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1 Abstract

The purpose of this study is to identify the factors that prominently affect the US COVID-19 mortality rate. We used a dataset comprising various information of 1739 different US counties, which contains the variable of interest- the mortality rate of each county, as well as over 300 potential explanatory variables, including but not limited to information on demographic and healthcare. The question of interest is to identify the most appropriate explanatory variables and to find the most suitable and statistically significant linear model to reflect their effects on the mortality rate. We started by identifying the best 9 explanatory variables that were the most reasonable and statistically significant in their respective single models. Then, using the automatic model selection method, we identified the best 2 models for each model size. Next, by comparing their R^2_{adj} , AIC values, BIC values, C_p values, and taking multicollinearity into consideration, we selected the final model consisting 4 explanatory variables, including the percentage of the population above 65 years old in the county, the total number of specialist in the county, the incoming number of International immigrants in the county for the past year, and the large-scale region to which the county belongs, which is a categorical variable of 4 large region bounds. Based on our dataset, the linear model consisting of these 4 variables best represent the trend and variation of the mortality rate. Further studies on the US COVID-19 mortality rate is recommended where more suitable explanatory variables are included in order to increase the explanatory power of the model.

2 Introduction

For the past 5 months, the coronavirus (COVID-19) pandemic has been raging all over the world. According to the World Health Organization, there are more than 9.44 million confirmed cases worldwide, and the total number of death cases is as high as 483,000 (World Health Organization (2020)). Therefore, we are interested in finding the factors that can potentially explain the COVID-19 mortality rate, as well as the degree to which those factors impact the mortality rate. Since the US has a large number of confirmed cases (USAFacts (2020)), we would use the COVID-19 cases from US and its corresponding counties' data (Killeen et al. (2020)) to analyze the causes of mortality rate of this pandemic.

From our previous report, we have found that there are some factors that presented statistically significant to the mortality rate of COVID-19, which are the factors of region, percentage of elder population, specialists and physicians. Thus, in this report, we would first extend our investigation, specially discovering in reasonable factors that are statistically significant to COVID-19 mortality rate. Based on all these results, we perform statistical analysis in comparing and fitting different models. Ultimately, we wish to gain some important insights from the mortality rate of COVID-19 by finding the best statistical significant model.

3 Dataset Description

The first dataset we found was the US COVID-19 data, which recorded the mortality rate under each county (USAFacts (2020)). Another machine-readable dataset (Killeen et al. (2020)) we have used contains socioeconomic, demographic, health care, education and transit data for each county in the 50 states in US. In total, there are 347 different factors in this dataset, such as the population estimate, migration rate, number of females, number of hospitals. Furthermore, both datasets include a key called Federal Information Processing Standard Publication (FIPS) code, which is a five-digit code uniquely identifying each area. Thus, by joining these two data sets together in Excel, we obtained our master data.

Furthermore, we are interested in the mortality rate and has chosen it to be our response variable. To satisfy the normality assumption, we created a column called Mortality, which from taking the natural log of mortality rate of each county. As such, we could use Mortality to be our response variable when computing the statistic models.

Table 1: P-values for Selected Explanatory Variables

Variable	p_value
ElderlyRate	0.0000007
Region	0.0247100
Specialist	0.0274500
population	0.0144000
Physician_rate	0.0460600
Unemployment_rate_2018	0.0484100
Poverty	0.0250100
Migration	0.0027500
Nurse	0.0140400

Table 2: Correlation Matrix

	ElderlyRate	Specialist	Physician_rate	Unemployment_rate_2018	Poverty	Migration	Nurse
ElderlyRate	1.000	-0.389	0.026	0.130	-0.371	-0.266	-0.391
Specialist	-0.389	1.000	0.127	-0.049	0.958	0.855	0.983
Physician_rate	0.026	0.127	1.000	0.028	0.041	0.080	0.106
Unemployment_rate_2018	0.130	-0.049	0.028	1.000	-0.026	-0.045	-0.055
Poverty	-0.371	0.958	0.041	-0.026	1.000	0.835	0.939
Migration	-0.266	0.855	0.080	-0.045	0.835	1.000	0.883
Nurse	-0.391	0.983	0.106	-0.055	0.939	0.883	1.000

4 Investigation

In the previous report, we have identified 6 individually significant explanatory variables, including Specialist, Physician_rate, ElderlyRate, Region, Population, Unemployment_rate_2018. Due to the low R^2_{adj} value in those models, we searched in our dataset for additional explanatory variables that reasonably affects the COVID-19 mortality rate. Among the variables that are reasonable to be included, we selected 3 of them whose single models were tested significant at $\alpha = 0.05$ level of significance. These additional variables are Poverty, Migration, and Nurse, making a total of 9 variables selected.

