STA 138: Final Project

Aman Singh & Jennifer Li
ID:915763034
ID:999339769
UC Davis
Instructor: Prabir Burman

3/09/2021

Question 1: Low Birth Rate

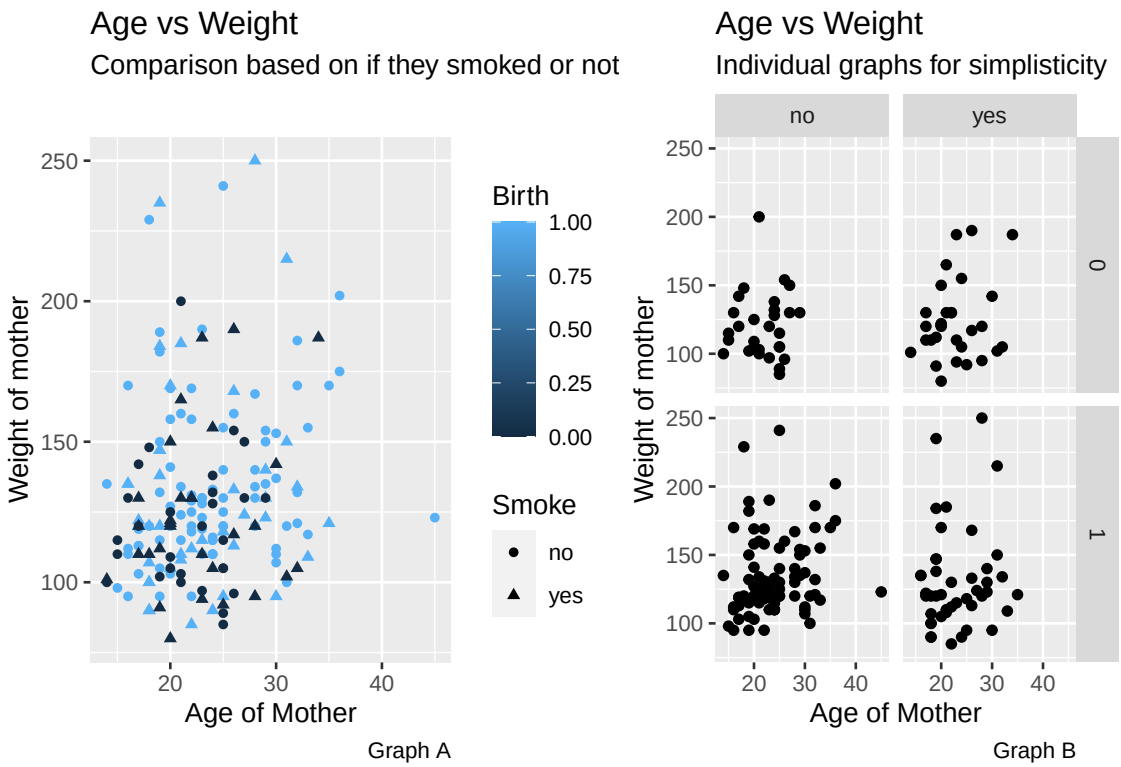
(I) Introduction

Smoking has been a huge issue since the 20^{th} century. There used to be advertisements all the time on the television where they would show as people having a great time and enjoying life. However, decades later, people found out that smoking leads to cancer and to horrible birth defects. Upon learning this, the government banned ads for smoking and started to limit the exposure of smoking to the public. Even when buying a cigarette, you have to be 18 years old as well as there is a huge caution warning on the box stating that it can lead to various defects in the body. The worst defect that we have seen so far has been when women who are pregnant are smoking at the same time. This can lead to some serious defects to the children and can affect them in the long run. While we do know that, what we want to investigate is whether the probability of low birth weight of infants is related to information on mother such as age, weight smoking status. We will be using the dataset called `Baby` provided by Professor Prabir Burman. `Baby` has 7 columns, `age`(age of the mother), `weight`(weight of the mother before pregnancy), `smoke`(smoking status during pregnancy), `pre`(history of premature labor), `hyp`(history of hypertension), `visits`(the number of visits during the first trimester), and `birth`(if the birth weight of the infant was low or not).

(II) Materials and Methods

Table 1: Summary Statistics

	Age	Weight	Visits	Birth
Min:	14	80	0	0
1st Qt.:	19	110	0	0
Median:	23	121	0	1
Mean:	23.24	129.8	.7937	.6878
3rd Qt:	26	140	1	1
Max:	45	250	6	1



We notice right away from the summary of the table that there seems to be multiple binomial variables in

this dataset. We see that `smoke`, `pre`, and `hyp` are all categorical variables with the 2 levels being `yes` or `no`. We wanted to make a way so we can start off with a regular logistic regression without any transformations or any interaction terms. What we will do next is to compare it to an interaction regression. We will then use an Goodness-of-Fit test to see if we can eliminate any variables and then proceed to use an stepwise regression to confirm if our regression is valid. We will then use that final regression to predict the birth column of the `Baby` dataset. After that we will compare our model with the dataset and see how accurate our model was.

