Data Analyzing with Logistic Regression and ANOVA

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1 Task 1: Logistic Regression

1.1 Introduction

In this task, we applied the logistic regression model to analyze the dataset of "prostate.csv" which contains the information from patients who are being assessed for prostate cancer.

Our goal is to build a binary-classification model to predict whether someone will be diagnosed with prostate cancer. The full model is as follows and we did some improvement to make our model more efficient.

$$\ln\left(\frac{\hat{\pi}}{1-\hat{\pi}}\right) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \beta_4 X_4 + \beta_5 X_5 + \beta_6 X_6 + \beta_7 X_7 + \varepsilon \tag{1}$$

A summary table is listed below to interpret these variables.

Name	Variable	Variable Kind	Units
`cancer`	Y	Response	0/1
`psa`	X_1	Numerical	mg/ml
`c.vol`	X_2	Numerical	cc
`weight`	X_3	Numerical	gm
`age`	X_4	Numerical	years
`benign`	X_5	Numerical	cm^2
`inv`	X_6	Categorical	invasion/no-invasion
`cap`	X_7	Numerical	cm

Table 1: A summary table for variables

	X_1	X_2	X_3	X_4	X_5	X_7
Min	0.651	0.2592	10.70	41.00	0.000	0.0000
Max	265.072	45.6042	450.34	79.00	10.278	18.1741

Table 2: Reasonable range for numeric variables

1.2 Model Fitting

Firstly, stepwise selection methods are employed to choose the best logistic regression model for the dataset, based on the criteria of AIC.

Method	Selected Model
`Forward`	$logit(\hat{\pi}) \sim X_2 + X_1 + X_4$
`Backward`	$logit(\hat{\pi}) \sim X_1 + X_2 + X_4$
`Forward/Backward`	$logit(\hat{\pi}) \sim X_2 + X_1 + X_4$
`Backward/Forward`	$logit(\hat{\pi}) \sim X_1 + X_2 + X_4$

Table 3: Stepwise selection results

The best model selected by all stepwise methods correspond with each other. As a result, `psa`, `c.vol` and `age` will be included in the candidate model.

$$\ln\left(\frac{\hat{\pi}}{1-\hat{\pi}}\right) = -9.0529 + 0.04064X_1 + 0.11788X_2 + 0.08779X_4 \tag{2}$$

	$\hat{\beta}$	$\exp(\hat{\beta})$	Pr(>|z|)
`Intercept`	-9.05285	0.00012	0.0145
`X1`	0.04064	1.04147	0.0596
`X2`	0.11788	1.12511	0.0244
`X4`	0.08779	1.09175	0.1073

Table 4: Coefficients of the candidate model

1.3 CI & HT for β_i's

Then we applied t test for each β_i, where $i = 1, 2, 3$, to see whether X_i can be dropped from the model or has a significant effect on Y.

- H_0: $\beta i = 0$.
- H_A: $\beta i \neq 0$.

Test-statistic is $ts = (\hat{\beta}_i - 0)/SE(\beta_i)$, corresponding confidence intervals are listed as follows,

	2.5%	97.5%
`X1`	0.0069	0.0878
`X2`	0.0169	0.2260
`X4`	-0.0128	0.2022

Table 5: 95% Confidence Intervals for $\hat{\beta}$'s

	2.5%	97.5%
`exp.X1`	1.0069	1.0918
`exp.X2`	1.0170	1.2536
`exp.X4`	0.9873	1.2240

Table 6: 95% Confidence Intervals for $\exp(\hat{\beta})$'s

1.4 Model Selection

P-value for $\hat{\beta}_3$ equals 0.1073, which is large enough for us to fail to reject H_0. Besides, CI for $\exp(\hat{\beta}_3)$ contains 1, which suggests X_4 may not have a significant effect on Y. So we used Likelihood Ratio Test to decide whether X_4 should be dropped from the model.

- H_0: X_4 can be dropped from the model.
- H_A: X_4 cannot be dropped from the model.

Test-statistic is $LR = -2(LL_0 - LL_A) \sim \chi^2(dof = 1)$. P-value equals 0.0896 which is larger than 0.05 but less than 0.10. It is not large enough for us to accept H_0. As a result, we decided not to drop X_4 from the final model.

Interpret of the p-value for Likelihood Ratio test above.

- It means if we used the smaller model without infomation on age to predict the diagnosis of prostate cancer, we would observe our data or more extreme with the probability of 0.0896.

