P8130 Final Project

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Abstract

Objective of this study is to predict the crime rate in counties. Data visualization and automatic search procedure combined with AIC and BIC are used for model selection. For model diagnostics, residuals plot and QQ-plot are applied to test the assumptions of linear regression. Model with influential points is compared by cross validation. Finally, our results show that the transformation model is the best with more significant variables, lower rmse, and higher adjusted r-squared . Our final linear regression model includes variables percent of population aged 18-34, percent of total population below poverty level, number of hospital beds, number of active physicians, and geographic region. Percent of population aged 18-34, percent of total population below poverty level, and number of hospital beds have positive correlation to crime rate, whereas number of active physicians have negative correlation to crime rate.

Introduction

According to Statista Research Department (Figure 1), the violent crime rate in the United States was 398.5 cases per 100,000 of the population. Even though the violent crime rate has been decreasing since 1990, the United States tops the ranking of countries with the most prisoners. The United States Federal Bureau of Investigation tracks the rate of reported violent crimes per 100,000 U.S. inhabitants. In the timeline above, rates are shown starting in 1990. The rate of reported violent crime has fallen since a high of 758.20 reported crimes in 1991 to a low of 361.6 reported violent crimes in 2014. Using the CDI data set, we want to analyze the potential relationship between crime rate and several variables like percent high school graduates and percent below poverty level. We will build a linear regression model to predict the crime rate, and use the coefficient to illustrate the influence of each variable on the crime rate.

Data Description

Firstly we had a general check of the data. The variable we would like to predict is the crime rate per 1000 population, which is not avalible in the data. The key variable to dirive the crime rate is the total serious crimes, and the total population. We ran a calculation to get the crime rate by using the formula $CrimeRate = \frac{TotalSeriousCrimes}{\frac{TotalPopulation}{1000}}$. After the creation of the variable crime rate, we checked if there are some unusual observations of crime rate, and the 4 city showed on (Table 1) represented unusual high crime rates, which are Kings in New York, Dade in Florida, Fulton in Georgia, and St. Louis in Missouri. The ID number, country name and state name cannot theoretically be used as predictors of crime rates, and we calculated the crime rate using total population and total serious crimes, so we dropped these variables for our future analysis.

We are also interested in the number observations of crime rate over regions, which is the only categorical variable, and created a table (Table 2) to visualize it. According to (Table 2), The number of observations around regions are similar.

Then, we checked the distribution of each numerical variables in the data, including crime rate, and the distribution is shown on (Figure 2). We discovered that the land area, percent Bachelor's degrees, number of hospital physicians, number of hospital beds, crime rate, number of poverty, total personal income, and percent of unemployment had left-skewed distributions, which means that most observations has low value of these variables. The percent of high school graduates had right-skewed distributions, which means that most of the observations have high percentage of high school graduates. The percent population aged between 18 and 34, percent population aged over 65, and per capita income are normally distributed.

Model Selection

After univariate analysis of the CDI data, the next step is fitting an appropriate and robust regression model that could predict the crime rate per 1000 people using other population characteristics in the data set. The final model should be small and good, so we cautiously select variables into the model.

First of all, we use data visualization to help us add or drop variables from the data set into the model. The pairwise scatter plots visualized the bi-variate relationship of crime rate with each numeric predictor variable(Figure 3). We do not detect any obvious curve-linear relationship with crime rate among these variables, so we would not consider any polynomial term. Some variables do not demonstrate the noticeable pattern in the pairwise plot, implying no correlation with the crime rate, so these predictors are out of

consideration. The rest of the numerical variables, including percent of population aged 18-34, number of active physicians, number of hospital beds, percent of poverty and total population income, are kept in the model. For the categorical variable, geographic region, we drew box-plots to visualize the distribution of crime rate by each region (Figure 4). There are significantly different distributions of crime rates among regions, so the geographic region is added to the model. Moreover, we consider adding interaction terms. For each numeric variable selected in the previous step, the Figure 5 checked whether its relationship with crime rate varies among different regions. Besides percent of the population aged 18-34, the other four numerical variables have substantially steeper slopes of regression of Northeast than those of West, suggesting a potentially different relationship with crime rate by region (Figure 5). Then, the interaction terms between these four variables and the region are added to the model.

The full model has six main effects and four interaction terms. It is necessary to reduce the number of predictors to avoid over-fitting. We used the automatic search procedure combined with criterions, AIC and BIC, to select some subset models that optimize the measure of goodness of fit. We perform backward elimination, forward selection and step-wise regression with each criterion and get four different models as candidates of our final model. The comparison of prediction ability is an appropriate method to select the final model from these candidates, and cross-validation is the efficient tool to measure. The original data set is randomly split into a 20/80 partition as testing and training sets pair respectively, and 500 random pairs are generated. For each pair, the training data is used to fit each candidate model, and then testing data is used to evaluate the performance for each fitted model by calculating the rooted mean square prediction error. The lower prediction error usually indicates higher prediction ability. Thus, we could estimate the overall prediction error distribution for each candidate model using 500 testing-training pairs shown in Figure 6 and examine its prediction ability. The model selected through AIC step-wise regression has the lowest prediction error across all candidate models, so we select this model as the final model before transformation which is processed in the model diagnostic part.