(III) Results

We made the categorical variables (`Smoke`,`Pre`,`Hyp`) an factor to accurately account for the response. The regression we started off with is the following:

$$Birth = Age + Weight + Factor(Smoke) + Factor(Pre) + Factor(Hyp) + Visits + \epsilon_t$$

Table 2: Logistic Regression 1 Results:

	Estimate	**Standard Error**	**Z-Value**	**P.Value**
Intercept:	-2.021488	1.113152	-1.816	0.06937
Age:	0.059091	0.036965	1.599	0.10992
Weight:	0.016086	0.006943	2.317	0.02051
Factor.Smoke.Yes:	-0.513740	0.349295	-1.471	0.14135
Factor.Pre.Yes:	-1.798908	0.510014	-3.527	0.00042
Factor.Hyp.Yes:	-1.772643	0.717756	-2.470	0.01352
Visits:	0.032113	0.178906	0.179	0.85755

Null deviance: 234.67 on 188 degrees of freedom
Residual deviance: 202.15 on 182 degrees of freedom
AIC: 216.15

Based on the rule of thumb, we see that `Weight`,`factor.pre.yes`,`factor.hyp.yes`, all seem to be statistically significant. We see here that the `factor.smoke.yes`, `factor.pre.yes`,and `factor.hyp.yes` all are accounted in the regression if the mother smokes,has a history of pre-mature labor, and has an history of hypertension.

We than try out an regression including the interaction terms stated in the problem. We add Weight & Pre together, Age & Weight together, and Weight & Hyp. We build an logistic regression that looks like the following:

$Birth = Age + Weight + Factor(Smoke) + Factor(Pre) + Factor(Hyp) + Visits + Age : Weight + Weight : Factor(Pre) + Weight : Factor(Hyp) + \epsilon_t$

Table 3: Logistic Regression 2 Results:

	Estimate	Standard Error	Z-Value	P.Value
Intercept:	-3.2742473	3.9295522	-0.833	0.405
Age:	0.1165393	0.1682394	0.693	0.488
Weight:	0.0258898	0.0304761	0.850	0.396
Factor.Smoke.Yes:	-0.5087686	0.3545077	-1.435	0.151
Factor.Pre.Yes:	-2.6303649	2.8680721	-0.917	0.359
Factor.Hyp.Yes:	-1.6168753	2.6785514	-0.604	0.546
Visits:	0.0292054	0.1802465	0.162	0.871
Age:Weight	-0.0004465	0.0012718	-0.351	0.726
Weight:Factor(pre)yes	0.0064942	0.0222361	0.292	0.770
Weight:Factor(hyp)yes	-0.0009711	0.0171863	-0.057	0.955

Null deviance: 234.67 on 188 degrees of freedom
Residual deviance: 201.96 on 179 degrees of freedom
AIC: 221.96

We immediately notice between the 2 regressions is that the AIC immediately increases between the 2 regressions.This is not a good look, which seems to be that we would have to drop some variables to lower the AIC. The AIC is basically an mathematical method to evaluate how well an model fits the data. We also notice that the Residual deviance goes down which means that we should also look at smaller variables in the regression. We also see that none of the variables are statistically significant.

We initially decided to try out an Goodness-of-Fit test on this data using categorical data, however we saw that the data doesn't seem to be good because the `age` variable is very widely dispersed as well as the `weight` variable leading us to perform the Likelihood ratio test instead.We then decide to carry out an likelihood ratio test to decide if we should drop the interaction terms. We will than reject or fail to reject based off the following hypothesis:

$$H_0 : B_{age:weight+weight:factor(pre)+weight:factor(hyp)} = 0$$
$$H_A : B_{age:weight+weight:factor(pre)+weight:factor(hyp)} \neq 0$$

As we can see testing the full model with the interactions compared to the reduced model, since the p-value is `.9789857`, we end up dropping the interaction variables as they do not provide any use to us. I also believe that we should test one more time for the variable `visits` as it doesn't seem to be that important of a variable. We use the following likelihood ratio hypothesis test:

$$H_0 : B_{visits} = 0$$

$$H_A : B_{visits} \neq 0$$

We also see that since the P-value is `.8572994`, we also fail to reject the Null Hypothesis which lets us drop the variable `visits` from the regression.

We will now use Stepwise regression to see if the model that we fit and tested is accurate to the Stepwise Regression fit, which uses the AIC values to calculate best fit. The backward model starts with the full model and goes to the null model to analyze best fit, while the forward model starts with the null model and goes to the full model. We will use both of them combined just for better analysis.

After running the model,we notice that the Front/Backward Step-wise regression function also provided the same regression as what we originally thought it was with all the interactions dropped as well as the variable `visits`. Our final regression looks like:

$$Birth = Age + Weight + Factor(Smoke) + Factor(Pre) + Factor(Hyp) + \epsilon_t$$

with the summary statistics being:

Table 4: Logistic Regression 3 Results:

	Estimate	**Standard Error**	**Z-Value**	**P.Value**
Intercept:	-3.2742473	3.9295522	-0.833	0.405
Age:	0.1165393	0.1682394	0.693	0.488
Weight:	0.0258898	0.0304761	0.850	0.396
Factor.Smoke.Yes:	-0.5087686	0.3545077	-1.435	0.151
Factor.Pre.Yes:	-2.6303649	2.8680721	-0.917	0.359
Factor.Hyp.Yes	-1.782710	0.716698	-2.487	0.012868

Null deviance: 234.67 on 188 degrees of freedom
Residual deviance: 202.19 on 183 degrees of freedom
AIC: 214.19

Comparing the last 3 regressions, we notice that this is the best fit model that we have tried so far. The reasons being that the AIC is at its lowest of the 3.

Using this final regression, we will then try to approximate our results by making a test dataset which has all the same columns as the `Baby` dataset except for the column Birth. We will then compare our results to the real world data to see how accurate our model is.

