

**THE
UNIVERSITY
OF RHODE ISLAND**

COLLEGE OF ARTS AND SCIENCES

CORONAVIRUS CASES IN THE UNITED STATES BY COUNTIES

Capstone Project Final Report

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ACKNOWLEDGEMENTS

First and foremost, I want to express my deepest gratitude and appreciation to my supervisor, Dr. Gavino Puggioni for his consistent support and guidance throughout these past several months especially when you factor the Coronavirus Pandemic and that I was and still an essential worker. I attribute his role to my growth and development in the Data Science field which is why I cannot thank him enough.

I want to give a special thanks to Kaggle for providing me with the dataset to use towards my capstone project for CSC 499. It was a tough start deciding which dataset would be fitting for the topic on time series as some of the other datasets I came across were complicated. I decided I wanted to do the dataset on the Coronavirus as my job has been helping in the COVID-19 relief efforts through the Air National Guard. It's my belief that analyzing this dataset has contributed to me better understanding the virus and its severity.

I want to also thank my family for their unwavering support and my friend Semere for his guidance and help throughout the different stages of this project. I attribute his help to the success of making this far.

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ABSTRACT

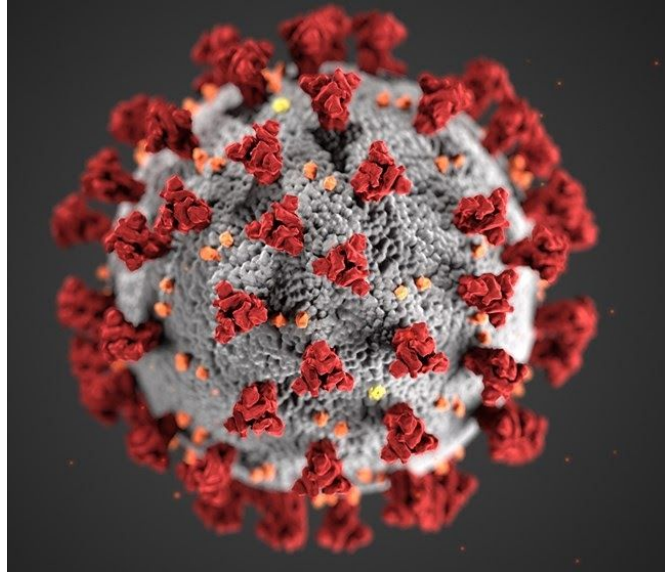
The main purpose of this capstone project is to thoroughly examine the dataset of the Coronavirus Cases in the United States by counties specifically in Rhode Island. Rhode Island has 5 counties: Bristol, Kent, Newport, Providence, and Washington.

The analysis conducted on the counties with regards to the cases and deaths takes note of their respective populations. It starts when determining the rate of growth of the county's cases. The growth of the counties are evaluated in absolute terms as well as per capita. Through making these calculations, we can compare and contrast the state and welfare of the counties. We can see which county is doing better or worse as well as taking into account the proportionality. It's noted when assessing the cumulative deaths for each county. Along with that, when plotting the data to visualize it, we plot the lines to compare the cases to deaths to understand the likelihood for the survival of the residents.

Through analyzing the data, we hope this may provide more insight about the Coronavirus's impact on Rhode Island. We may determine if there was a relationship between the number of cases and the socioeconomic status of the residents of each respective county. Since time series is being utilized in analyzing the dataset, we can see whether the mask mandate and stay at home order played a significant role and to what extent.

COVID-19 ORIGIN

Coronaviruses are a group of viruses that cause diseases in both animals and humans. An example of the Coronavirus would be Severe Acute Respiratory Syndrome (SARS) otherwise known as SARS-CoV. In December 2019, the Coronavirus, known as the COVID-19 was first identified in Wuhan, a city in the Hubei province of China with experts believing that it originated in bats or pangolins although they are common in animals such as cattles and camels. It spread to humans through one of Wuhan's open-air "wet markets" where wild animals such as cobras, wild boars, and raccoon dogs. As the markets are crowded, the conditions have allowed the viruses from different animals to interchange genes. In the dataset provided, the cases started happening on January 21, 2020. It was about 2 months later that the World Health Organization (WHO) designated the COVID-19 epidemic as a Pandemic on March 11, 2020. A Pandemic occurs when a disease that people are not immune to spreads across large regions. The last global Pandemic the world saw was the 1918 Spanish Flu which was caused by an H1N1 virus with genes of avian origin.



(The image above is a COVID-19 particle provided by the CDC)

It is important to note that the Coronavirus spreads through respiratory droplets, such as through coughing, sneezing, or even speaking. The picture above is a visual illustration of the COVID-19. A virus is just a frame around genetic material and a few proteins that makes more of itself by entering a living cell. There are many ways that Corona can spread: via surfaces, if you touch someone who is ill and then your face, rubbing your eyes or nose. Most of the time, Corona spreads through droplet infection when people cough, sneeze or talk. The destination of this virus are the intestines and the spleen of the lungs, which can lead to a very damaging effect.

Biology explains the COVID-19 virus as such:

“Corona connects to a specific receptor on its victim’s membranes to inject its genetic material. The cell then copies and reassembles the virus. It fills up with more and more copies of the original virus until it reaches a critical point and finally self-destructs”. The cell melts away, releasing new corona particles ready to attack more

cells. The number of infected cells grows and after 10 days, millions of body cells are infected and billions of viruses swarm the lungs” (Jason Kottke) .

Our immune system protects us from illnesses but when immune cells pour into the lungs to fight the virus, Corona infects some of them which leads to more damage. Two specific cells that inflict havoc are: neutrophils which kill both healthy and unhealthy cells. The other type of cell are killer T- cells which usually order infected cells to “commit controlled suicide”, they get confused and start ordering healthy cells to kill themselves too.

In many cases, the immune system slowly regains control and kills infected cells, prohibits the virus from infecting new ones and recovery begins. The majority of people infected by the Corona will get through it with mild symptoms: fever, dry cough. However, some people who have contracted the virus have really severe or critical cases. COVID-19 is very harmful towards our body given that millions of epithelial cells have died when Coronavirus enters our body which erases the protective lining of the lungs. Respiration becomes very difficult, and a lot of patients need ventilators to survive.

Unfortunately, this is a fast spreading pandemic and there is a shortage of resources, like medical staff or equipment like ventilators needed to help everybody which leaves patients at risk to death.

Most importantly, this is why everyone must practice social distance- 6ft apart, wear masks, and wash your hands. Coronavirus is wrapped with a Lipid Envelope, which is basically a layer of fat; soap breaks that fat apart, and leaves it unable to infect you. The virus has shown to be capable of causing permanent irreversible damage leading to lifelong disabilities if CDC guidelines are not followed carefully.