In conclusion, the final model is $logit(\hat{\pi}) \sim X_1 + X_2 + X_4$.

1.5 Model Diagnostics

1.5.1 Normality

Because Y is binomially distributed, standardized residuals should be approximately normally distributed.

$$r_i = \frac{y_i - \hat{\pi}_i}{\sqrt{\hat{\pi}_i(1-\hat{\pi}_i)(1-h_{ii})n_1}} \sim N(0,1) \tag{3}$$

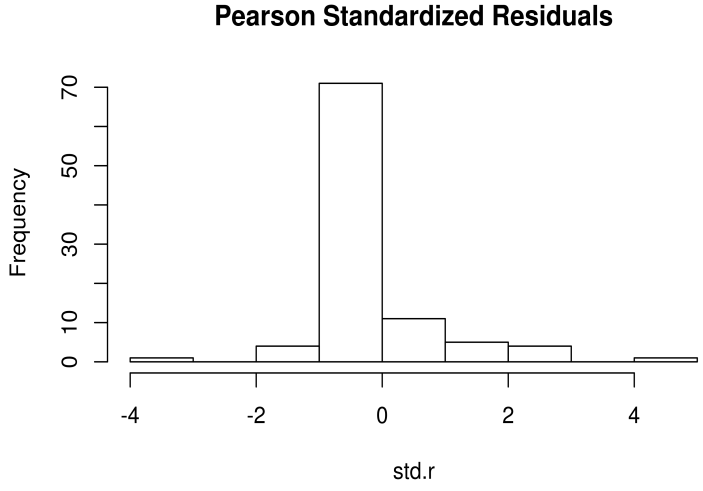


Figure 1: Plot of standardized residuals

Judging from the plot, we can conclude that the standardized residuals of pearson is approximately normally distributed.

Besides, in general, $|r_i| > 3$ can be an outlier. Therefore, there are several outliers in the dateset.

1.5.2 ROC and AUC

Since sensitivity and specificity rely on the cutoff value π_0, ROC and AUC are usually used as a better criteria to judge if a model fits well and how good the model is.

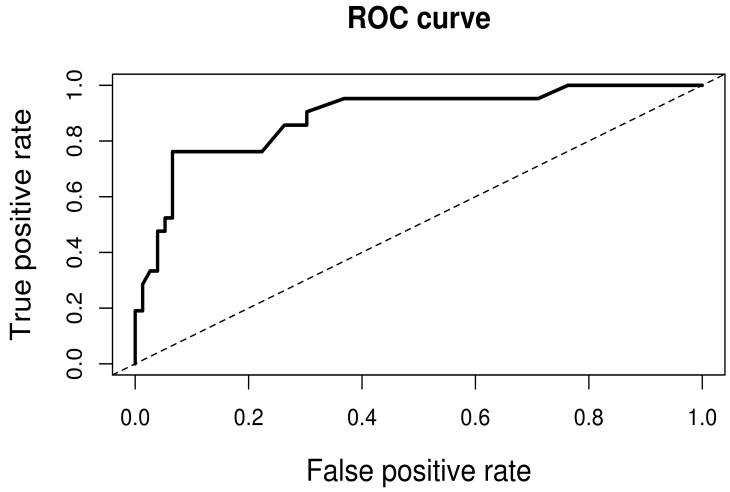
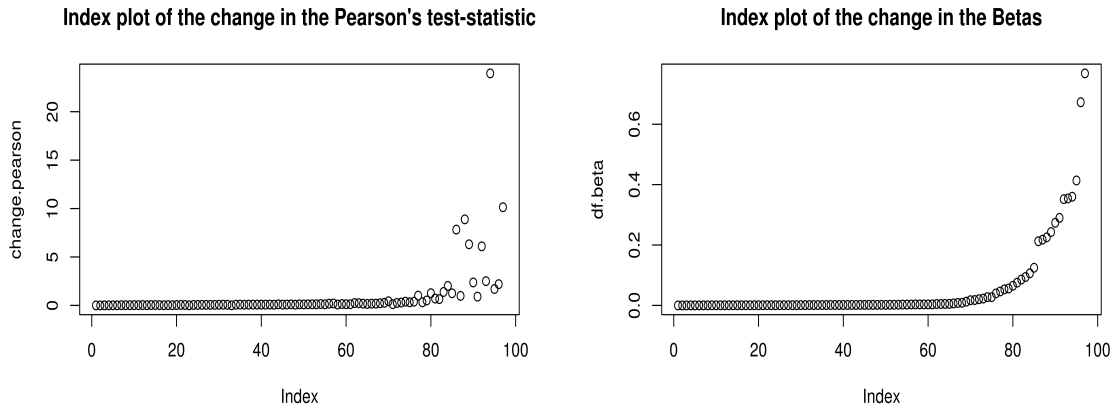


Figure 2: ROC

AUC equals 0.8835, 95% CI for AUC is $[0.7977, 0.9693]$ and does not contain 0.5. We can conclude that the model is very well fit.

