Analyzing Hospital Dataset Using Linear Regression

Wangqian Miao*
Kuang Yaming Hornors School, Biophysics, Nanjing University
Mingyi Xue
School of Chemistry and Chemical Engineering, Nanjing University
Instructor: Dr. Erin K. Melcon
Department of Statistics, University of California, Davis

Contents

*The two authors are all exchange students from Nanjing university

1 Introduction

In this article, we use the linear regression model to analyze the dataset of "Hospfull.csv" which describes characteristics of the United States Hospitals. The source of this data is the text: "Applied Linear Statistical Models, fifth edition, Kutner, Nachtsheim, Neter, and Li."

Our goal is predicting the average estimated probability of acquiring infection in hospital (in percantage) by finding the important explanary variables. Depending on the tools and techniques we learn in linear regression, we will build a "correct" model and make the prediction.

Firstly, we will use the full model and make the improvement later. In the dataset, we choose "Infect" as our response variable Y and let other variables be the explanary variables X_i. So, the linear regression model is:

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \beta_4 X_4 + \beta_5 X_5 + \varepsilon \tag{1}$$

We make a summary table as following to intepret the variables.

Name	Variable	Variable Kind	Units
Indfect	Y	Response	Percentage
Length	X_1	Numerical	Days
Culture	X_2	Numerical	Ratio
Bed	X_3	Numerical	Number
Medschool	X_4	Categorical	Y/N
Region	X_5	Categorical	NE/NC/S/W

Table 1: A summary table for the variables

2 Summary

2.1 Analyzing the Sample Correlation Coeffient

Firstly,we analyze the correlaytion coeffient between Y and numerical variables to find whether the linear relationship between Y and X_i is strong enough.

Y v.s. X_i	Correlation Coeffient	Linear Relationship Strength
X_1	0.5334	Moderate & Positive
X_2	0.5592	Moderate & Positive
X_3	0.3598	Weak & Positive

