STAT 707 Homework 1

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```
library(matlib)
library(GGally)
library(lubridate)
library(tidyverse)
library(ggpubr)
library(faraway)
library(knitr)
opts_chunk$set(tidy.opts=list(width.cutoff=60),tidy=TRUE)
```

6.27. In a small-scale regression study, the following data were obtained:

```
num_data <- matrix(c(7, 33, 42, 4, 41, 33, 16, 7, 75, 3, 49,
    28, 21, 5, 91, 8, 31, 55), nrow = 6, ncol = 3, byrow = TRUE)
num_data
```

```
##      [,1] [,2] [,3]
## [1,]    7   33   42
## [2,]    4   41   33
## [3,]   16    7   75
## [4,]    3   49   28
## [5,]   21    5   91
## [6,]    8   31   55
```

```
data1 <- as.data.frame(num_data)
```

We begin by isolating our matrices

```
Y <- matrix(matrix(num_data[, 3], nrow = 6, ncol = 1), nrow = 6,
    ncol = 1)
Y
```

```
##      [,1]
## [1,]   42
## [2,]   33
## [3,]   75
## [4,]   28
## [5,]   91
## [6,]   55
```

```
X <- matrix(c(1, 7, 33, 1, 4, 41, 1, 16, 7, 1, 3, 49, 1, 21,
    5, 1, 8, 31), nrow = 6, ncol = 3, byrow = T)
X
```

```
##      [,1] [,2] [,3]
## [1,]    1    7   33
## [2,]    1    4   41
## [3,]    1   16    7
## [4,]    1    3   49
## [5,]    1   21    5
## [6,]    1    8   31
```

```
Xtran <- t(X)
Xtran
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]    1    1    1    1    1    1
## [2,]    7    4   16    3   21    8
## [3,]   33   41    7   49    5   31
```

Assume that the regression model (6.1) with independent normal error terms is appropriate.

$$Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2}$$

Using matrix methods, obtain

(a) b

$$b = (X'X)^{-1}X'Y$$

```
b <- inv(Xtran %*% X) %*% Xtran %*% Y
b
```

```
##             [,1]
## [1,] 33.9321020
## [2,]  2.7847707
## [3,] -0.2643979
```

Here, $\beta_0, \beta_1, \beta_2$ are 33.932, 2.2784, and -0.264, respectively.

(b) e

The fitted values are represented by $\hat{Y} = Xb$ and the residual terms by

$$e = Y - \hat{Y} = Y - Xb$$

```
e <- Y - X %*% b
e
```

```
##             [,1]
## [1,] -2.70036663
## [2,] -1.23087135
## [3,] -1.63764825
## [4,] -1.33091751
## [5,] -0.09029763
## [6,]  6.98606687
```

(c) H

Define the matrix **H** as follows $\mathbf{H} = X(X'X)^{-1}X'$

```
H <- X %*% inv(Xtran %*% X) %*% Xtran
H
```

```
##             [,1]        [,2]        [,3]       [,4]        [,5]       [,6]
## [1,]  0.23143639  0.25168006  0.21178834  0.1488734 -0.05475455 0.21099418
## [2,]  0.25168006  0.31240977  0.09437951  0.2662835 -0.14787196 0.22314063
## [3,]  0.21178834  0.09437951  0.70442097 -0.3191731  0.10446756 0.20412257
## [4,]  0.14887339  0.26628346 -0.31917314  0.6142637  0.14143589 0.14834214
## [5,] -0.05475455 -0.14787196  0.10446756  0.1414359  0.94040059 0.01632796
## [6,]  0.21099418  0.22314063  0.20412257  0.1483421  0.01632796 0.19708945
```

(d) SSR

Let **J** denote a n x n matrix of 1's. In this exercise, we would have a 6 x 6 matrix.

```
J <- matrix(1, nrow = 6, ncol = 6)
```

$$SSR = bX'Y - (\frac{1}{n})Y'JY = Y'[H - \frac{1}{n}J]Y, \ \textit{(df = p-1)}$$

```
t(Y) %*% (H - J * (1/6)) %*% Y
```

```
##          [,1]
## [1,] 3010.107
```

Thus, our residual sum of squares is approximately equal to 3010.107.

(e) s^2{b}

$s^2b = MSE(X'X)^{-1}$ where $MSE = \frac{SSE}{n-p}$ and $SSE = Y'Y - b'X'Y$

First lets find our SSE.

```
SSE <- t(Y) %*% Y - t(b) %*% t(X) %*% Y
SSE
```

```
##          [,1]
## [1,] 61.89313
```

Now lets find our MSE value.

```
# n = 6 and p = 3
MSE <- SSE/(6 - 3)
MSE
```

```
##          [,1]
## [1,] 20.63104
```

The estimated variance-covariance matrix s^2b now is equal to

```
s_squared_b <- 20.631 * inv(t(X) %*% X)
s_squared_b
```

```
##            [,1]        [,2]        [,3]
## [1,] 713.39022 -34.0595669 -13.5553968
## [2,] -34.05957   1.6568335   0.6421941
## [3,] -13.55540   0.6421941   0.2617044
```

(f) $\hat{Y}_h$ **when** $X_{h1} = 10, X_{h2} = 30$

Our new matrix of values X_h

```
X_h <- matrix(c(1, 10, 30), nrow = 3, ncol = 1)
X_h
```

```
##      [,1]
## [1,]    1
## [2,]   10
## [3,]   30
```

The estimated mean response corresponding to X_h, denoted by $\hat{Y}_h$, is $\hat{Y}_h = X_h'b$

```
t(X_h) %*% b
```

```
##          [,1]
## [1,] 53.84787
```

Thus $\hat{Y}_h$ is equal to 53.848

(g) $s^2(\hat{Y}_h)$ **when** $X_{h1} = 10, X_{h2} = 30$

The estimated variance $s^2(\hat{Y}_h)$ is given by:

$$s^2(\hat{Y}_h) = MSE(X_h'(X'X)^{-1}X_h) = X_h's^2(b)X_h$$

