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Assignment on Regression and Classification

1. Simple regression. Get a univariate dataset from sources 1.

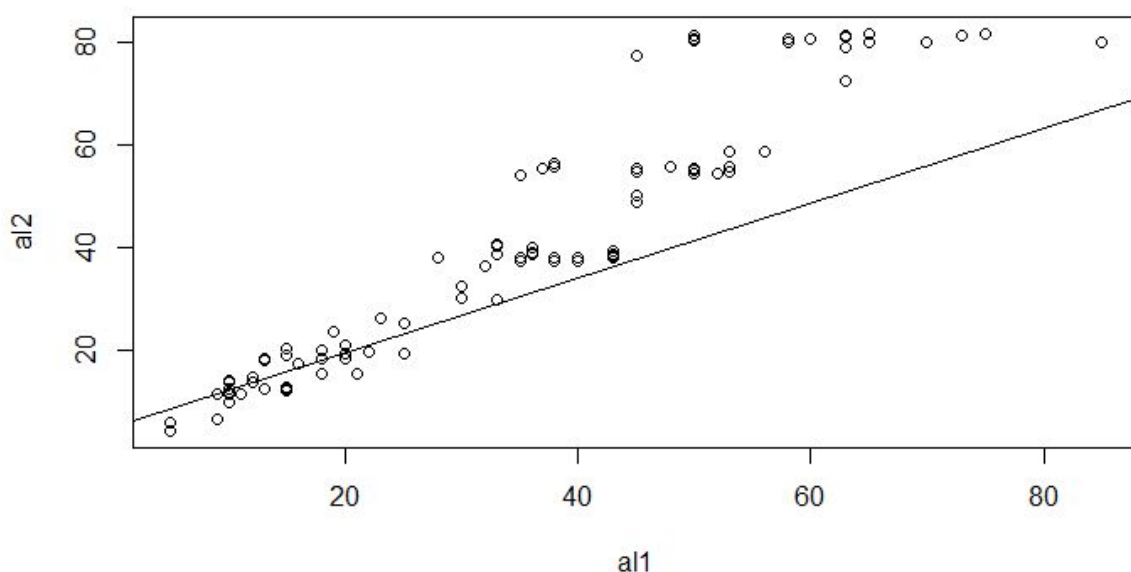
I have chosen data frame "alaska.pipeline" from UsingR. This data frame contains the following columns: field.defect (depth of defect as measured in field), lab.defect (depth of defect as measured in lab), batch (one of 6 batches). Length of data frame is 107.

```
al1 = alaska.pipeline$field.defect
al2 = alaska.pipeline$lab.defect
al3 = alaska.pipeline$batch
length(al1)
[1] 107
length(al2)
[1] 107
length(al3)
[1] 107
```

(a) Build a simple regression model (command lm). Provide the estimates of the model's parameters. Draw the scatter plot and the regression line.

I use data about depth of defect as measured in field and about depth of defect as measured in lab for to build a simple regression model.

```
al = lm(al1~al2)
plot(al1, al2)
abline(al)
```



(b) Analyze the summary statistics (command summary()) focusing on:

- i. The t-test for the slope. Explain.
- ii. The F-test. Explain.
- iii. R² coefficient. Explain.

```
> summary(al)
```

Call:

```
lm(formula = al1 ~ al2)
```

Residuals:

Min	1Q	Median	3Q	Max
-16.5817	-3.8259	0.1283	3.7432	21.5174

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	4.99368	1.12566	4.436	2.26e-05 ***
al2	0.73111	0.02455	29.778	< 2e-16 ***