Table 2: A summary table for the variables

2.2 Scatter Plot

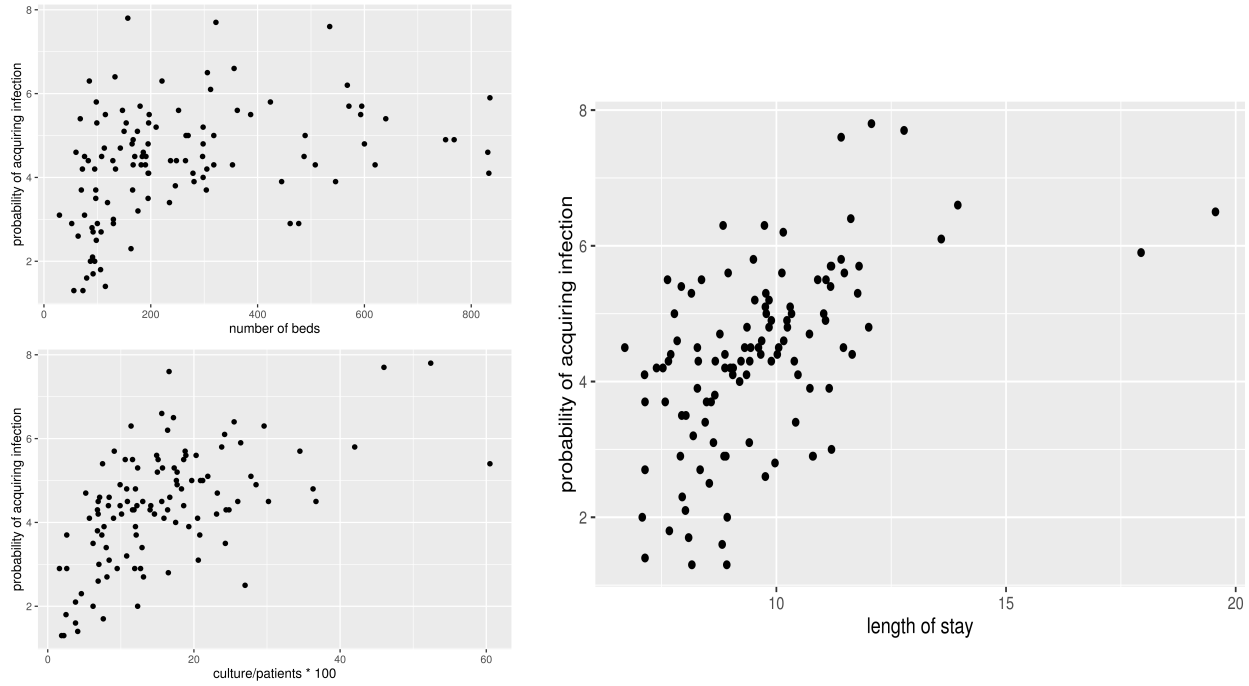


Figure 1: Scatter plots by different numerical variables

2.3 Five Number Summary

Region	Min	Q_1	Median	Mean	Q_3	Max
NC	1.300	3.8500	4.400	4.394	5.225	7.800
NE	2.500	4.200	4.850	4.861	5.750	7.700
S	1.300	2.900	4.200	3.927	4.700	7.600
W	2.600	4.075	4.450	4.381	4.850	5.600

Table 3: A summary table for the variables

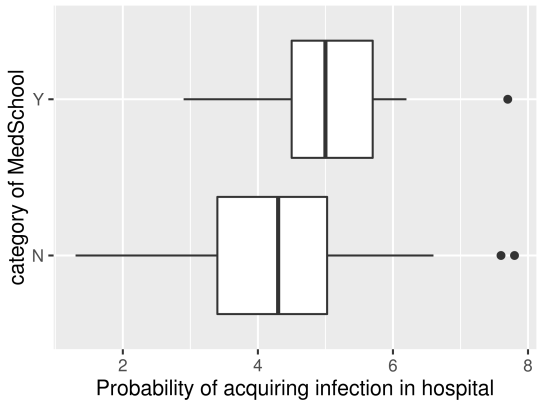
Medschool	Min	Q_1	Median	Mean	Q_3	Max
N	1.300	3.400	4.300	4.224	5.025	7.800000
Y	2.900	4.500	5.000	5.094	5.700	7.700

Table 4: A summary table for the variables

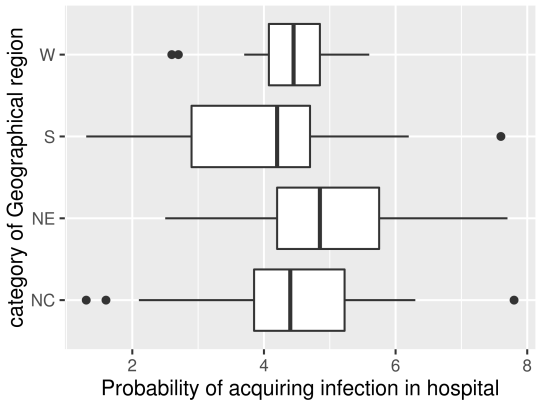
3 Data Preparation

3.1 Boxplots

According to the Boxplot by different catogorical, we find there exists some outliers in the dataset.



(a) the first subfigure



(b) the second subfigure

3.2 Remove Outliers

The outliers are shown in the following table. We remove 10 outliers and the ratio of the full dataset is 8.850%.

Index	Length	Infect	Culture	Bed	MedSchool	Region
2	8.82	1.6	3.8	80	N	NC
8	11.18	5.4	60.5	640	Y	NC
13	12.78	7.7	46	322	Y	NE
47	19.56	6.5	17.2	306	N	NE
53	11.41	7.6	16.6	535	N	S
54	12.07	7.8	52.4	157	N	NC
93	8.92	1.3	2.2	56	N	NC
101	9.76	2.6	6.9	64	N	W
103	7.14	2.7	13.1	92	N	W
112	17.94	5.9	26.4	835	Y	NE

Table 5: The information of outliers

4 Model Fitting

4.1 Using A.I.C & B.I.C

Based on the criatia of A.I.C or B.I.C, the "correct" model can be found.