Model Diagnotics

Transformation:

Lamda = 0.5 is in the confidence level, thus we can fit the model with transformation. To verify the assumptions of linear regression, fitted values vs residuals plot and qq-plot are applied. Based on Figure 7, after transformation, residuals have more constant variance since the dots are more scattered around 0.

QQ plot implies normality is met because most points roughly form a straight line. In addition, adj-r squared is higher (0.44 vs 0.43), which shows higher correlation and better prediction results. Thus, a transformed model is chosen. Influential point: Based on Cook's distance plot (Figure 8), there are three influential points such as row 1,2,6. Their Di > 0.5. By checking the value, the value seems correct and we decide to keep those influential points in the model. Multicollinearity:
From Table 3, VIF scores above 1 implies that there is some correlation between variables. However, since VIF scores are small (<5), there is not enough to be concerned about multicollinearity.

Results

Finally we get to the following regression model.

$$\sqrt{CRM_1000} = 4.15189 + 0.08105 \times poverty + 0.00066 \times beds - 0.93004 \times I\{region = Northeast\} + 0.99089 \times I\{region = South\} + 1.03623 \times I\{region = West\} + 0.05991 \times pop18 - 0.00062 \times docs + 0.00018 \times beds \times I\{region = Northeast\} - 0.00027 \times beds \times I\{region = South\} - 0.00082 \times beds \times I\{region = West\} + 0.00016 \times docs \times I\{region = Northeast\} + 0.00062 \times doc \times I\{region = South\} + 0.00090 \times docs \times I\{region = West\}$$

According to our final outcome, percent below poverty level, number of hospital beds, percent of the population aged between 18 and 34, geographic region, number of active physicians, have a significant influence on the crime rate of the county. As for the region. This dummy variable shows that counties in the South and West have about 1% greater $\sqrt{CRM1000}$ than North Central. And counties in the Northeast are expected to have the least crime rate among four geographic regions. As for all continuous variables in the final model, poverty has the most positive impact on the crime rate. The estimated coefficient is 0.081, which increase $\sqrt{CRM1000}$ by 0.081 percent if the percent below the poverty level increases 1 percent in the county. The second primary influential variable is the percent of the population aged between 18 and 34(pop18), pop18 also shows a positive relationship with the crime rate. The estimated coefficient is 0.0599, which means we will expect to see about 0.0599% additional $\sqrt{CRM1000}$ if the percent below the poverty level increases 1 percent in the county. The number of active physicians, number of hospital beds show a different relationship with the crime rate. 10000 additional active physicians will reduce the $\sqrt{CRM1000}$ in the county by 6.23% percent, on the other hand, 10000 additional hospital beds will increase the $\sqrt{CRM1000}$ in the county by 6.62% percent. Finally, there are 6 interaction terms that

show 10000 additional active physicians will increase the $\sqrt{CRM1000}$ by 1.57%, 6.24%, and 8.97% in Northeast, South, and West compared with North Central. 10000 additional hospital beds will increase the $\sqrt{CRM1000}$ by 1.8% in the Northeast and decrease the $\sqrt{CRM1000}$ by 2.67%, 8.22% in the South and West compared with NorthCentral.

Conclusions and Discussion

Based on the final model, we find out that several factors have a significant impact on crime rate and thus can be used to predict crime rate in counties of the United States. These factors are percent of population aged 18-34, percent of total population below poverty level, number of hospital beds, number of active physicians, and geographic region. Among those factors, the number of active physicians, the region of Northeast compared to North Central, the number of hospital beds in the region of South and West have a negative association on the crime rate. The remaining factors have a positive association on the crime rate. During the modeling process, we have some findings. First, we perform backward elimination, forward selection and stepwise regression with AIC and BIC criterions separately based on the set of potential predictors. Among these six models, we find out that models built by forward selection and stepwise regression with BIC are the same. Models built by backward elimination with AIC and with BIC are the same. Therefore, we only remain one of the same models as the candidate model. The four candidate models are built with backward elimination with AIC, forward selection with AIC, stepwise regression with AIC, and forward selection with BIC. Second, by separately arranging column area and pop in the original dataset from the smallest to the largest, we find that the area and population of row 6 has the rank 11th and 435th in a total of 440 counties, respectively. This indicates that row 6, Kings of NY, has a very high population density, and that's the reason row 6 is a very influential observation for our model. We have no idea whether there is a data error of this observation.

The strength of our project is that we choose models based on automatic search procedures instead of merely subjective judgement based on visualization. Also, we use the transformed model as our final result to satisfy the assumptions of residuals to the greatest extent. We only consider linear association between crime rate and factors that influence crime rate. However, it is possible that crime rate and those factors have a nonlinear association. If we consider nonlinear association, the model might predict the crime rate in 440 counties in the United States more accurately than the model we built in this project.