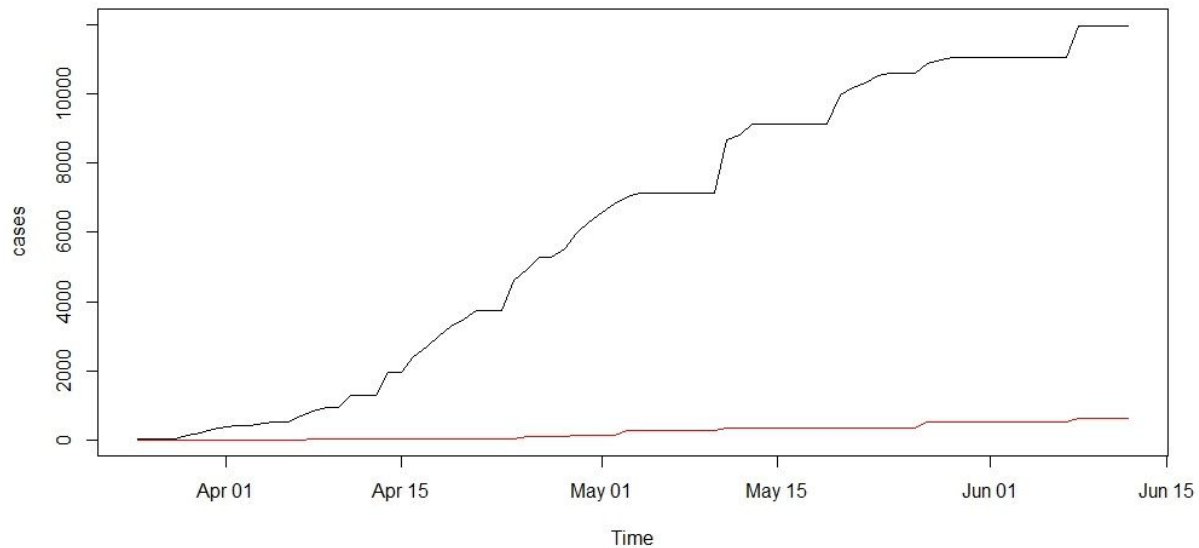
```
> table(Coronavirus_Cases$state)
```

Alabama	Alaska	Arizona	Arkansas
5413	1183	1347	5851
California	Colorado	Connecticut	Delaware
5141	4907	791	332
District of Columbia	Florida	Georgia	Guam
98	5770	12889	90
Hawaii	Idaho	Illinois	Indiana
393	2626	7509	7483
Iowa	Kansas	Kentucky	Louisiana
7074	5961	8590	5403
Maine	Maryland	Massachusetts	Michigan
1375	2143	1414	6424
Minnesota	Mississippi	Missouri	Montana
6324	6695	7751	2342
Nebraska	Nevada	New Hampshire	New Jersey
4598	1073	943	2017
New Mexico	New York	North Carolina	North Dakota
2311	5089	7808	2858
Northern Mariana Islands	Ohio	Oklahoma	Oregon
77	7063	5440	2720
Pennsylvania	Puerto Rico	Rhode Island	South Carolina
5542	92	504	3888
South Dakota	Tennessee	Texas	Utah
3576	7565	16363	2055
Vermont	Virgin Islands	Virginia	Washington
1258	91	10040	3456
West Virginia	Wisconsin	Wyoming	
3799	5458	1711	

The table here shows the number of cases state by state and unincorporated territory (Guam, Puerto Rico, Northern Mariana Islands, Virgin, Islands) from January 21, 2020 to June 12, 2020. Texas has the most cases followed by Georgia and Virginia. Hawaii has the least amount of cases followed by Delaware and Rhode Island. While it should not be surprising that the smaller states have less cases as opposed to the larger states, it's worth noting that California seemed to fare well proportionally considering it is the biggest state by population in the United States. They were the first state to go on a lockdown in an effort to contain the spread.

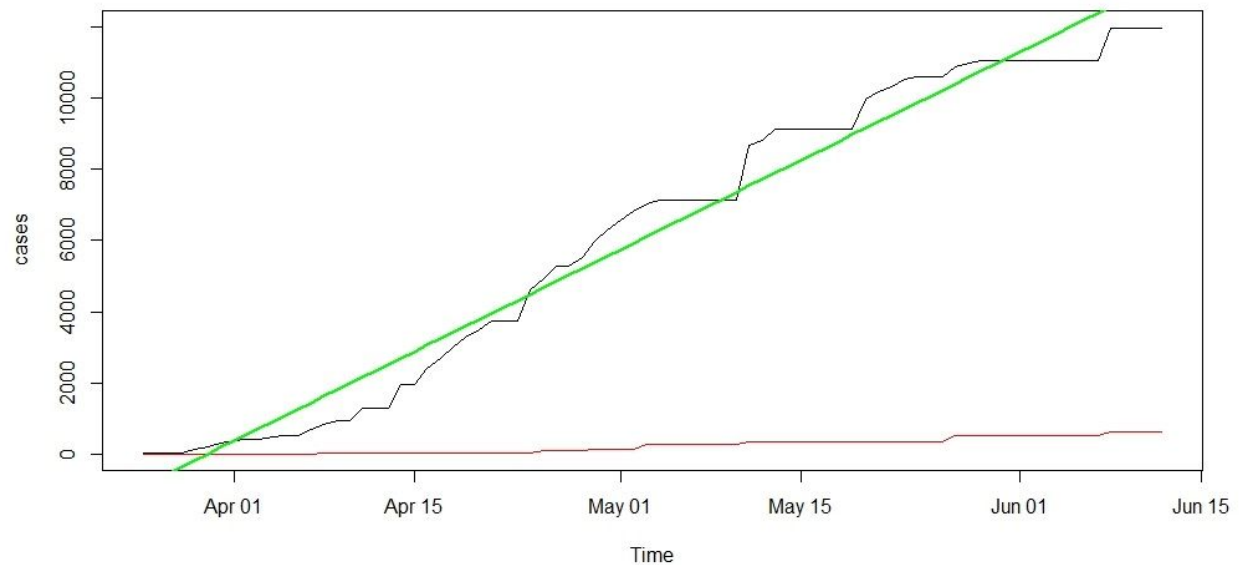
PROVIDENCE COUNTY

```
> # Providence County
> Coronavirus_Cases.RI.PVD <- Coronavirus_Cases %>% filter(state == 'Rhode Island', county=='Providence')
> plot(as.Date(Coronavirus_Cases.RI.PVD$date, format="%m/%d/%y"), Coronavirus_Cases.RI.PVD$cases, type
="l", xlab="Time", ylab="cases")
> lines(as.Date(Coronavirus_Cases.RI.PVD$date, format = "%m/%d/%y"), Coronavirus_Cases.RI.PVD$deaths, col
="red")
> |
```



This illustration shows the Coronavirus Cases in Providence County from April to June with the deaths as the red line. For every 6,192 cases, the deaths were 229.3 on average.