Without considering the interaction term, we find that the full model has the lowest A.I.C. based on the all subsets of the full model.The model we build is

$$\begin{aligned}\hat{y_1} = &-0.4536 + 0.3962X_1 + 0.0586X_2 + 0.0013X_3 - 0.4005X_{4Y} \\ &- 0.4577X_{5NE} - 0.3619X_{5S} + 0.9163X_{5W}\end{aligned} \tag{2}$$

Without considering the interaction term, we find that the full model has the lowest B.I.C. based on the all subsets of the full model.The model we build is

$$\begin{aligned}\hat{y_2} = &-0.5573 + 0.4389X_1 + 0.0565X_2 \\ &- 0.5097X_{5NE} - 0.3471X_{5S} + 0.9048X_{5W}\end{aligned} \tag{3}$$

There are some differences between the two models, we will use some techniques to compare them.

4.2 C.I. & H.T. for β_i

We analyze the full model's βs C.I.($\alpha = 0.5$) for the first model. The table is as following.

	2.5 %	97.5 %
(Intercept)	-1.8014	0.8942
X_1	0.2507	0.5417
X_2	0.0371	0.0802
X_3	0.0001	0.0024
X_{4Y}	-0.9805	0.1796
X_{5NE}	-0.9469	0.0316
X_{5S}	-0.7823	0.0585
X_{5W}	0.3422	1.4905

Table 6: C.I. of βs of the first model

The C.I. of X_4 contains 0. We will consider that X_4 should be dropped.

	Coefficients:	Estimate Std. Error	t value	Pr($>\|t\|$)
(Intercept)	-0.453605	0.678888	-0.6680	0.50565
X_1	0.396160	0.073290	5.405	4.79e-07
X_2	0.058650	0.010860	5.401	4.89e-07
X_3	0.001265	0.000568	2.227	0.02833
X_{4Y}	-0.400484	0.292175	-1.371	0.17370
X_{5NE}	-0.457657	0.246435	-1.857	0.06639
X_{5S}	-0.361916	0.211761	-1.709	0.09070
X_{5W}	0.916322	0.289204	3.168	0.00206

Table 7: H.T. for βs of the first model

The p-value of β_4 is big enough for us to accept H_0 which means $\beta_4 = 0$, we can drop X_4. Now we have a model " Y X_1, X_2, X_3, X_5". We find that $\beta_3' s$ value is quite small. How much error we will reduce by adding X_3 in our model "$Y \sim X_1, X_2, X_5$" ?

4.3 Partial R^2

We use partial R^2 to estimate how much error we will reduce by adding X_3.

$$R^2 = \frac{SSE_S - SSE_L}{SSE_S} = 3.156\% \tag{4}$$

Our goal is to find a "correct" model, so we can drop X_3 and choose the second model $Y \sim X_1, X_2, X_5$ which is the best under the B.I.C criteria.

4.4 Add Interavtion Term

At last we consider that wether we should add the interaction term analyzing the C.I. of βs, we find there is no need to add interaction term, because the C.I. all contain 0.

4.5 Model Selection

Based on the discussion above, we find the most important variables X_1, X_2, X_5 and our final model is that

$$Y \sim X_1 + X_2 + X_5 \tag{5}$$

5 Model Diagnotics

There are some assumptions we should obey by using linear regression. Mostly, we care about the normality of e_i and whether the variance is a constant.

5.1 e_i Normality

The assumption is that $\varepsilon \sim \mathcal{N}(0, \sigma_\varepsilon)$. We use e_i to estimate ε in practice. There are two popular ways which are QQ plot and Shapiro-Wilk Normality Test.

5.1.1 QQ Plot

Accoding to the figure below, most points are near to $y = x$ which suggests e_i is normarly distributed.