Reference

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Appendix I: Figure and Table

Figure 1: Crime Rate between 1990-2020

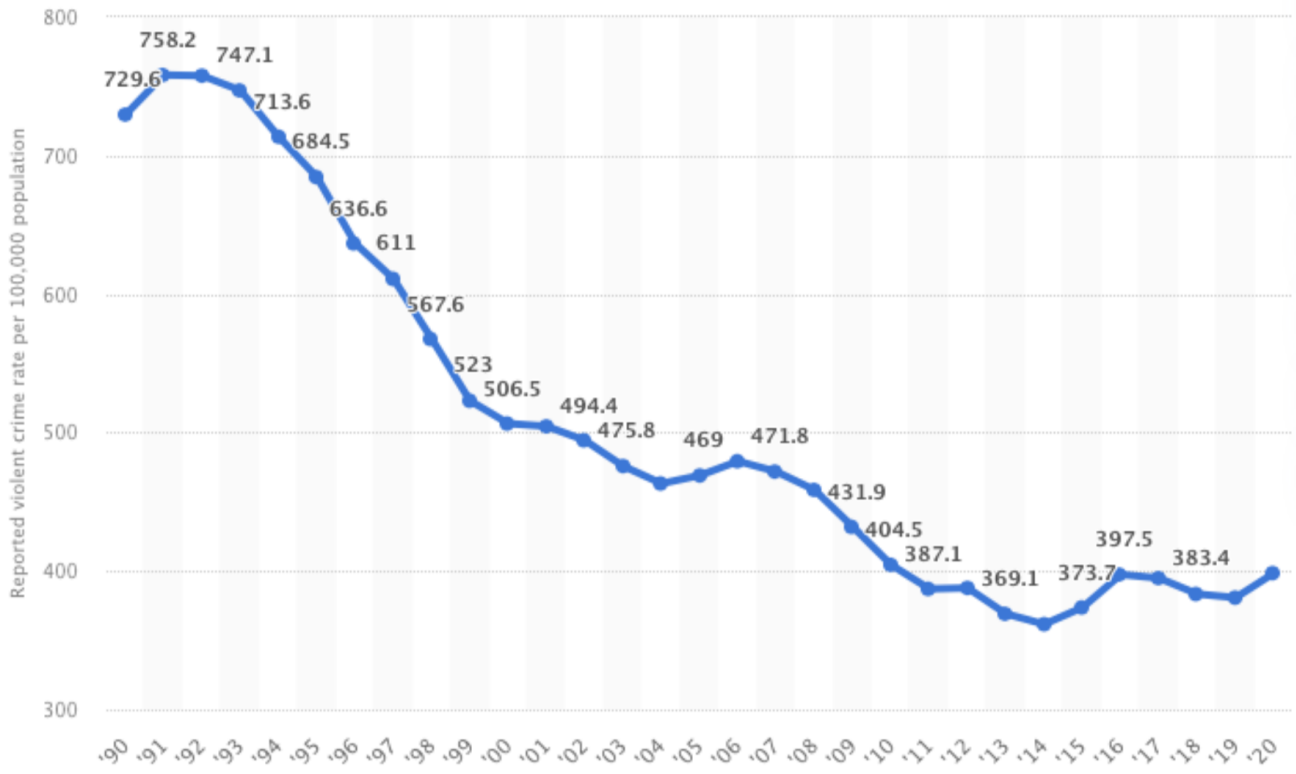


Table 1: Outliers in Crime Rate

state	crime_rate	cty
NY	295.9867	Kings
FL	126.3362	Dade
GA	143.3467	Fulton
MO	161.5967	St._Loui