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

Residual standard error: 6.081 on 105 degrees of freedom

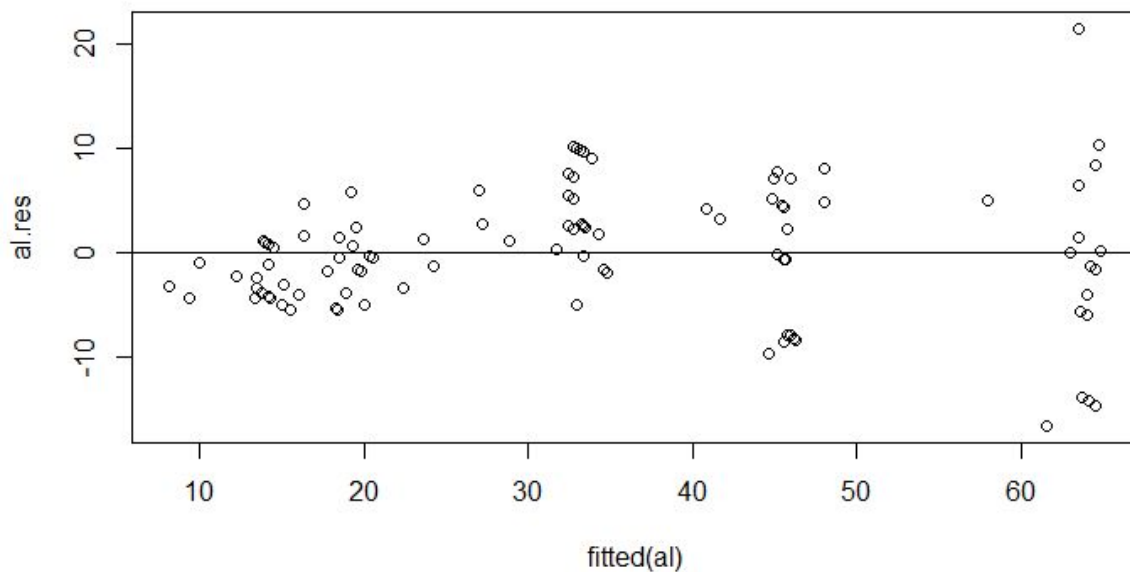
Multiple R-squared: 0.8941, Adjusted R-squared: 0.8931

F-statistic: 886.7 on 1 and 105 DF, p-value: < 2.2e-16

As we can see t-test value is 29.778 and p-value is < 2e-16, it means that al2 isn't significant R² is 0.8931, It means that we have a good model with correlated values. Estimate show us positive correlation.

(c) Plot the residuals against fitted values and comment on the model's adequacy. Examine the qq-plot for the residuals. Plot Cook's distances of the model. Explain.

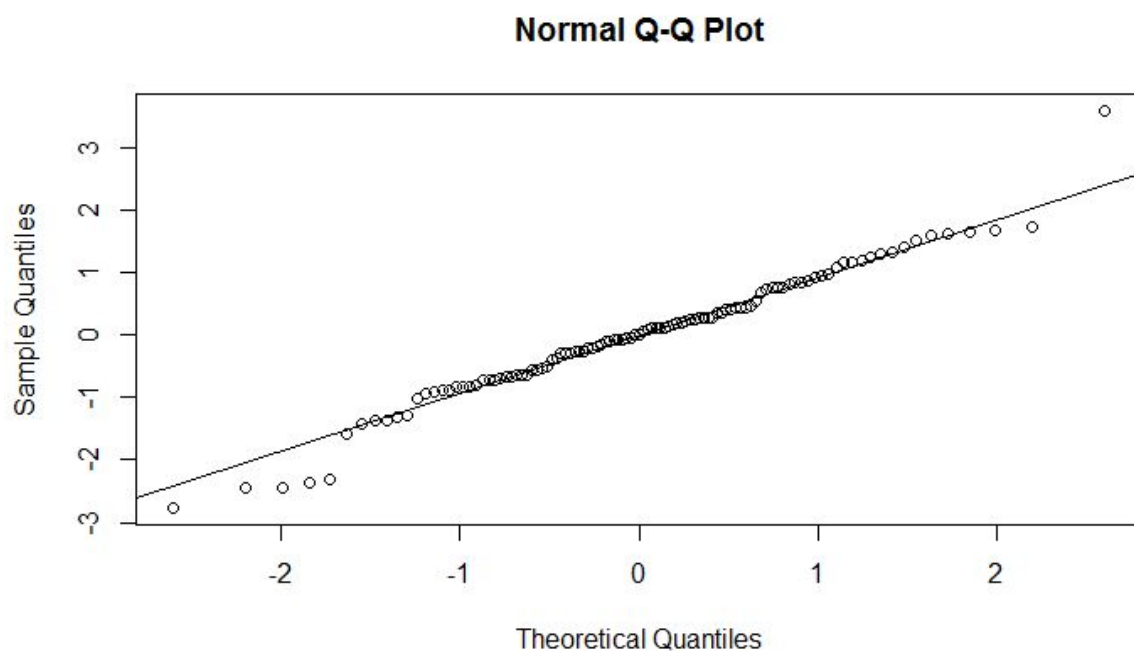
```
al.res = resid(al)
plot(fitted(al), al.res)
abline(0,0)
```