cases	deaths	trend
Min: 37	Min: 0.0	Min: 1.0
1st Qu: 1787	1st Qu: 20.0	1st Qu: 20.75
Median: 7083	Median: 265.0	Median: 40.50
Mean: 6192	Mean: 229.3	Mean: 40.50
3rd Qu: 10541	3rd Qu: 342.0	3rd Qu: 60.25
Max: 11959	Max: 637.0	Max: 80.00



```
> # Trend for Providence County Cases Absolute
> Coronavirus_Cases.RI.PVD$trend <- 1:80
> mod <- lm(cases ~ trend, data = Coronavirus_Cases.RI.PVD)
> summary(mod)

Call:
lm(formula = cases ~ trend, data = Coronavirus_Cases.RI.PVD)

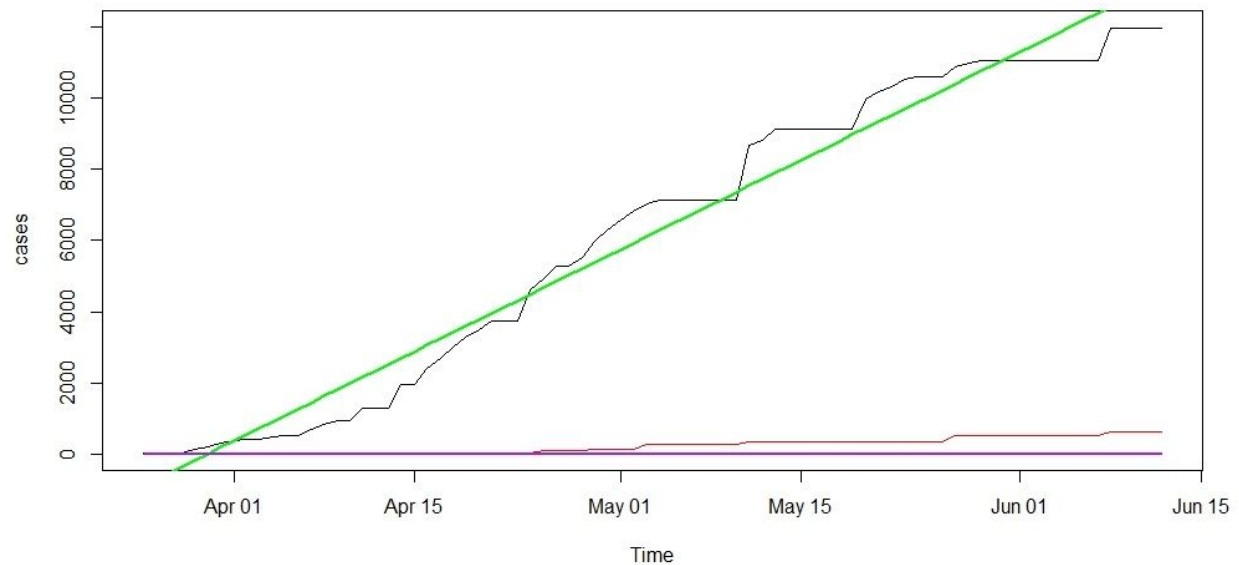
Residuals:
    Min       1Q   Median       3Q      Max
-1315.4  -590.4   114.2   570.1  1219.7

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1057.692    158.866  -6.658  3.5e-09 ***
trend         179.001      3.408  52.529 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 703.8 on 78 degrees of freedom
Multiple R-squared:  0.9725,    Adjusted R-squared:  0.9722
F-statistic: 2759 on 1 and 78 DF,  p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.PVD$date, format = "%m/%d/%y"), mod$fitted.values, col="green", lwd=
2)
```

This graph is for the Providence County plot regarding the cases in absolute terms. Looking at the trend analysis, Providence saw 179 cases occurring on a daily basis from April to June for 80 days.



```
> # Trend for Providence County cases Relative
> mod <- lm(cases/638931 ~ trend, data = Coronavirus_Cases.RI.PVD)
> summary(mod)

Call:
lm(formula = cases/638931 ~ trend, data = Coronavirus_Cases.RI.PVD)

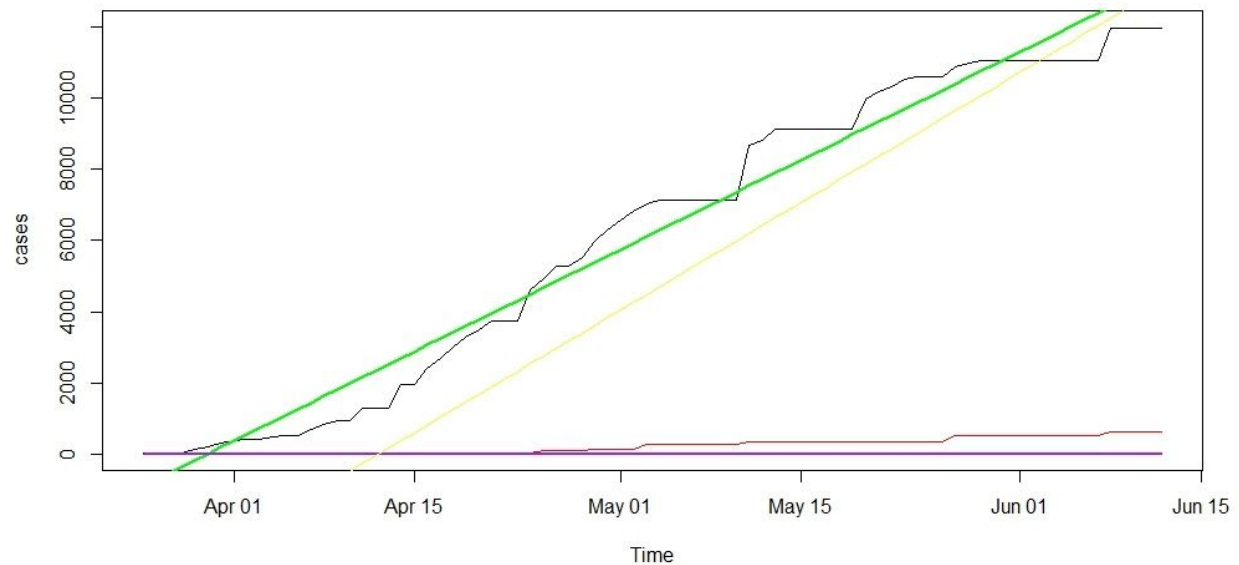
Residuals:
    Min       1Q   Median       3Q      Max
-0.0020587 -0.0009240  0.0001787  0.0008923  0.0019089

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.655e-03  2.486e-04  -6.658  3.5e-09 ***
trend        2.802e-04  5.333e-06  52.529 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.001102 on 78 degrees of freedom
Multiple R-squared:  0.9725,    Adjusted R-squared:  0.9722
F-statistic: 2759 on 1 and 78 DF,  p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.PVD$date, format = "%m/%d/%y"), mod$fitted.values, col="purple", lwd
=2)
```