```
s_squared_yhat <- t(X_h) %*% s_squared_b %*% X_h
s_squared_yhat
```

```
##          [,1]
## [1,] 5.408904
```

The estimated variance, $s^2(\hat{Y}_h) \approx 5.409$.

Exercise 6.28

You have been asked to evaluate two alternative models for predicting the number of active physicians (Y) in a CDI. Proposed model I includes as predictor variables total population (X_1), land area (X_2), and total personal income (X_3). Proposed model II includes as predictor variables population density (X_1, the total population divided by land area), percent of population greater than 65 years old (X_2), and total personal income (X_3)

```
CD1 <- read.csv("/Users/daniel421/Desktop/R/STAT707/STAT_707_GLM2/CDI_Data.csv",
    header = FALSE)
```

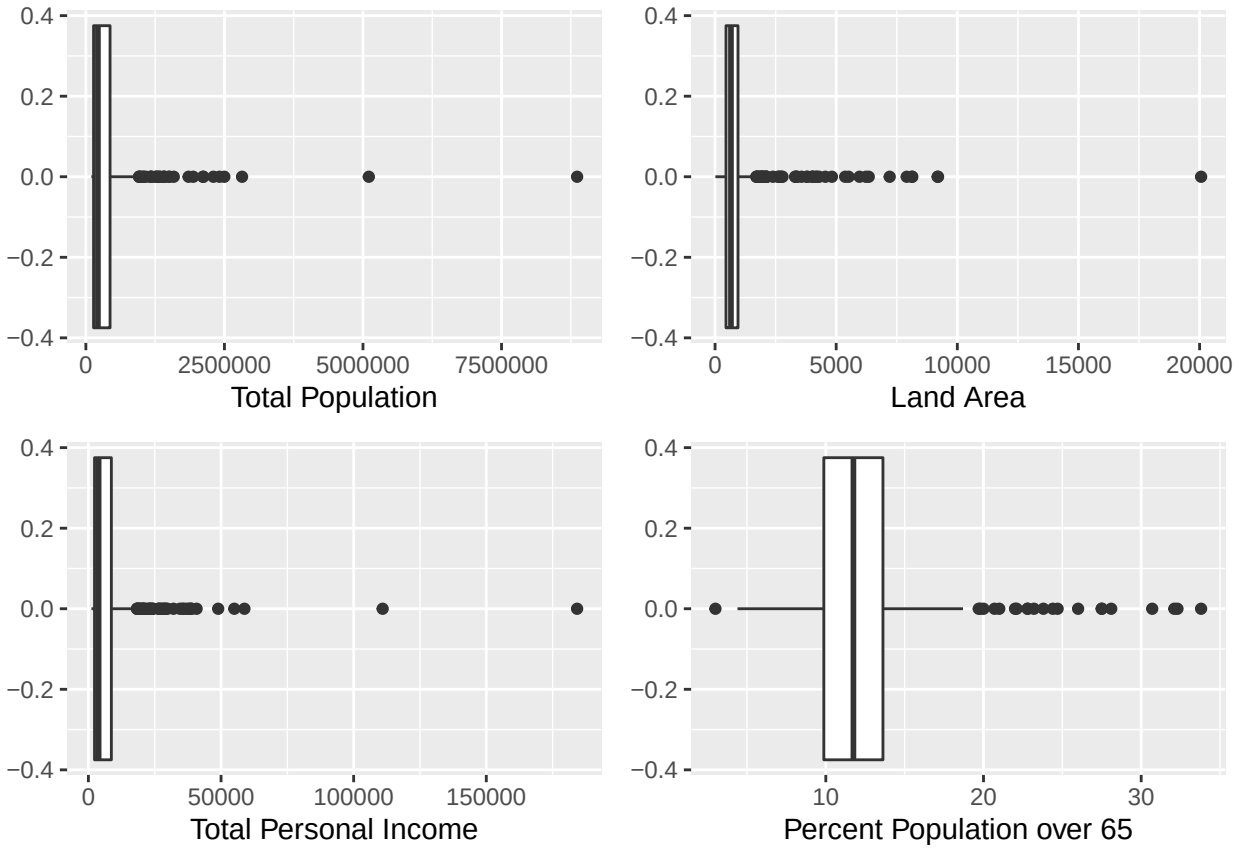
```
names(CD1) <- c("ID", "county", "state", "land_area", "total_pop",
    "percent_pop_18_34", "percent_pop_65", "num_physicians",
    "n_hos_beds", "total_crimes", "percent_hs_grads", "percent_bach",
    "percent_pov", "percent_unemp", "per_capita", "total_income",
    "geographic_region")
```

```
CDI <- CD1
rm(CD1)
```

a. Prepare a boxplot for each of the predictor variables. What noteworthy information is provided by your plots?

```
a1 <- ggplot(data = CDI, mapping = aes(x = total_pop)) + geom_boxplot() +
    labs(x = "Total Population")
a2 <- ggplot(data = CDI, mapping = aes(x = land_area)) + geom_boxplot() +
    labs(x = "Land Area")
a3 <- ggplot(data = CDI, mapping = aes(x = total_income)) + geom_boxplot() +
    labs(x = "Total Personal Income")
a4 <- ggplot(data = CDI, mapping = aes(x = percent_pop_65)) +
    geom_boxplot() + labs(x = "Percent Population over 65")
```