The p-value of the global F-tests for the corresponding 9 single-model fittings are listed below. Full single-model summaries are included in the appendix.

As shown above, all 9 of those explanatory variables are statistically significant; we then select the best model based on those 9 variables. Firstly, we will observe the correlation matrix and VIF of those variables to spot red flags for multicollinearity.

Observe the correlation matrix. Using 0.8 as a cutoff, we see signs of multicollinearity issues in the following pairs of variables: Specialist & Poverty, Specialist & Migration, Specialist & Nurse, Poverty & Migration, Poverty & Nurse, Migration & Nurse.

Observe the GVIF values. Using the value 5 as a cutoff, we see signs of multicollinearity issues in Specialist, Poverty, Migration, and Nurse.

Table 3: VIF Values

	GVIF	Df	$\text{GVIF}^{1/(2 \cdot \text{Df})}$
ElderlyRate	1.357739	1	1.165221
factor(Region)	1.924274	3	1.115264
Specialist	50.404208	1	7.099592
factor(population)	1.311527	1	1.145219
Physician_rate	1.986869	1	1.409563
Unemployment_rate_2018	18.091201	1	1.044606
Poverty	13.701774	1	3.701591
Migration	5.028916	1	2.242524
Nurse	41.407467	1	6.434863

5 Model Selection

5.1 Automatic model selection method

To start our model selection process, we used the stepwise selection method first given the full model as the initial model to find the best model based on algorithm.

```
##
## Call:
## lm(formula = Mortality ~ ElderlyRate + factor(Region) + Specialist +
##     Physician_rate + Unemployment_rate_2018 + Migration)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.8599 -0.5010  0.1324  0.6692  3.5356
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -4.051e+00  2.057e-01 -19.690 < 2e-16 ***
## ElderlyRate     2.519e+00  5.377e-01   4.684 3.04e-06 ***
## factor(Region)Northeast -1.827e-01  1.056e-01  -1.730  0.08386 .
## factor(Region)South    -1.338e-01  6.226e-02  -2.149  0.03176 *
## factor(Region)West     -2.880e-01  9.211e-02  -3.127  0.00180 **
## Specialist        3.348e-05  1.599e-05   2.095  0.03636 *
## Physician_rate    9.720e-04  6.566e-04   1.480  0.13894
## Unemployment_rate_2018  3.337e-02  1.993e-02   1.674  0.09422 .
## Migration        -2.206e-05  8.203e-06  -2.690  0.00722 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.034 on 1722 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.0282, Adjusted R-squared:  0.02369
## F-statistic: 6.247 on 8 and 1722 DF, p-value: 5.454e-08

## Stepwise Model Path
## Analysis of Deviance Table
##
```

```
## Initial Model:
## Mortality ~ ElderlyRate + factor(Region) + Specialist + factor(population) +
##     Physician_rate + Unemployment_rate_2018 + Poverty + Migration +
##     Nurse
##
## Final Model:
## Mortality ~ ElderlyRate + factor(Region) + Specialist + Physician_rate +
##     Unemployment_rate_2018 + Migration
##
##
```

	Step	Df	Deviance	Resid. Df	Resid. Dev	AIC
## 1				1719	1839.327	129.0726
## 2	- Poverty	1	0.03228038	1720	1839.359	127.1030
## 3	- Nurse	1	0.06151220	1721	1839.421	125.1609
## 4	- factor(population)	1	1.03274628	1722	1840.454	124.1325

The stepwise method gives the model: Mortality ~ ElderlyRate + factor(Region) + Specialist + Physician_rate + Unemployment_rate_2018 + Migration) as the final model. However, we noticed the p-value for Physician_rate = 0.13894 > $\alpha = 0.05$ and the p-value for Unemployment_rate_2018 = 0.09422 > $\alpha = 0.05$, which do not indicate statistical significance. Thus, the model is not the most suitable model for our dataset.

5.2 Model selection process

In order to find the best fitting model, we performed another model selection process by fitting all possible combinations.

