

project 2

Group 11

```
#packages library
#|echo: false
library(tidyverse)
library(moderndiver)
library(gapminder)
library(sjPlot)
library(stats)
library(jtools)
```

1 Introduction

(include research question)

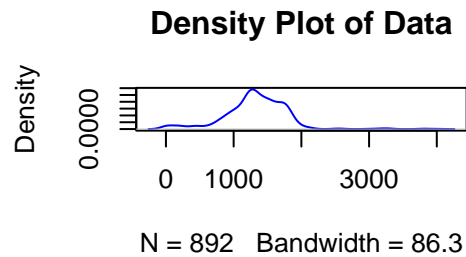
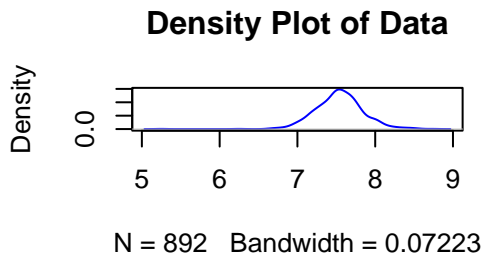
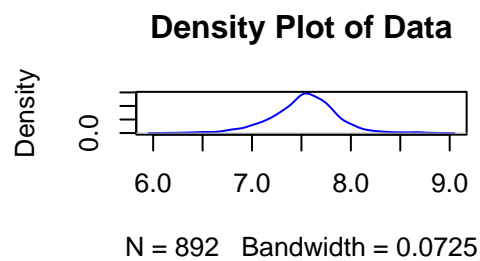
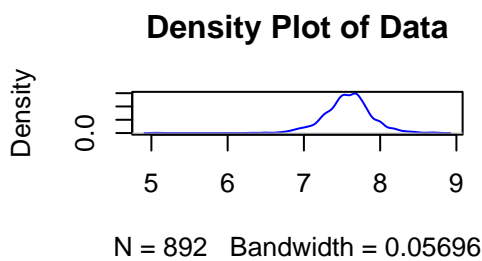
2 Data preparing & Cleaning

```
#data cleaning
data<-read.csv("dataset11.csv")
data<-na.omit(data)
data$Qualityclass_dummy<-ifelse(data$Qualityclass=="Good",1,0) #for "Good"=1
  ↪ "Poor"=0
data$Qualityclass <- as.factor(data$Qualityclass)
data$harvested <- as.factor(data$harvested)
data$category_two_defects<-as.factor(data$category_two_defects)
#Outlier in altitude_mean_meters
sum(data$altitude_mean_meters>8848)+sum(data$altitude_mean_meters<0)
```

[1] 2

```
data=data%>%
  filter(data$altitude_mean_meters<8848 & data$altitude_mean_meters>0)

#standardized
par(mfrow=c(2,2))
plot(density(data$aroma), col = "blue", main = "Density Plot of Data")
plot(density(data$flavor), col = "blue", main = "Density Plot of Data")
plot(density(data$acidity), col = "blue", main = "Density Plot of Data")
plot(density(data$altitude_mean_meters), col = "blue", main = "Density Plot
↵ of Data")
```



```
#Min-Max standardized
min_max_norm=function(x){
  return((x-min(x))/(max(x)-min(x)))
}
data[,2:4]=lapply(data[,2:4],min_max_norm)
data$altitude_mean_meters=min_max_norm(data$altitude_mean_meters)
```

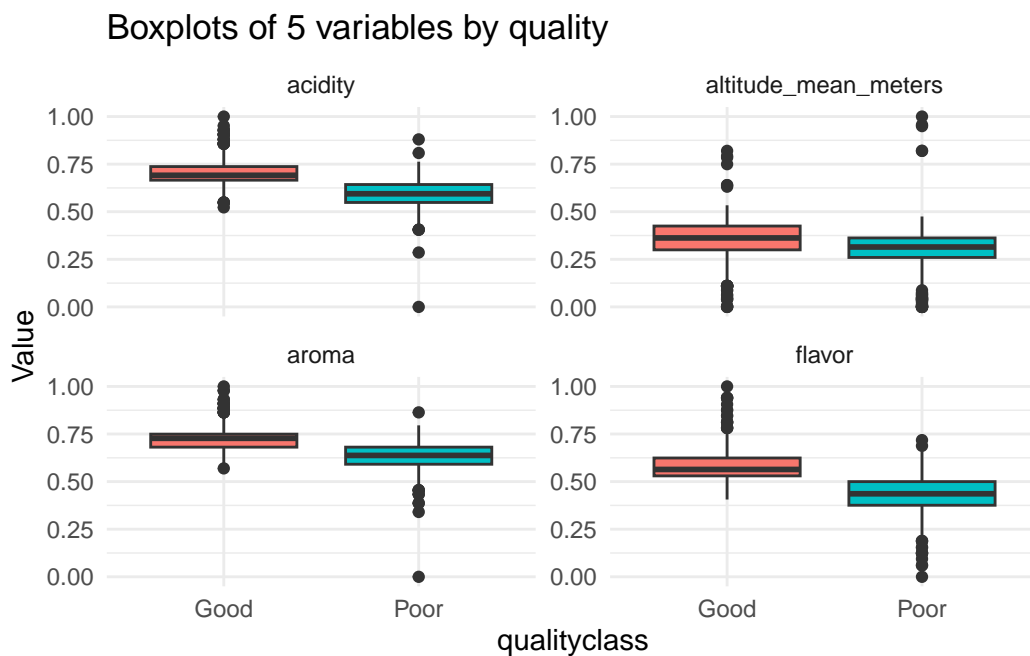
in this dataset aroma,flavor,acidity and altitude_mean_meters are continuous variables, category_two_defects, Qualityclass and harvested are categorical variables. #Exploratory Data Analysis # Illuminating visualizations of the data

```

library(tidyr)
#change formula
data_long <- data %>%
  pivot_longer(cols = c(aroma,flavor,acidity,altitude_mean_meters),
               names_to = "Variable",
               values_to = "Value")
library(ggplot2)

#boxplot
#continuous
ggplot(data = data_long, aes(x = Qualityclass, y = Value, fill =
  ↪ Qualityclass)) +
  geom_boxplot() +
  facet_wrap(~Variable, scales = "free_y") +
  theme_minimal() +
  labs(title = "Boxplots of 5 variables by quality",
       x = "qualityclass",
       y = "Value") +
  theme(legend.position = "none")