```
figure <- ggarrange(a1, a2, a3, a4, ncol = 2, nrow = 2)
figure
```

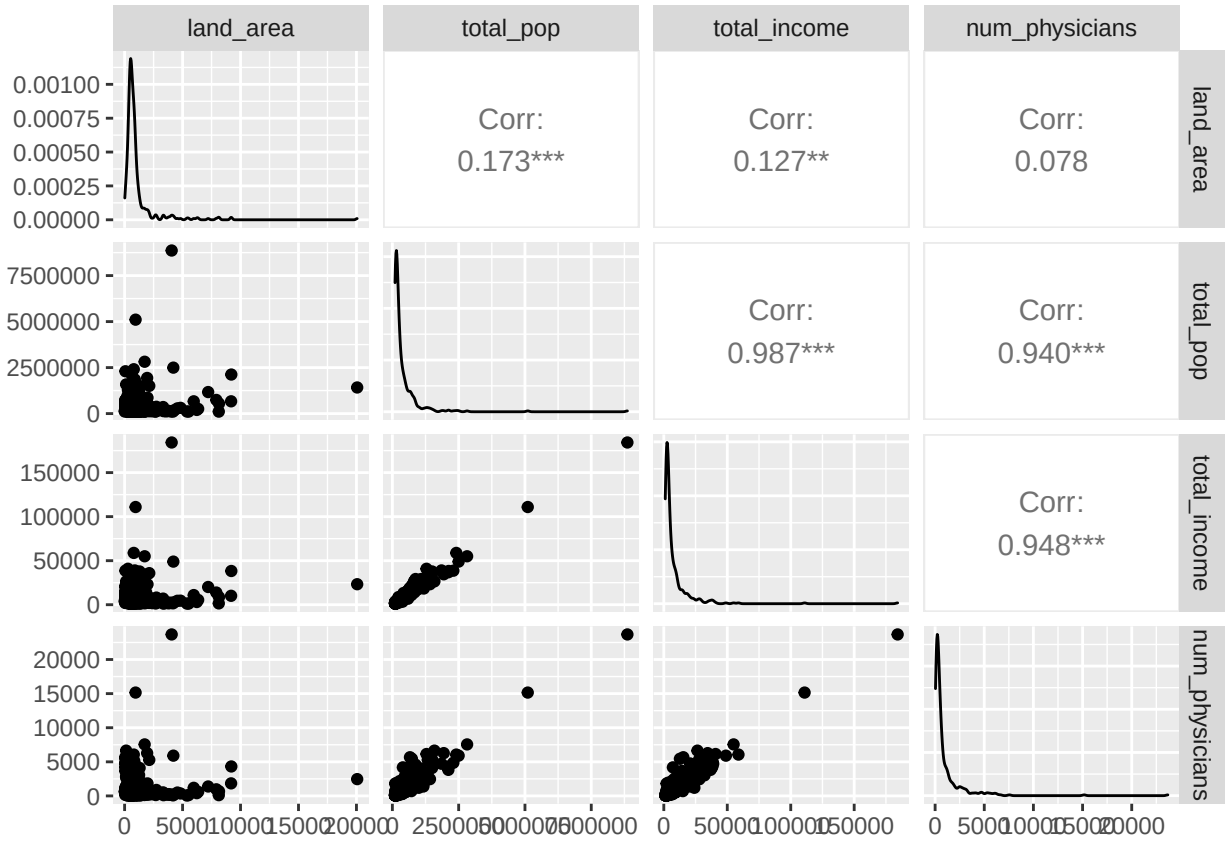


Three of the variables appear to be skewed to the right, many of the values fall out of range of the 4 quartiles.

b. Obtain the scatter plot matrix and the correlation matrix for each proposed model. Summarize the information provided.

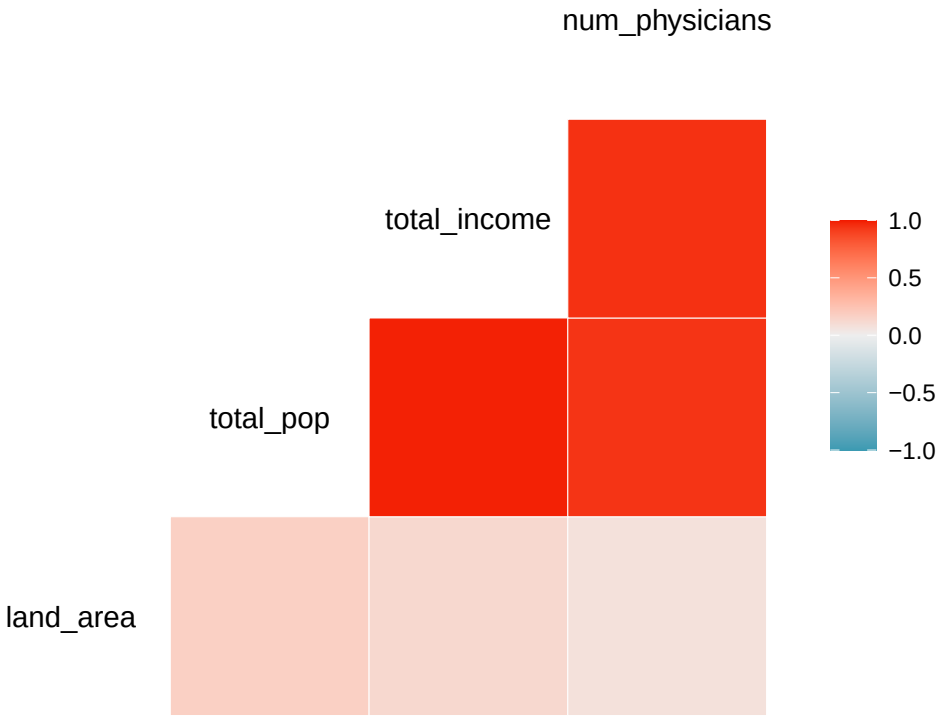
We will first begin with a combination of a scatter plot, density plot and the correlation values of the variables.