The plot shows the mean residual doesn't change with the fitted values, but the spread of the residuals is increasing as the fitted values changes. That is, the spread is not constant. Heteroskedasticity.

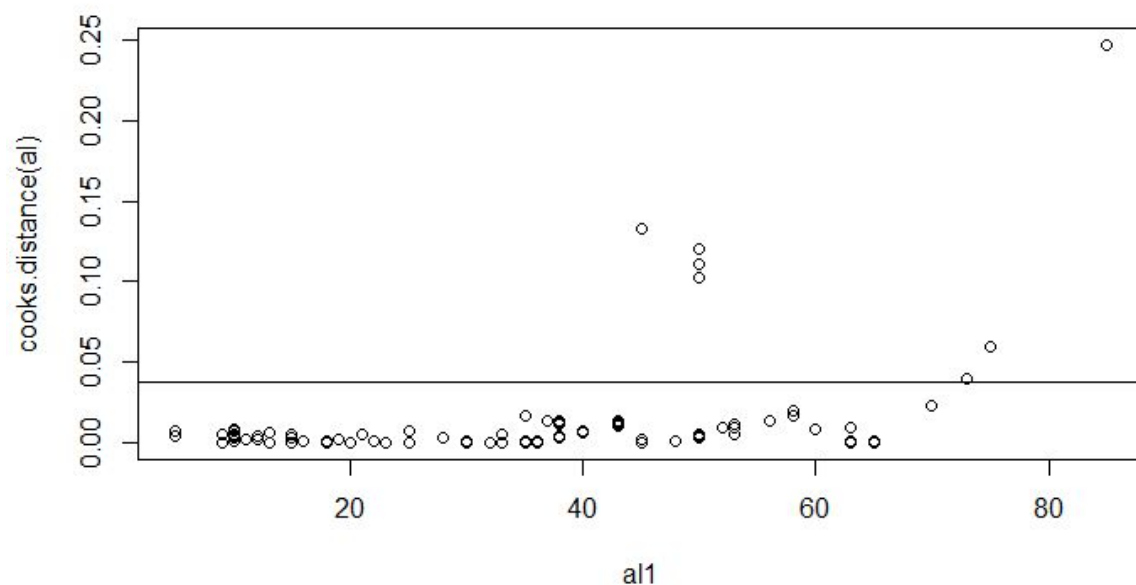
```
al.stdres = rstandard(al)
qqnorm(al.stdres)
qqline(al.stdres)
```

We can observe heavy-tailed distribution on qqplot.



```
plot(al1, cooks.distance(al))
n = 4/107
abline(n,0)
```

Ly



The cut off is 0.037. We can see that model has 7 outliers which can negatively affect regression model.

(d) Make predictions for several new values of the explanatory (independent) variable. For each predicted value, compute and plot the confidence intervals for the mean and single value.

```
> al1P= seq(0, 53, 0.5)
> predict(al, new = data.frame(al1 = al1P))
```