```

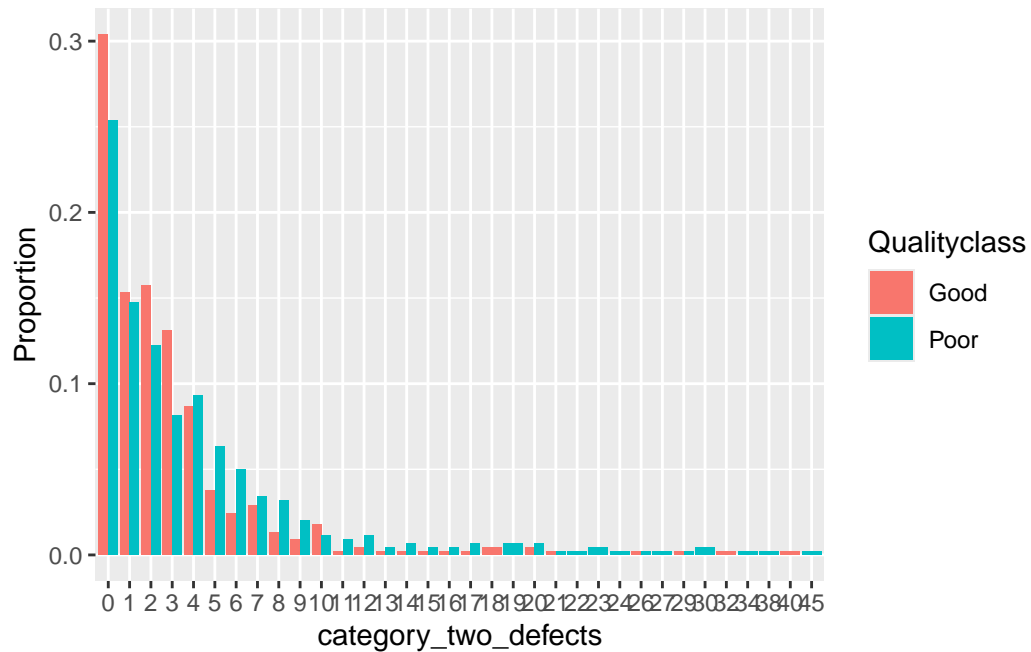


```

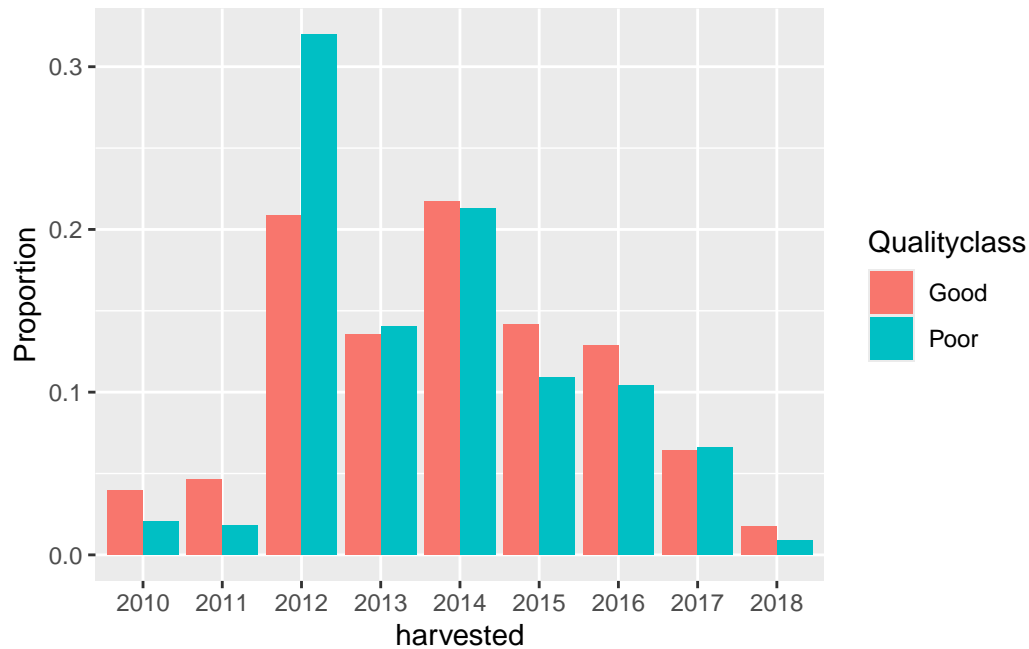
#categorical
#category_two_defects