```
ggpairs(CDI, columns = c(4, 5, 16, 8))
```



We then look at a more visual correlation plot, detailing that the number of physicians, total personal income and the total population of the county are highly correlated with each other.

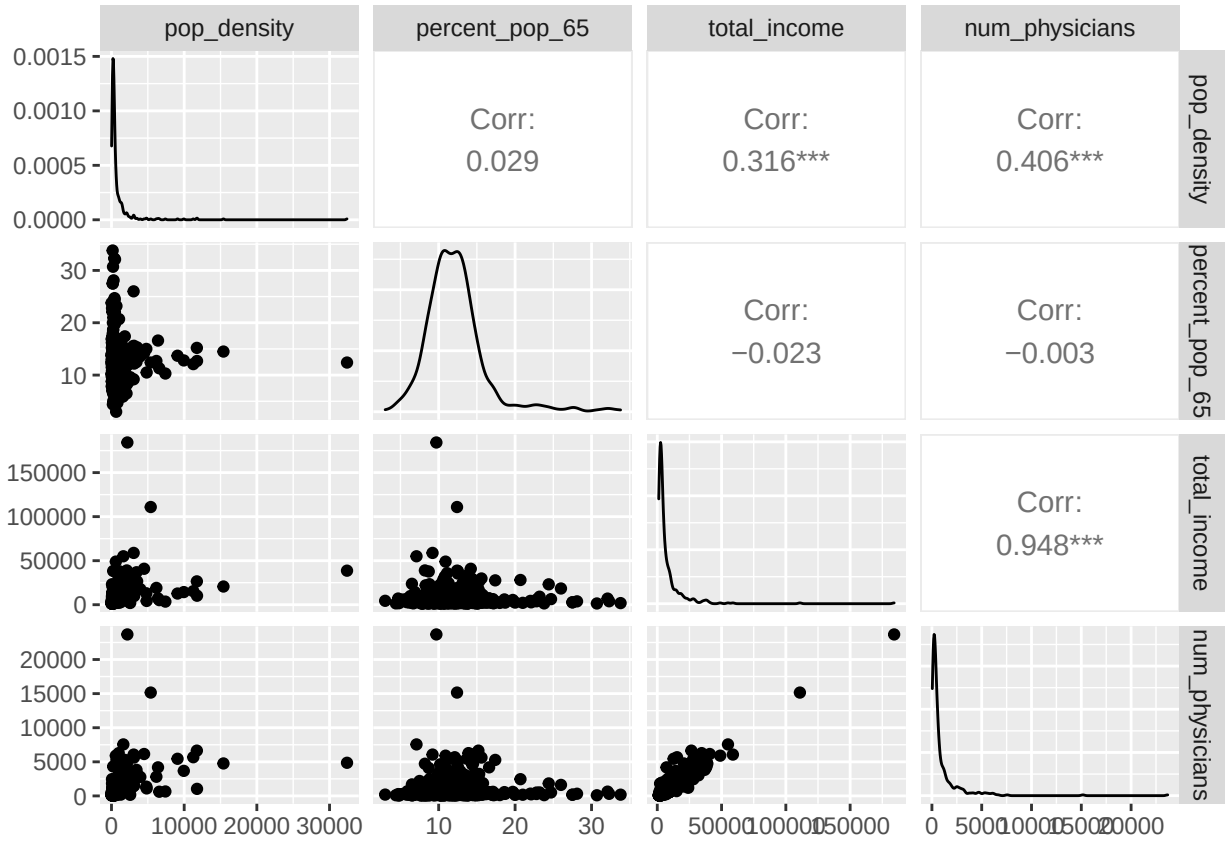
```
ggcorr(data = CDI[, c(4, 5, 16, 8)], method = c("everything",
    "pearson"))
```



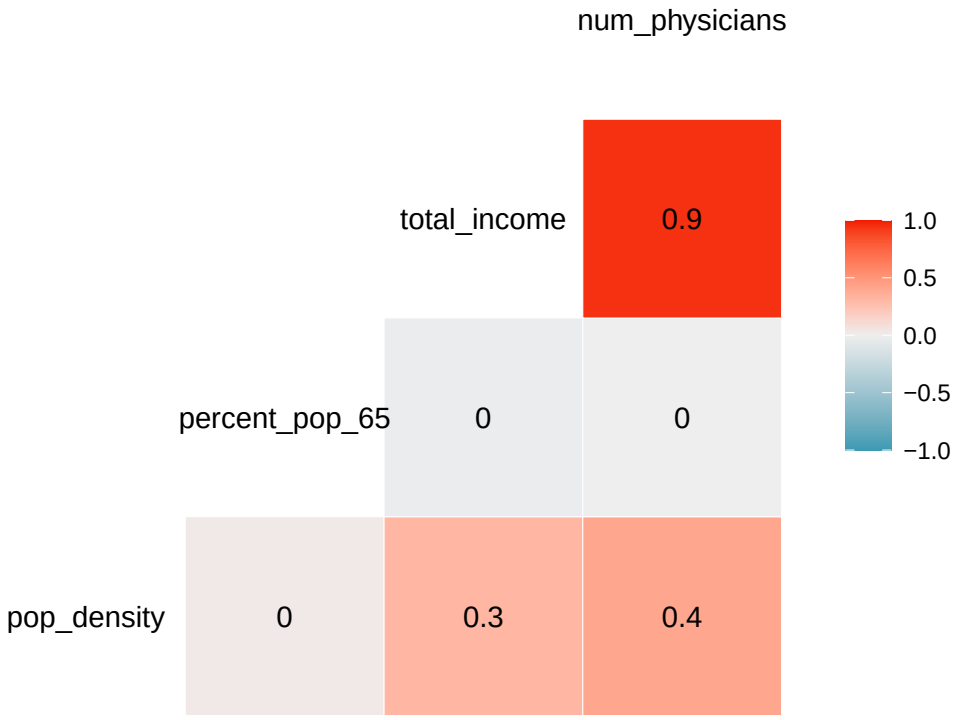
We will now look at the second model. A new variable "pop_density" will need to be created, to represent the total population divided by the land area.

```
CDI["pop_density"] <- CDI$total_pop/CDI$land_area
```

```
ggpairs(data = CDI[, c(18, 7, 16, 8)])
```




```
ggcorr(data = CDI[, c(18, 7, 16, 8)], method = c("everything",
    "pearson"), label = TRUE)
```



We see that most of the variables are skewed to the right, with the "percent of population 65 or older", being the only variable who appears to approach a normal distribution. Two pairs, "percent_pop_65" with "total_income" and "percent_pop_65" with "num_physicians" have low negative correlation values. The number of physicians again, appears to be highly correlated with total income.

c. For each proposed model, fit the first-order regression model (6.5) with three predictor variables.

For both models, we will fit the regression:

$$Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \epsilon_i$$

using our indicated predicted variables.

Model 1

```
model_1 <- glm(num_physicians ~ total_pop + land_area + total_income,
    data = CDI)
```

$$\hat{Y_1} = -13.3162 + 0.000836618 X_1 - 0.065523 X_2 + 0.094132 X_3$$

Model 2

```
model_2 <- glm(num_physicians ~ pop_density + percent_pop_65 +
    total_income, data = CDI)
```

$$\hat{Y_2} = -170.574 + 0.0961589X_1 + 6.33984X_2 + 0.126566X_3$$

d. Calculate R^2 for each model. Is one model clearly preferable in terms of this measure?