1	2	3	4	5	6	7	8	9
19.762123	45.935900	14.132568	20.493234	16.325901	33.507011	20.347012	32.922123	45.643455
10	11	12	13	14	15	16	17	18
64.871676	33.872567	46.228344	34.603678	15.448568	64.579232	15.009902	64.579232	19.981457
19	20	21	22	23	24	25	26	27
45.935900	63.994343	19.615901	46.301455	13.840124	19.323457	16.325901	33.360789	19.250346
28	29	30	31	32	33	34	35	36

```

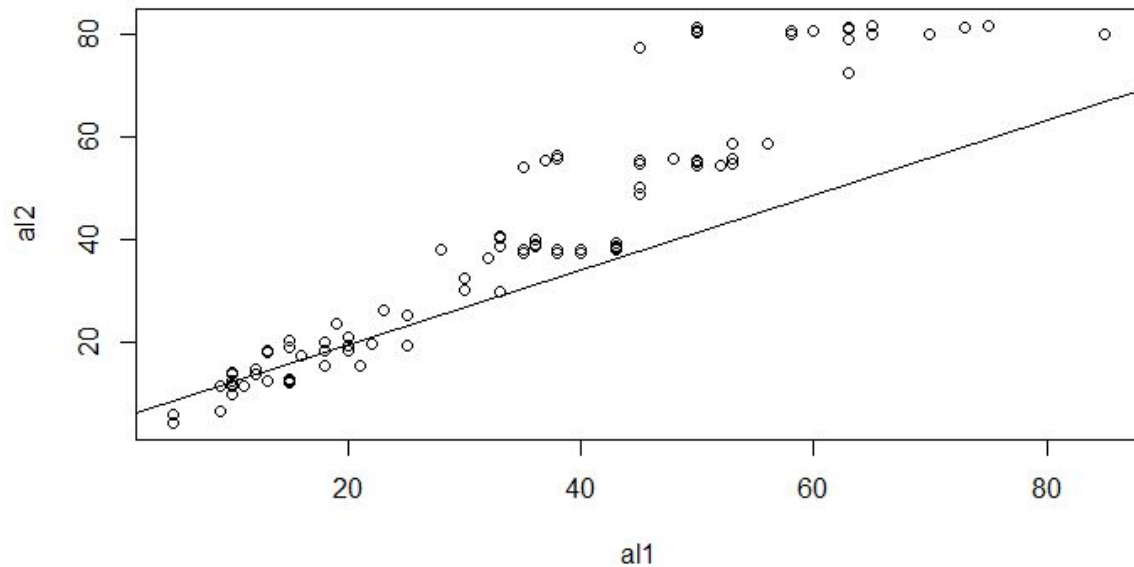
32.775900 45.204788 63.482565 33.141456 45.789677 33.360789 14.132568 63.775009
14.278790
  37    38    39    40    41    42    43    44    45
64.140565 19.981457 45.204788 18.884790 45.570344 13.986346 18.446124 13.401457
32.775900
  46    47    48    49    50    51    52    53    54
18.519235 32.775900 45.424122 33.287678 44.839233 32.775900 13.767013 64.725454
13.401457
  55    56    57    58    59    60    61    62    63
63.482565 18.373012 45.424122 63.628787 63.994343 45.789677 15.960346 64.213676
13.767013
  64    65    66    67    68    69    70    71    72
64.506121 14.132568 32.922123 44.619900 62.970787 18.299901 45.570344 13.328346
19.250346
  73    74    75    76    77    78    79    80    81
16.325901 32.410345 19.250346 32.410345 45.570344 63.482565 32.410345 16.325901
22.321012
  82    83    84    85    86    87    88    89    90
12.158568 34.823011 17.788124 8.137458 31.679234 24.221901 27.219456 41.695455
27.000123
  91    92    93    94    95    96    97    98    99
23.637012 15.083013 48.056122 34.238122 9.380346 57.999232 33.360789 19.177235
64.579232
 100   101   102   103   104   105   106   107
61.581676 44.912344 9.965235 28.827901 19.469679 47.983010 14.425013 40.818122

```

```

> conf = predict(al, new = data.frame(al1 = al1P), int = "conf")
> prdct = predict(al, new = data.frame(al1 = al1P), int = "predict")
> plot(al1, al2)
> abline(al)

```



2. Multivariate regression. Get a multivariate dataset (at least 3 variables) from 2.

I have chosen data frame Efficiency of Muscle Work - Case 2: Algerian Subjects from <http://www.stat.ufl.edu>. Measurements of Heat Production (calories) at various Body Masses (kgs) and Work levels (Calories/hour) on a stationary bike. This data frame contains the following columns: Body Mass(V1), Work Level(V2), Heat Output(V3). Length of data frame is 37.