```

```
ggplot(data, aes(x=category_two_defects , y = ..prop.., group=Qualityclass,
  ↪ fill=Qualityclass)) +
  geom_bar(position="dodge", stat="count") +
  labs(y = "Proportion")
```



```
#harvested
ggplot(data, aes(x=harvested , y = ..prop.., group=Qualityclass,
  ↪ fill=Qualityclass)) +
  geom_bar(position="dodge", stat="count") +
  labs(y = "Proportion")
```



#Numerical Summaries

```
#summary
summary(data)
```

country_of_origin	aroma	flavor	acidity
Length:892	Min. :0.0000	Min. :0.0000	Min. :0.0000
Class :character	1st Qu.:0.6376	1st Qu.:0.4361	1st Qu.:0.5943
Mode :character	Median :0.6812	Median :0.5301	Median :0.6429
	Mean :0.6797	Mean :0.5098	Mean :0.6535
	3rd Qu.:0.7275	3rd Qu.:0.5940	3rd Qu.:0.7143
	Max. :1.0000	Max. :1.0000	Max. :1.0000

category_two_defects	altitude_mean_meters	harvested	Qualityclass
0 :249	Min. :0.0000	2012 :235	Good:451
1 :134	1st Qu.:0.2747	2014 :192	Poor:441
2 :125	Median :0.3274	2013 :123	
3 : 95	Mean :0.3302	2015 :112	
4 : 80	3rd Qu.:0.3997	2016 :104	
5 : 45	Max. :1.0000	2017 : 58	
(Other):164		(Other): 68	

Qualityclass_dummy
Min. :0.0000

```

1st Qu.:0.0000
Median :1.0000
Mean   :0.5056
3rd Qu.:1.0000
Max.   :1.0000

```

```
#####need to add a table for summary use gt()
```

```
#Formal Data Analysis #Model fitted original model
```

$$\ln\left(\frac{p}{1-p}\right) = \alpha + \beta_1 \cdot \text{aroma} + \beta_2 \cdot \text{flavor} + \beta_3 \cdot \text{acidity} + \beta_4 \cdot \text{defects} + \beta_5 \cdot \text{meters} + \beta_6 \cdot \text{harvested}$$

(each variable need to be explain)

```

#model fitted for original
model <- glm(Qualityclass_dummy ~
  ↪ aroma+flavor+acidity+category_two_defects+altitude_mean_meters+harvested,
  ↪ data = data, family = binomial(link = "logit"))
summary(model)

```

Call:

```

glm(formula = Qualityclass_dummy ~ aroma + flavor + acidity +
  category_two_defects + altitude_mean_meters + harvested,
  family = binomial(link = "logit"), data = data)

```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-3.247e+01	2.778e+00	-11.691	< 2e-16 ***
aroma	1.810e+01	2.735e+00	6.618	3.64e-11 ***
flavor	2.025e+01	2.494e+00	8.120	4.65e-16 ***
acidity	1.376e+01	2.533e+00	5.432	5.56e-08 ***
category_two_defects1	-1.527e-01	3.649e-01	-0.418	0.67572
category_two_defects2	-8.175e-02	3.825e-01	-0.214	0.83075
category_two_defects3	4.523e-01	4.053e-01	1.116	0.26444
category_two_defects4	4.698e-01	4.452e-01	1.055	0.29131
category_two_defects5	6.914e-02	5.687e-01	0.122	0.90323
category_two_defects6	-5.740e-01	6.216e-01	-0.924	0.35574
category_two_defects7	-1.043e+00	8.714e-01	-1.197	0.23123
category_two_defects8	2.646e-03	8.002e-01	0.003	0.99736