The blue line highlights the relative cases where the cases in Providence are divided by the population of Providence.



```
> # Trend for Providence County deaths Absolute
> deaths_Providence <- cumsum(Coronavirus_Cases.RI.PVD$deaths)
> mod <- lm(deaths_Providence ~ trend, data = Coronavirus_Cases.RI.PVD)
> summary(mod)

Call:
lm(formula = deaths_Providence ~ trend, data = Coronavirus_Cases.RI.PVD)

Residuals:
    Min       1Q   Median       3Q      Max
-2911.0 -2039.2  -536.6   1824.6   5251.4

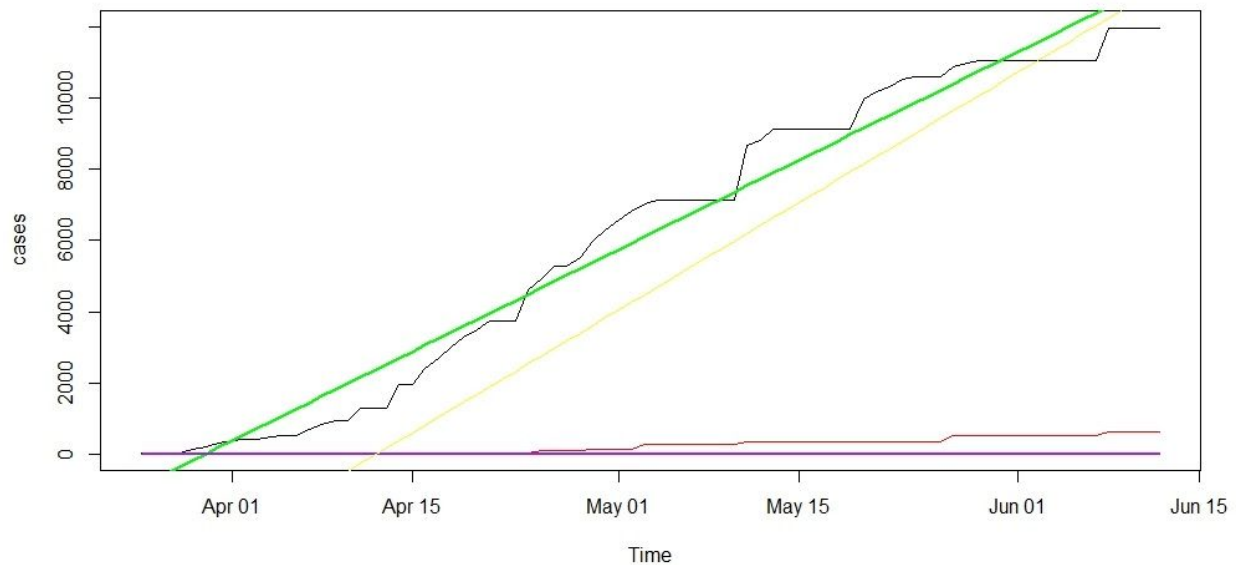
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -4137.71     517.91  -7.989 9.87e-12 ***
trend         215.38       11.11  19.388 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2294 on 78 degrees of freedom
Multiple R-squared:  0.8281,    Adjusted R-squared:  0.8259
F-statistic: 375.9 on 1 and 78 DF,  p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.PVD$date, format = "%m/%d/%y"), mod$fitted.values, col = "yellow")
> 
```

The trend analysis for the deaths in absolute deaths shows 215 deaths occurring on a daily basis.

The number of deaths exceed the number of cases which is why the yellow line is steeper than the green line.



```
> # Trend for Providence County deaths Relative
> mod_deaths <- lm(deaths_Providence/638931 ~ trend, data = Coronavirus_Cases.RI.PVD)
> summary(mod_deaths)

Call:
lm(formula = deaths_Providence/638931 ~ trend, data = Coronavirus_Cases.RI.PVD)

Residuals:
    Min       1Q   Median       3Q      Max
-0.0045561 -0.0031916 -0.0008398  0.0028557  0.0082191

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -6.476e-03  8.106e-04  -7.989 9.87e-12 ***
trend        3.371e-04  1.739e-05  19.388 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

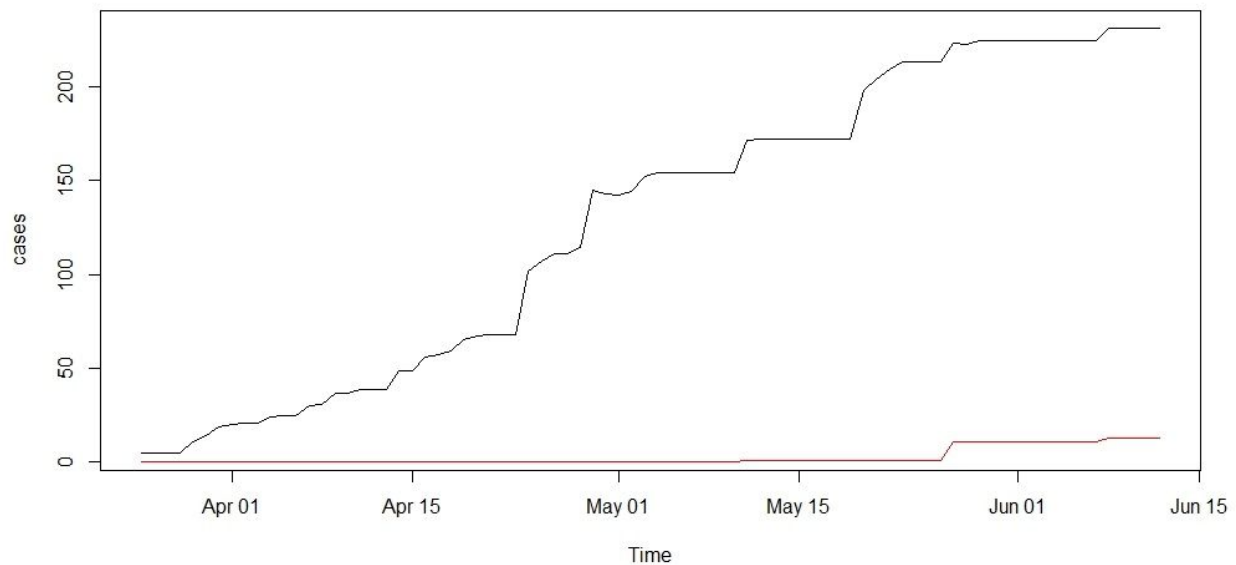
Residual standard error: 0.003591 on 78 degrees of freedom
Multiple R-squared:  0.8281,    Adjusted R-squared:  0.8259
F-statistic: 375.9 on 1 and 78 DF, p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.PVD$date, format = "%m/%d/%y"), mod_deaths$fitted.values, col="blue", lwd=2)
```

The blue line represents the trend for Providence deaths in relative terms. The CumSum function is utilized to accumulate the deaths and divide by the population. The population of Providence County is 638,931. The trend is multiplied by 100,000 and it is found that Providence saw about 34 deaths a day.

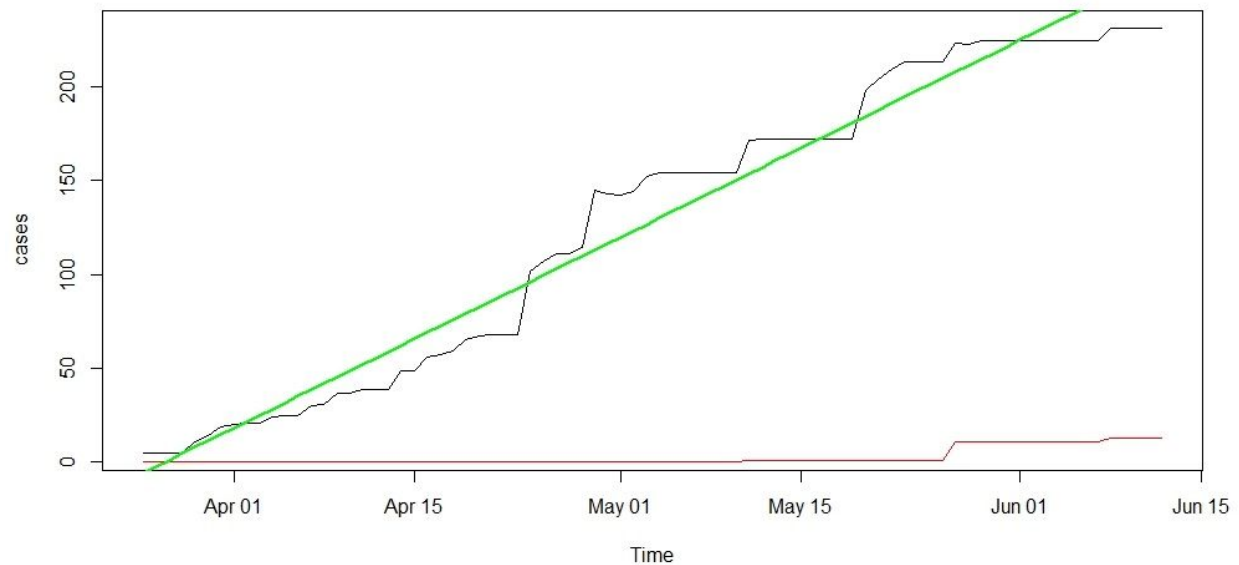
BRISTOL

```
> # Bristol County
> Coronavirus_Cases.RI.Bristol <- Coronavirus_Cases %>% filter(state == 'Rhode Island', county=='Bristol')
> plot(as.Date(Coronavirus_Cases.RI.Bristol$date, format="%m/%d/%y"), Coronavirus_Cases.RI.Bristol$cases,
type="l", xlab="Time", ylab="cases")
> lines(as.Date(Coronavirus_Cases.RI.Bristol$date, format = "%m/%d/%y"), Coronavirus_Cases.RI.Bristol$deaths, col="red")
> |
```