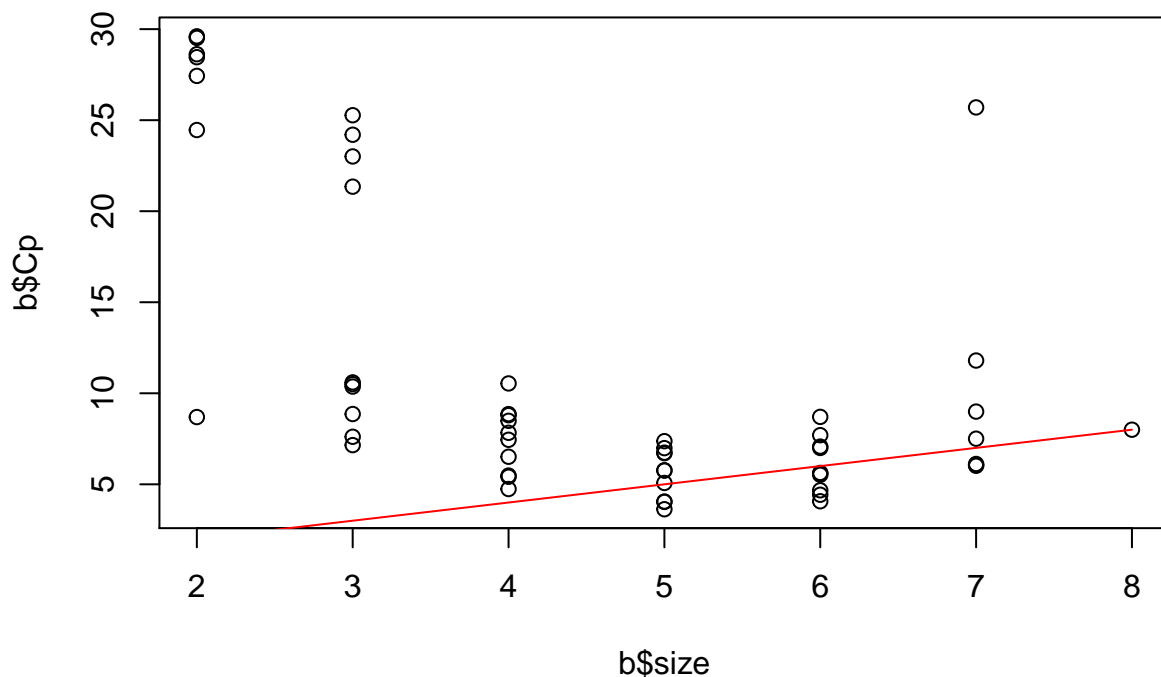


Table 4: Model Selection with CP values

	(Intercept)	ElderlyRate	RegionNortheast	RegionSouth	RegionWest	Specialist	populationSmall
1	1	1	0	0	0	0	0
1	1	0	0	0	0	0	0
2	1	1	0	0	1	0	0
2	1	1	0	0	0	0	0
3	1	1	0	1	1	0	0
3	1	1	0	0	0	1	0
4	1	1	0	1	1	0	0
4	1	1	0	0	1	1	0
5	1	1	0	1	1	1	0
5	1	1	0	1	1	0	0
6	1	1	0	1	1	1	0
6	1	1	0	1	1	0	0
7	1	1	1	1	1	1	0
7	1	1	0	1	1	1	1
8	1	1	1	1	1	1	0
8	1	1	1	1	1	0	0
9	1	1	1	1	1	1	1
9	1	1	1	1	1	0	1
10	1	1	1	1	1	1	1
10	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1

From the result, we noticed that models containing at least five variables have a fair Cp value and as the number of variables increases the R_{adj}^2 increases. Then, we consider the following models:

By comparing this result, we notice that model1, model2, model3, and model4 have the lowest AIC and BIC values. Since model1 is included in model3, and model2 is included in model4. First, to compare model1 and model3, we use backward elimination procedure.

Step 1: start by fitting Model3: Mortality~ElderlyRate + Specialist + Migration + Unemployment_rate_2018 + factor(Region), and consider the partial t tests for each explanatory variable.

```
##
## Call:
## lm(formula = Mortality ~ ElderlyRate + Specialist + Migration +
##     Unemployment_rate_2018 + factor(Region))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.8914 -0.4922  0.1263  0.6632  3.5146
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -3.810e+00  1.263e-01 -30.179  < 2e-16 ***
## ElderlyRate    2.566e+00  5.370e-01   4.779 1.92e-06 ***
## Specialist     3.561e-05  1.593e-05   2.236  0.02549 *
## Migration     -2.253e-05  8.200e-06  -2.747  0.00607 **
## Unemployment_rate_2018  3.528e-02  1.990e-02   1.773  0.07634 .
```