category_two_defects9	-7.248e-01	8.452e-01	-0.858	0.39117
category_two_defects10	1.499e+00	9.563e-01	1.568	0.11694
category_two_defects11	5.490e-01	1.324e+00	0.415	0.67838
category_two_defects12	3.154e+00	1.915e+00	1.647	0.09964
category_two_defects13	-8.069e-01	2.143e+00	-0.377	0.70652
category_two_defects14	6.154e-01	1.684e+00	0.365	0.71484
category_two_defects15	-1.016e+00	1.489e+00	-0.682	0.49504
category_two_defects16	2.320e+00	6.870e+00	0.338	0.73556
category_two_defects17	1.791e+00	1.357e+00	1.320	0.18675
category_two_defects18	1.306e+01	1.536e+03	0.009	0.99321
category_two_defects19	-1.128e+01	1.284e+03	-0.009	0.99299
category_two_defects20	3.653e+00	3.341e+00	1.093	0.27422
category_two_defects21	2.356e+00	6.836e+00	0.345	0.73034
category_two_defects22	-1.048e+01	2.400e+03	-0.004	0.99652
category_two_defects23	-1.407e+01	1.312e+03	-0.011	0.99144
category_two_defects24	-5.145e+00	2.400e+03	-0.002	0.99829
category_two_defects26	-3.092e-01	3.468e+00	-0.089	0.92895
category_two_defects27	-3.219e+00	2.400e+03	-0.001	0.99893
category_two_defects29	1.180e+00	1.288e+01	0.092	0.92701
category_two_defects30	-7.186e+00	1.686e+03	-0.004	0.99660
category_two_defects32	1.495e+01	2.400e+03	0.006	0.99503
category_two_defects34	-7.445e+00	2.400e+03	-0.003	0.99752
category_two_defects38	-6.458e+00	2.400e+03	-0.003	0.99785
category_two_defects40	1.388e+01	2.400e+03	0.006	0.99538
category_two_defects45	-9.804e+00	2.400e+03	-0.004	0.99674
altitude_mean_meters	2.696e+00	1.033e+00	2.611	0.00902 **
harvested2011	-1.790e-01	1.121e+00	-0.160	0.87312
harvested2012	-8.377e-01	9.387e-01	-0.892	0.37220
harvested2013	-2.441e-01	9.480e-01	-0.258	0.79678
harvested2014	8.853e-02	9.450e-01	0.094	0.92535
harvested2015	-4.161e-01	9.534e-01	-0.436	0.66252
harvested2016	3.715e-01	9.871e-01	0.376	0.70668
harvested2017	1.888e-01	9.839e-01	0.192	0.84779
harvested2018	1.378e+00	1.284e+00	1.073	0.28331

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1236.46 on 891 degrees of freedom
Residual deviance: 495.99 on 846 degrees of freedom
AIC: 587.99

Number of Fisher Scoring iterations: 15

```
summ(model)
```

MODEL INFO:

Observations: 892

Dependent Variable: Qualityclass_dummy

Type: Generalized linear model

Family: binomial

Link function: logit

MODEL FIT:

$\chi^2(45) = 740.47$, $p = 0.00$

Pseudo- R^2 (Cragg-Uhler) = 0.75

Pseudo- R^2 (McFadden) = 0.60

AIC = 587.99, BIC = 808.49

Standard errors:MLE

	Est.	S.E.	z val.	p
(Intercept)	-32.47	2.78	-11.69	0.00
aroma	18.10	2.73	6.62	0.00
flavor	20.25	2.49	8.12	0.00
acidity	13.76	2.53	5.43	0.00
category_two_defects1	-0.15	0.36	-0.42	0.68
category_two_defects2	-0.08	0.38	-0.21	0.83
category_two_defects3	0.45	0.41	1.12	0.26
category_two_defects4	0.47	0.45	1.06	0.29
category_two_defects5	0.07	0.57	0.12	0.90
category_two_defects6	-0.57	0.62	-0.92	0.36
category_two_defects7	-1.04	0.87	-1.20	0.23
category_two_defects8	0.00	0.80	0.00	1.00
category_two_defects9	-0.72	0.85	-0.86	0.39
category_two_defects10	1.50	0.96	1.57	0.12
category_two_defects11	0.55	1.32	0.41	0.68
category_two_defects12	3.15	1.92	1.65	0.10
category_two_defects13	-0.81	2.14	-0.38	0.71
category_two_defects14	0.62	1.68	0.37	0.71
category_two_defects15	-1.02	1.49	-0.68	0.50
category_two_defects16	2.32	6.87	0.34	0.74
category_two_defects17	1.79	1.36	1.32	0.19

category_two_defects18	13.06	1535.80	0.01	0.99
category_two_defects19	-11.28	1284.07	-0.01	0.99
category_two_defects20	3.65	3.34	1.09	0.27
category_two_defects21	2.36	6.84	0.34	0.73
category_two_defects22	-10.48	2399.54	-0.00	1.00
category_two_defects23	-14.07	1312.39	-0.01	0.99
category_two_defects24	-5.14	2399.54	-0.00	1.00
category_two_defects26	-0.31	3.47	-0.09	0.93
category_two_defects27	-3.22	2399.55	-0.00	1.00
category_two_defects29	1.18	12.88	0.09	0.93
category_two_defects30	-7.19	1686.23	-0.00	1.00
category_two_defects32	14.95	2399.54	0.01	1.00
category_two_defects34	-7.44	2399.54	-0.00	1.00
category_two_defects38	-6.46	2399.54	-0.00	1.00
category_two_defects40	13.88	2399.54	0.01	1.00
category_two_defects45	-9.80	2399.54	-0.00	1.00
altitude_mean_meters	2.70	1.03	2.61	0.01
harvested2011	-0.18	1.12	-0.16	0.87
harvested2012	-0.84	0.94	-0.89	0.37
harvested2013	-0.24	0.95	-0.26	0.80
harvested2014	0.09	0.94	0.09	0.93
harvested2015	-0.42	0.95	-0.44	0.66
harvested2016	0.37	0.99	0.38	0.71
harvested2017	0.19	0.98	0.19	0.85
harvested2018	1.38	1.28	1.07	0.28

find p-value of category_two_defects and altitude_mean_meters and harvested are higher than 0.05

```
#del category_two_defects variabile
model_ctd <- glm(Qualityclass_dummy ~
  ↪ aroma+flavor+acidity+altitude_mean_meters+harvested, data = data, family
  ↪ = binomial(link = "logit"))
summary(model_ctd)
```