1.6 Remove Outliers

We know that in logistic regression repeated rows may be diagnosed as influential points using leave-one-out measures like DfBeta and $\Delta\chi^2$. However, considering that there are 6 numeric explanatory variables in this dataset, it is almost impossible to have repeated rows. As a result, we treated all selected influential points as outliers. We removed 3 outliers, the ratio of which to the number of samples in the whole dataset is 3.09%, thus would not affect the dataset too much.



(a) Index plot of the change in the Pearson's test-statistics

(b) Index plot of the change in the Betas

Figure 3: Plots to identify outliers

criteria	cutoff
change.pearson	15
df.beta	0.50

Table 7: Cutoff

According to standardized residuals and Figure 3, outliers are as follows.

index	Y	X1	X2	X3	X4	X5	X6	X7
41	1	9.974	1.8589	23.104	60	0	no-invasion	0
55	1	14.880	23.3361	33.784	59	0	no-invasion	0
91	0	56.261	25.7903	60.340	68	0	no-invasion	0

Table 8: Outliers of the dataset

1.7 Final Model

Finally, `psa`, `c.vol` and `age` are included in the final model. The logistic regression model is fitted using the dataset removed outliers.

$$\ln\left(\frac{\hat{\pi}}{1-\hat{\pi}}\right) = -13.5201 + 0.0648X_1 + 0.1285X_2 + 0.1428X_4 \tag{4}$$

	$\hat{\beta}$	$\exp(\hat{\beta})$	Pr(>|z|)
`Intercept`	-13.52014	1.3436×10^{-6}	0.0049
`X1`	0.06481	1.06695	0.0230
`X2`	0.12850	1.13712	0.0449
`X4`	0.14279	1.15349	0.0376

Table 9: Coefficients of the final model

Interpretation of p-values for t-test of $\hat{\beta}_i$'s.

- p-value for $\hat{\beta}_1$: If the infomation on serum prostate-specific antigen level was dropped from the model, we would observe our data or more extreme with the probability of 0.0230.
- p-value for $\hat{\beta}_2$: If the infomation on cancer volume was dropped from the model, we would observe our data or more extreme with the probability of 0.0449.
- p-value for $\hat{\beta}_3$: If the infomation on age was dropped from the model, we would observe our data or more extreme with the probability of 0.0376.

	2.5%	97.5%
`exp.X1`	1.0174	1.1374
`exp.X2`	1.0086	1.3029
`exp.X4`	1.0192	1.3397

Table 10: 95% Confidence Intervals for $\exp(\hat{\beta})$'s in the final model

1.7.1 Error Matrix

We set the value of cutoff π_0 to 0.30, and get the following matrix, with a sensitivity of 0.7895, a specificity of 0.9200 and an error-rate of 0.1064.

	$\hat{y}=0$	$\hat{y}=1$
$y=0$	69	6
$y=1$	4	15

Table 11: Error Matrix

1.7.2 Predictive Power

$$\begin{aligned} 1-\frac{SSE}{SSTO} &= 1-\sum_{i=0}^{n}(y_i-\hat{\pi}_i)^2/\sum_{i=0}^{n}(y_i-\bar{y})^2 \\ &= 0.5069 \end{aligned} \tag{5}$$

When we use Logistic Regression instead of $\bar{y}$ to predict the probability of a patient who is being assessed for prostate cancer, we can reduce the error by 50.69%.

1.8 Interpretation

In this section, we are going to interpret $\hat{\beta}_i$'s and CI's of test-statistics in terms of the problem. (Note that p-values of test-statistics have already been interpreted in the context)

1.8.1 $\hat{\beta}_i$'s

- $\exp(\hat{\beta}_0)$: It is inappropriate to interpret $\hat{\beta}_0$, since 0 is not within the reasonable range for X_1, X_2 and X_4.
- $\exp(\hat{\beta}_1)$: The odds of diagnosis with prostate cancer are multiplied by 1.0670 when serum prostate-specific antigen level increases by 1 mg/mL, holding all other variables constant.
- $\exp(\hat{\beta}_2)$: The odds of diagnosis with prostate cancer are multiplied by 1.1371 when prostate cancer volume increases by 1 cc, holding all other variables constant.
- $\exp(\hat{\beta}_3)$: The odds of diagnosis with prostate cancer are multiplied by 1.1535 when age of patient incrases by 1 year, holding all other variables constant.