Table 5: Figure 4: Models

Model	Regression_Equation
1	Log of Mortality Rate vs. ElderlyRate + Specialist + Migration + Region
2	Log of Mortality Rate vs. ElderlyRate + Nurse + Migration + Region
3	Log of Mortality Rate vs. ElderlyRate + Specialist + Migration + Unemployment_rate_2018 + Region
4	Log of Mortality Rate vs. ElderlyRate + Nurse + Migration + Unemployment_rate_2018 + Region
5	Log of Mortality Rate vs. ElderlyRate + Specialist + Migration + Unemployment_rate_2018 + Region + P
6	Log of Mortality Rate vs. ElderlyRate + Specialist + Migration + Unemployment_rate_2018 + Physician_rat
7	Log of Mortality Rate vs. ElderlyRate + Nurse + Migration + Unemployment_rate_2018 + Physician_rat
8	Log of Mortality Rate vs. ElderlyRate + Specialist + Migration + Unemployment_rate_2018 + Physician_rat
9	Log of Mortality Rate vs. ElderlyRate + Nurse + Migration + Unemployment_rate_2018 + Physician_rat
10	Log of Mortality Rate vs. ElderlyRate + Specialist + Nurse + Migration + Unemployment_rate_2018 + P
11	Log of Mortality Rate vs. ElderlyRate + Specialist + Migration + Unemployment_rate_2018 + Physician_rat
12	Log of Mortality Rate vs. ElderlyRate + Specialist + Nurse + Migration + Unemployment_rate_2018 + P

Table 6: Figure 5: AIC and BIC values

	df	AIC	BIC
model1	8	5039.856	5083.508
model2	8	5040.714	5084.366
model3	9	5038.699	5087.807
model4	9	5039.464	5088.573
model5	10	5040.188	5094.752
model6	10	5038.498	5093.062
model7	10	5038.847	5093.412
model8	11	5039.526	5099.547
model9	11	5039.804	5099.825
model10	12	5041.468	5106.946
model11	12	5041.507	5106.985
model12	13	5043.438	5114.372

```
## factor(Region)Northeast -1.016e-01  9.036e-02  -1.125  0.26080
## factor(Region)South     -1.588e-01  5.995e-02  -2.648  0.00816 **
## factor(Region)West      -2.942e-01  9.205e-02  -3.196  0.00142 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.034 on 1723 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.02697,    Adjusted R-squared:  0.02301
## F-statistic: 6.821 on 7 and 1723 DF,  p-value: 5.179e-08
```

According to the result, the p-value for $\text{Unemployment_rate_2018} = 0.07634 > \alpha = 0.05$ which means $\text{Unemployment_rate_2018}$ is not statistically significant. Then, we omit the variable $\text{Unemployment_rate_2018}$ from the model.

```
##
## Call:
## lm(formula = Mortality ~ ElderlyRate + Specialist + Migration +
##     factor(Region))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.8565 -0.5003  0.1307  0.6712  3.5013
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -3.700e+00  1.099e-01 -33.666 < 2e-16 ***
## ElderlyRate      2.699e+00  5.320e-01   5.073 4.33e-07 ***
## Specialist       3.641e-05  1.593e-05   2.285 0.02241 *
## Migration       -2.297e-05  8.201e-06  -2.801 0.00516 **
## factor(Region)Northeast -8.959e-02  9.016e-02  -0.994 0.32053
## factor(Region)South    -1.422e-01  5.926e-02  -2.400 0.01650 *
## factor(Region)West     -2.641e-01  9.054e-02  -2.917 0.00358 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.035 on 1724 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.02519,    Adjusted R-squared:  0.0218
## F-statistic: 7.425 on 6 and 1724 DF,  p-value: 7.282e-08
```

Step 2: Repeat the procedure in step 1 with a simplified model excluding the $\text{Unemployment_rate_2018}$, which is the our model1. The p-value for $\text{ElderlyRate} = 4.33e-07 < \alpha = 0.05$, the p-value for $\text{Specialist} = 0.02241 < \alpha = 0.05$, p-value for $\text{Migration} = 0.00516 < \alpha = 0.05$, and the p-values for most categories under Region are under $\alpha = 0.05$. This suggests that all variables inside this model are statistically significant. Thus we cannot further simplify this model and this model would be one of our best models to consider.