Call:

```
glm(formula = Qualityclass_dummy ~ aroma + flavor + acidity +
  altitude_mean_meters + harvested, family = binomial(link = "logit"),
  data = data)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-31.90576	2.70450	-11.797	< 2e-16 ***
aroma	18.43367	2.69614	6.837	8.08e-12 ***
flavor	19.27574	2.37645	8.111	5.01e-16 ***
acidity	13.40118	2.46435	5.438	5.39e-08 ***
altitude_mean_meters	2.43429	0.97737	2.491	0.0128 *
harvested2011	-0.05273	1.08890	-0.048	0.9614
harvested2012	-0.58227	0.90349	-0.644	0.5193
harvested2013	-0.19932	0.92158	-0.216	0.8288
harvested2014	0.10122	0.91885	0.110	0.9123
harvested2015	-0.40804	0.92349	-0.442	0.6586
harvested2016	0.44626	0.95346	0.468	0.6398
harvested2017	0.22480	0.95680	0.235	0.8142
harvested2018	1.66547	1.25028	1.332	0.1828

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1236.46 on 891 degrees of freedom
Residual deviance: 513.89 on 879 degrees of freedom
AIC: 539.89

Number of Fisher Scoring iterations: 7

```
summ(model_ctd)
```

MODEL INFO:

Observations: 892

Dependent Variable: Qualityclass_dummy

Type: Generalized linear model

Family: binomial

Link function: logit

MODEL FIT:

$\chi^2(12) = 722.58$, $p = 0.00$

Pseudo- R^2 (Cragg-Uhler) = 0.74

Pseudo- R^2 (McFadden) = 0.58

AIC = 539.89, BIC = 602.20

Standard errors:MLE

	Est.	S.E.	z val.	p
(Intercept)	-31.91	2.70	-11.80	0.00
aroma	18.43	2.70	6.84	0.00
flavor	19.28	2.38	8.11	0.00
acidity	13.40	2.46	5.44	0.00
altitude_mean_meters	2.43	0.98	2.49	0.01
harvested2011	-0.05	1.09	-0.05	0.96
harvested2012	-0.58	0.90	-0.64	0.52
harvested2013	-0.20	0.92	-0.22	0.83
harvested2014	0.10	0.92	0.11	0.91
harvested2015	-0.41	0.92	-0.44	0.66
harvested2016	0.45	0.95	0.47	0.64
harvested2017	0.22	0.96	0.23	0.81
harvested2018	1.67	1.25	1.33	0.18

AIC decreased

```
#del altitude_mean_meters variable
model_0 <- glm(Qualityclass_dummy ~
  ↪ aroma+flavor+acidity+altitude_mean_meters, data = data, family =
  ↪ binomial(link = "logit"))
summary(model_0)
```

Call:

```
glm(formula = Qualityclass_dummy ~ aroma + flavor + acidity +
  altitude_mean_meters, family = binomial(link = "logit"),
  data = data)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-31.0176	2.4204	-12.815	< 2e-16 ***
aroma	17.0856	2.5335	6.744	1.54e-11 ***
flavor	18.7270	2.2919	8.171	3.06e-16 ***
acidity	14.0064	2.4087	5.815	6.06e-09 ***
altitude_mean_meters	1.8539	0.9269	2.000	0.0455 *

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1236.46 on 891 degrees of freedom
Residual deviance: 528.38 on 887 degrees of freedom
AIC: 538.38

Number of Fisher Scoring iterations: 7

```
summ(model_0)
```

MODEL INFO:

Observations: 892

Dependent Variable: Qualityclass_dummy

Type: Generalized linear model

Family: binomial

Link function: logit

MODEL FIT:

$\chi^2(4) = 708.08, p = 0.00$

Pseudo- R^2 (Cragg-Uhler) = 0.73

Pseudo- R^2 (McFadden) = 0.57

AIC = 538.38, BIC = 562.35

Standard errors:MLE

	Est.	S.E.	z val.	p
(Intercept)	-31.02	2.42	-12.82	0.00
aroma	17.09	2.53	6.74	0.00
flavor	18.73	2.29	8.17	0.00
acidity	14.01	2.41	5.81	0.00
altitude_mean_meters	1.85	0.93	2.00	0.05

AIC decreased

```
#del harvested variable
model1 <- glm(Qualityclass_dummy ~ aroma+flavor+acidity, data = data, family
  ↪ = binomial(link = "logit"))
summary(model1)
```

```
Call:
glm(formula = Qualityclass_dummy ~ aroma + flavor + acidity,
     family = binomial(link = "logit"), data = data)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-30.711	2.398	-12.806	< 2e-16 ***
aroma	17.647	2.531	6.972	3.14e-12 ***
flavor	18.328	2.256	8.123	4.55e-16 ***
acidity	14.202	2.388	5.948	2.72e-09 ***

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1236.46 on 891 degrees of freedom
Residual deviance: 532.32 on 888 degrees of freedom
AIC: 540.32

Number of Fisher Scoring iterations: 7