This is the plot of the COVID-19 cases in Bristol Rhode Island from April to June. The deaths are represented in the red line. The deaths seemed consistent on a flat line until the later part of May, we see a slight increase and that is around the time, there seemed to be a noticeable increase in the cases based on the steepness with the slope.

cases	deaths	trend
Min: 5	Min. : 0.000	Min: 1.00
1st Qu: 46.5	1st Qu.: 0.000	1st Qu: 20.75
Median: 153.0	Median : 0.000	Median: 40.50
Mean: 128.2	Mean : 2.663	Mean: 40.50
3rd Qu: 213.0	3rd Qu.: 1.000	3rd Qu: 60.25
Max: 231.0	Max. : 13.000	Max: 80.00



```
> # Trend for Bristol County Cases Absolute
> Coronavirus_Cases.RI.Bristol$trend <- 1:80
> mod = lm(cases ~ trend, data = Coronavirus_Cases.RI.Bristol) # The slope is in absolute terms
> summary(mod)

Call:
lm(formula = cases ~ trend, data = Coronavirus_Cases.RI.Bristol)

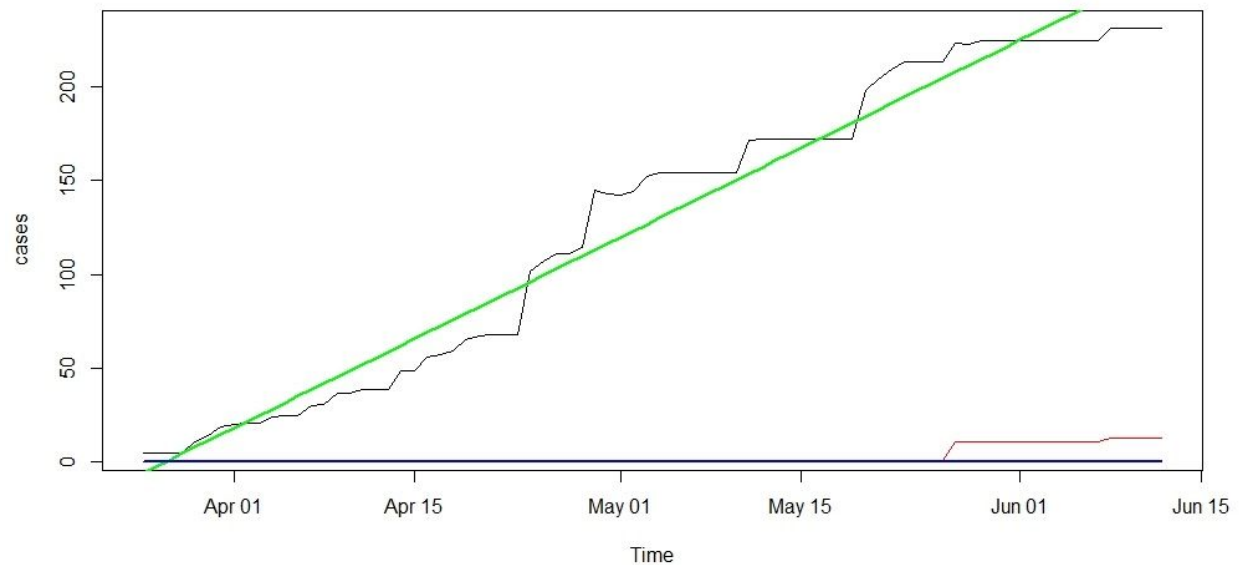
Residuals:
    Min       1Q   Median       3Q      Max
-30.915 -12.996   2.181  10.631  32.019

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -8.87468    3.32304  -2.671  0.00921 **
trend         3.38487    0.07128  47.488 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 14.72 on 78 degrees of freedom
Multiple R-squared:  0.9666,    Adjusted R-squared:  0.9661
F-statistic: 2255 on 1 and 78 DF,  p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.Bristol$date, format = "%m/%d/%y"), mod$fitted.values, col="green",
+       lwd=2)
> |
```

This plot is for the Bristol County's cases in absolute terms. The trend analysis shows Bristol sees around 3 cases occurring on a daily basis for the given time period shown by the green line.



```
> # Trend for Bristol County Cases Relative
> mod <- lm(cases/48479 ~ trend, data = Coronavirus_Cases.RI.Bristol)
> summary(mod)

Call:
lm(formula = cases/48479 ~ trend, data = Coronavirus_Cases.RI.Bristol)

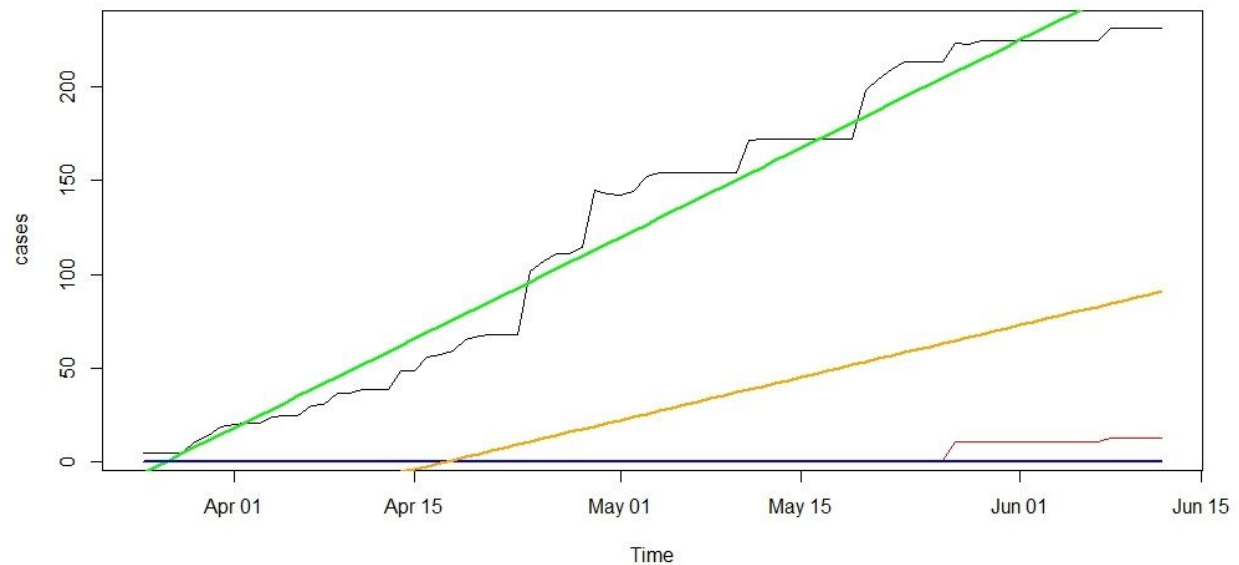
Residuals:
    Min       1Q   Median       3Q      Max
-6.377e-04 -2.681e-04  4.498e-05  2.193e-04  6.605e-04

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.831e-04  6.855e-05  -2.671  0.00921 **
trend        6.982e-05  1.470e-06  47.488  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.0003037 on 78 degrees of freedom
Multiple R-squared:  0.9666,    Adjusted R-squared:  0.9661
F-statistic: 2255 on 1 and 78 DF,  p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.Bristol$date, format = "%m/%d/%y"), mod$fitted.values, col = "blue",
+       lwd = 2)
> |
```

