Analyzing Hospital Dataset Using Linear Regression

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Contents

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1 Introduction

In this article, we applied the linear regression model to analyze the dataset of "Hospfull.csv", which describes characteristics of 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 to predict 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 decided to build a "correct" model instead of "predict" model and make the prediction.

We started at the full model and would make improvements and adjustments step by step. In the dataset, we chose "Infect" as the response variable Y and other variables as explanary variables X_i. So the linear regression model is:

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

A summary table is listed as follows to intepret these 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 Coefficients

Firstly,we analyzed the correlation coefficient between Y and numeric variables to find whether there is a significant linear relationship between Y and X_i. A summary table and explanation of correlation coeffients is listed in the following table.

Y v.s. X_i	Correlation Coefficient	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 of correlation coefficients

2.2 Scatter Plots

Scatter plots can also help us find whether there is a linear pattern or some trend between Y and X_i. According to following plots, it is obvious that Y increases when X_1 and X_2 inreases.

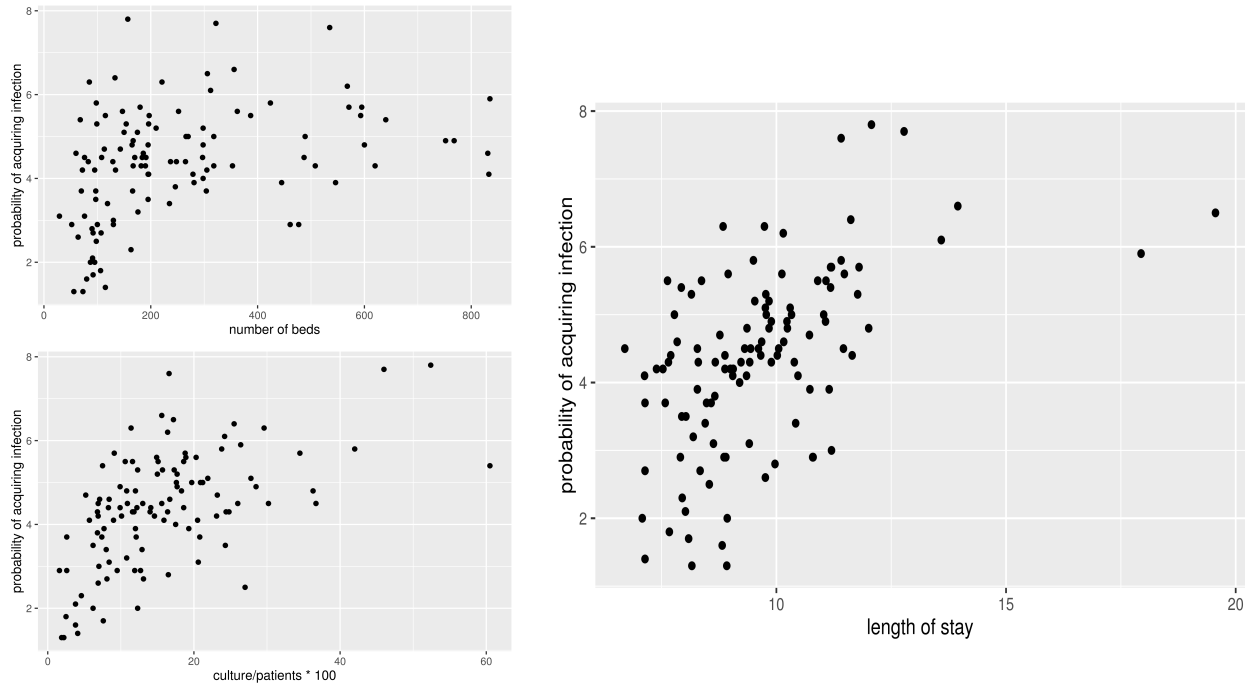


Figure 1: Scatter plots of different numerical variables

2.3 Five Number Summary

Five statistics numbers give a brief review of basic information on our dataset. As shown in the table below, differences exist between varied categories, which suggests categorical variables are supposed to be included in the target model.

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: Five number table of Region

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

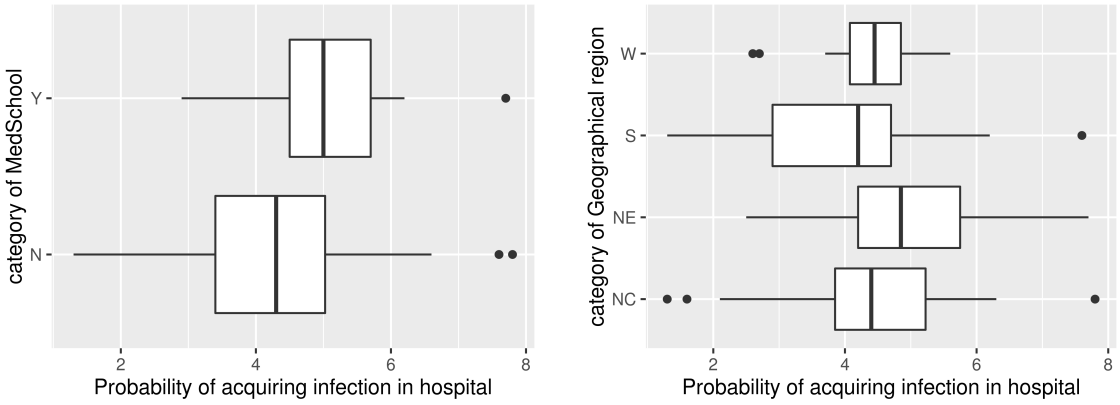
Table 4: Five number table of Medschool

3 Data Preparation

Outliers are inevitable in any dataset, which have an effect on outcomes of coefficients and prediction. R is able to find and remove these values.