```
summ(model1)
```

MODEL INFO:

Observations: 892
Dependent Variable: Qualityclass_dummy
Type: Generalized linear model
Family: binomial
Link function: logit

MODEL FIT:

$\chi^2(3) = 704.14$, $p = 0.00$
Pseudo- R^2 (Cragg-Uhler) = 0.73
Pseudo- R^2 (McFadden) = 0.57
AIC = 540.32, BIC = 559.50

Standard errors:MLE

	Est.	S.E.	z val.	p
(Intercept)	-30.71	2.40	-12.81	0.00

aroma	17.65	2.53	6.97	0.00
flavor	18.33	2.26	8.12	0.00
acidity	14.20	2.39	5.95	0.00

```
##### need a table for summ
```

aroma flavor acidity significant this three varibales will be saved and AIC decreased to min.
optimization model (final model)

$$\ln \left(\frac{p}{1-p} \right) = \alpha + \beta_1 \cdot \text{aroma} + \beta_2 \cdot \text{flavor} + \beta_3 \cdot \text{acidity} + \beta_4 \cdot \text{harvested}$$

```
#####model1
```

```
levels(data$Qualityclass) #base on "good"
```

```
[1] "Good" "Poor"
```

```
#for original model
mod1coefs <- round(coef(model), 2)
library(knitr)
confint(model) %>%
  kable()
```

	2.5 %	97.5 %
(Intercept)	-38.1854338	-27.2711993
aroma	12.8982348	23.6359497
flavor	15.5380009	25.3372050
acidity	8.8898953	18.8349218
category_two_defects1	-0.8694362	0.5639448
category_two_defects2	-0.8312538	0.6710736
category_two_defects3	-0.3364056	1.2559917
category_two_defects4	-0.3960145	1.3537865
category_two_defects5	-1.0634771	1.1720588
category_two_defects6	-1.8281503	0.6249114
category_two_defects7	-2.6861160	0.7122507
category_two_defects8	-1.5780035	1.5897154
category_two_defects9	-2.5195019	0.8658394

	2.5 %	97.5 %
category_two_defects10	-0.3228813	3.4391795
category_two_defects11	-2.6381797	3.0713435
category_two_defects12	-0.5229555	6.4090166
category_two_defects13	-4.8848764	2.6926501
category_two_defects14	-2.9873634	3.7271785
category_two_defects15	-4.3434076	2.3157523
category_two_defects16	-4.0840962	8.8195512
category_two_defects17	-1.4210880	4.4165181
category_two_defects18	-227.4871279	NA
category_two_defects19	NA	154.8072880
category_two_defects20	-0.8322924	8.4077228
category_two_defects21	-4.0348970	8.8394569
category_two_defects22	NA	477.9443385
category_two_defects23	NA	191.2042648
category_two_defects24	NA	482.2000562
category_two_defects26	-5.3327893	4.8223827
category_two_defects27	NA	482.8918280
category_two_defects29	-7.1169297	9.5218187
category_two_defects30	NA	254.7657979
category_two_defects32	-473.8564449	NA
category_two_defects34	NA	480.4074862
category_two_defects38	NA	480.9510968
category_two_defects40	-474.8441203	NA
category_two_defects45	NA	478.4965206
altitude_mean_meters	0.6578071	4.7241363
harvested2011	-2.4669518	1.9719426
harvested2012	-2.8197380	0.9105193
harvested2013	-2.2390861	1.5293781
harvested2014	-1.9001820	1.8585887
harvested2015	-2.4223610	1.3662790
harvested2016	-1.6916394	2.2290361
harvested2017	-1.8647301	2.0434207
harvested2018	-1.1584341	3.9710165

```
#for optimization model
mod1coefs_0 <- round(coef(model_0), 2)
library(knitr)
confint(model_0) %>%
  kable()
```

	2.5 %	97.5 %
(Intercept)	-36.0129131	-26.509287
aroma	12.2631820	22.208218
flavor	14.3901620	23.388516
acidity	9.3719109	18.830611
altitude_mean_meters	0.0249537	3.672661

log-odds