We made our column into a logical class where it displayed true if the prediction was equal to the Birth column in `Baby` and we found the length of the True which ended up being $\frac{141}{189} = 74.6\%$. This means our model accurately explains 74.6% of the data in the `Baby` dataset.

(IV) Conclusion

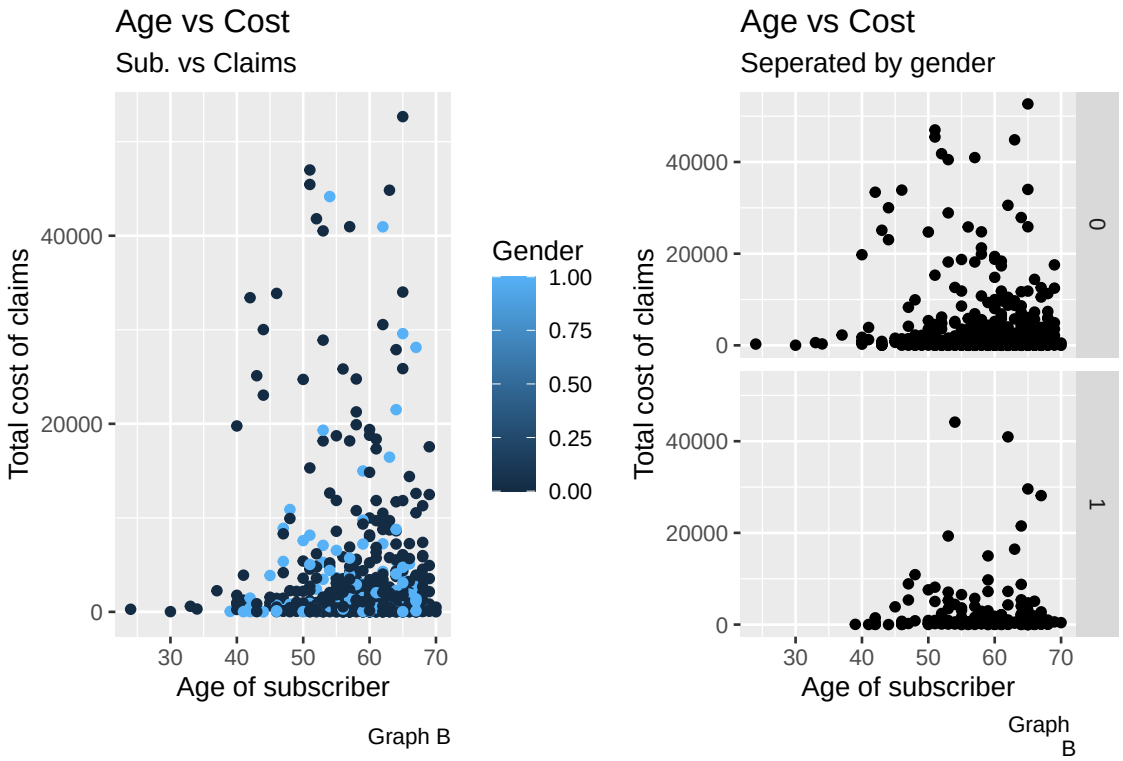
Seeing that our data accurately predicted 74.6% of the data in the dataset, we think that it's a result of a pretty accurate and good model. It is possible to increase the validity and accuracy of this model maybe if we added transformations and of course other variables such as whether they attended college, if their parents smoked, etc. While our model works pretty well on this dataset, it remains to be seen if it can do the same on another dataset with different variables. Another reasoning behind the predictability of it being 74.6% is largely because of outside influences on people. Everyone is different and is not bound by the variables described in the dataset. Thus, no model can 100% accurately describe a dataset, thus describing the error term at the end of a regression, ϵ_t. We also highly recommend not to base any claims off of this final regression model as the dataset is not that big as well as not that good in the amount of variables they should account for.

Question 2: Ischemic Heart Disease

(I) Introduction

Heart disease is one of the most common diseases which can lead to death. It is in fact an very serious disease and is an type of disease which starts off by having an buildup of plaque. This leads to the coronary arteries thus having to narrow, which limits the blood flow to the heart. Some symptoms of coronary artery disease can really range from no symptoms, to chest pain and even an heart attack depending on the person. Some treatment can help but ultimately there is no cure and would have to deal with for the rest of your life. In this paper, we are looking into an dataset called `ischemic` given to us by Professor Prabir Burman which contains 9 columns. The 9 columns are `cost`(the total cost of claims made by the subscriber), `age`(age of the subscriber), `gender`(gender of subscriber),`inter`(total number of interventions or procedures carried out),`drugs`(number of tracked drugs prescribed), `complications`(number of other complications that came from the heart treatment), `comorbidities` (number of other diseases that the subscriber had during the period), `duration` (number of days of duration of treatment condition), and `visits` (number of emergency room visits). We will be using this data set to perform a Poisson regression that will perform an data summary, goodness-of-fit and model selection to model the mean of visits as an function of 8 other variables.