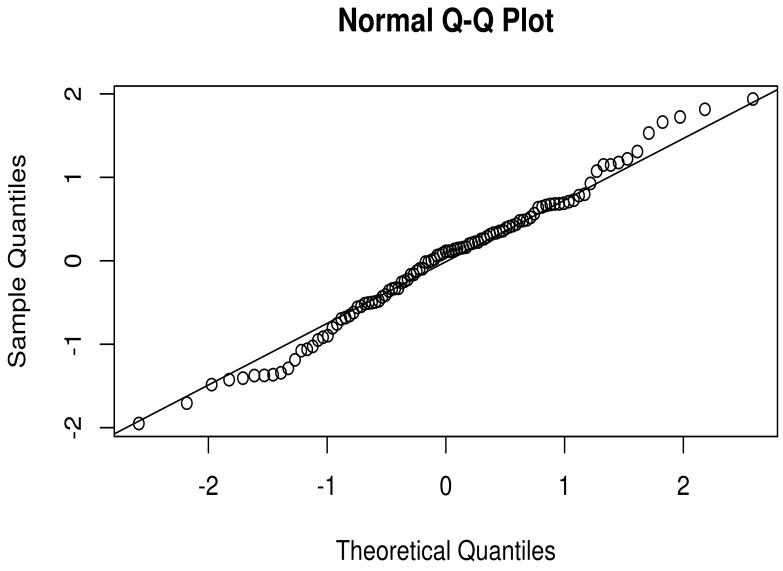


Figure 2: best

5.1.2 Shapiro-Wilk Normality Test

We use Shapiro-Wilk Test to find whether the error is normaly distributed.

- H_0: The error is normaly distributed.
- H_A: The error is not normaly distributed.

Accoding to R, the p-value=0.5181. Is is large enough for us to accept null which means the error is normaly distributed under any significance.

5.1.3 Conclusion

Our model obey the assumption that $\varepsilon \sim \mathcal{N}(0, \sigma_\varepsilon)$.

5.2 Constant Variance

The assumption is that σ_ε is constant. There are two popular ways which are plotting $e_i v.s. \hat{y}_i$ and Fligner-Killeen Test.

5.2.1 e_i v.s. $\hat{y}_i$ Plot

Accoding to the figure below , there is no clear pattern in the plot, so the conclusion is that the variance is constant.

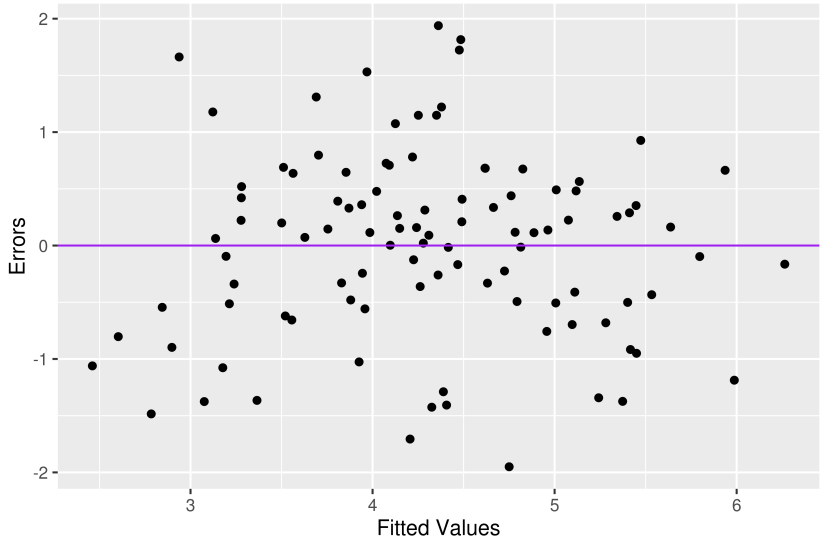


Figure 3: best

5.2.2 Fligner-Killeen Test

We use Fligner-Killeen Test to find whether the variance is constant.

- H_0: $\sigma^2_{lower} = \sigma^2_{higher}$.
- H_A: $\sigma^2_{lower} \neq \sigma^2_{higher}$.

Accoding to R, the p-value=0.2361. Is is large enough for us to accept null which means the variance is constant under any significance.

5.2.3 Conclusion

The conclusion is that our model obey the assumption that the variance is constant.

5.3 Remove Outliers Again

We use the method of "Cooks Distance" to find wether there still exists some outliers in the dataset. As shown in the figure below, The "Cooks Distance" is so small that there is no need to move any points out of our dataset.