```
mod.coef.logodds<-model_0 %>%
  summary() %>%
  coef()
```

```
plot_model(model_0, show.values = TRUE, transform = NULL,
  title = "Log-Odds (quality-good)", show.p = FALSE)
```

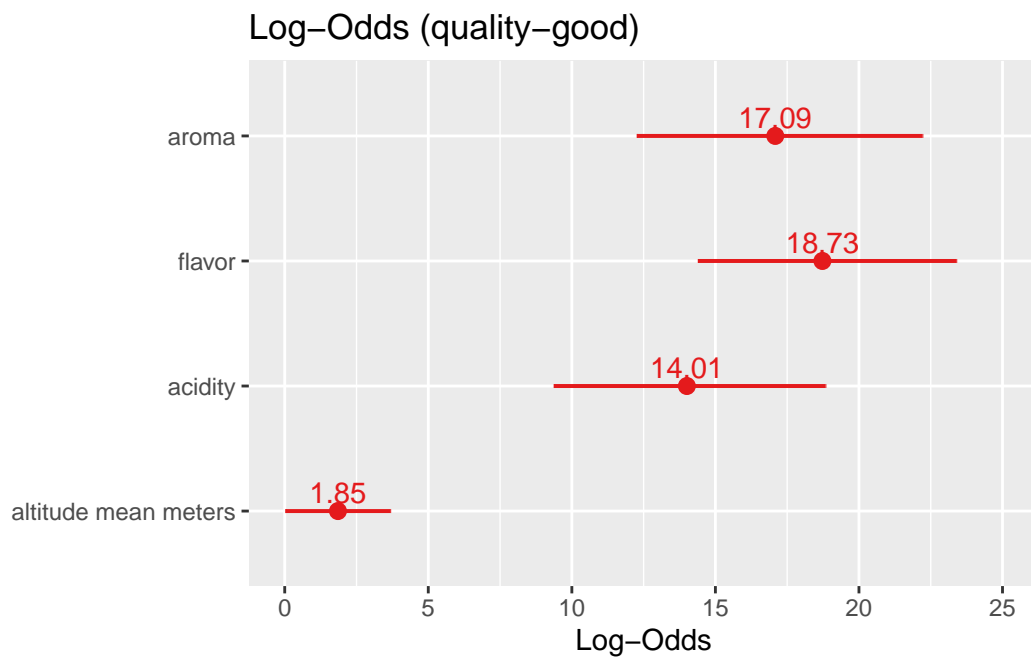


Figure 1: the log-odds of explanatory variables for quality good


```
data<- data%>%
  mutate(logodds.good = predict(model_0))
```

odds

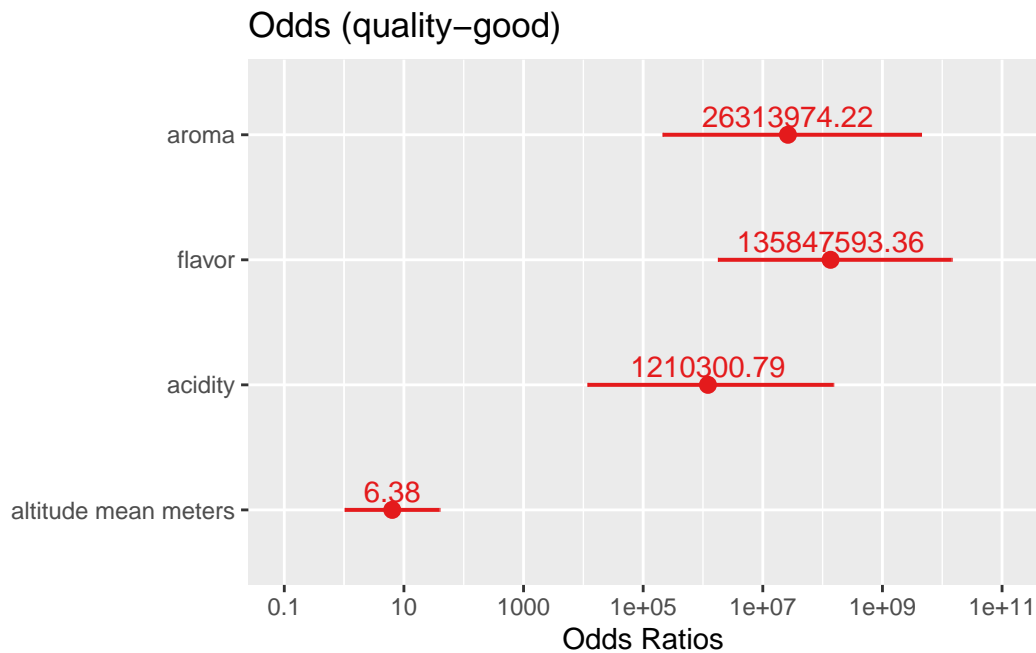
```
model_0 %>%
  coef() %>%
  exp()
```

(Intercept)	aroma	flavor
3.382473e-14	2.631397e+07	1.358476e+08
acidity	altitude_mean_meters	
1.210301e+06	6.384407e+00	