(II) Materials and Methods



The full model that includes all predictor variables is:

$$log(\mu) = \beta_0 + \beta_1 x_{complications} + \beta_2 x_{comorbidities} + \beta_3 x_{duration} + \beta_4 x_{age} + \beta_5 x_{gender} + \beta_6 x_{cost} + \beta_7 x_{drugs} + \beta_8 x_{inter}$$

From the summary of the full model, we can see the estimated parameters and their relatively low standard errors, which results in the estimated regression function:

$$log(\hat{\mu}) = (4.994e-01) + (6.125e-02)x_{complications} - (8.999e-04)x_{comorbidities} + (3.529e-04)x_{duration} + (6.724e-03)x_{age} + (1.819e-01)x_{gender} + (1.495e-05)x_{cost} + (1.932e-01)x_{drugs} + (1.007e-02)x_{inter}$$

It makes sense to see that from our estimated regression function of the full model, the variable `comorbidities` (the number of other diseases that the subscriber had during the period) has a negative correlation with the average number of emergency room visits related to heart disease, as the subscriber may have visited the emergency room because of another disease unrelated to heart disease.

Going by model selection using stepwise regression, we can see that the reduced model that results in the lowest AIC = 3268.1 and drop the variables `complications` and `comorbidities`:

$log(\mu) = \beta_0 + \beta_3 x_{duration} + \beta_4 x_{age} + \beta_5 x_{gender} + \beta_6 x_{cost} + \beta_7 x_{drugs} + \beta_8 x_{inter}$

From the summary of the reduced model, we can see the estimated parameters and their relatively low standard errors, which results in the estimated regression function:

$log(\hat{\mu}) = (5.208e-01) + (3.453e-04)x_{duration} + (6.334e-03)x_{age} + (1.857e-01)x_{gender} + (1.493e-05)x_{cost} + (1.963e-01)x_{drugs} + (1.025e-02)x_{inter}$

From both summary statistics and diagnostic plots for the transformed full model and transformed reduced model, we can see that there appears to be constant variance with few outliers, and a majority of the standardized residuals fall within +/- 3 standard deviations of 0.

We will be using the likelihood ratio test to determine whether the variable ($x_{complications}$) should be dropped from the model. Here, $H_0 : \beta_1 = 0$ and $H_1 : \beta_1 \neq 0$.

The likelihood-ratio test statistic where G_2 = {residual deviance of the reduced model} - {residual deviance of the full model} = 1044.6 - 1043.6 = with degrees of freedom = 781 - 780 = 1. Since the p-value, which is the area to the right of 0.05 under the X_1^2 curve, is about 0.3, which is larger than $\alpha = 0.05$, we fail to reject the null hypothesis, and may drop the variable complications from the full model.

We will again be using the likelihood ratio test to determine whether the variable ($x_{comorbidities}$) should be dropped from the model. Here, $H_0 : \beta_2 = 0$ and $H_1 : \beta_2 \neq 0$.

The likelihood-ratio test statistic where G_2 = {residual deviance of the reduced model} - {residual deviance of the full model} = 1043.7 - 1043.6 = with degrees of freedom = 781 - 780 = 1. Since the p-value, which is the area to the right of 0.05 under the X_1^2 curve, is about 0.8, which is larger than $\alpha = 0.05$, we fail to reject the null hypothesis, and may drop the variable comorbidities from the full model.

We will again be using the likelihood ratio test to determine whether the variables ($x_{complications}$) and ($x_{comorbidities}$) should be dropped from the model. Here, $H_0 : \beta_1 = \beta_2 = 0$ and $H_1 : \beta_1 \neq 0$ *or* $\beta_2 \neq 0$.

The likelihood-ratio test statistic where G_2 = {residual deviance of the reduced model} - {residual deviance of the full model} = 1044.7 - 1043.6 = with degrees of freedom = 781 - 779 = 2. Since the p-value, which is the area to the right of 0.05 under the X_2^2 curve, is about 0.57, which is larger than $\alpha = 0.05$, we fail to reject the null hypothesis, and may drop both variables comorbidities and complications from the full model.

We also performed the likelihood-ratio test on all other predictor variables to see if they should be dropped from the model. We saw that the p-values for all other reduced models was lower than $\alpha = 0.05$, and therefore, we should choose the aforementioned model that dropped both variables complications and comorbidities.

Dropping the variables complication and comorbidities does not make much sense for our model, since complications that arose during the heart disease treatment can lead a subscriber to visiting the emergency room, and symptoms from the number of other diseases that the subscriber had during the period can lead to the subscriber visiting the emergency room because of another disease (hence its negative correlation with the average number of visits to the emergency room related to heart disease). Because of this, we are transforming all of the predictor variables (except gender) by the square root to see if we can get a more accurate model to represent our data.

The full model that includes all predictor variables after being transformed by square root (except gender) is:

$log(\mu) = \beta_0 + \beta_1 x_{newcomp} + \beta_2 x_{newcomorb} + \beta_3 x_{newdur} + \beta_4 x_{newage} + \beta_5 x_{gender} + \beta_6 x_{newcost} + \beta_7 x_{newdrug} + \beta_8 x_{newinter}$

From the summary of the full transformed model, we can see the estimated parameters and their relatively low standard errors, which results in the estimated regression function:

$log(\hat{\mu}) = (-0.0370823) + (0.1006946)x_{newcomp} - (0.0243875)x_{newcomorb} + (0.0083841)x_{newdur} + (0.1026150)x_{newage} + (0.1724272)x_{gender} + (0.0039905)x_{newcost} + (0.4195931)x_{newdrug} + (0.0159633)x_{newinter}$

Going by model selection using stepwise regression, we can see that the reduced model that results in the lowest AIC = 3217.91 is when we transform the variables by square root (except for gender) and drop the variable inter:

$log(\mu) = \beta_0 + \beta_1 x_{newcomp} + \beta_2 x_{newcomorb} + \beta_3 x_{newdur} + \beta_4 x_{newage} + \beta_5 x_{gender} + \beta_6 x_{newcost} + \beta_7 x_{newdrug}$