Next, to compare model2 and model4, we use the extra sum of squares principle since model2 is nested within model4. So, we performed a hypothesis test on the variable $\text{Unemployment_rate_2018}$.

```
##
## Call:
## lm(formula = Mortality ~ ElderlyRate + Nurse + Migration + factor(Region))
##
```



```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.8555 -0.5041  0.1376  0.6711  3.4571
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -3.698e+00  1.109e-01 -33.352 < 2e-16 ***
## ElderlyRate      2.695e+00  5.371e-01   5.017 5.79e-07 ***
## Nurse           2.056e-04  9.837e-05   2.090 0.03680 *
## Migration       -2.390e-05  9.150e-06  -2.612 0.00907 **
## factor(Region)Northeast -9.286e-02  9.037e-02  -1.028 0.30427
## factor(Region)South   -1.446e-01  5.924e-02  -2.441 0.01475 *
## factor(Region)West    -2.611e-01  9.052e-02  -2.885 0.00396 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.035 on 1724 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.02471,    Adjusted R-squared:  0.02131
## F-statistic: 7.279 on 6 and 1724 DF,  p-value: 1.076e-07

##
## Call:
## lm(formula = Mortality ~ ElderlyRate + Nurse + Migration + Unemployment_rate_2018 +
##     factor(Region))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.8908 -0.4927  0.1311  0.6602  3.4712
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -3.811e+00  1.273e-01 -29.942 < 2e-16 ***
## ElderlyRate      2.562e+00  5.418e-01   4.730 2.43e-06 ***
## Nurse           2.023e-04  9.832e-05   2.058 0.03975 *
## Migration       -2.355e-05  9.146e-06  -2.575 0.01012 *
## Unemployment_rate_2018  3.580e-02  1.990e-02   1.799 0.07214 .
## factor(Region)Northeast -1.051e-01  9.056e-02  -1.161 0.24582
## factor(Region)South   -1.613e-01  5.993e-02  -2.692 0.00717 **
## factor(Region)West    -2.917e-01  9.204e-02  -3.169 0.00155 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.034 on 1723 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.02653,    Adjusted R-squared:  0.02258
## F-statistic: 6.709 on 7 and 1723 DF,  p-value: 7.293e-08
```

Hypothesis test:

$$(1) H_0: \beta_{unemployment} = 0 \text{ vs. } H_a: \beta_{unemployment} \neq 0$$

$$(2) f_0 = \frac{(1.035 - 1.034) / (1724 - 1723)}{1.034 / 1723} = 1.66634$$

```
## [1] 0.1969227
```

(3) p-value = $P(F_{1,1723} > 1.66634) = 0.197$

(4) Since p-value $> \alpha = 0.05$, then we do not reject H_0 at a 5% level of significance, which suggests the addition variable Unemployment_rate_2018 is not useful.

Thus we choose model2 as one of our best models to consider.

