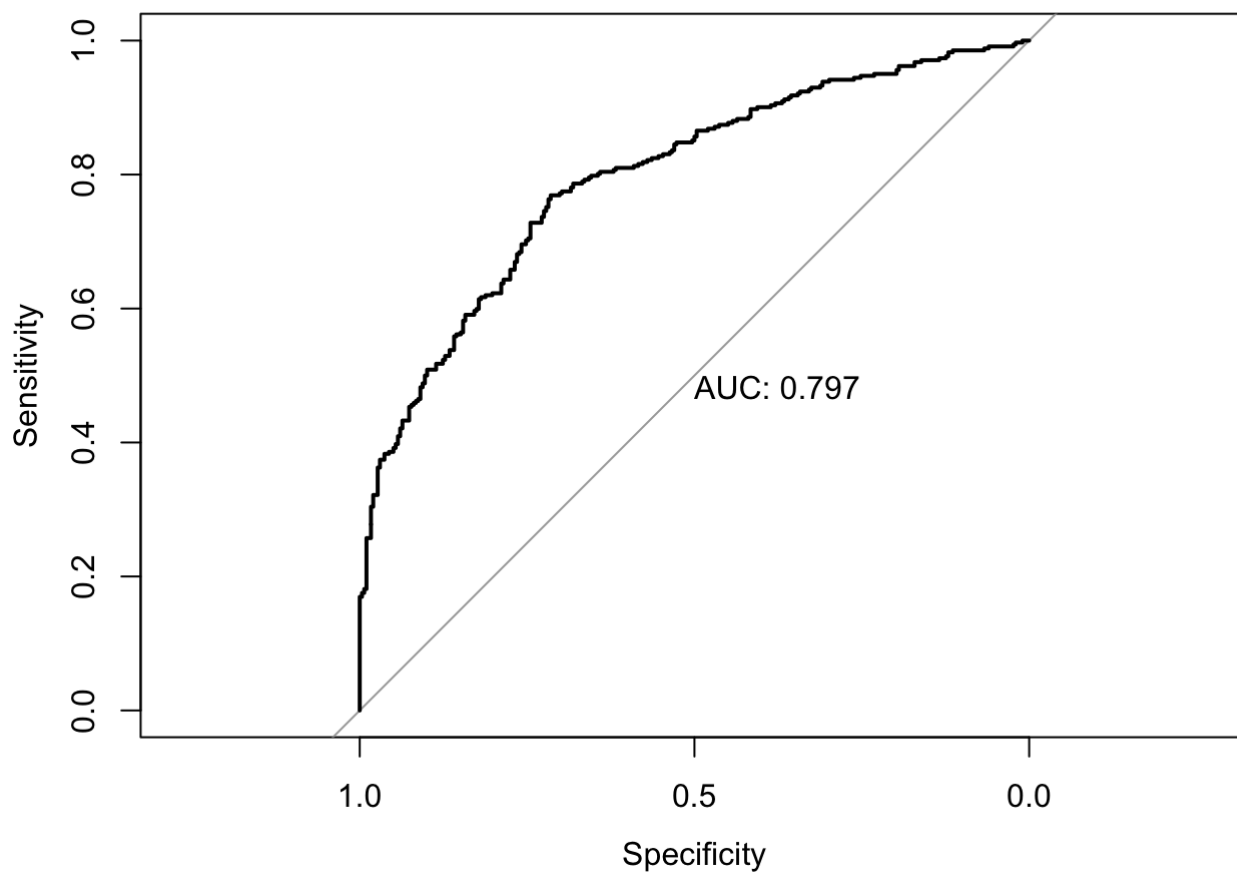
```
##  
## Attaching package: 'pROC'
```

```
## 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] 0.7968425
```

AUC and ROC with just one variable

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

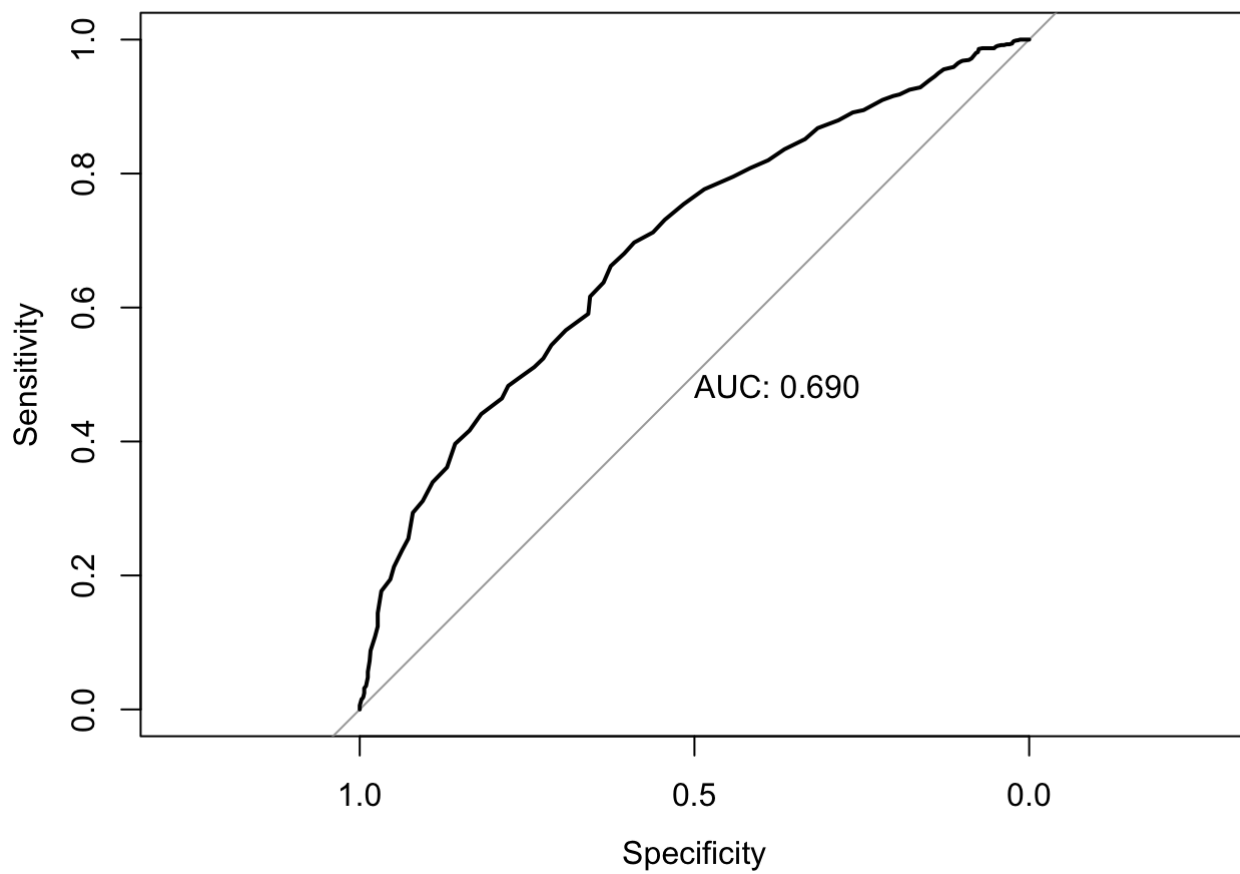
```
##
## Call:
## glm(formula = highquality ~ vol_acidity, family = binomial(link = "logit"),
##      data = red)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8697  -1.1148   0.7156   1.0375   2.0349
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (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
```

```
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
```