From the summary of the reduced transformed model, we can see the estimated parameters and their relatively low standard errors, which results in the estimated regression function:

$log(\hat{\mu}) = (-0.0202454) + (0.1026728)x_{newcomp} - (0.0249671)x_{newcomorb} + (0.0088116)x_{newdur} + (0.1020661)x_{newage} + (0.1742938)x_{gender} + (0.0042954)x_{newcost} + (0.4221196)x_{newdrug}$

It makes sense to see that from our estimated regression function of the full transformed model and reduced transformed model, the transformed by square root variable comorbidities (the number of other diseases that the subscriber had during the period) has a negative correlation with the average number of emergency room visits related to heart disease, as the subscriber may have visited the emergency room because of another disease unrelated to heart disease. From both summary statistics and diagnostic plots for the transformed full model and transformed reduced model, we can see that there appears to be constant variance with few outliers, and a majority of the standardized residuals fall within +/- 3 standard deviations of 0.

We will be using the likelihood-ratio test to determine whether the variable inter transformed by the square root ($x_{newinter}$) should be dropped from the model. Here, $H_0 : \beta_8 = 0$ and $H_1 : \beta_8 \neq 0$.

The likelihood-ratio test statistic where G_2 = {residual deviance of the reduced model} - {residual deviance of the full model} = 992.5 - 992.01 = 0.49 with degrees of freedom = 780 - 779 = 1. Since the p-value, which is the area to the right of .05 under the X_1^2 curve, is about 0.48, which is larger than $\alpha = 0.05$, we fail to reject the null hypothesis, and may drop newinter from the full (transformed) model.

We also performed the likelihood-ratio test on all other predictor variables transformed by the square root (except gender) to see if they should be dropped from the model. We saw that although the p-values for 2 other reduced models (one that did not include the variable comorbidities and another that did not include the variable complications) were greater than $\alpha = 0.05$, these models still resulted in a higher AIC (with the lowest being 3218.2 by dropping variables newcomorb and newcomp in addition to dropping newinter from the model), and therefore, we should choose the aforementioned model that solely dropped the transformed variable inter.

(III) Results

After the model's transformation by square root, we can see that the total number of interventions or procedures carried out (inter) has no impact on the model, as the p-value of the model not including this variable is greater than $\alpha = 0.05$, so we can drop it from the model.

We also wanted to see if adding the untransformed variable inter to the fully transformed reduced model would result in a lower AIC and could be added to the model, but it resulted in having a slightly higher AIC = 3218.8. Because the reduced model after transforming all of the predictor variables results in the lowest AIC, we will use this reduced transformed model to represent the mean of number of emergency room visits as a function of these 7 other variables.

Dropping the transformed variable inter makes sense because the total number of procedures or interventions carried out as these tasks are carried out after the subscriber's visit to the emergency room and are done either in the emergency room or in a different part of the hospital, A.K.A. these tasks happen as a result of the subscriber's visit to the emergency room, and do not affect the number of emergency room visits.

(IV) Conclusion

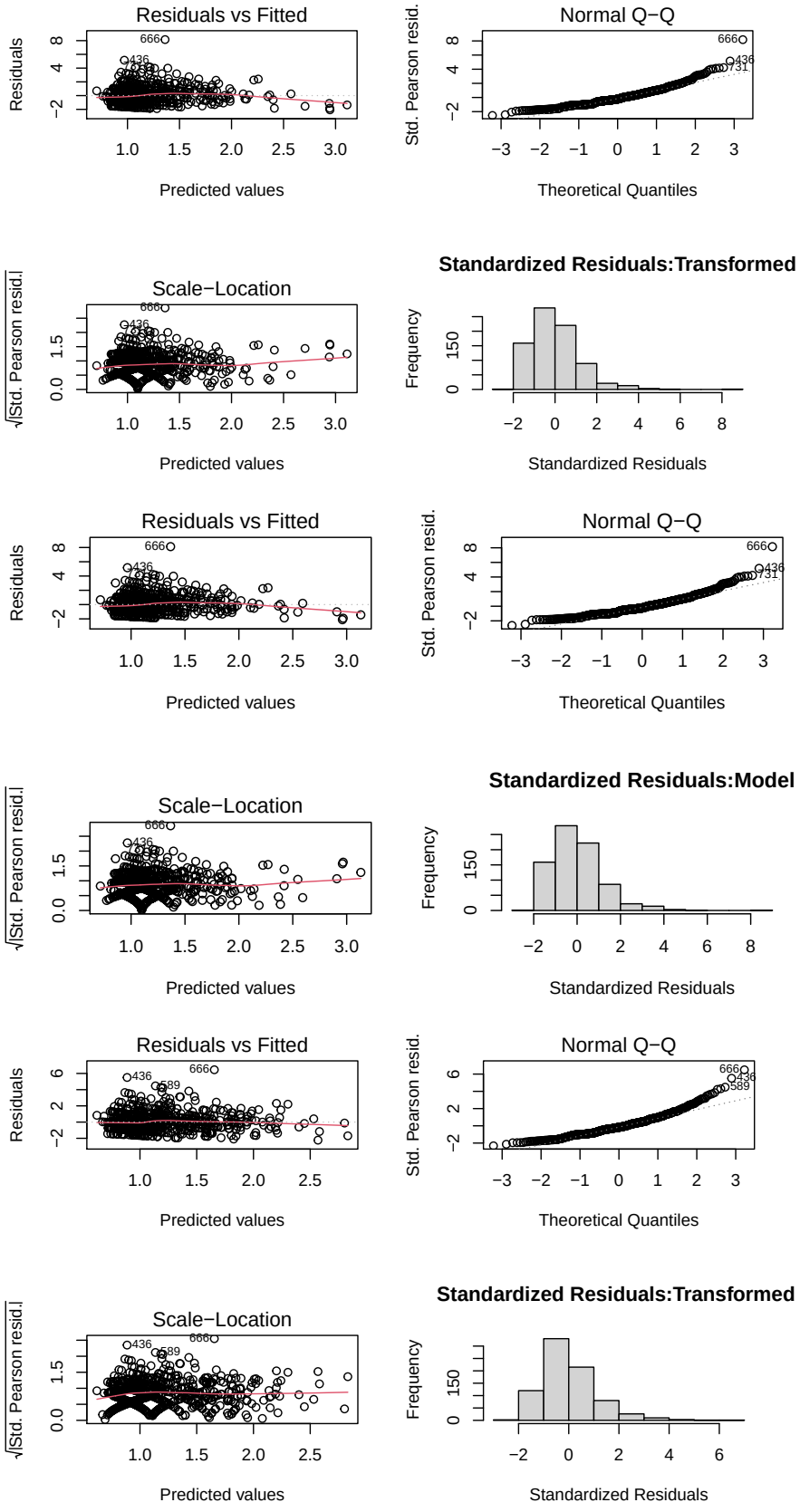
In conclusion, our final model had the best fit to model the average number of emergency room visits related to heart disease as a function of 7 other variables (all transformed by square root): `cost` (total cost of claims made by subscriber in dollars), `age` (age of subscriber in years), `gender of subscriber` (1 = male, 0 = otherwise), `drugs` (number of tracked drugs prescribed), `complications` (number of other complications