Then, we compare model1 and model2 results. We notice model1 and model2 have the same standard error, but model1 has a lower p-value and higher R_{adj}^2 compared to model2. Thus, we choose model1 to further investigate on. Moreover, we want to investigate on the collinearity of these two variables.

```
##
## Call:
## lm(formula = Mortality ~ ElderlyRate + Specialist + Migration +
##     factor(Region) + Specialist * Migration)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.8525 -0.5057  0.1349  0.6702  3.4808
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -3.715e+00  1.113e-01 -33.373  < 2e-16 ***
## ElderlyRate      2.768e+00  5.384e-01   5.141 3.04e-07 ***
## Specialist       3.605e-05  1.594e-05   2.262  0.0238 *
## Migration      -1.429e-05  1.322e-05  -1.081  0.2797
## factor(Region)Northeast -9.857e-02  9.081e-02  -1.086  0.2778
## factor(Region)South    -1.428e-01  5.927e-02  -2.410  0.0160 *
## factor(Region)West     -2.676e-01  9.064e-02  -2.952  0.0032 **
## Specialist:Migration  -1.801e-10  2.151e-10  -0.837  0.4025
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.035 on 1723 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.02559,    Adjusted R-squared:  0.02163
## F-statistic: 6.463 on 7 and 1723 DF,  p-value: 1.548e-07

## Analysis of Variance Table
##
## Response: Mortality
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ElderlyRate    1  28.05  28.0523  26.1915 3.437e-07 ***
## Specialist      1   0.06   0.0583   0.0545  0.815509
## Migration       1   8.65   8.6463   8.0728 0.004546 **
## factor(Region)  3  10.95   3.6492   3.4071 0.016987 *
## Specialist:Migration  1   0.75   0.7511   0.7013 0.402473
## Residuals     1723 1845.41   1.0710
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The overall p-value = $1.548e-07 < \alpha = 0.05$, which is higher than the model1. The adjusted $R^2 = 0.02163$ which is lower than 0.0218 from model1, which means the model that includes the interaction term explains less variability. Besides, the p-values for Migration increases to $0.2797 > \alpha = 0.05$ which do not indicate statistically significant. Besides, the global F-statistic = 6.463 which is lower than 7.425 from model1. Thus, adding the interaction term does not contribute to our study, and we decide to stay with model1.

We notice from previous analysis that Specialist and Migration have a correlation of 0.855, which shows they are highly correlated. Also, Specialist has a VIF value more than 50, and Migration has a VIF value of 5 indicating multicollinearity issue between these two variables. However, for the current dataset, we choose to stay with model1 as our best model, and will need to investigate on this using a larger dataset.

Based on the method we used and models we discussed, we select model1: Mortality \sim ElderlyRate + Specialist + Migration + factor(Region) as the most suitable model for the given COVID-19 dataset.

6 Assumption Checking

6.1 Mean of 0:

Looking at the plot of Residuals vs. Fitted values the residuals do appear randomly scatter around the value 0, whereas there are some points are far away (such as observation 99, 898 & 1114) from the majority which results the mean scatter around 0. However, overall it appears to fairly satisfy the assumption of mean of 0.

6.2 Independence:

Again the plot of Residuals vs. Fitted values shows the residuals randomly scattered with no apparent trend and thus satisfied.

6.3 Constant Variance:

The scale location plot suggests that the majority of residuals are randomly scattered within an upper and lower band around the value 0, which suggests a constant variance. However, since there is a few larger residuals at the bottom and on the left hand side, the red line bulges up and down in the middle of the plot, causing a slightly increase and decrease in variability. However, in general, it is still considered fairly satisfied.