The blue line highlights the relative cases where the cases in Bristol are divided by the population of Bristol.



```
> # Trend for Bristol County Deaths Absolute
> deaths_Bristol <- cumsum(Coronavirus_Cases.RI.Bristol$deaths)
> mod_deaths <- lm(deaths_Bristol ~ trend, data = Coronavirus_Cases.RI.Bristol)
> summary(mod_deaths)
```

```
Call:
lm(formula = deaths_Bristol ~ trend, data = Coronavirus_Cases.RI.Bristol)
```

```
Residuals:
    Min       1Q   Median       3Q      Max
-47.219 -32.630  -5.304   22.022  122.047
```

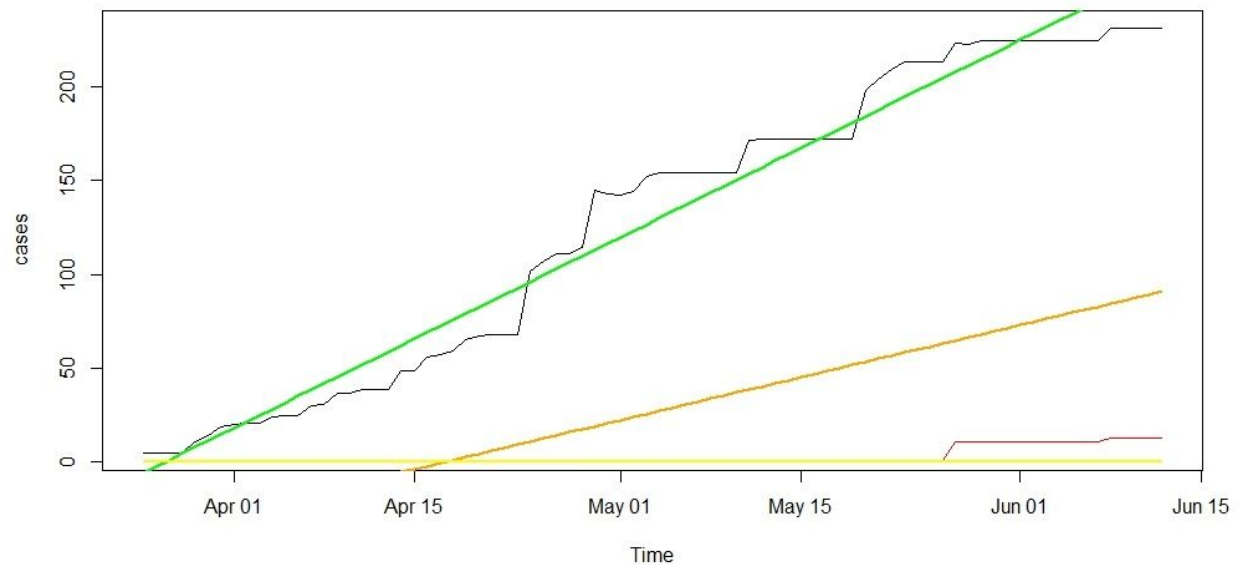
```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -39.5592     8.7584  -4.517 2.20e-05 ***
trend         1.6314     0.1879   8.684 4.43e-13 ***
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 38.8 on 78 degrees of freedom
Multiple R-squared:  0.4916,    Adjusted R-squared:  0.485
F-statistic: 75.41 on 1 and 78 DF,  p-value: 4.433e-13
```

```
> lines(as.Date(Coronavirus_Cases.RI.Bristol$date, format = "%m/%d/%y"), mod_deaths$fitted.values, col="orange", lwd=2)
> |
```

The trend analysis for the deaths in absolute deaths shows about 2 deaths occurring on a daily basis. It is highlighted by the orange line where since the deaths are much lower than Providence, the line is much flatter.



```
> # Trend for Bristol County Deaths Relative
> mod_deaths2 <- lm(deaths_Bristol/48479 ~ trend, data = Coronavirus_Cases.RI.Bristol)
> summary(mod_deaths2)

Call:
lm(formula = deaths_Bristol/48479 ~ trend, data = Coronavirus_Cases.RI.Bristol)

Residuals:
    Min       1Q   Median       3Q      Max
-0.0009740 -0.0006731 -0.0001094  0.0004543  0.0025175

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -8.160e-04  1.807e-04  -4.517 2.20e-05 ***
trend        3.365e-05  3.875e-06   8.684 4.43e-13 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

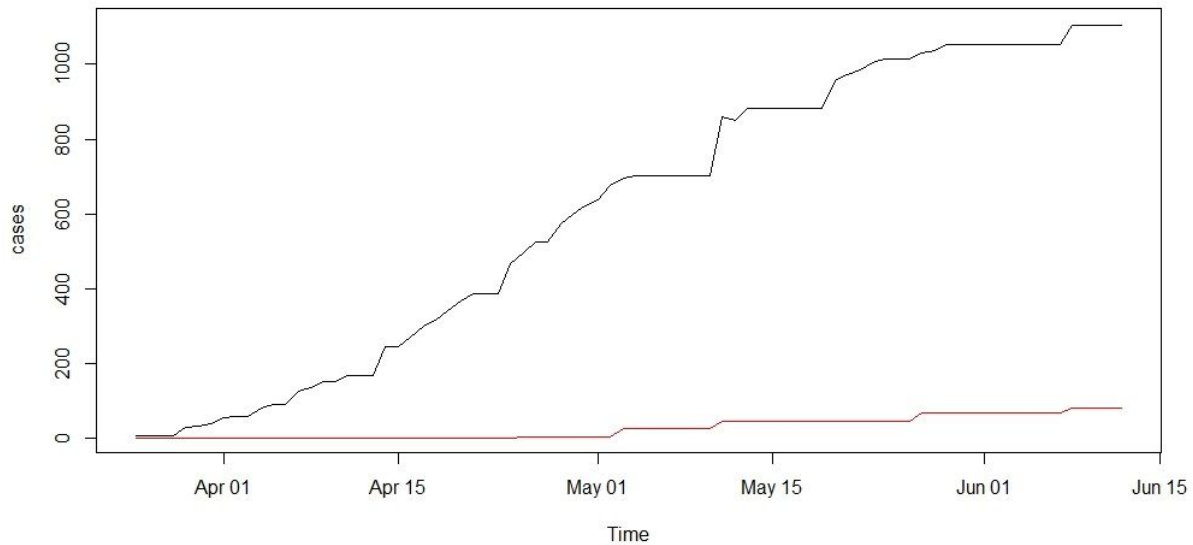
Residual standard error: 0.0008004 on 78 degrees of freedom
Multiple R-squared:  0.4916,    Adjusted R-squared:  0.485
F-statistic: 75.41 on 1 and 78 DF,  p-value: 4.433e-13

> lines(as.Date(Coronavirus_Cases.RI.Bristol$date, format = "%m/%d/%y"), mod_deaths2$fitted.values, col
="yellow", lwd=2)
```

The yellow line represents the trend for Bristol in relative terms. The cumulative sum of the deaths in Bristol is divided by the population followed by the percentage multiplied by 100,000. The relative deaths are 444 deaths.