1.8.2 CI's for $\hat{\beta}_i$'s

- CI for $\exp(\hat{\beta}_1)$: We are 95% confident that the odds of diagnosis with prostate cancer tend to be multiplied by between 1.0174 and 1.1374 when serum prostate-specific antigen level increases by 1 mg/mL, holding all other variables constant.
- CI for $\exp(\hat{\beta}_2)$: We are 95% confident that the odds of diagnosis with prostate cancer tend to be multiplied by between 1.0086 and 1.3029 when prostate cancer volume increases by 1 cc, holding all other variables constant.
- CI for $\exp(\hat{\beta}_3)$: We are 95% confident that the odds of diagnosis with prostate cancer tend to be multiplied by between 1.01922 and 1.3397 when age of patient increases by 1 year, holding all other variables constant.

1.9 Predict

We used our model to answer this question, "Predict the probability of prostate cancer diagnosis for someone with 10 psa, 5 c.vol, age 67."

Name	Result
$\hat{\pi}_i$	0.0652
$\hat{y}$	0

Table 12: Prediction

The probability of prostate cancer diagnosis for someone with 10 psa, 5 c.vol, age 67 is 0.0652, and it is small enough for us to conclude that he would not be diagnosed with prostate cancer.

1.10 Conclusion

It is safe to conclude that the infomation on age of patient has the most significant effect on the prediction of prostate cancer diagnosis since the coefficient of $\exp(\hat{\beta}_i)$ is the largest positive value.

2 Task 2: ANOVA

2.1 Introduction

In this task, we applied ANOVA to analyze the dataset of "cows.csv" which contains the information from cows fed different types of grass.

Our goal is to build a model to tell whether there exist significant differences between groups. The full model is as follows and we did some improvement to make our model more efficient.

$$Y_{ij} = \mu_i + \varepsilon_{ij} \tag{6}$$

A summary table is listed below to interpret these variables.

Name	Variable	Variable Kind	Units
`Weight`	Y	Response	kg
`Grass`	X	Catogorical	A/B/C

Table 13: A summary table for variables

2.2 Data Preparation

2.2.1 Summary Table

Some useful statistics give us a brief review of basic information on our dataset. As shown in the table below, it is apparent that differences exist between varied categories.

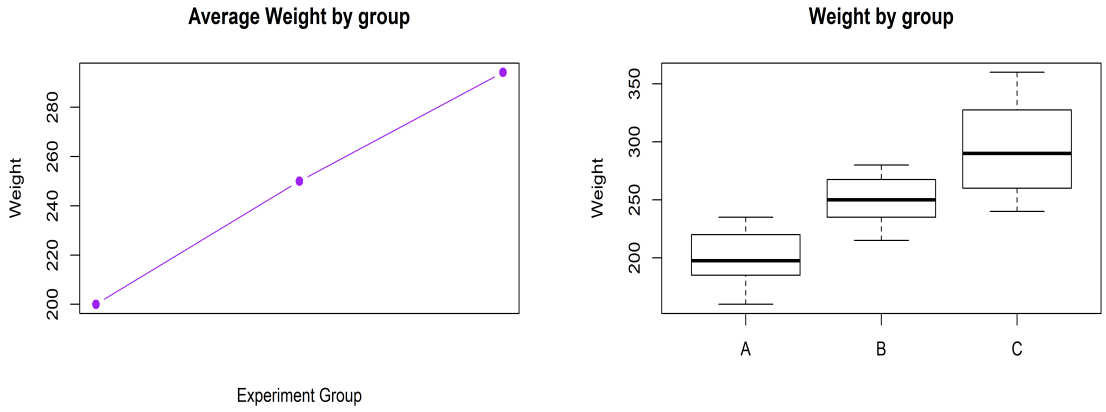
	A	B	C
Means	200.0	250.0	294.2
Std. Dev	22.46	20.45	40.44
Sample Size	12	12	12

Table 14: Summary Table for data

2.2.2 Visualizing the Data

By visualizing the data, it is obvious that the mean weight varies from group to group , which suggests the factor that different types of grass the cows were fed have a significant effect on the weight of cows.