```
model_1_R2 <- with(summary(model_1), 1 - deviance/null.deviance)
model_2_R2 <- with(summary(model_2), 1 - deviance/null.deviance)
```

The coefficient of multiple determination, R^2 for model 1 is approximately equal to 0.903, while the R^2 for model 2 is approximately equal to 0.912. You can't determine which model is more preferable in terms of their R^2, other tests of normality should be conducted.

e. For each model, obtain the residuals and plot them against $\hat{Y}$, each of the three predictor varaibles, and each of the two-factor interaction terms.

We will first obtain the residuals of both models, and concatenate them to our CDI data frame.

```
CDI["model_1_resid"] <- residuals(model_1)
CDI["model_2_resid"] <- residuals(model_2)
```

Model 1 diagnostics

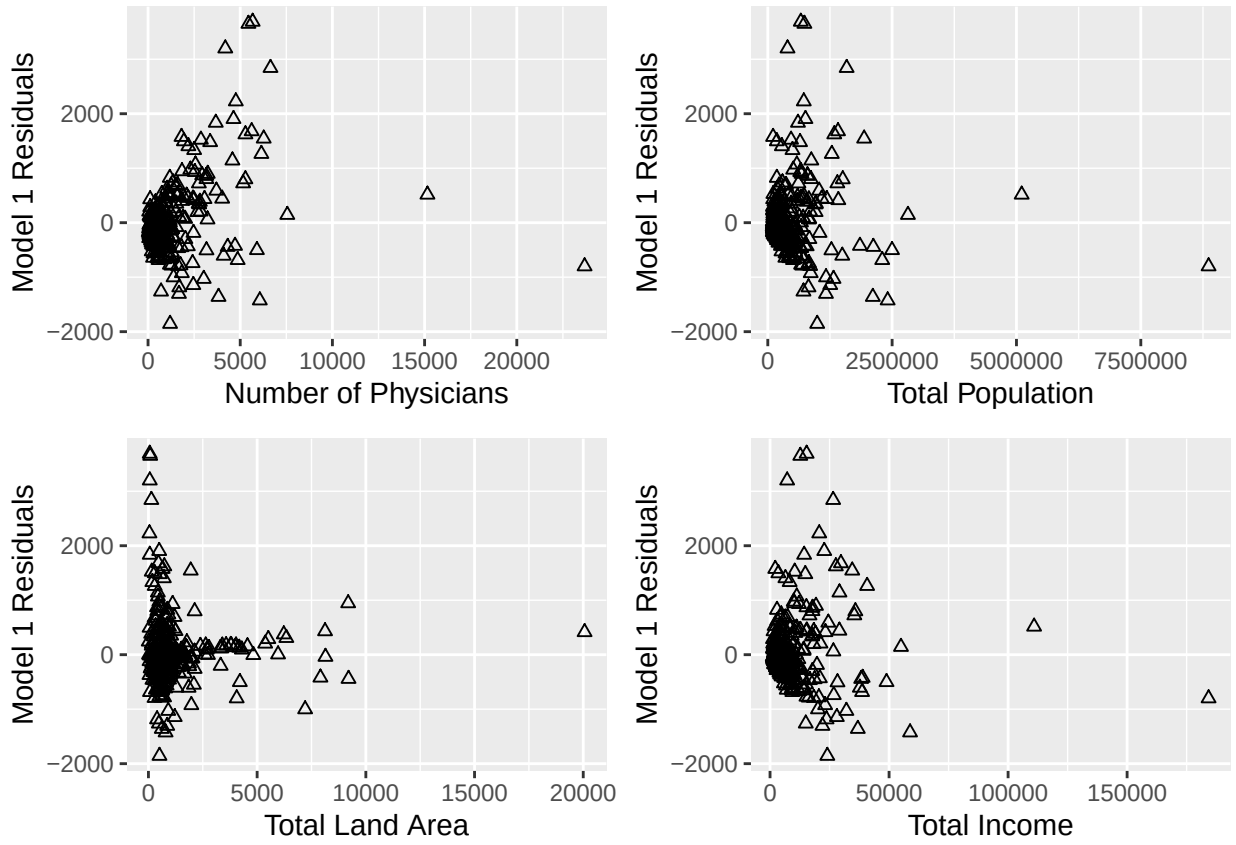
```
b1 <- ggplot(data = CDI, mapping = aes(x = num_physicians, y = model_1_resid)) +
    geom_point(shape = 24) + labs(y = "Model 1 Residuals", x = "Number of Physicians")
```

```
b2 <- ggplot(data = CDI, mapping = aes(x = total_pop, y = model_1_resid)) +
    geom_point(shape = 24) + labs(y = "Model 1 Residuals", x = "Total Population")
```

```
b3 <- ggplot(data = CDI, mapping = aes(x = land_area, y = model_1_resid)) +
    geom_point(shape = 24) + labs(y = "Model 1 Residuals", x = "Total Land Area")
```

```
b4 <- ggplot(data = CDI, mapping = aes(x = total_income, y = model_1_resid)) +
    geom_point(shape = 24) + labs(y = "Model 1 Residuals", x = "Total Income")
```