3.1 Boxplots

Outliers are apparent to pick out according to boxplots below.



(a) Boxplot by Meddschool

(b) Boxplot by Region

Figure 2: Boxplots by different categorical variables

3.2 Remove Outliers

We removed 10 outliers, the ratio of which to the number of samples in the whole dataset is 8.850%, thus would not affect the dataset too much. Outliers are shown in the following table.

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: Detailed information of outliers

4 Model Fitting

4.1 Model Selection

The “correct” model can be found based on the criatia of A.I.C or B.I.C. R gives us two candidate models without considering any interaction term.

We found that the full model has the lowest A.I.C. compared to all subset models. Therefore,

the first model we built is

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

We also found that the model with the lowest B.I.C. compared to all other models. Therefore, the second model we built is

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

Because A.I.C usually provides us with a larger "correct" model while B.I.C usually favors the "smaller" one, we were able to find our final model somewhere between the first model based on A.I.C and the second model based on B.I.C. Using some techniques to compare different models is of great necessity, as what we did in the next.

4.2 C.I. & H.T. for β_i

Because the first model is larger than the second one, at the same time, a "correct" model is needed in the end. By analyzing C.I. and H.T. of βs, we could decide whether we should drop some variables from the first model.

	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

We were considering to drop X_4 at this moment since confidence intervals containing 0 do not suggest a significant relationship with the response variable Y. Though indicate variables like X_{5NE} and X_{5S} contain 0 as well, we could not drop X_5 from the first model because X_{5W} does not contain 0 and suggests a strong relationship with Y.

	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 $\beta_4 = 0$, so we could drop X_4. Now we have a new candidate model " $Y \sim X_1, X_2, X_3, X_5$" and dismiss the full one.

4.3 Partial R^2

We found that the value of β_3 is quite small. We used partial R^2 to estimate how much error we could reduce by adding X_3 to our second model "$Y \sim X_1, X_2, X_5$". If partial R^2 is small, we would consider dropping X_3.

$$R^2\{X_1, X_2, X_3, X_5 | X_1, X_2, X_5\} = \frac{SSE_S - SSE_L}{SSE_S} = 3.156\% \tag{4}$$

$R^2\{X_1, X_2, X_3, X_5 | X_1, X_2, X_5\}$ is not large enough to overweigh the additional cost a large model will bring about. Besides, considering the correlation coefficient between X_3 and Y and the scatter plot of X_3 and Y in section 2.2 only suggests a weak relationship, we dropped X_3 and chose the second model "$Y \sim X_1, X_2, X_5$" temporarily as our final model.

4.4 Add Interaction Terms

At last, to figure out whether interaction terms should be added, we analyzed the C.I. of βs of relavant interaction terms and found that there was no need to add these terms because the C.I. all contain 0.

	2.5 %	97.5%
(Intercept)	-2.2187	3.2553
X_1	0.0451	0.6108
X_2	0.0336	0.0778
X_{5NE}	-5.7841	1.3486
X_{5S}	-5.6676	1.3708
X_{5W}	-2.3968	7.2876
$X_1 : X_{5NE}$	-0.1829	0.5292
$X_1 : X_{5S}$	-0.1798	0.5627
$X_1 : X_{5W}$	-0.7801	0.3557

Table 8: H.T. for βs of interaction terms with X_1

	2.5 %	97.5%
(Intercept)	-1.5605	1.3035
X_1	0.2868	0.5552
X_2	-0.00532	0.0815
X_{5NE}	-1.7807	0.4531
X_{5S}	-1.8586	-0.1378
X_{5W}	0.1689	2.6083
$X_2 : X_{5NE}$	-0.0452	0.0732
$X_2 : X_{5S}$	-0.0068	0.1038
$X_2 : X_{5W}$	-0.1208	0.0405