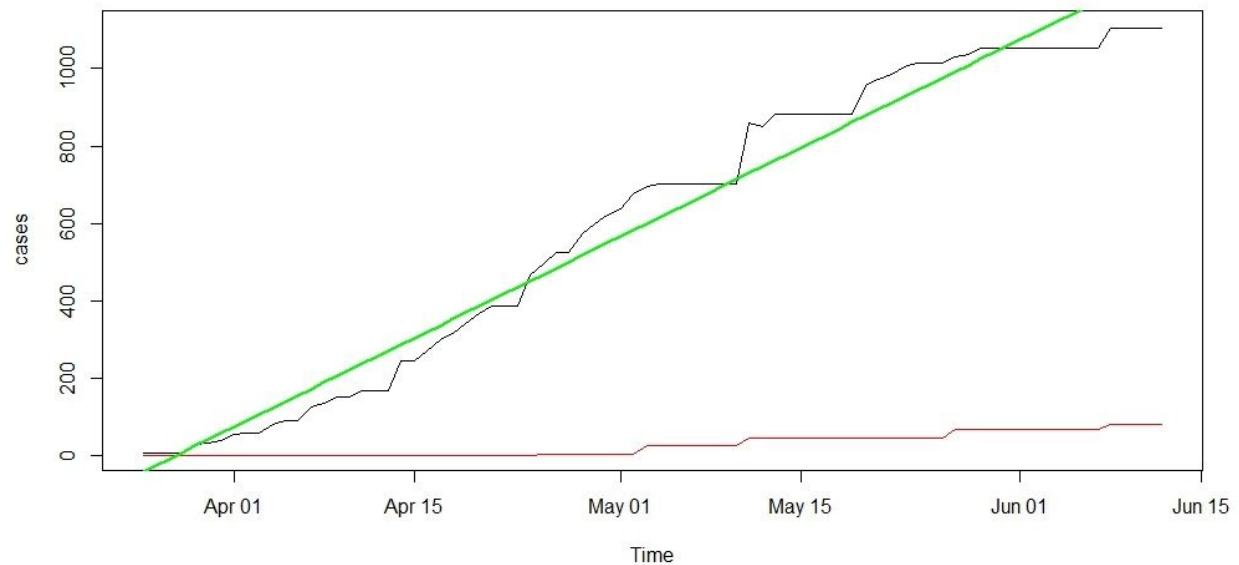
KENT

```
> # Kent County
> Coronavirus_Cases.RI.Kent = Coronavirus_Cases %>% filter(state == 'Rhode Island', county=='Kent')
> plot(as.Date(Coronavirus_Cases.RI.Kent$date, format="%m/%d/%y"), Coronavirus_Cases.RI.Kent$cases, type
="l", xlab="Time", ylab="cases")
> lines(as.Date(Coronavirus_Cases.RI.Kent$date, format = "%m/%d/%y"), Coronavirus_Cases.RI.Kent$deaths, c
ol="red")
```



This illustration shows the Coronavirus Cases in Kent County from April to June with the deaths as the red line. For every 607 cases, the deaths were 27 on average.

cases	deaths	trend
Min: 7.0	Min: 0.0	Min: 1.0
1st Qu: 225.2	1st Qu: 0.00	1st Qu: 20.75
Median: 700.0	Median: 25.00	Median: 40.50
Mean: 607.3	Mean: 27.32	Mean: 40.50
3rd Qu: 1007.0	3rd Qu: 46.00	3rd Qu: 60.25
Max: 1105.0	Max: 82.00	Max: 80.00



```
> # Trend for Kent County Cases Absolute
> Coronavirus_Cases.RI.Kent$trend <- 1:80
> mod <- lm(cases ~ trend, data = Coronavirus_Cases.RI.Kent)
> summary(mod)

call:
lm(formula = cases ~ trend, data = Coronavirus_Cases.RI.Kent)

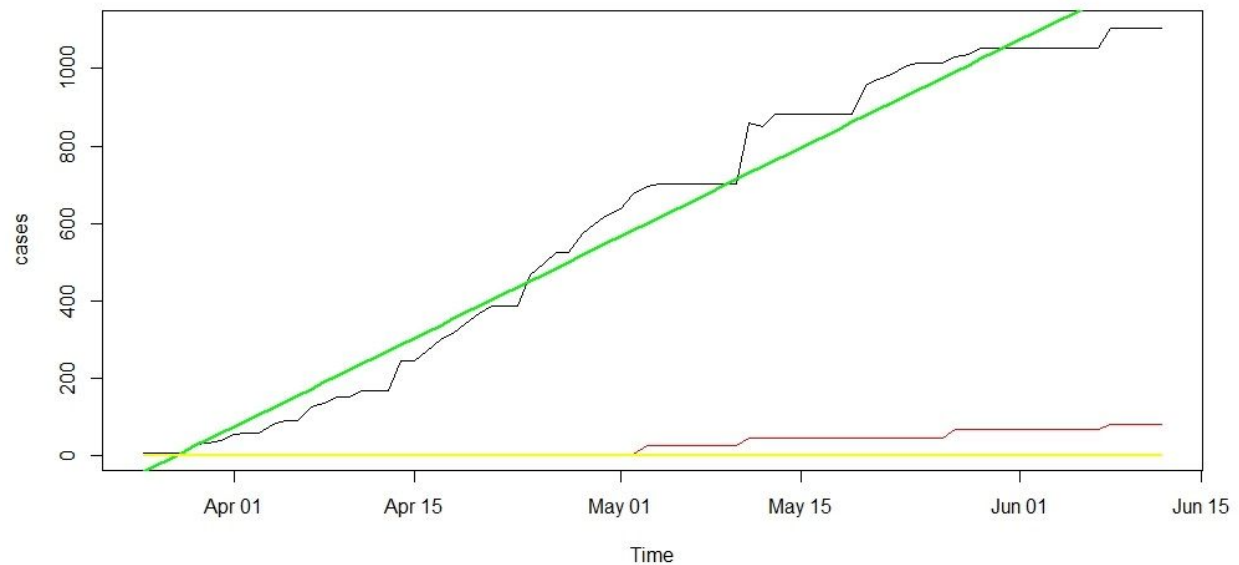
Residuals:
    Min       1Q   Median       3Q      Max
-150.516  -47.884    0.955   54.278  128.611

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -57.3009    15.0146  -3.816  0.00027 ***
trend          16.4102     0.3221  50.954  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 66.52 on 78 degrees of freedom
Multiple R-squared:  0.9708,    Adjusted R-squared:  0.9705
F-statistic: 2596 on 1 and 78 DF,  p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.Kent$date, format = "%m/%d/%y"), mod$fitted.values, col="green", lwd
=2)
> |
```