```
figure2 <- ggarrange(b1, b2, b3, b4, ncol = 2, nrow = 2)
figure2
```



Model 2 Diagnostics

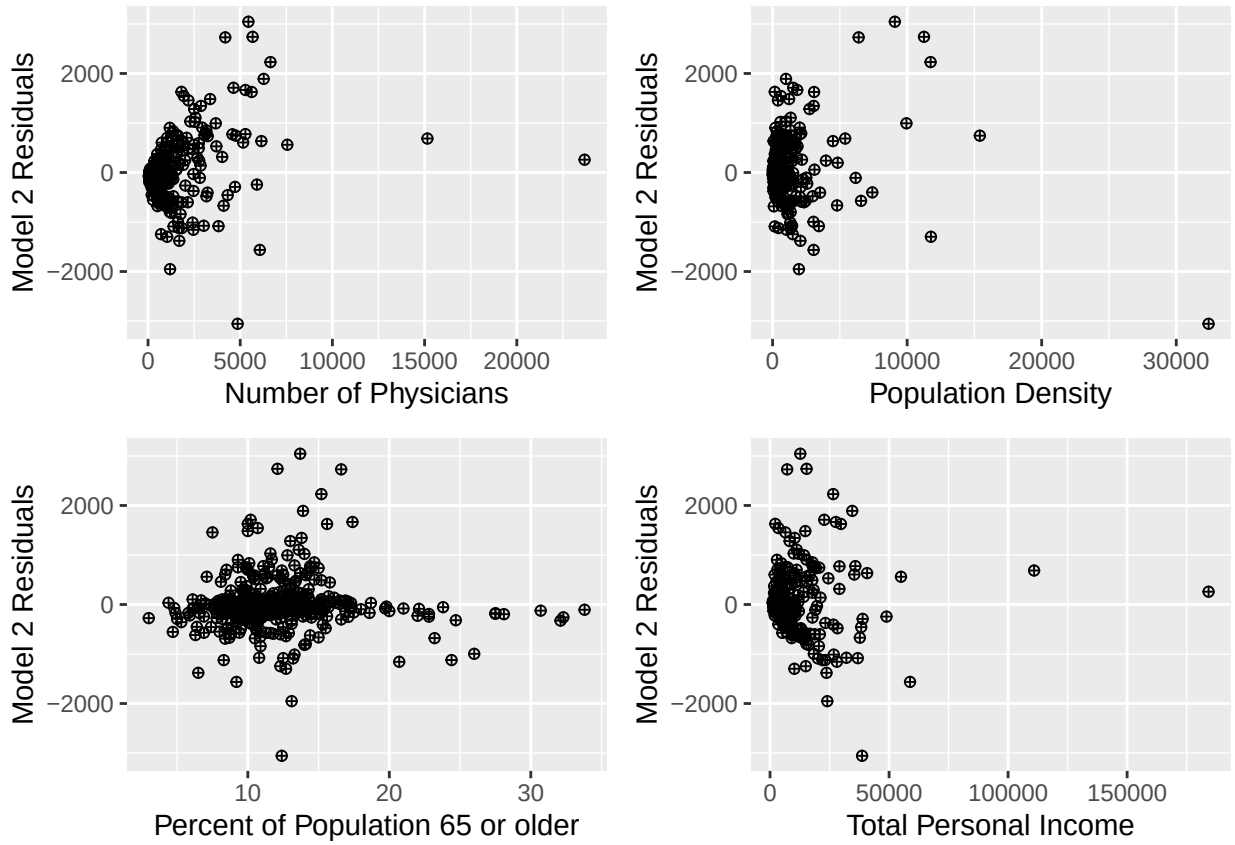
```
c1 <- ggplot(data = CDI, mapping = aes(x = num_physicians, y = model_2_resid)) +
    geom_point(shape = 10) + labs(y = "Model 2 Residuals", x = "Number of Physicians")
```

```
c2 <- ggplot(data = CDI, mapping = aes(x = pop_density, y = model_2_resid)) +
    geom_point(shape = 10) + labs(y = "Model 2 Residuals", x = "Population Density")
```

```
c3 <- ggplot(data = CDI, mapping = aes(x = percent_pop_65, y = model_2_resid)) +
    geom_point(shape = 10) + labs(y = "Model 2 Residuals", x = "Percent of Population 65 or older")
```

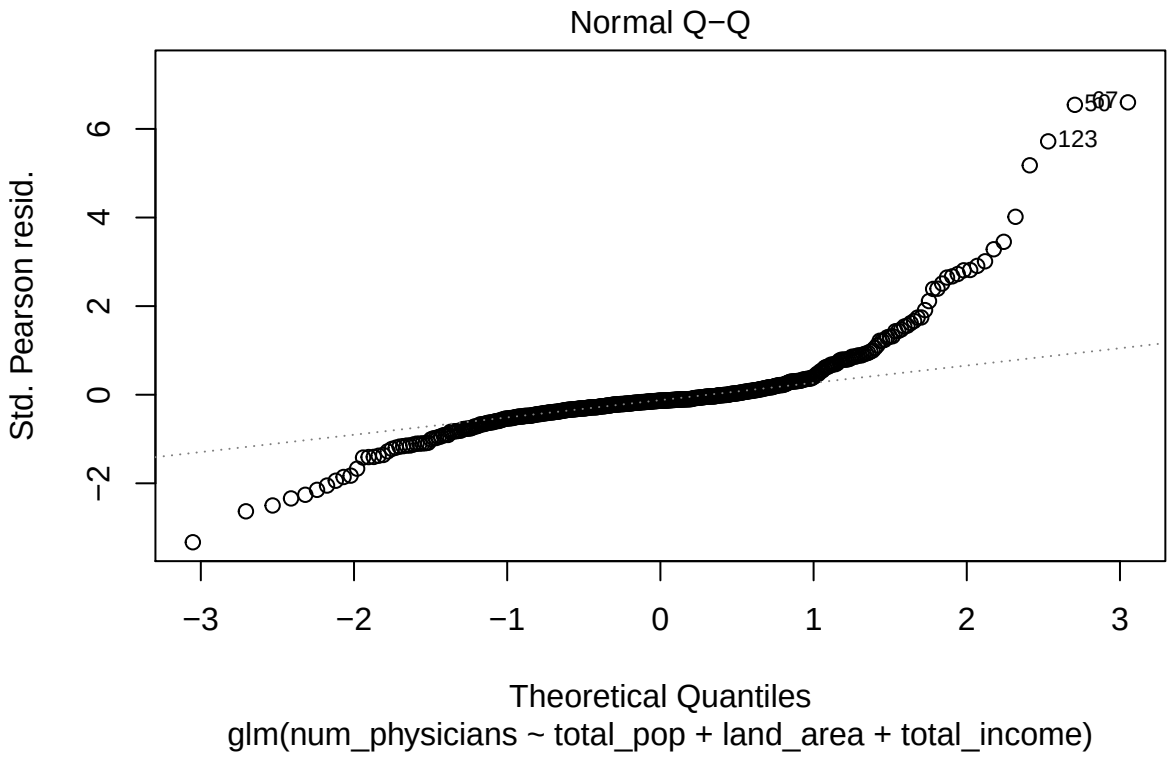
```
c4 <- ggplot(data = CDI, mapping = aes(x = total_income, y = model_2_resid)) +
    geom_point(shape = 10) + labs(y = "Model 2 Residuals", x = "Total Personal Income")
```