Table 2: Number of Observations in Each Region

region	n
North Central	108
Northeast	103
South	152
West	77

Figure 2: Marginal Distribution of Numerical Variables

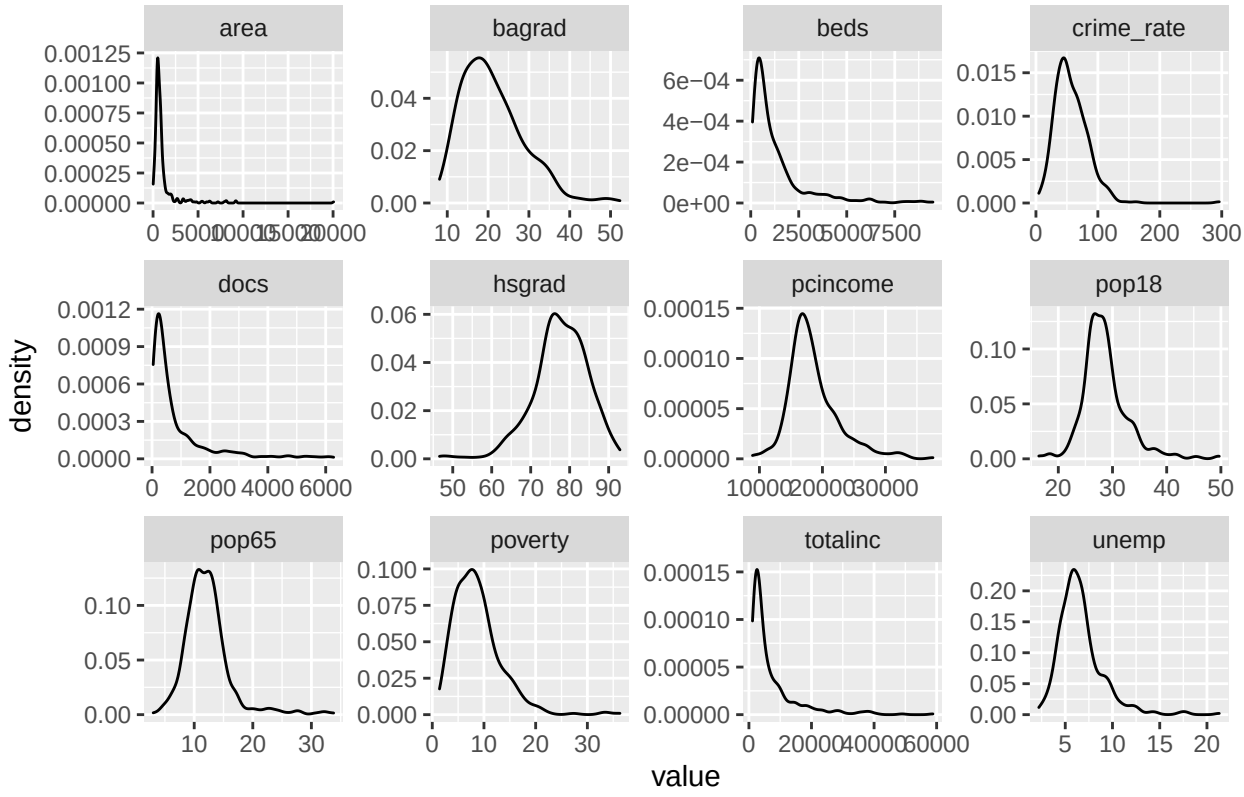