From the grouped boxplot, we are convinced that there is no obvious outliers in our dataset.



(a) Mean of different groups

(b) Boxplot of weight vs Grass

Figure 4: Review of the dataset

2.3 Simple one-way ANOVA

2.3.1 F-test

We first use F-test to find whether type of grass is an important factor in the model.

- H_0: $\mu_A = \mu_B = \mu_C$.
- H_A: Not all $\mu_i (i = A, B, C)$ are equal.

According to R, the p-value for F-tset is almost 0. So we reject H_0 and conclude that the Grass group has a significant effect on cows' weight.

Interpret the p-value of F-test above.

- It means that if $\mu_A = \mu_B = \mu_C$ was true (types of grass had no significant difference on the weight of cows), we would observe our data or more exteme with the probability of almost 0%.

2.3.2 ANOVA Table

	difference	95 % C.I.	p-value
$\mu_A - \mu_B$	-50.00	[-80.07,-19.93]	0.00058
$\mu_A - \mu_C$	-94.17	[-124.2,-64.10]	0
$\mu_B - \mu_C$	-44.17	[-74.24,-14.10]	0.002314

Table 15: ANOVA table for the data

The C.I.'s based on Bonferroni does not contain 0 which means there exists significant difference between different groups.

Interpretation for p-values of F-test.

- p-value for $\mu_A - \mu_B$: If there was no significant difference between the mean weight of cows fed grass A and grass B, we would observe our data or more extreme with the probability of 0.00058.
- p-value for $\mu_A - \mu_C$: If there was no significant difference between the mean weight of cows fed grass A and grass C, we would observe our data or more extreme with the probability of 0.
- p-value for $\mu_B - \mu_C$: If there was no significant difference between the mean weight of cows fed grass B and grass C, we would observe our data or more extreme with the probability of 0.002314.

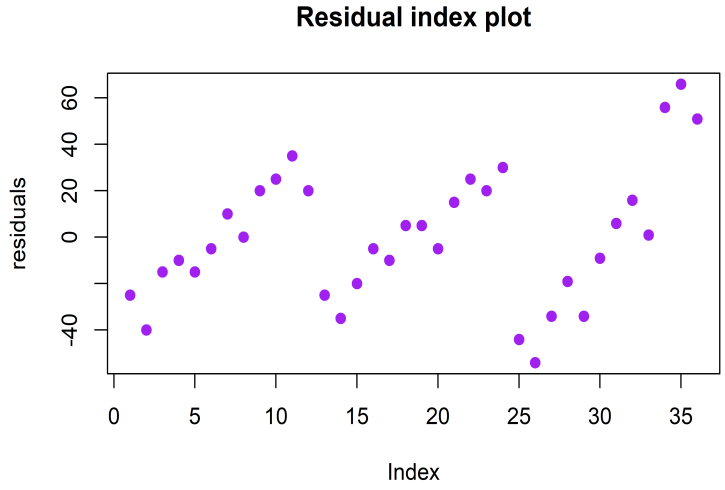
Interpret $\mu_i - \mu_j$ and the CI's for $\mu_i - \mu_j$.

- $\mu_A - \mu_B$: The estimated weight gain (kg) in the cows fed grass A is 50.00kg smaller than the cows fed grass B.
- $\mu_A - \mu_C$: The The estimated weight gain (kg) in the cows fed grass A is 94.17kg smaller than the cows fed grass C.
- $\mu_B - \mu_C$: The The estimated weight gain (kg) in the cows fed grass B is 44.17kg smaller than the cows fed grass C.

- CI for $\mu_A - \mu_B$: We are 95% confident that weight gain (kg) in the cows fed grass A is smaller than the cows fed grass B by between 19.93kg and 80.07kg.
- CI for $\mu_A - \mu_C$: We are 95% confident that weight gain (kg) in the cows fed grass A is smaller than the cows fed grass C by between 64.10kg and 124.2kg.
- CI for $\mu_B - \mu_C$: We are 95% confident that weight gain (kg) in the cows fed grass B is smaller than the cows fed grass C by between 14.10kg and 74.24kg.

2.4 Diagnostics for the model

2.4.1 Independence of Y



Index is just a subjective order of samples in the dataset, points on the plot can be randomly shuffled. Since there is no apparent pattern along the vertical axis, we can conclude that each sample is independently selected.