(a) Choose the response and explanatory variables.

Response variable is Heat Production. Explanatory variables are Body Masses and Work levels.

```
v1 = musc.data$V1
v2 = musc.data$V2
v3 = musc.data$V3
```

(b) Build a multivariate linear model (command lm). Provide the estimates of the model's parameters.

```
musc.lm = lm(v3~v1+v2)
```

(c) Analyze the summary statistics (command summary()) with the emphasis on:

- i. t-test for slopes. Explain.
- ii. Overall F-test. Explain.
- iii. R2 and adjusted R2 coefficients. Explain.

```
> summary(musc.lm)
```

Call:

```
lm(formula = v3 ~ v1 + v2)
```

Residuals:

Min	1Q	Median	3Q	Max
-282.0	-109.2	9.1	123.9	235.9

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	977.425	376.053	2.599	0.013723 *
v1	17.778	4.943	3.597	0.001011 **
v2	6.244	1.522	4.102	0.000242 ***

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

Residual standard error: 147.1 on 34 degrees of freedom

Multiple R-squared: 0.4922, Adjusted R-squared: 0.4624

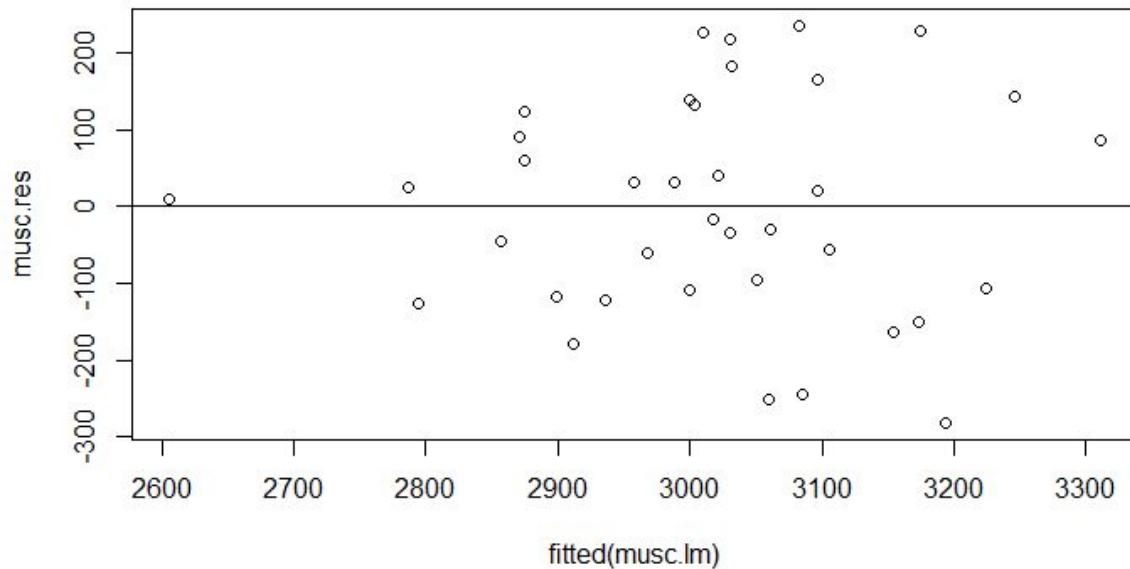
F-statistic: 16.48 on 2 and 34 DF, p-value: 9.914e-06

v2 isn't significant, v1 has not good value of significant

R² is 0.4624, It means that we have not good model with low correlated values. Estimate show us positive correlation.

(d) Plot the residuals against fitted values and comment on the model's adequacy.

```
musc.res = resid(musc.lm)
plot(fitted(musc.lm),musc.res)
abline(0,0)
```



The plot shows the mean residual doesn't change with the fitted values, but the spread of the residuals is increasing as the fitted values changes. That is, the spread is not constant. Heteroskedasticity.