Figure 3: Scatterplots of crime rate vs. numerical predictor variables

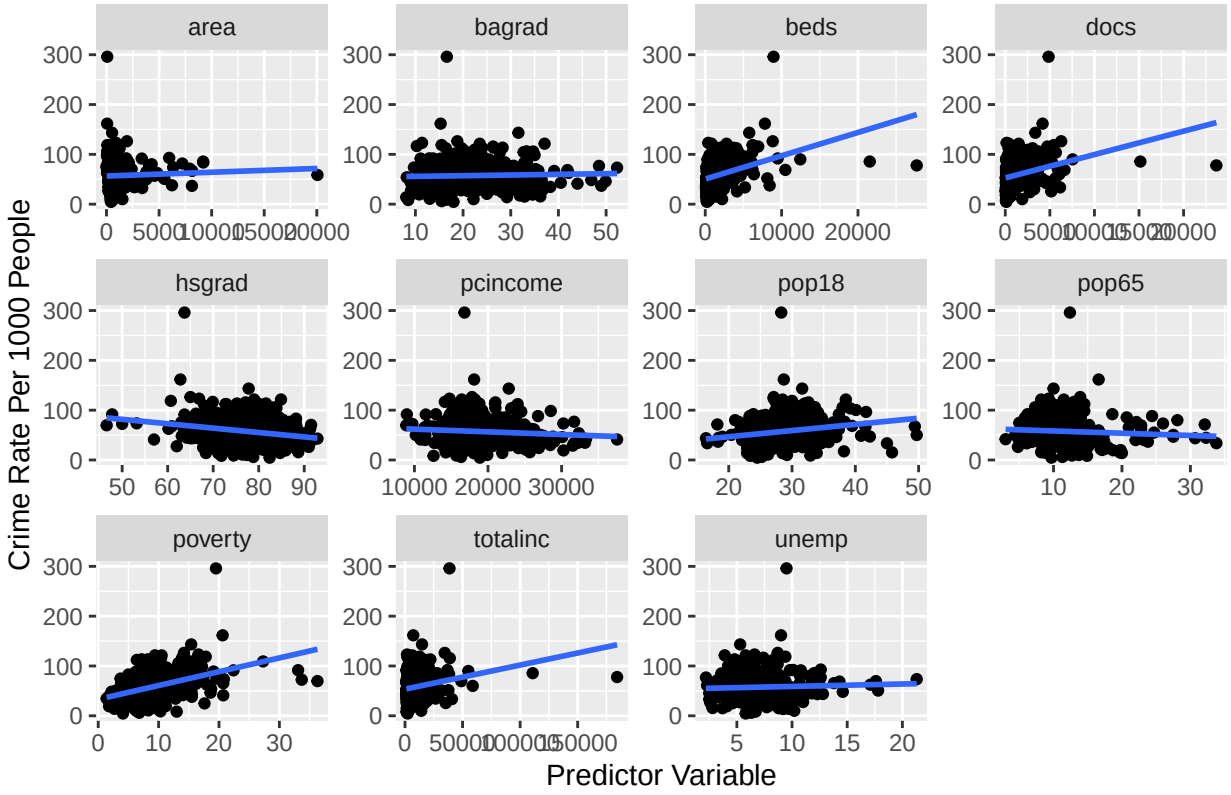
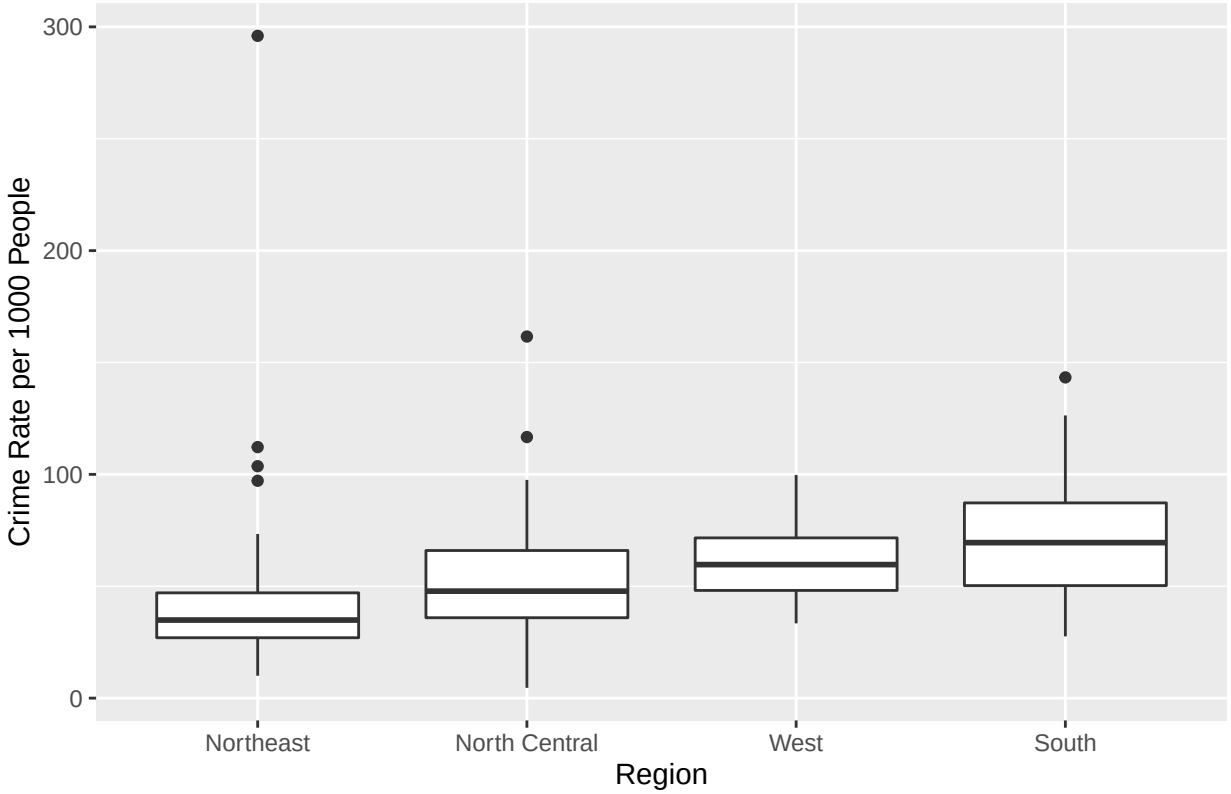
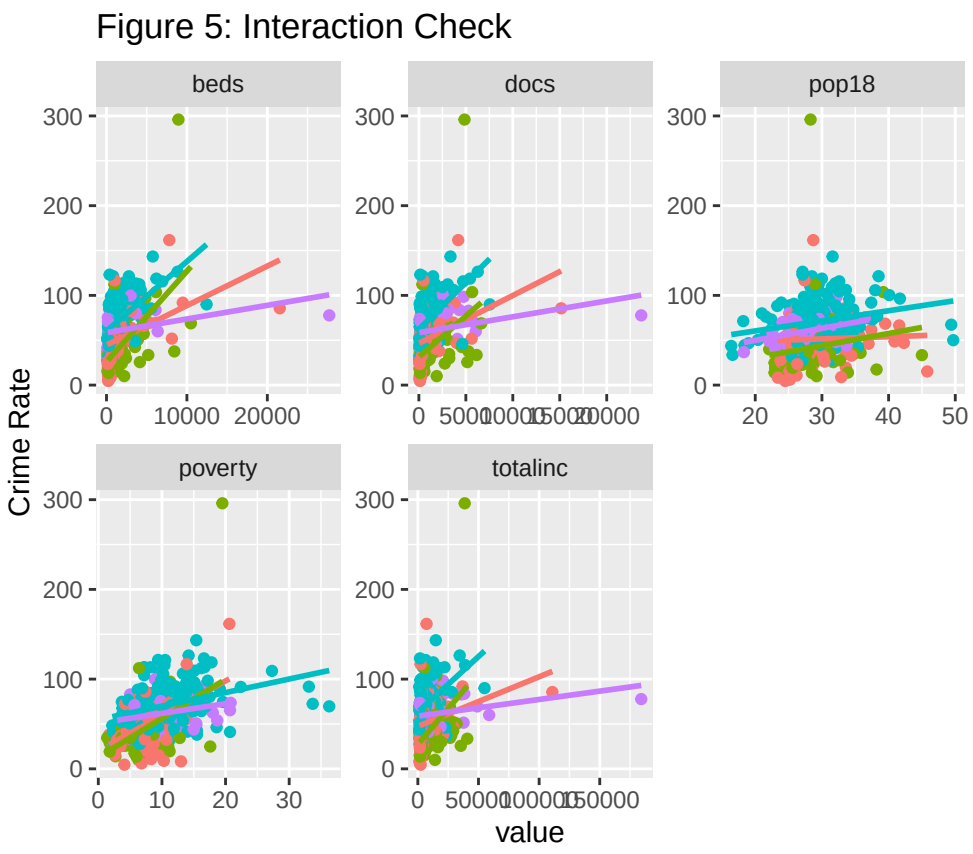