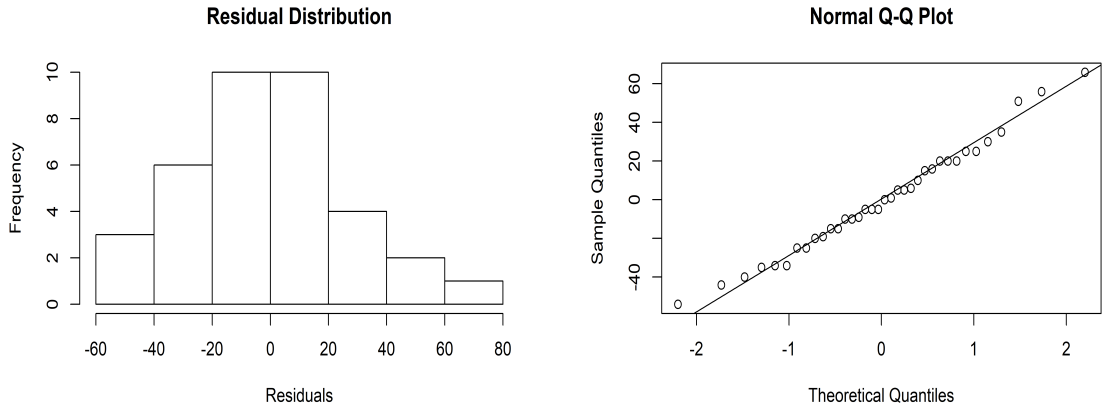
2.4.2 Normality of errors

We used Shapiro-Wilks test for error normality. According to R, the p-value is 0.8852. So we fail to reject the null hypothesis and conclude that the errors are normally distributed.

Interpret p-value of the shapiro test .

- If the errors were normally distributed, we would observe the data or more extreme 88.52% of the time.

Secondly, based on the Normal QQ Plot and the distribution of the residuals, we are convinced that the errors are normal.



(a) Residual Distribution Plot (b) Normal QQ Plot

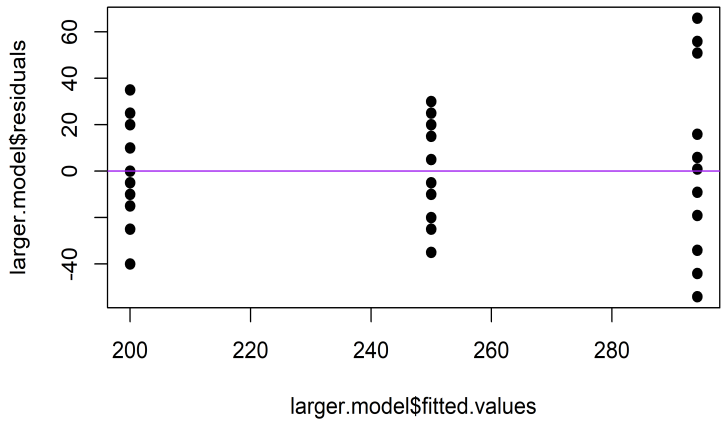
Figure 5: Plots of model diagnostics

2.4.3 Test for equal variance

We used Modified-Levene test for equal variances. According to R, the p-value is 0.03931. It is small enough for us to reject the null hypothesis at $\alpha = 0.05$ and conclude that the variance is not constant. What is more, the plot below also shows the variance is not constant.

Interpret the p-value of Modified-Levene test.

- If the variance was constant, we would observe the data or more extreme 3.931% of the time.



2.5 Choose cutoff and remove outliers

Based on the analysis of the standardized residuals in R, using the cutoff based on t-distribution, which is 2.733, there is no outlier in the dataset.

2.6 Final Model and Predict

The final model and the estimated y in each group is as follows.

$$\begin{aligned} \hat{y}_A &= \mu_A = 200.0 \\ \hat{y}_B &= \mu_B = 250.0 \\ \hat{y}_C &= \mu_C = 294.2 \end{aligned} \tag{7}$$

2.7 Conclusion

It is safe for us to conclude that types of grass are of great importance on the weight of cows. For this question, cows that were fed grass C weighed most.