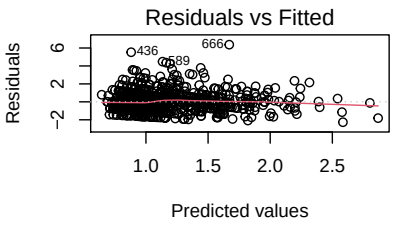
that arose during the heart disease treatment), `comorbidities` (number of other diseases that the subscriber had during the period), `duration` (number of days of duration of treatment condition):

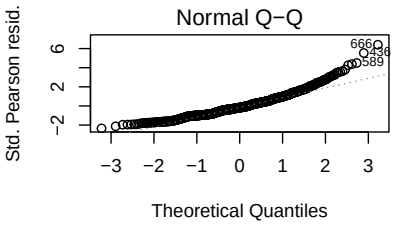
$log(\hat{\mu}) = (-0.0202454) + (0.1026728)x_{newcomp} - (0.0249671)x_{newcomorb} + (0.0088116)x_{newdur} + (0.1020661)x_{newage} + (0.1742938)x_{gender} + (0.0042954)x_{newcost} + (0.4221196)x_{newdrug}$

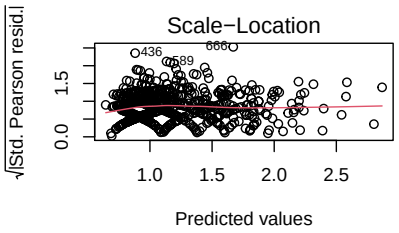
This model resulted in the lowest AIC, which is ideal for model selection using stepwise regression. We also saw from doing a likelihood-ratio statistic test that we could drop the transformed variable inter from the model, as it had no impact on the transformed reduced model. As mentioned above, dropping the transformed variable inter makes sense because the average number of emergency room visits is not affected by the total number of procedures or interventions carried out as these tasks are carried out after the subscriber's visit to the emergency room and are done either in the emergency room or in a different part of the hospital, A.K.A. these tasks happen as a result of the subscriber's visit to the emergency room, and do not affect the number of emergency room visits.

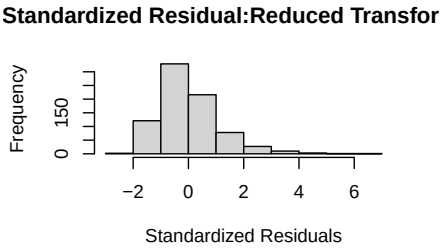
Graphs of Residuals of different GLM models




Residuals vs Fitted
Residuals
436
589
666
−2
2
6
1.0
1.5
2.0
2.5
Predicted values


Normal Q−Q
Std. Pearson resid.
666
436
589
−2
2
6
−3
−2
−1
0
1
2
3
Theoretical Quantiles


Scale−Location
√|Std. Pearson resid.|
436
589
666
0.0
1.5
1.0
1.5
2.0
2.5
Predicted values


Standardized Residual:Reduced Transfor
Frequency
0
150
−2
0
2
4
6
Standardized Residuals