Figure 4: Boxplot of Crime Rate over Region





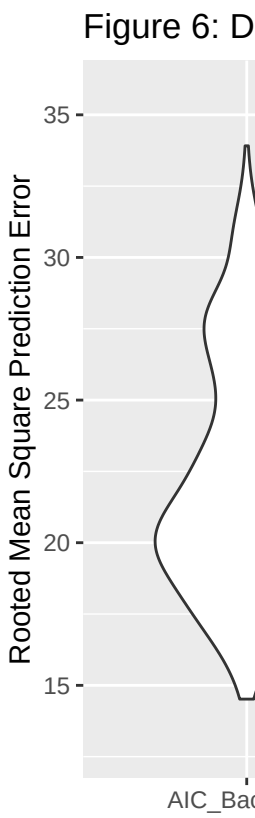


Figure 7. Assumptions of linear regression check before and after transformation

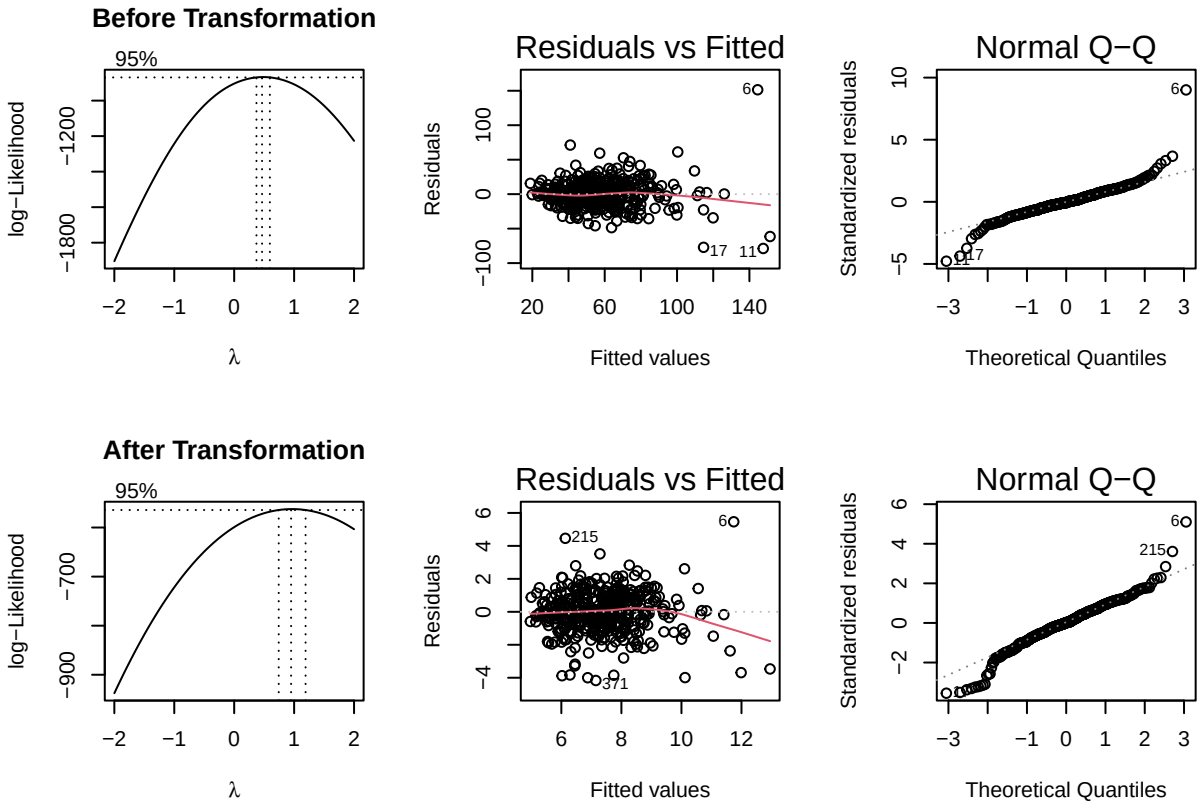


Figure 8: Cook's Distance to Check Influential Points

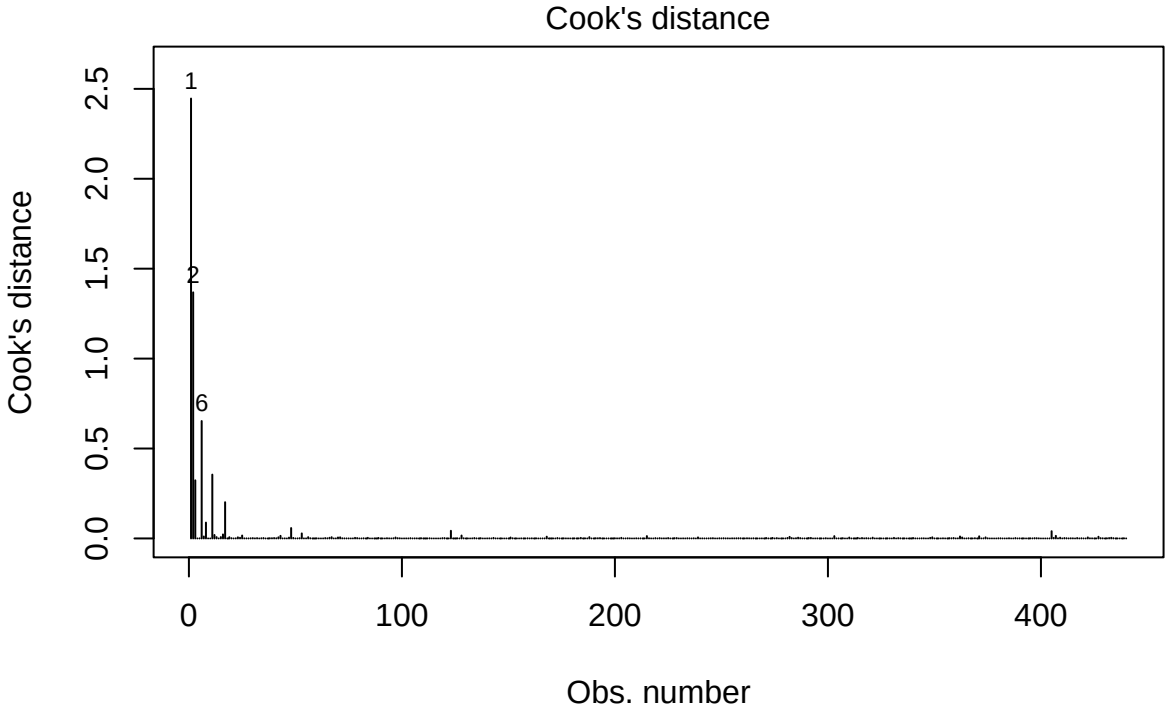


Table 3: Table 3: Multicolinearity Check

Term	VIF	SE_factor
poverty	2.149675	1.466177
beds	1.773850	1.331859
region	1.761193	1.327100
pop18	1.183588	1.087928
docs	2.407664	1.551665