```
figure3 <- ggarrange(c1, c2, c3, c4, ncol = 2, nrow = 2)
figure3
```



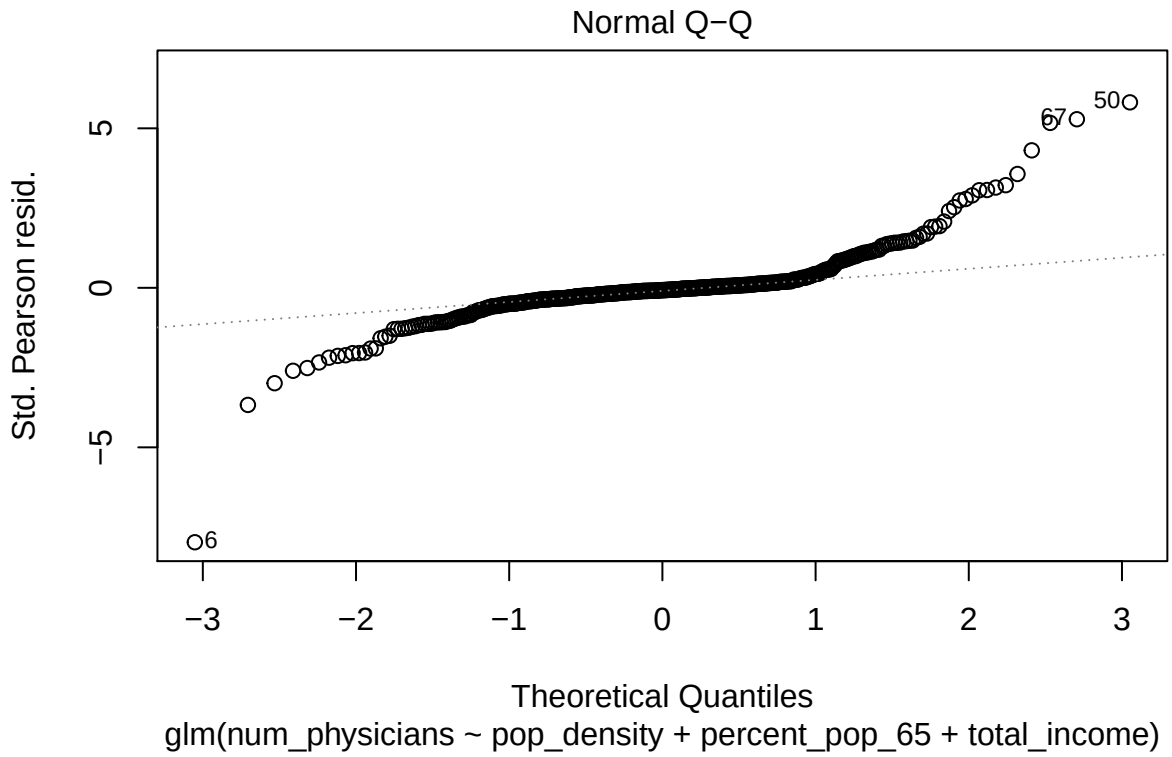
QQ-plot for Model 1

```
plot(model_1, which = 2)
```



QQ-plot for Model 2

```
plot(model_2, which = 2)
```



We will conduct the Shapiro-Wilk test for as our first test for normality. We will be testing the null hypothesis H_0, that our residuals ε_i are normally distributed.

```
shapiro.test(CDI$model_1_resid)
```

Model I

```
##
##  Shapiro-Wilk normality test
##
## data:  CDI$model_1_resid
## W = 0.75754, p-value < 2.2e-16
```