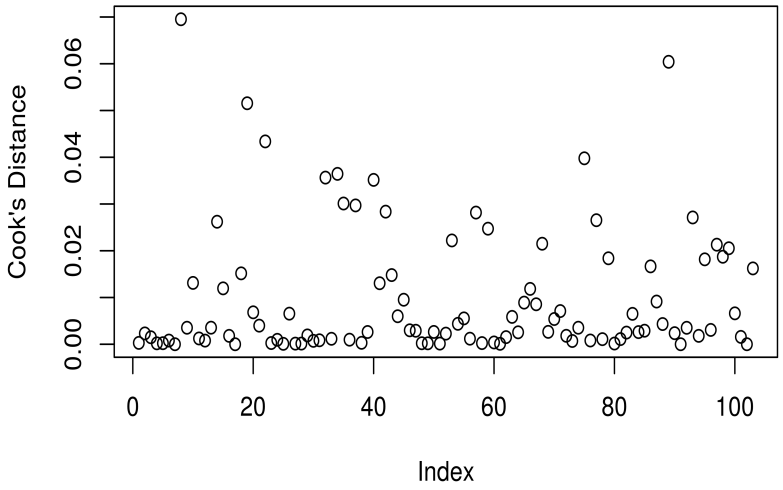


Figure 4: best

5.4 Final model

Our final model is a "correct"" model and it is appropriate.

$$\begin{aligned} Y = &- 0.5573 + 0.4389X_1 + 0.0565X_2 - 0.5097X_{5NE} \\ &- 0.3471X_{5S} + 0.9048X_{5W} + \varepsilon \end{aligned} \tag{6}$$

6 Interpretation

In this section, we will interpret the meaning of βs according to this problem.

- β_0: Since the probability of acquring infection in hospital cannot be negative, it is inappropriate to predict the probability of acquiring infection at all X's equal 0.
- β_1: When the length of stay of all patients in the hospital increases by 1 day, the probability of acquring infection in hospital tends to increase by 0.4389 percentage on average, holding all other variables constant.
- β_2: When the ratio of number of cultures performed to number of patients increases by 1, the probability of acquring infection in hospital tends to increase by 0.05648 percentage on average, holding all other variables constant.
- β_3: The probability of acquring infection in hospital tends to decrease by 0.5097 percentage on average when patients are in category of North East compared to patients in category of North Central, holding all other variables constant.
- β_4: The probability of acquiring infection in hospital tends to decrease by 0.3471 percentage on average when patients are in category of South compared to patients in category of North Central, holding all other variables constant.
- β_5: bThe probability of acquiring infection in hospital tends to increase by 0.9048 percentage on average when patients are in category of West compared to patients in category of North Central, holding all other variables constant.