Apendix II: R Code

```
# data clean (calculate crime_rate (1000 people))
crime_rate_df = read_csv("data/cdi.csv") %>%
  mutate(crime_rate = crimes /(pop/1000),
         region = case_when(
    region == 1 ~ "Northeast",
    region == 2 ~ "North Central",
    region == 3 ~ "South",
    region == 4 ~ "West"
  ),
  region = factor(region))
# check outliers
OutVals = boxplot(crime_rate_df$crime_rate)$out
```

```
crime_rate_df %>%
  dplyr::filter(crime_rate %in% OutVals) %>%
  dplyr::select(state, crime_rate, cty) %>%
  knitr::kable(caption = "Outliers in Crime Rate")


crime_rate_df %>%
  group_by(region) %>%
  count() %>%
  knitr::kable(caption = "Number of Observations in Each Region")


# numeric variables
crime_rate_df_numeric  =
  crime_rate_df%>%
  dplyr::select(area,pop18,pop65,docs,beds,hsgrad,bagrad,poverty,unemp,
                pcincome,totalinc,crime_rate)%>%
  filter(beds<10000,docs<10000)
```

```r
# marginal distribution
crime_rate_df_numeric %>%
  pivot_longer(area:crime_rate,names_to = "predictors",values_to = "value")%>%
  ggplot(aes(x = value))+
  geom_density()+
  facet_wrap(.~predictors,scales = "free") +
  labs(
    title = "Figure 2: Marginal Distribution of Numerical Variables"
  )


## Variable Selection
# numerical variables
crime_rate_df %>%
  dplyr::select(crime_rate,area,pop18,pop65,docs,beds,hsgrad,bagrad,
                poverty,unemp,totalinc,pcincome) %>%
  pivot_longer(area:pcincome, names_to = "predictor", values_to = "value") %>%
  ggplot(aes(x = value, y = crime_rate)) +
  geom_point() +
  geom_smooth(method = "lm", se = F) +
  facet_wrap(.~predictor, scales = "free") +
  labs(title = "Figure 3: Scatterplots of crime rate vs. numerical predictor variables",
       x = "Predictor Variable",
       y = "Crime Rate Per 1000 People")


#categorical variable
crime_rate_df%>%
  ggplot(aes(x = fct_reorder(region,crime_rate),y=crime_rate))+
  geom_boxplot() +
  labs(
    title = "Figure 4: Boxplot of Crime Rate over Region",
    x = "Region",
```

```
    y = "Crime Rate per 1000 People"
  )


crime_rate_df_all = crime_rate_df %>%
  dplyr::select(crime_rate,pop18,docs,beds,poverty,totalinc,region)


#interaction term
crime_rate_df_all %>%
  pivot_longer(pop18:totalinc, names_to = "predictor", values_to = "value") %>%
  ggplot(aes(x = value,y = crime_rate,color = region)) +
  geom_point() +
  geom_smooth(method = "lm",se = F) +
  facet_wrap(.~predictor, scales = "free") +
  labs(
    title = "Figure 5: Interaction Check",
    y = "Crime Rate"
  )
```

```
#stepwise procedure with AIC and BIC
lm0 = lm(data = crime_rate_df_all, crime_rate ~ pop18 + docs + beds +
           poverty + totalinc + region + docs*region + beds*region +
           poverty*region + totalinc*region)


step(lm0 , direction = "backward", scope = ~pop18 + docs + beds +
       poverty + totalinc + region + docs*region + beds*region +
       poverty*region + totalinc*region)
lm1_AIC_Backward = lm(formula = crime_rate ~ pop18 + docs + beds +
                        poverty + totalinc + region + docs:region +
                        poverty:region + totalinc:region,
    data = crime_rate_df_all)
```

```
lm_null = lm(crime_rate ~ NULL, data = crime_rate_df_all)

step(lm_null,direction = "forward", scope = ~pop18 + docs + beds +
       poverty + totalinc + region + docs*region + beds*region +
       poverty*region + totalinc*region)

lm2_AIC_Forward = lm(formula = crime_rate ~ poverty + beds + region +
                       pop18 + docs + beds:region + poverty:region +
                       region:docs, data = crime_rate_df_all)

step(lm_null,direction = "both", scope = ~pop18 + docs + beds +
       poverty + totalinc + region + docs*region + beds*region +
       poverty*region + totalinc*region)

lm3_AIC_Both = lm(formula = crime_rate ~ poverty + beds + region +
                    pop18 + docs +
    beds:region + region:docs, data = crime_rate_df_all)