(e) Play with your model by adding or removing the explanatory variables. Alternatively, add a non-linear term(s) to your model:

i. Choose the best one by the partial F-test criterion (command anova), see p. 294 of [1].

```
> musc.lm1 = lm(v3~v1)
> musc.lm2 = lm(v3~v2)
> anova(musc.lm1)
Analysis of Variance Table
```

```
Response: v3
      Df Sum Sq Mean Sq F value    Pr(>F)
v1      1 349284 349284 11.111 0.002037 **
Residuals 35 1100259 31436
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> anova(musc.lm2)
Analysis of Variance Table
```

```
Response: v3
      Df Sum Sq Mean Sq F value    Pr(>F)
v2      1 433482 433482 14.932 0.0004616 ***
Residuals 35 1016061 29030
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
anova(musc.lm1, musc.lm2)
Analysis of Variance Table
```

```
Model 1: v3 ~ v1
```

```
Model 2: v3 ~ v2
```

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	35	1100259				
2	35	1016061	0	84198		

ii. Choose the best one by the AIC criterion (command `stepAIC`), see p. 295 of [1].

```
> stepAIC(musc.lm1)
```

```
Start: AIC=385.11
```

```
v3 ~ v1
```

	Df	Sum of Sq	RSS	AIC
<none>		1100259	385.11	
- v1	1	349284	1449544	393.31

```
Call:
```

```
lm(formula = v3 ~ v1)
```

```
Coefficients:
```

(Intercept)	v1
1668.97	19.76

```
> stepAIC(musc.lm2)
```

```
Start: AIC=382.16
```

```
v3 ~ v2
```

	Df	Sum of Sq	RSS	AIC
<none>		1016061	382.16	
- v2	1	433482	1449544	393.31

```
Call:
```

```
lm(formula = v3 ~ v2)
```

```
Coefficients:
```

(Intercept)	v2
2118.255	6.779

iii. For each model, watch the value of the adjusted R² .

```
> summary(musc.lm1)
```

Call:

```
lm(formula = v3 ~ v1)
```

Residuals:

Min	1Q	Median	3Q	Max
-333.04	-137.55	3.78	118.78	321.07

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1668.970	405.072	4.120	0.00022 ***
v1	19.759	5.928	3.333	0.00204 **

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

Residual standard error: 177.3 on 35 degrees of freedom

Multiple R-squared: 0.241, Adjusted R-squared: 0.2193

F-statistic: 11.11 on 1 and 35 DF, p-value: 0.002037

```
> summary(musc.lm2)
```

Call:

```
lm(formula = v3 ~ v2)
```

Residuals:

Min	1Q	Median	3Q	Max
-303.90	-132.51	-30.33	151.04	318.10

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2118.255	233.930	9.055	1.07e-10 ***
v2	6.779	1.754	3.864	0.000462 ***

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

Residual standard error: 170.4 on 35 degrees of freedom

Multiple R-squared: 0.299, Adjusted R-squared: 0.279

F-statistic: 14.93 on 1 and 35 DF, p-value: 0.0004616

We can see that model with different variables have close values of R^2 : 0.2193 and 0.279. It means that choice of explanatory variable has not affect the quality of the model.

3. Logistic regression. Get a binary response regression dataset from 1 or 2. Briefly describe the data.

I have chosen data frame Presence of Growth of CRA7152 in Apple Juice from

<http://www.stat.ufl.edu>. Absence of growth of CRA7152 in apple juice

as a function of pH (3.5-5.5), Brix (11-19), temperature (25-50C), and Nisin concentration

(0-70).

```
apple.ph = apple.data$V1
apple.nisin = apple.data$V2
apple.temp = apple.data$V3
apple.brix = apple.data$V4
apple.growth = apple.data$V5
```

(a) Build a logistic regression model (command glm). Comment on the significance of the coefficients.

```
apple.log = glm(apple.growth~apple.ph+apple.nisin+apple.temp+apple.brix, family =
binomial)
> summary(apple.log)
```

Call:

```
glm(formula = apple.growth ~ apple.ph + apple.nisin + apple.temp +
    apple.brix, family = binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.3614	-0.3990	-0.1585	0.6306	1.6200

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-7.24633	3.21864	-2.251	0.024362 *
apple.ph	1.88595	0.54123	3.485	0.000493 ***
apple.nisin	-0.06628	0.01905	-3.479	0.000503 ***
apple.temp	0.11042	0.04769	2.316	0.020585 *
apple.brix	-0.31173	0.14317	-2.177	0.029458 *

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 95.945 on 73 degrees of freedom
Residual deviance: 52.331 on 69 degrees of freedom
AIC: 62.331

Number of Fisher Scoring iterations: 6

We can see that apple.ph, apple.temp, apple.brix correlated, but without good value.
Apple.nisin and apple.ph don't correlated.

(b) Use stepAIC command to select the best model.