Ⓥ

Code Appendix

```
# cuttingoffcode
library(knitr)
opts_chunk$set(tidy.opts = list(width.cutoff = 70), tidy = TRUE)
# library & importing data
library(readxl)
library(tidyverse)
library(patchwork)
library(MASS)
baby <- read_excel("baby.xls")
summary(baby)
# analysis for question 1
p = baby %>% ggplot() + geom_point(mapping = aes(x = age, y = weight, color = birth,
    shape = smoke)) + labs(title = "Age vs Weight", subtitle = "Comparison based on if they smoked or n
    x = "Age of Mother", y = "Weight of mother", color = "Birth", caption = "Graph A",
    shape = "Smoke")

b = baby %>% ggplot(aes(age, weight)) + geom_point() + facet_grid(vars(birth),
    vars(smoke)) + labs(title = "Age vs Weight", subtitle = "Individual graphs for simplisticity",
    x = "Age of Mother", y = "Weight of mother", caption = "Graph B")

p + b
z = glm(birth ~ age + weight + factor(smoke) + factor(pre) + factor(hyp) +
    visits, data = baby, family = "binomial")
summary(z)
x = glm(birth ~ age + weight + factor(smoke) + factor(pre) + factor(hyp) +
    visits + age:weight + weight:factor(pre) + weight:factor(hyp), data = baby,
    family = "binomial")
summary(x)
fit_full = glm(birth ~ age + weight + factor(smoke) + factor(pre) + factor(hyp) +
    visits + age:weight + weight:factor(pre) + weight:factor(hyp), data = baby,
    family = "binomial")
fit_reduced = glm(birth ~ age + weight + factor(smoke) + factor(pre) +
    factor(hyp) + visits, data = baby, family = "binomial")
G2 = fit_reduced$deviance - fit_full$deviance
1 - pchisq(G2, df = 3)
fit_full = glm(birth ~ age + weight + factor(smoke) + factor(pre) + factor(hyp) +
    visits, data = baby, family = "binomial")
fit_reduced = glm(birth ~ age + weight + factor(smoke) + factor(pre) +
    factor(hyp), data = baby, family = "binomial")
G2 = fit_reduced$deviance - fit_full$deviance
1 - pchisq(G2, df = 1)
step.model <- stepAIC(x, direction = "both", trace = FALSE)
summary(step.model)
final = glm(formula = birth ~ age + weight + factor(smoke) + factor(pre) +
    factor(hyp), family = "binomial", data = baby)

summary(final)
test <- data.frame(baby[1:189, 1:6])
prediction = predict(final, test, type = "response")
lol = ifelse(prediction > 0.5, 1, 0)
```

```
cbind(prediction, lol, baby$birth)
cool = lol == baby$birth
length(cool[cool == TRUE])
# Question 2
ischemic <- read_excel("ischemic.xlsx")

summary(ischemic)

a = ischemic %>% ggplot() + geom_point(mapping = aes(x = age, y = cost,
    color = gender)) + labs(title = "Age vs Cost", subtitle = "Sub. vs Claims",
    x = "Age of subscriber", y = "Total cost of claims", color = "Gender",
    caption = "Graph B", shape = "Smoke")

b = ischemic %>% ggplot(aes(age, cost)) + geom_point() + facet_grid(vars(gender)) +
    labs(title = "Age vs Cost", subtitle = "Seperated by gender", x = "Age of subscriber",
        y = "Total cost of claims", caption = "Graph
       B")

a + b


fit_full = glm(visits ~ cost + age + gender + inter + drugs + complications +
    comorbidities + duration, data = ischemic, family = poisson)

fit_reduced1 = glm(visits ~ age + gender + inter + drugs + complications +
    comorbidities + duration, data = ischemic, family = poisson)

G2 = fit_reduced1$deviance - fit_full$deviance  #df=1

1 - pchisq(G2, df = 1)  #keep cost

fit_reduced2 = glm(visits ~ cost + gender + inter + drugs + complications +
    comorbidities + duration, data = ischemic, family = poisson)

G2 = fit_reduced2$deviance - fit_full$deviance  #df=1

1 - pchisq(G2, df = 1)  #keep age

fit_reduced3 = glm(visits ~ cost + age + inter + drugs + complications +
    comorbidities + duration, data = ischemic, family = poisson)

G2 = fit_reduced3$deviance - fit_full$deviance  #df=1

1 - pchisq(G2, df = 1)  #keep gender

fit_reduced4 = glm(visits ~ cost + age + gender + drugs + complications +
    comorbidities + duration, data = ischemic, family = poisson)

G2 = fit_reduced4$deviance - fit_full$deviance  #df=1

1 - pchisq(G2, df = 1)  #keep inter

fit_reduced5 = glm(visits ~ cost + age + gender + inter + complications +
```

```
    comorbidities + duration, data = ischemic, family = poisson)

G2 = fit_reduced5$deviance - fit_full$deviance  #df=1

1 - pchisq(G2, df = 1)  #keep drugs

fit_reduced6 = glm(visits ~ cost + age + gender + inter + drugs + comorbidities +
    duration, data = ischemic, family = poisson)

G2 = fit_reduced6$deviance - fit_full$deviance  #df=1

1 - pchisq(G2, df = 1)  #drop complications

fit_reduced7 = glm(visits ~ cost + age + gender + inter + drugs + complications +
    duration, data = ischemic, family = poisson)

G2 = fit_reduced7$deviance - fit_full$deviance  #df=1

1 - pchisq(G2, df = 1)  #drop comorbidities

fit_reduced8 = glm(visits ~ cost + age + gender + inter + drugs + complications +