7 Prediction

We will use our model to do a prediction.b

8 Conclusion

R Appendix

Listing 1: R script for Project 1

```
##### set work directory and load dataset #####
setwd("/home/xmy/STA 101/Projects/P1")
HospFull<-read.csv("HospFull.csv", header = TRUE)
head(HospFull, n = 3)

##### load packages #####
library("ggplot2")
library("leaps")
library("MPV")

##### define functions #####
Partial.R2 = function(small.model,big.model){
SSE1 = sum(small.model$residuals^2)
SSE2 = sum(big.model$residuals^2)
PR2 = (SSE1 - SSE2)/SSE1
return(PR2)
}
All.Criteria = function(the.model){
p = length(the.model$coefficients)
n = length(the.model$residuals)
the.BIC = BIC(the.model)
the.LL = logLik(the.model)
the.AIC = AIC(the.model)
the.PRESS = PRESS(the.model)
the.R2adj = summary(the.model)$adj.r.squared
# the.CP = summary(the.model)$cp
the.results = c(the.LL,p,n,the.AIC,the.BIC,the.PRESS,the.R2adj)
names(the.results) = c("LL","p","n","AIC","BIC","PRESS","R2adj")
return(the.results)
}


##### correlation #####
cor(HospFull$Length, HospFull$Infect)
cor(HospFull$Culture, HospFull$Infect)
cor(HospFull$Bed, HospFull$Infect)


##### Infect summary #####
summary(HospFull$Infect)
# grouped by MedSchool
aggregate(Infect ~ MedSchool, data = HospFull, summary)
# grouped by Region
aggregate(Infect ~ Region, data = HospFull, summary)

# plot(HospFull)
##### boxplots of Infect #####
require(ggplot2)
# boxplot grouped by MedSchool
ppi = 600
# Calculate the height and width (in pixels) for a 4x3-inch image at 600 ppi
png("group_boxplot_medschool.png", width=6*ppi, height=4*ppi, res=ppi)
ggplot(HospFull, aes(y=Infect, x = MedSchool))+ theme_gray() + geom_boxplot() + ylab("Probability of acquiring infection in hospital") +
xlab("category of MedSchool")+ coord_flip()
#ggtitle("Boxplot of Infect grouped by Medchool")
dev.off()

# boxplot grouped by Region
png("group_boxplot_region.png", width=6*ppi, height=4*ppi, res=ppi)
ggplot(HospFull, aes(y=Infect, x = Region))+ theme_gray() + geom_boxplot() + ylab("Probability of acquiring infection in hospital") +
xlab("category of Geographical region")+ coord_flip()
#ggtitle("Boxplot of Infect grouped by Region")
dev.off()


##### scatter plots of Infect #####
# scatter plot of Infect vs. Length
png("scatter_plot_length.png", width=6*ppi, height=4*ppi, res = ppi)
qplot(HospFull$Length, HospFull$Infect, data = HospFull) +xlab("length of stay") + ylab("probability of acquiring infection")
dev.off()

# scatter plot of Infect vs. Culture
```

```
png("scatter_plot_culture.png",  width=6*ppi, height=4*ppi, res = ppi)
qplot(HospFull$Culture, HospFull$Infect, data = HospFull) +xlab("culture/patients * 100") + ylab("probability of acquiring infection")
dev.off()

# scatter plot of Infect vs. Bed
png("scatter_plot_bed.png", width=6*ppi, height=4*ppi, res = ppi)
qplot(HospFull$Bed, HospFull$Infect, data = HospFull) +xlab("number of beds") + ylab("probability of acquiring infection")
dev.off()



##### remove outliers according to plots #####
# cover HospFull
the.original = HospFull
HospFull=HospFull[-which(HospFull$Length>15),]
HospFull=HospFull[-which(HospFull$Culture>60),]
HospFull=HospFull[-which(HospFull$MedSchool=="Y" & HospFull$Infect > 7),]
HospFull=HospFull[-which(HospFull$MedSchool=="N" & HospFull$Infect > 7),]
HospFull=HospFull[-which(HospFull$Region=="W" & HospFull$Infect < 3),]
HospFull=HospFull[-which(HospFull$Region=="NC" & HospFull$Infect < 2),]
length(the.original$Infect)
length(HospFull$Infect)
the.ratio = (length(the.original$Infect)-length(HospFull$Infect))/length(the.original$Infect)
the.ratio

##### subset models of Infect~. #####
# rename dataset for convenience
names(HospFull) = c("X1","Y","X2","X3","X4","X5")
full.model = lm(Y~ X1 + X2 + X3 + X4 + X5,data = HospFull)
round(full.model$coefficients,4)
bic.model = lm(Y~X1+X2+X5, data = HospFull)
round(bic.model$coefficients, 4)
all.models = c("Y~1","Y~X1","Y~X2","Y~X3","Y~X4","Y~X5",