```
> stepAIC(apple.log)
Start: AIC=62.33
apple.growth ~ apple.ph + apple.nisin + apple.temp + apple.brix
```

	Df	Deviance	AIC
<none>		52.331	62.331
- apple.brix	1	58.153	66.153
- apple.temp	1	59.219	67.219
- apple.ph	1	70.148	78.148
- apple.nisin	1	73.637	81.637

```
Call: glm(formula = apple.growth ~ apple.ph + apple.nisin + apple.temp +
  apple.brix, family = binomial)
```

Coefficients:

(Intercept)	apple.ph	apple.nisin	apple.temp	apple.brix
-7.24633	1.88595	-0.06628	0.11042	-0.31173

Degrees of Freedom: 73 Total (i.e. Null); 69 Residual

Null Deviance: 95.95

Residual Deviance: 52.33 AIC: 62.33

We observe model with lowest AIC 62.33 and optimal model with considering AIC will be
formula = apple.growth ~ apple.ph + apple.temp

(c) Make a prediction based on the entire dataset. State the threshold of acceptance.
Compare the forecast with the actual observations. Comment on the results.

Threshold of acceptance is 0.5

```
> predict(apple.log, type = "response")
```

1	2	3	4	5	6	7	8
0.640865388	0.063703458	0.624390499	0.269213240	0.721189987	0.615292098		
0.938462821	0.770470752						
9	10	11	12	13	14	15	16
0.005417622	0.007774388	0.076511360	0.002429956	0.367785386	0.071650011		
0.021713675	0.012476633						
17	18	19	20	21	22	23	24
0.023025058	0.429165305	0.013483055	0.272967506	0.819688780	0.974717132		
0.932083860	0.008631542						
25	26	27	28	29	30	31	32
0.010669862	0.154826624	0.024486574	0.300339180	0.023000986	0.048209979		
0.591373886	0.729702272						
33	34	35	36	37	38	39	40
0.447747132	0.675506680	0.970759620	0.128449650	0.211818044	0.640865388		
0.063703458	0.624390499						

41	42	43	44	45	46	47	48
0.269213240	0.721189987	0.615292098	0.938462821	0.770470752	0.005417622		
0.007774388	0.076511360						
49	50	51	52	53	54	55	56
0.002429956	0.367785386	0.071650011	0.021713675	0.012476633	0.023025058		
0.429165305	0.013483055						
57	58	59	60	61	62	63	64
0.272967506	0.819688780	0.974717132	0.932083860	0.008631542	0.010669862		
0.154826624	0.024486574						
65	66	67	68	69	70	71	72
0.300339180	0.023000986	0.048209979	0.591373886	0.729702272	0.447747132		
0.675506680	0.970759620						
73	74						
0.128449650	0.211818044						

```

> apple.growth
[1] 0 0 1 1 1 0 0 1 0 0 0 0 0 0 0 0 1 0 0 1 1 1 0 0 0 0 1 0 0 1 1 0 1 1 0 0 0 0 1 1 1 0 0 1 0
[47] 0 0 0 0 0 0 0 0 1 0 0 1 1 1 0 0 0 0 1 0 0 1 1 0 1 1 0 0

```

More than 80% of predicted values correspond to actual observations.

(d) Divide the entire set into training and test subsets. Rebuild the model using only the training subset. Make predictions for the test subset. Comment.