```
shapiro.test(CDI$model_2_resid)
```

Model II

```
##
```

```
##  Shapiro-Wilk normality test
##
## data:  CDI$model_2_resid
## W = 0.80268, p-value < 2.2e-16
```

Our p-values < 0.05 indicates that we should reject the H_0 and conclude the residuals are not normally distributed.

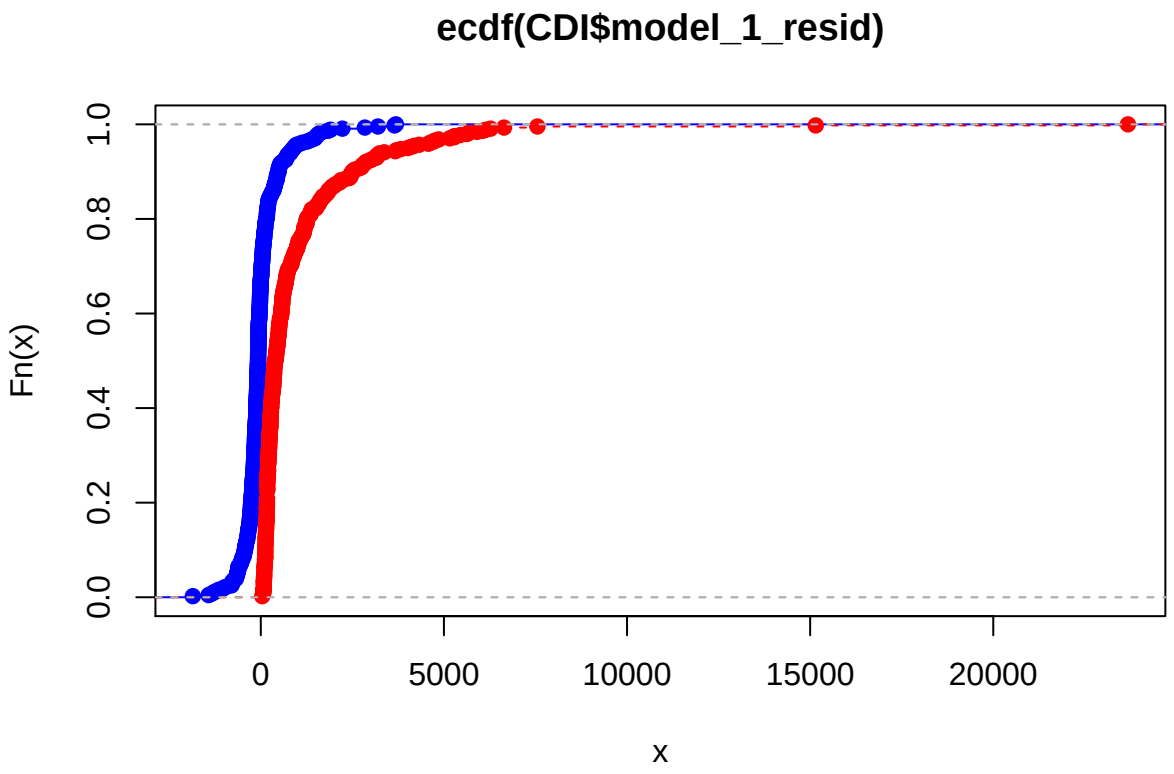
We will conduct Kolmogorov-Smirnov Tests on both model residuals. Does ε_i and the number of physicians come from the same distribution? "A K-S Test quantifies a distance between the cumulative distribution function of the given reference distribution and the empirical distributions of given two samples, or between the empirical distribution of given two samples."

```
ks.test(CDI$model_1_resid, CDI$num_physicians)
```

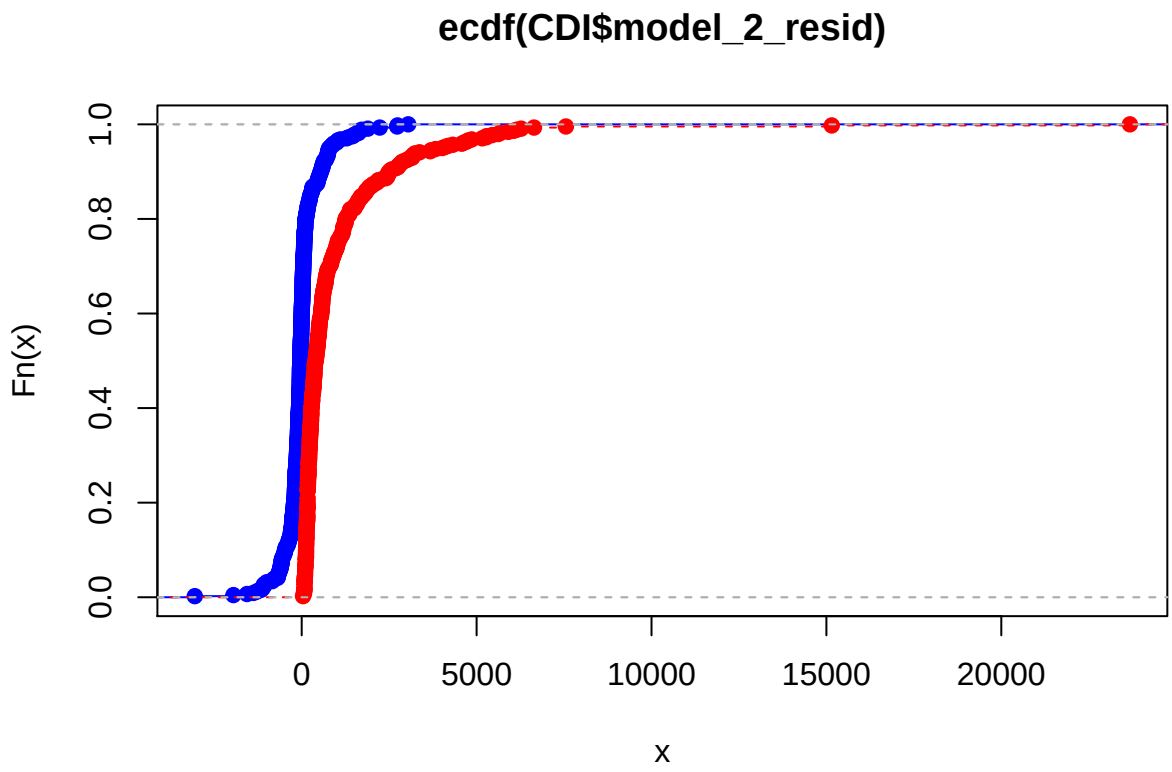
Model I

```
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  CDI$model_1_resid and CDI$num_physicians
## D = 0.73636, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

```
plot(ecdf(CDI$model_1_resid), xlim = range(c(CDI$model_1_resid,
    CDI$num)), col = "blue")
plot(ecdf(CDI$num_physicians), add = TRUE, col = "red", lty = "dashed")
```




```
plot(ecdf(CDI$model_2_resid), xlim = range(c(CDI$model_2_resid,
    CDI$num)), col = "blue")
plot(ecdf(CDI$num_physicians), add = TRUE, col = "red", lty = "dashed")
```



Model II

```
ks.test(CDI$model_2_resid, CDI$num_physicians)
```

```
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  CDI$model_2_resid and CDI$num_physicians
## D = 0.74091, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

This test for both model residuals gives us a distance ≤ 0.73. Our p-values are again less than our $\alpha = 0.05$, we fail our test for normality. We state with 95% confidence that the model residuals do not fit a normal distribution.

```
# knitr::purl('HW_1_Lupercio_Daniel.Rmd','HW_1_Lupercio_Daniel.R',documentation
# = 2)
```