```
#check value
exp(coef(model_0))
```

(Intercept)	aroma	flavor
3.382473e-14	2.631397e+07	1.358476e+08
acidity	altitude_mean_meters	
1.210301e+06	6.384407e+00	

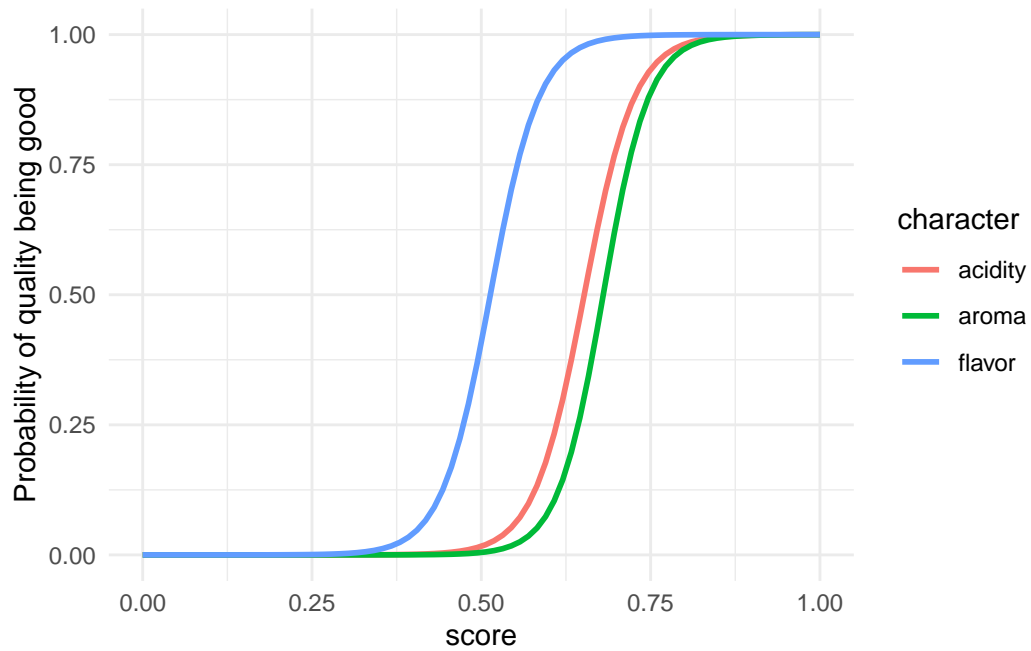
```
#odd ratio for quality good
plot_model(model_0, show.values = TRUE,
  title = "Odds (quality-good)", show.p = FALSE)
```



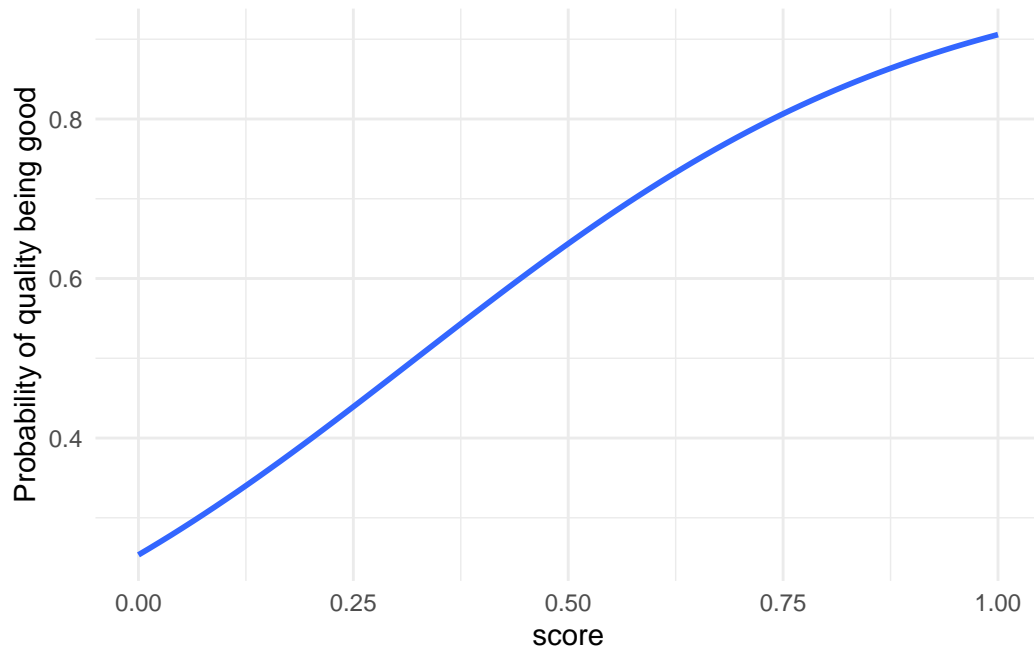
```
data<- data%>%
  mutate(odds.good = exp(logodds.good))
data<- data%>%
  mutate(prob.good = fitted(model_0))
```

probability continuous

```
#aroma/acidity/flavor prob
library(ggplot2)
library(tidyr)
library(dplyr)
data_long1 <- data %>%
  pivot_longer(cols = c(aroma, flavor, acidity), names_to = "Type", values_to =
    ↪ "Value")
# plot
ggplot(data = data_long1, aes(x = Value, y = prob.good, color = Type)) +
  geom_smooth(method = "glm", method.args = list(family = "binomial"), se =
    ↪ FALSE) +
  labs(x = "score", y = "Probability of quality being good", color =
    ↪ "character") +
  theme_minimal()
```



```
ggplot(data = data, aes(x =altitude_mean_meters, y =prob.good)) +  
  geom_smooth(method = "glm", method.args = list(family = "binomial"), se =  
    ↪ FALSE) +  
  labs(x = "score", y = "Probability of quality being good", color =  
    ↪ "character") +  
  theme_minimal()
```



```
library(grid)
library(gridExtra)
#plot

p1=plot_model(model_0, type = "pred",terms = "aroma" ,title = "Aroma",
              axis.title = c("aroma", "Prob. of quality being good"))
p2=plot_model(model_0, type = "pred", terms="flavor",title = "Flavor",
              axis.title = c("flavor", "Prob. of quality being good"))
p3=plot_model(model_0, type = "pred",terms = "acidity", title = "Acidity",
              axis.title = c("acidity", "Prob. of quality being good"))
p4=plot_model(model_0, type = "pred",terms = "altitude_mean_meters", title =
  ↪ "altitude_mean_meters",
              axis.title = c("altitude_mean_meters", "Prob. of quality being
  ↪ good"))
#merge
grid.arrange(p1,p2,p3,p4,nrow=2)
```