6.4 Normality:

The Q-Q plot overall appears good, since most of the residuals are lying on a straight line. However, the normality assumption can only be considered as fairly satisfied, since there are some points at the tails are off the line (such as observation 99, 898 & 1549), suggesting some potential outliers.

6.5 Outliers:

It could be seen that there are some potential outliers, as we could find that there are some points off the straight at the tails in Q-Q plot, which appears to be outliers.

In terms of the leverage and Standard Residual plot, it could seen that there is a point on the very right side and a few other points are far away compared to the rest of majority of observations (observations that are greater than the leverage 0.1). As such, those points are considered to have a high leverage, whereas they are all within the Cook's Distance. Thus, these points are considered not to be influential.

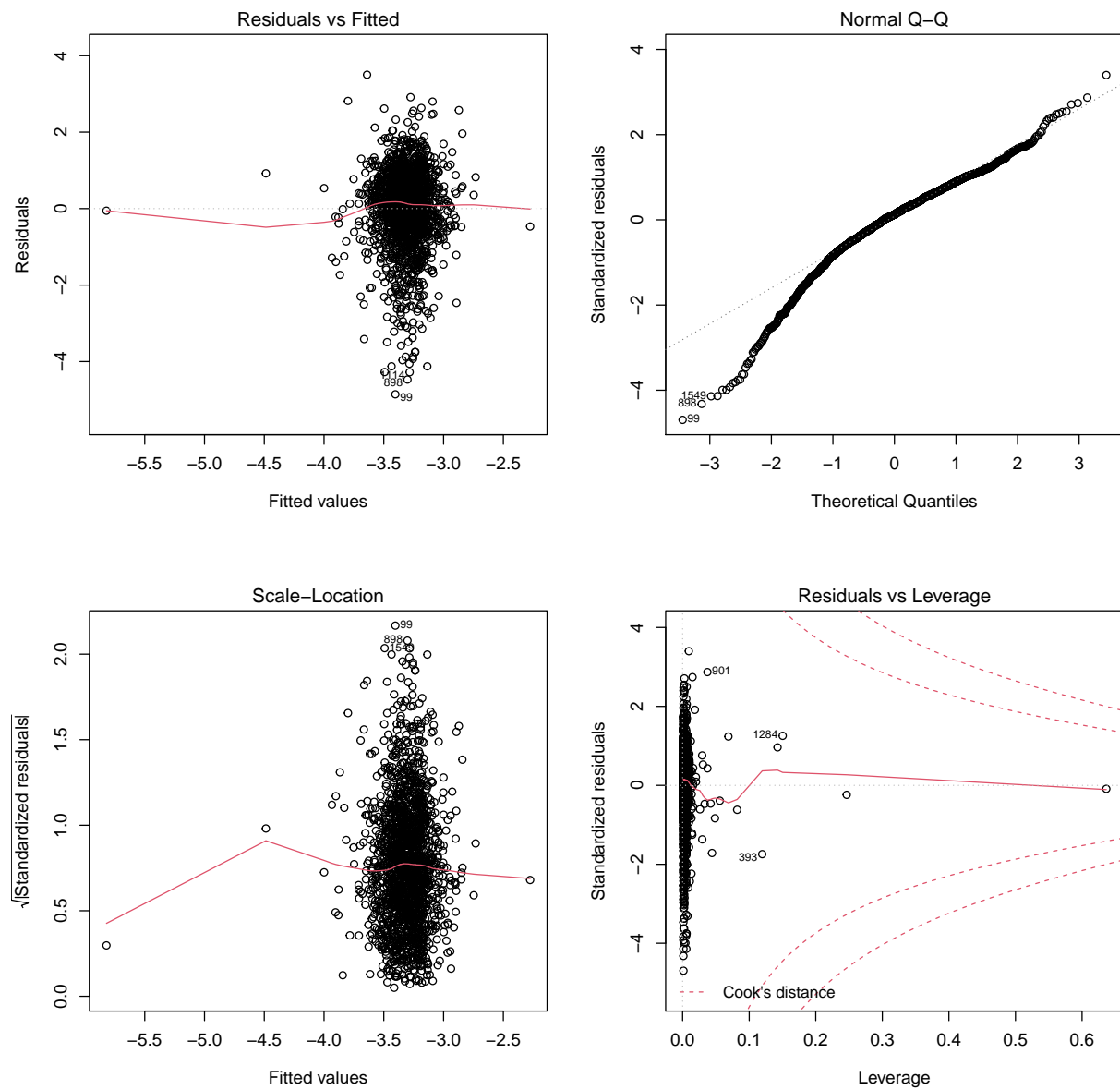


Figure 1: Plot for Model Checking

7 Results

We found that Elderly rate, number of Specialists, number of international migrations, and region are four variables that have major impacts to COVID-19 mortality rate given the dataset. This result matches with our initial speculation. Based on above discussion, the final model is selected to be $Mortality \sim ElderlyRate + Specialist + Migration + factor(Region)$ as it has high R_{adj}^2 compared to other models and is overall statistically significant. Besides, the hypothesis tests for individual variables indicate statistical significance. Further, the best linear model fitting for these variables is $Mortality = -3.700e + 00 + (2.699e + 00)x_{ElderlyRate} + (3.641e - 05)x_{Specialist} - (2.297e - 05)x_{Migration} - (8.959e - 02)x_{Northeast} - (1.422e - 01)x_{South} - (2.641e - 01)x_{West}$. However, there can several limitations of this study and will be discussed below.

8 Limitation of Study

Even though we have considered model 1: $Mortality \sim ElderlyRate + Specialist + Migration + factor(Region)$ as our best model, there are still a great degree of limitation from using this model to analyze the mortality rate of COVID-19. First, model 1 has a low explanatory power. Specially, $R_{adj}^2 = 0.0218$, which means model 1 could only explain 2.18% percentage of variability of the mortality rate of COVID-19. This indicates that there is a large room for model improvement. Thus, a further investigation on factors are desired.

Secondly, multicollinearity issue is presented, which not only undermines the statistical significance of an independent variable, but also violates our model independence assumption. For instance, the correlation between Specialist & Migration is as high as 0.855, highlighting a strong positive linear association in this pair variable. In addition, a very high VIF value (50.404208) of Specialist, suggesting that the association will affect the standard errors. Since the multicollinearity issue is considered very severe in this case, we would need to do further investigation and study about the cause of this issue. The solution for this problem could be varied by situation. If it is structural multicollinearity, centering the variables could be helpful. (Frost (2017)). Another potential solution could be linearly combining the independent variables together, such as adding them together. The solution could also depends on our interest. Therefore, this will all required further discussion, since it could also be a situation that is very difficult to resolve.

9 Conclusion

Appendix