    comorbidities, data = ischemic, family = poisson)

G2 = fit_reduced8$deviance - fit_full$deviance  #df=1

1 - pchisq(G2, df = 1)  #keep duration

step(fit_full)

summary(fit_full)

resfull = residuals(fit_full, "pearson")
# par(mfrow = c(2,2)) plot(fit_full ,which= 1) plot(fit_full,which= 2)
# plot(fit_full,which= 3)

# hist(resfull, main = 'Standardized Residuals:Transformed', xlab =
# 'Standardized Residuals')

redmod = glm(visits ~ cost + age + gender + inter + drugs + duration, data = ischemic,
    family = poisson)

summary(redmod)

step(redmod)

# plot(redmod)

resredmod = residuals(redmod, "pearson")


# par(mfrow = c(2,2)) plot(redmod ,which= 1) plot(redmod,which= 2)
# plot(redmod,which= 3) hist(resredmod, main = 'Standardized
# Residuals:Model', xlab = 'Standardized Residuals')
```

```
newcost = sqrt(ischemic$cost)

newage = sqrt(ischemic$age)

newinter = sqrt(ischemic$inter)

newdrug = sqrt(ischemic$drugs)

newcomp = sqrt(ischemic$complications)

newcomorb = sqrt(ischemic$comorbidities)

newdur = sqrt(ischemic$duration)

newmod = glm(visits ~ newcost + newage + gender + newinter + newdrug +
    newcomp + newcomorb + newdur, data = ischemic, family = poisson)

fit_red1 = glm(visits ~ newage + gender + newinter + newdrug + newcomp +
    newcomorb + newdur, data = ischemic, family = poisson)

G2 = fit_red1$deviance - newmod$deviance  #df=1

1 - pchisq(G2, df = 1)  #keep cost

fit_red2 = glm(visits ~ newcost + gender + newinter + newdrug + newcomp +
    newcomorb + newdur, data = ischemic, family = poisson)

G2 = fit_red2$deviance - newmod$deviance  #df=1

1 - pchisq(G2, df = 1)  #keep age

fit_red3 = glm(visits ~ newcost + newage + newinter + newdrug + newcomp +
    newcomorb + newdur, data = ischemic, family = poisson)

G2 = fit_red3$deviance - newmod$deviance  #df=1

1 - pchisq(G2, df = 1)  #keep gender

fit_red4 = glm(visits ~ newcost + newage + gender + newdrug + newcomp +
    newcomorb + newdur, data = ischemic, family = poisson)

G2 = fit_red4$deviance - newmod$deviance  #df=1

1 - pchisq(G2, df = 1)  #drop inter

fit_red5 = glm(visits ~ newcost + newage + gender + newinter + newcomp +
    newcomorb + newdur, data = ischemic, family = poisson)

G2 = fit_red5$deviance - newmod$deviance  #df=1

1 - pchisq(G2, df = 1)  #keep drugs

fit_red6 = glm(visits ~ newcost + newage + gender + newinter + newdrug +
```

```
    newcomorb + newdur, data = ischemic, family = poisson)

G2 = fit_red6$deviance - newmod$deviance  #df=1

1 - pchisq(G2, df = 1)  #drop complications

fit_red7 = glm(visits ~ newcost + newage + gender + newinter + newdrug +
    newcomp + newdur, data = ischemic, family = poisson)

G2 = fit_red7$deviance - newmod$deviance  #df=1

1 - pchisq(G2, df = 1)  #drop comorbidities

fit_red8 = glm(visits ~ newcost + newage + gender + newinter + newdrug +
    newcomp + newcomorb, data = ischemic, family = poisson)

G2 = fit_red8$deviance - newmod$deviance  #df=1

1 - pchisq(G2, df = 1)  #keep duration

redmod2 = glm(visits ~ newcost + newage + gender + newdrug + newcomp +
    newcomorb + newdur, data = ischemic, family = poisson)

redmod3 = glm(visits ~ newcost + newage + gender + newdrug + newdur, data = ischemic,
    family = poisson)

summary(newmod)

summary(redmod2)

summary(redmod3)

step(newmod)

step(redmod2)

step(redmod3)

# plot(newmod)


resnewmod = residuals(newmod, "pearson")

# par(mfrow = c(2,2)) plot(newmod ,which= 1) plot(newmod,which= 2)
# plot(newmod,which= 3)

# hist(resnewmod, main = 'Standardized Residuals:Transformed ', xlab =
# 'Standardized Residuals')

# plot(redmod2) par(mfrow = c(2,2)) plot(redmod2 ,which= 1)
# plot(redmod2,which= 2) plot(redmod2,which= 3)
resmod2 = residuals(redmod2, "pearson")
```

```r
# hist(resmod2, main = 'Standardized Residual:Reduced Transformed',
# xlab = 'Standardized Residuals')

redmod4 = glm(visits ~ newcost + newage + gender + newdrug + newcomp +
    newcomorb + newdur + inter, data = ischemic, family = poisson)

step(redmod4)


par(mfrow = c(2, 2))
plot(fit_full, which = 1)
plot(fit_full, which = 2)
plot(fit_full, which = 3)

hist(resfull, main = "Standardized Residuals:Transformed", xlab = "Standardized Residuals")

par(mfrow = c(2, 2))
plot(redmod, which = 1)
plot(redmod, which = 2)
plot(redmod, which = 3)
hist(resredmod, main = "Standardized Residuals:Model", xlab = "Standardized Residuals")

par(mfrow = c(2, 2))
plot(newmod, which = 1)
plot(newmod, which = 2)
plot(newmod, which = 3)

hist(resnewmod, main = "Standardized Residuals:Transformed ", xlab = "Standardized Residuals")

par(mfrow = c(2, 2))
plot(redmod2, which = 1)
plot(redmod2, which = 2)
plot(redmod2, which = 3)

hist(resmod2, main = "Standardized Residual:Reduced Transformed", xlab = "Standardized Residuals")
```