R Appendix

Listing 1: R script for Project 2

```
##### Logistic Regression #####
##### set work directory and load dataset #####
setwd("/home/xmy/STA_101/Projects/P2")
prostate <- read.csv("prostate.csv", header = TRUE)
head(prostate, n = 3)

##### load packages #####
library(ggplot2)
library(pROC)
library(EnvStats)
library(bestglm)
library(nnet)
library(LogisticDx)
library(asbio)

##### set default parameters #####
ppi = 600

##### rename columns of datasets #####
names(prostate) = c("Y", "X1", "X2", "X3", "X4", "X5", "X6", "X7")
head(prostate, n = 3)
summary(prostate)

##### define functions #####

##### prostate summary #####

##### preparation of data #####
# filename = "group_boxplot_X1.png"
# png(filename, width=6*ppi, height=4*ppi, res=ppi)
# ggplot(prostate, aes(y=X1, x = as.factor(Y)))+ theme_gray() + geom_boxplot() + ylab("Serum prostate-specific antigen level") +
#  xlab("Indicator of prostate cancer")
# dev.off()


##### model selection #####
empty.model = glm(Y~1, data=prostate, family = binomial(link=logit))
full.model = glm(Y~., data=prostate, family = binomial(link=logit))
### Forward stepwise
F.model = step(empty.model, scope = list(lower=empty.model,upper=full.model),trace = FALSE, direction = "forward", criteria = "AIC")
### Backward stepwise
B.model = step(full.model, scope = list(lower=empty.model,upper=full.model),trace = FALSE, direction = "backward", criteria = "AIC")
### Forward/Backward stepwise
FB.model = step(empty.model, scope = list(lower=empty.model,upper=full.model),trace = FALSE, direction = "both", criteria = "AIC")
### Backward/Forward stepwise
BF.model = step(full.model, scope = list(lower=empty.model,upper=full.model),trace = FALSE, direction = "both", criteria = "AIC")
### display selected models
F.model
B.model
FB.model
BF.model

##### final model #####
final.model = glm(Y~X1+X2+X4, data=prostate, family = binomial(link=logit))
summary(final.model)
the.betas = final.model$coefficients
round(the.betas,4)
exp.betas = exp(the.betas)
names(exp.betas) = c("(Intercept)", "exp.X1", "exp.X2", "exp.X4")
round(exp.betas,4)
```

```
# display final model
### CI for betas
alpha = 0.05
the.CI = confint(final.model, level = 1 - alpha)
round(the.CI,4)
exp.CI = exp(the.CI)
rownames(exp.CI) = c("(Intercept)", "exp.X1", "exp.X2", "exp.X4")
round(exp.CI,4)


##### if X4 can be dropped #####
model.A = final.model
model.0 = glm(Y~X1+X2, data=prostate, family = binomial(link=logit))
LLA = logLik(model.A)
LL0 = logLik(model.0)
pA = length(model.A$coefficients)
p0 = length(model.0$coefficients)
LR = -2*(LL0-LLA)
p.value = pchisq(LR, df = pA-p0, lower.tail = FALSE)
p.value
# interpret p-value


##### Diagnostics #####
### Pearson residuals
good.stuff = dx(final.model)
pear.r = good.stuff$Pr
std.r = good.stuff$sPr
plot.name = "pearson_std_e.png"
png(plot.name, width=6*ppi, height=4*ppi, res=ppi)
hist(std.r, main = "Pearson Standardized Residuals")
dev.off()
cutoff.std = 3.0
good.stuff[abs(std.r)>cutoff.std]
### dfbeta
df.beta = good.stuff$dBhat
plot.name = "dfbeta.png"
png(plot.name, width=6*ppi, height=4*ppi, res=ppi)
plot(df.beta, main = "Index plot of the change in the Betas")
dev.off()
cutoff.beta = 0.50
good.stuff[df.beta>cutoff.beta]
### dchisq
change.pearson = good.stuff$dChisq
plot.name = "dchisq.png"
png(plot.name, width=6*ppi, height=4*ppi, res=ppi)
plot(change.pearson, main = "Index plot of the change in the Pearson's test-statistic")
dev.off()
cutoff.pearson = 15
good.stuff[change.pearson>cutoff.pearson]

##### ROC and AUC #####
plot.name = "auc.png"
png(plot.name, width=6*ppi, height=4*ppi, res=ppi)
my.auc = auc(final.model$y, fitted(final.model), plot = TRUE)
dev.off()
my.auc
auc.CI = ci(my.auc, level = 0.95)
auc.CI
# interpret auc.CI

##### remove outliers #####
new.prostate  = prostate