```
##
## Call:
## lm(formula = Mortality ~ ElderlyRate)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.8993 -0.4917  0.1336  0.6605  3.6109
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -3.74966    0.09149 -40.982 < 2e-16 ***
## ElderlyRate  2.40160    0.48247   4.978 7.07e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.039 on 1737 degrees of freedom
## Multiple R-squared:  0.01406,    Adjusted R-squared:  0.0135
## F-statistic: 24.78 on 1 and 1737 DF,  p-value: 7.072e-07

##
## Call:
## lm(formula = Mortality ~ Region)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.9109 -0.4914  0.1316  0.6785  3.0620
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -3.20073    0.04848 -66.017 < 2e-16 ***
## RegionNortheast -0.07649    0.09046  -0.846  0.39790
## RegionSouth    -0.14826    0.05972  -2.482  0.01314 *
## RegionWest     -0.24041    0.09116  -2.637  0.00843 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.044 on 1727 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.005412,    Adjusted R-squared:  0.003684
## F-statistic: 3.132 on 3 and 1727 DF,  p-value: 0.02471

##
## Call:
## lm(formula = Mortality ~ Specialist)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.9596 -0.4855  0.1351  0.6562  3.2403
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept) -3.299e+00  2.565e-02 -128.642  <2e-16 ***
## Specialist  -1.728e-05  7.828e-06   -2.207   0.0274 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.045 on 1737 degrees of freedom
## Multiple R-squared:  0.002796,    Adjusted R-squared:  0.002222
## F-statistic: 4.871 on 1 and 1737 DF,  p-value: 0.02745
```

```
##
## Call:
## lm(formula = Mortality ~ population)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.9877 -0.4918  0.1333  0.6649  3.2686
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -3.40734    0.04648  -73.31  <2e-16 ***
## populationSmall  0.13515    0.05518   2.45   0.0144 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.044 on 1737 degrees of freedom
## Multiple R-squared:  0.003442,    Adjusted R-squared:  0.002869
## F-statistic:      6 on 1 and 1737 DF,  p-value: 0.0144
```

```
##
## Call:
## lm(formula = Mortality ~ Physician_rate)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.8957 -0.4926  0.1193  0.6658  3.1942
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -3.5697674  0.1318121 -27.082  <2e-16 ***
## Physician_rate  0.0009903  0.0004961   1.996   0.0461 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.045 on 1737 degrees of freedom
## Multiple R-squared:  0.002289,    Adjusted R-squared:  0.001715
## F-statistic: 3.985 on 1 and 1737 DF,  p-value: 0.04606
```

```
##
## Call:
## lm(formula = Mortality ~ Unemployment_rate_2018)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```

## -4.9849 -0.4643  0.1295  0.6592  3.2247
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -3.46670    0.08251 -42.016  <2e-16 ***
## Unemployment_rate_2018  0.03688    0.01867   1.975   0.0484 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.045 on 1737 degrees of freedom
## Multiple R-squared:  0.002241, Adjusted R-squared:  0.001666
## F-statistic: 3.901 on 1 and 1737 DF, p-value: 0.04841

##
## Call:
## lm(formula = Mortality ~ Poverty)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.9570 -0.4868  0.1355  0.6550  3.2323
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -3.300e+00  2.555e-02 -129.168  <2e-16 ***
## Poverty      -3.448e-07  1.537e-07  -2.243   0.025 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.045 on 1737 degrees of freedom
## Multiple R-squared:  0.002888, Adjusted R-squared:  0.002314
## F-statistic: 5.032 on 1 and 1737 DF, p-value: 0.02501

##
## Call:
## lm(formula = Mortality ~ Migration)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.9585 -0.4795  0.1358  0.6560  3.2221
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -3.301e+00  2.526e-02 -130.691  < 2e-16 ***
## Migration    -1.269e-05  4.232e-06  -2.999   0.00275 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.044 on 1737 degrees of freedom
## Multiple R-squared:  0.00515, Adjusted R-squared:  0.004577
## F-statistic: 8.992 on 1 and 1737 DF, p-value: 0.00275

##
## Call:

```



```
## lm(formula = Mortality ~ Nurse)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.9610 -0.4833  0.1338  0.6569  3.2986
##
## Coefficients:
##              Estimate Std. Error  t value Pr(>|t|)
## (Intercept) -3.298e+00  2.566e-02 -128.519  <2e-16 ***
## Nurse       -1.063e-04  4.324e-05   -2.459    0.014 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.044 on 1737 degrees of freedom
## Multiple R-squared:  0.003468,    Adjusted R-squared:  0.002895
## F-statistic: 6.046 on 1 and 1737 DF,  p-value: 0.01404
```

R Code

Reference

Frost, Jim. 2017. "Multicollinearity in Regression Analysis: Problems, Detection, and Solutions," September. <https://statisticsbyjim.com/regression/multicollinearity-in-regression-analysis/>.

Killeen, Benjamin D., Jie Ying Wu, Kinjal Shah, Anna Zapaishchykova, Philipp Nikutta, Aniruddha Tamhane, Shreya Chakraborty, et al. 2020. "A County-Level Dataset for Informing the United States' Response to COVID-19," April.

USAFacts. 2020. "Coronavirus Locations: COVID-19 Map by County and State," March. <https://usafacts.org/visualizations/coronavirus-covid-19-spread-map/>.

World Health Organization. 2020. "Coronavirus Disease (Covid-19) Outbreak Situation." <https://www.who.int/emergencies/diseases/novel-coronavirus-2019>.