"Y~X1+X2","Y~X1+X3","Y~X1+X4","Y~X1+X5","Y~X2+X3","Y~X2+X4","Y~X2+X5","Y~X3+X4","Y~X3+X5","Y~X4+X5",
"Y~X1+X2+X3","Y~X1+X2+X4","Y~X1+X2+X5","Y~X1+X3+X4","Y~X1+X3+X5","Y~X1+X4+X5","Y~X2+X3+X4","Y~X2+X3+X5","Y~X2+X4+X5","Y~X3+X4+X5",
"Y~X1+X2+X3+X4","Y~X1+X2+X3+X5","Y~X1+X2+X4+X5","Y~X1+X3+X4+X5","Y~X2+X3+X4+X5",
"Y~X1+X2+X3+X4+X5")
Infect.all.model.crit = t(sapply(all.models,function(M){
current.model = lm(M,data = HospFull)
All.Criteria(current.model)
}))
Infect.all.model.crit
Infect.all.model.crit = data.frame(Infect.all.model.crit)
# find the model with lowest BIC
Infect.all.model.crit[which(Infect.all.model.crit$BIC == min(Infect.all.model.crit[,5])),]
# find the model with lowest AIC
Infect.all.model.crit[which(Infect.all.model.crit$AIC == min(Infect.all.model.crit[,4])),]


##### anova analysis of X4 #####
summary(full.model)
summary(bic.model)
alpha = 0.05
the.CIs = confint(full.model,level = 1-alpha)
round(the.CIs, 4)
# drop X4
smaller.model = lm(Y~X1+X2+X3+X5, data = HospFull)
anova.small = anova(smaller.model)
larger.model = lm(Y~X1+X2+X3+X4+X5, data = HospFull)
anova.large = anova(larger.model)
anova(smaller.model,larger.model)


##### anova analysis of X3 #####
smaller.model = lm(Y~X1+X2+X5, data = HospFull)
anova.small = anova(smaller.model)
larger.model = lm(Y~X1+X2+X3+X5, data = HospFull)
anova.large = anova(larger.model)
anova(smaller.model,larger.model)
##### partial r2 of X3 #####
partial.R2=Partial.R2(smaller.model, larger.model)
partial.R2


##### considering interaction terms #####
# interaction term between X1 and X5
final.model = lm(Y~X1+X2+X5, data = HospFull)
final.model
X1.interation.model = lm(Y~X1+X2+X5+X1*X5, data = HospFull)
summary(X1.interation.model)
confint(X1.interation.model,level = 1-alpha)
anova(final.model,X1.interation.model)
partial.R2=Partial.R2(final.model,X1.interation.model)
partial.R2
# interaction term between X2 and X5
X2.interation.model = lm(Y~X1+X2+X5+X2*X5, data = HospFull)
X2.interation.model
summary(X2.interation.model)
confint(X2.interation.model,level = 1-alpha)
anova(final.model,X2.interation.model)
```

```
partial.R2=Partial.R2(final.model,X2.interation.model)
partial.R2


##### diagnose of model #####
final.model = lm(Y~X1+X2+X5, data = HospFull)
final.model
HospFull$ei = final.model$residuals
HospFull$yhat = final.model$fitted.values
## nomality
# qqplot
png("qqplot.png", width=6*ppi, height=4*ppi, res = ppi)
qqnorm(final.model$residuals)
qqline(final.model$residuals)
dev.off()
# S-W test
the.SWtest = shapiro.test(final.model$residuals)
the.SWtest

## constant variance
# ei-yi plot
png("scatter_plot_constant_variance.png", width=6*ppi, height=4*ppi, res = ppi)
qplot(yhat, ei, data = HospFull) +
xlab("Fitted Values") + ylab("Errors") + geom_hline(yintercept = 0,col = "purple")
dev.off()
# F-K test
HospFull$ei = final.model$residuals
Group = rep("Lower",nrow(HospFull))
Group[HospFull$Y < median(HospFull$Y)] = "Upper"
Group = as.factor(Group)
HospFull$Group = Group
the.FKtest= fligner.test(HospFull$ei, HospFull$Group)
the.FKtest

## outliers
# cook's distance
cutoff = 0.10
CD = cooks.distance(final.model)
HospFull$CD = cooks.distance(final.model)
HospFull[which(HospFull$CD>cutoff),]
# no outliers
png("cooks_distance.png", width=6*ppi, height=4*ppi, res = ppi)
plot(CD,ylab = "Cook's Distance")
abline(h = cutoff,color = "purple")
dev.off()

SR = stdres(final.model)
HospFull$SR = SR
cutoff= 3
png("standardized_error.png", width=6*ppi, height=4*ppi, res = ppi)
ggplot(HospFull,aes(x = SR))+geom_histogram(binwidth = 0.5,color = "black",fill = "white")+ xlab("standardized error")
dev.off()
SR[which(abs(SR) > cutoff)]

##### final model #####
final.model
R2 = summary(final.model)$r.squared
R2

##### predict estimated values of Y #####
alpha = 0.05
x.star = data.frame(X1 = 8, X2 = 14, X5 = 'W')
predict(final.model, x.star, interval = "confidence", level = 1-alpha)
predict(final.model, x.star, interval = "prediction", level = 1-alpha)
```