```

apple.data = read.table("apple_juice_dat.txt")
names(apple.data) = c('ph','nisin', 'temp', 'brix', 'growth')
apple.log = glm(growth ~ ph + nisin + temp + brix, data = apple.data, family =
binomial)
set.seed(101)
tr.index = sample(1:nrow(apple.data), nrow(apple.data)*0.8)
trSet = apple.data[tr.index, ]
testSet = apple.data[-tr.index, ]
apple.log1 = glm(growth ~ ph+ nisin + temp + brix, trSet, family = binomial)
fitted_results_test = predict(apple.log1, newdata= testSet, type = "response")
fitted_results_test = ifelse(fitted_results_test > 0.5,1,0)
fitted_results_test
5 6 17 20 26 27 29 37 43 44 49 54 56 58 70
1 1 0 0 0 0 0 0 1 1 0 0 0 1 1

```

4. Discriminant analysis. Use the same dataset as for the logistic regression.

(a) Conduct the linear discriminant analysis (command `lda`, package `MASS`) using training and test subsets. Compare the forecast with the actual observations. Comment on the

results.

```
> apple.log2 = lda(growth ~ ph+ nisin + temp + brix, trSet)
```

```
> apple.log2
```

```
Call:
```

```
lda(growth ~ ph + nisin + temp + brix, data = trSet)
```

Prior probabilities of groups:

```
      0      1
0.5932203 0.4067797
```

Group means:

```
      ph  nisin  temp  brix
0 4.2000 47.42857 38.97143 15.00
1 4.8125 17.50000 40.91667 13.25
```

Coefficients of linear discriminants:

```
      LD1
ph  1.14212031
nisin -0.03855885
temp  0.03817777
brix -0.16672426
```

```
> apple.log2 = lda(growth ~ ph+ nisin + temp + brix, testSet)
```

```
> apple.log2p = predict(apple.log2, trSet)$class
```

```
> apple.log2p
```

```
[1] 0 0 0 0 1 1 1 0 0 0 0 0 0 0 1 0 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 1 0
```

```
[47] 1 0 0 0 0 0 1 0 0 1 0 0 0
```

```
Levels: 0 1
```

The LDA output is 0.593 and 0.406, it means that 59,3% of the training observations correspond presence of Growth of CRA7152.

(b) Conduct the quadratic discriminant analysis (command qda). Comment.

```
> apple.qda = qda(growth ~ ph+ nisin + temp + brix, trSet)
```

```
> predict(apple.qda, testSet)
```

```
$class
```

```
[1] 1 1 0 0 0 0 0 0 1 0 0 0 0 1 0
```

```
Levels: 0 1
```

```
$posterior
```

```
      0      1
5 0.02246616 9.775338e-01
6 0.10345915 8.965409e-01
17 0.99958814 4.118634e-04
20 0.97856839 2.143161e-02
```

```
26 0.99686579 3.134205e-03
27 0.99999911 8.854489e-07
29 0.99809355 1.906453e-03
37 0.99739444 2.605557e-03
43 0.10345915 8.965409e-01
44 0.99988304 1.169638e-04
49 0.99996654 3.345766e-05
54 0.99958814 4.118634e-04
56 0.99866290 1.337101e-03
58 0.07475746 9.252425e-01
70 0.83690817 1.630918e-01
```

5. The KNN classifier. Use the same dataset as for the logistic regression and discriminant analysis.

- (a) Conduct the KNN classification (command `knn()`, package `class`) using training and test subsets. Compare the forecast with the actual observations. Comment on the results.
- (b) Play with a number of nearest neighbors K .
-

```
> apple.label = apple.data[1:59, 1]
> knn(trSet, testSet, apple.label, 3)
[1] 3.5 3.5 5.5 5 5 3.5 3.5 3.5 5 5 3.5 5.5 5 4 4
Levels: 3.5 4 5 5.5
> knn(trSet, testSet, apple.label, 5)
[1] 5 5 5.5 5 5 3.5 5 3.5 5 5 5.5 5.5 3.5 5 5.5
Levels: 3.5 4 5 5.5
> knn(trSet, testSet, apple.label, 1)
[1] 3.5 5 5 3.5 5 3.5 5 3.5 4 4 5 5 4 5.5 5.5
Levels: 3.5 4 5 5.5
```