step(lm_null,direction = "forward", k = log(nrow(crime_rate_df)),
     scope = ~pop18 + docs + beds + poverty + totalinc + region +
       docs*region + beds*region + poverty*region + totalinc*region)

lm4_BIC_Forward_Both = lm(formula = crime_rate ~ poverty + beds + region +
                            pop18 + beds:region,
    data = crime_rate_df_all)
```

```
library(modelr)
set.seed(1200)
#cross-validation
cv_df <-
  crossv_mc(crime_rate_df_all, 500)
```

```r
cv_df <-
  cv_df %>%
  mutate(
    train = map(train, as_tibble),
    test = map(test, as_tibble)
  )


cv_df_result <-
  cv_df %>%
  mutate(
    lm1_AIC_Backward = map(.x = train, ~lm(crime_rate ~ pop18 +
                                             docs + beds + poverty +
                                             totalinc + region + docs:region +
                                             poverty:region + totalinc:region,
                                           data = .x)),
    lm2_AIC_Forward = map(.x = train, ~lm(crime_rate ~ pop18 + docs +
                                            beds + poverty + totalinc +
    region + docs:region + beds:region + poverty:region + totalinc:region,
    data = .x, )),
    lm3_AIC_Both = map(.x = train, ~lm(crime_rate ~ poverty + beds + region +
                                         pop18 + docs +
    beds:region + region:docs, data = crime_rate_df_all)),
    lm4_BIC_Forward_Both = map(.x = train, ~lm(crime_rate ~ poverty + beds +
                                                 region + pop18 + beds:region,
                                               data = .x))
    ) %>%
  mutate(
    rmse_AIC_Backward = map2_dbl(.x = lm1_AIC_Backward,
                                 .y = test,
                                 ~rmse(model = .x, data = .y)),
    rmse_AIC_Forward = map2_dbl(.x = lm2_AIC_Forward, .y = test,
```

```
                                ~rmse(model = .x, data = .y)),
    rmse_AIC_Both = map2_dbl(.x = lm3_AIC_Both, .y = test,
                             ~rmse(model = .x, data = .y)),
    rmse_BIC_Forward_Both = map2_dbl(.x = lm4_BIC_Forward_Both,
                                     .y = test,
                                     ~rmse(model = .x, data = .y))
  )


cv_df_result %>%
  dplyr::select(starts_with("rmse")) %>%
  pivot_longer(
    rmse_AIC_Backward:rmse_BIC_Forward_Both,
    names_to = "model",
    values_to = "rmse",
    names_prefix = "rmse_"
  ) %>%
  ggplot(aes(x = model, y = rmse)) +
  geom_violin() +
  labs(
    title = "Figure 6: Distribution of RMSPE over Candidate Models",
    x = "Model",
    y = "Rooted Mean Square Prediction Error"
  )
```

```
## Model Diagnostic
lm3_AIC_Both = lm(formula = crime_rate ~ poverty + beds + region +
                    pop18 + docs +
    beds:region + region:docs, data = crime_rate_df_all)


crime_rate_df_transform = crime_rate_df_all %>%
  mutate(crime_rate = sqrt(crime_rate))
```

```
lm3_AIC_Both_transform = lm(formula = crime_rate ~ poverty +
                              beds + region + pop18 + docs +
    beds:region + region:docs, data = crime_rate_df_transform)


lm3_without_interaction = lm(formula = crime_rate ~ poverty +
                               beds + region + pop18 + docs,
                             data = crime_rate_df_all)
```

```
#transformation
par(mfrow = c(2,3))
boxcox(lm3_AIC_Both)
title("Before Transformation")
plot(lm3_AIC_Both ,which = 1)
plot(lm3_AIC_Both ,which = 2)
boxcox(lm3_AIC_Both_transform)
title("After Transformation")
plot(lm3_AIC_Both_transform,which = 1)
plot(lm3_AIC_Both_transform,which = 2)
```

```
#influential points
plot(lm3_AIC_Both_transform,which = 4,sub.caption = "")
title("Figure 8: Cook's Distance to Check Influential Points")
```

```
#multicolinearity
check_collinearity(lm3_without_interaction) %>%
  knitr::kable(caption = "Table 3: Multicolinearity Check")
```