# remove outliers
new.prostate = new.prostate[-which(prostate$X1 == 14.880|prostate$X1 == 56.261|prostate$X1 == 9.974),]
the.ratio = (length(prostate$Y)-length(new.prostate$Y))/length(prostate$Y)
the.ratio

##### final best model #####
final.model = glm(Y~X1+X2+X4, data=new.prostate, family = binomial(link=logit))
final.model
summary(final.model)
the.betas = final.model$coefficients
the.betas
exp.betas = exp(the.betas)
names(exp.betas) = c("(Intercept)", "exp.X1", "exp.X2", "exp.X4")
exp.betas
# display final model
### CI for betas
alpha = 0.05
the.CI = confint(final.model, level = 1 - alpha)
the.CI
exp.CI = exp(the.CI)
rownames(exp.CI) = c("(Intercept)", "exp.X1", "exp.X2", "exp.X4")
exp.CI

##### error matrix #####
pi.0=0.30
truth = new.prostate$Y
```

```
predicted = ifelse(fitted(final.model)>pi.0,1,0)
my.table = table(truth, predicted)
my.table
sens = sum(predicted == 1 & truth ==1)/sum(truth ==1)
spec = sum(predicted == 0 & truth ==0)/sum(truth ==0)
error = sum(predicted!=truth)/length(predicted)
results = c(sens,spec,error)
names(results) = c("Sensitivity","Specificity","Error-Rate")
results
# interpret error matrix



##### predictive power #####
r = cor(final.model$y, final.model$fitted.values)
r
prop.red = 1-sum((final.model$y - final.model$fitted.values)^2)/sum((final.model$y - mean(final.model$y))^2)
prop.red
# interpret predictive power

##### predict #####
x.star = data.frame(X1 = 10, X2 = 5, X4 = 67)
the.predict = predict(final.model, x.star, type = "response")
the.predict

#### ANOVA ####
cows =read.csv("cows.csv")
head(cows)
ppi = 600
group.means = by(cows$Weight,cows$Grass,mean)  # First argument is Y, second is grouping column/s
png("1.png", width=6*ppi, height=4*ppi, res=ppi)
plot(group.means,xaxt = "n",pch = 19,col = "purple",xlab = "Experiment Group",ylab = "Weight",main = "Average Weight by group",type = "b") #Addinf xax
dev.off()

png("2.png", width=6*ppi, height=4*ppi, res=ppi)
boxplot(cows$Weight ~ cows$Grass, main = "Weight by group",ylab = "Weight")
dev.off()

group.means = by(cows$Weight,cows$Grass,mean)
group.sds = by(cows$Weight,cows$Grass,sd)
group.nis = by(cows$Weight,cows$Grass,length)
the.summary = rbind(group.means,group.sds,group.nis)
the.summary = round(the.summary,digits = 4)
colnames(the.summary) = names(group.means)
rownames(the.summary) = c("Means","Std. Dev","Sample Size")
the.summary

library(asbio)
options(scipen = 8)
larger.model = lm(Weight ~ Grass , data = cows)
smaller.model = lm(Weight ~1 , data = cows)
anova.table = anova(smaller.model, larger.model)
anova.table
bonfCI(cows$Weight,cows$Grass, conf.level = 0.95)
bonfCI

p = length(larger.model$coefficients) #Counts the number of betas
alpha = 0.01 # You may change this to whatever you like
t.cutoff = qt(1- alpha/2, n-p)
ei.s = larger.model$residuals/sqrt(sum(larger.model$residuals^2)/(length(larger.model$residuals) - length(larger.model$coefficients)))
outliers = which(abs(ei.s) > t.cutoff)
outliers
t.cutoff

png("3.png", width=6*ppi, height=4*ppi, res=ppi)
plot(larger.model$residuals,main = "Residual index plot",xlab = "Index",ylab = "residuals",pch = 19, col = "purple")
dev.off()
par(mfrow=c(1,2))
png("4.png", width=6*ppi, height=4*ppi, res=ppi)
hist(larger.model$residuals,main = "Residual Distribution",xlab = "Residuals")
dev.off()
png("5.png", width=6*ppi, height=4*ppi, res=ppi)
qqnorm(larger.model$residuals)
qqline(larger.model$residuals)
dev.off()

shap.test = shapiro.test(larger.model$residuals)
shap.test$p.value
ML.test = modlevene.test(larger.model$residuals,cows$Grass)
ML.test$'Pr(>F)'
png("6.png", width=6*ppi, height=4*ppi, res=ppi)
plot(larger.model$fitted.values,larger.model$residuals,pch = 19)
abline(h= 0 , col = "purple")
dev.off()
```