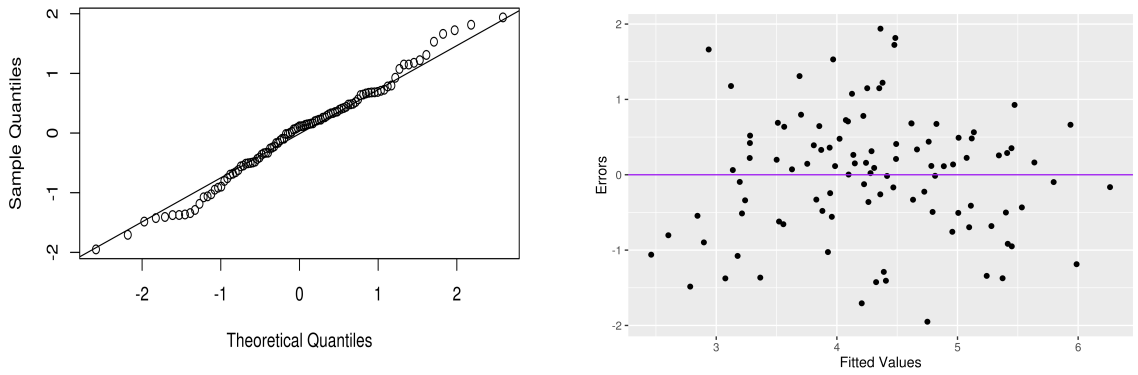
Table 9: H.T. for βs of interaction terms with X_2

4.5 Final Model

Based on the discussion above, we have found the most important variables X_1, X_2, X_5 and reached our final model "$Y \sim X_1 + X_2 + X_5$".

5 Model Diagnostics

There are a few assumptions we have to obey when using linear regression. Mostly, we care about the normality of e_i and whether the variance is constant.



(a) Normal qqplot

(b) e_i v.s. $\hat{y_i}$ plot

Figure 3: Plots of model diagnostics

5.1 e_i Normality

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

5.1.1 QQ Plot

Accoding to the figure in Figure3(a), except several deviations, most points are near the expected line $y = x$, which suggests e_i is normally distributed.

5.1.2 Shapiro-Wilk Normality Test

We also used Shapiro-Wilk Test to find whether the error is normaly distributed at a given significance.

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

Accoding to R, the p-value of S-W test statistics is 0.5181. It is large enough for us to accept the null hypothesis, which means the error is normally distributed under any significance we usually use.

5.1.3 Conclusion

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

5.2 Constant Variance

The assumption is that σ_ε is constant in linear regression. There are two popular ways to verify this assumption, 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 in Figure3(b), there is similar pattern vertical spread across the plot, so we concluded that the variance is constant.

5.2.2 Fligner-Killeen Test

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

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

Accoding to R, the p-value of F-K test statistics is 0.2361. It is large enough for us to accept the null hypothesis, which means the variance is constant under any significance we usually use.

5.2.3 Conclusion

Our final model obeys the assumption that the variance is constant.

5.3 Remove Outliers Again

We used the method "Cooks Distance" to find whether there are still some outliers in the dataset. As shown in the figure below, The "Cooks Distance" is so small (less than the frequently used cutoff = 0.50) that there is no need to remove any points out of the current dataset.

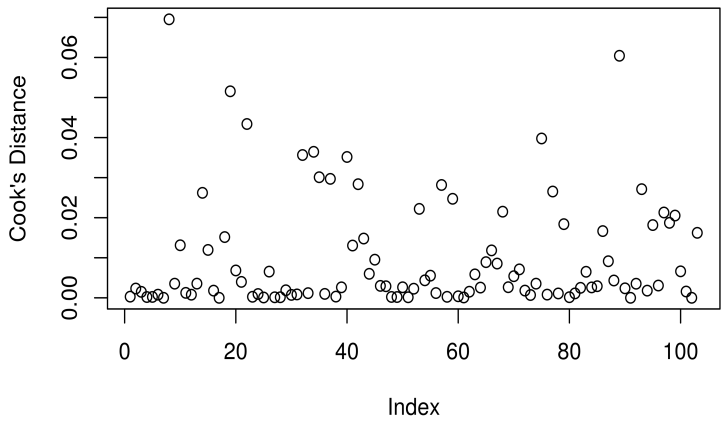


Figure 4: cook's distance

5.4 Final model

Our final model is a "correct"" model and it is appropriate, obeying linear regression assumptions, and there's no need to include interaction terms.

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

This model can be written to four parallel lines due to the categorical variable X_5 and no interaction terms.

Category	Linear Regression function
North Central	$\hat{y} = -0.5573 + 0.4389X_1 + 0.0565X_2$
North East	$\hat{y} = -1.0670 + 0.4389X_1 + 0.0565X_2$
South	$\hat{y} = -0.9044 + 0.4389X_1 + 0.0565X_2$
West	$\hat{y} = 0.3475 + 0.4389X_1 + 0.0565X_2$

Table 10: Linear regression function for different regions

6 Interpretation

In this section, the meaning of every single β is interpreted 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: The 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 used our final model to answer this question, "Predict the probability of infection in hospital with Stay=8, Culture=14, Region='W'. "

	point estimate	prediction intervals
$\bar{y}^*$	4.6493	[4.2042, 5.0945]
y^*	4.6493	[2.9272, 6.3715]

Table 11: Estimated value of Infect for x^*

8 Conclusion

We have found that the average length of stay of all patients in the hospital(X_1), the ratio of number of cultures performed to number of patients(X_2) and geographical region(X_5) have the most important effect on the prabability of acquiring infection in hospital.

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)
```