This is the plot for Kent County's absolute cases. Through the summary statistics, we see from the trend that the county sees 16 cases occurring on a daily basis during the given time period.



```

> # Trend for Kent County Cases Relative
> mod <- lm(cases/164292 ~ trend, data = Coronavirus_Cases.RI.Kent)
> summary(mod)

Call:
lm(formula = cases/164292 ~ trend, data = Coronavirus_Cases.RI.Kent)

Residuals:
    Min       1Q   Median       3Q      Max
-9.162e-04 -2.915e-04  5.810e-06  3.304e-04  7.828e-04

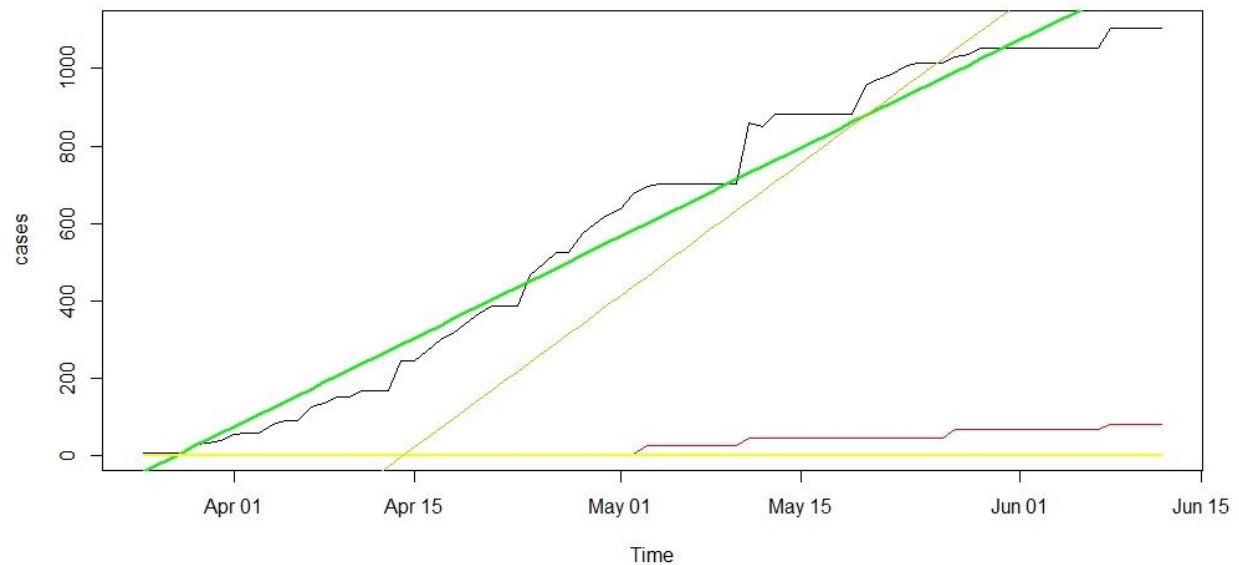
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -3.488e-04  9.139e-05  -3.816  0.00027 ***
trend        9.988e-05  1.960e-06  50.954 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.0004049 on 78 degrees of freedom
Multiple R-squared:  0.9708,    Adjusted R-squared:  0.9705
F-statistic: 2596 on 1 and 78 DF, p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.Kent$date, format = "%m/%d/%y"), mod$fitted.values, col = "yellow",
+       lwd = 2)
>

```

The yellow line represents Kent county's cases where it is divided by 164,292 people. The slope shown in the trend is about 10.



```
> # Trend for Kent County Deaths Absolute
> deaths_Kent <- cumsum(Coronavirus_Cases.RI.Kent$deaths)
> mod <- lm(deaths_Kent ~ trend, data = Coronavirus_Cases.RI.Kent)
> summary(mod)

Call:
lm(formula = deaths_Kent ~ trend, data = Coronavirus_Cases.RI.Kent)

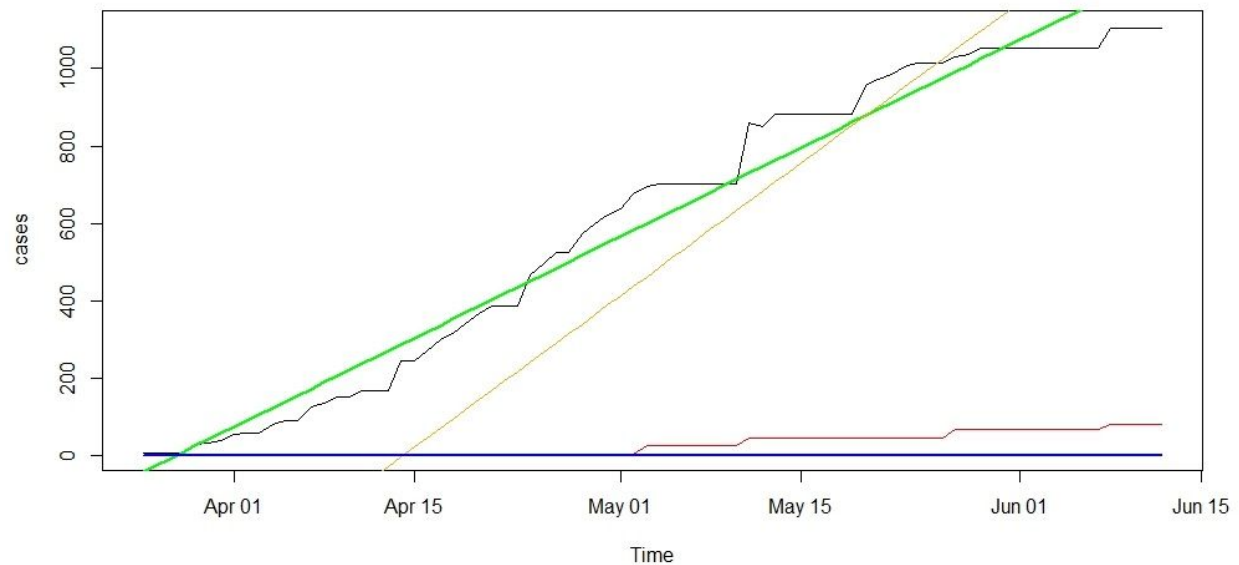
Residuals:
    Min       1Q   Median       3Q      Max
-413.7 -282.2  -55.7   254.2   744.1

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -517.428     72.770   -7.11 4.85e-10 ***
trend         24.491      1.561    15.69 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 322.4 on 78 degrees of freedom
Multiple R-squared:  0.7594,    Adjusted R-squared:  0.7563
F-statistic: 246.2 on 1 and 78 DF,  p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.Kent$date, format = "%m/%d/%y"), mod$fitted.values, col = "orange")
> |
```

The orange line signifies the absolute deaths in Kent county where the county sees 24 deaths daily. The deaths exceed the number of cases which is why the orange line is steeper than the green line (16 cases).



```
> # Trend for Kent County Deaths Relative
> mod_deaths3 <- lm(deaths_Kent/164292 ~ trend, data = Coronavirus_Cases.RI.kent)
> summary(mod_deaths3)

Call:
lm(formula = deaths_Kent/164292 ~ trend, data = Coronavirus_Cases.RI.kent)

Residuals:
    Min       1Q   Median       3Q      Max
-0.0025183 -0.0017174 -0.0003391  0.0015469  0.0045292

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -3.149e-03  4.429e-04  -7.11 4.85e-10 ***
trend        1.491e-04  9.501e-06  15.69 < 2e-16 ***
---
signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

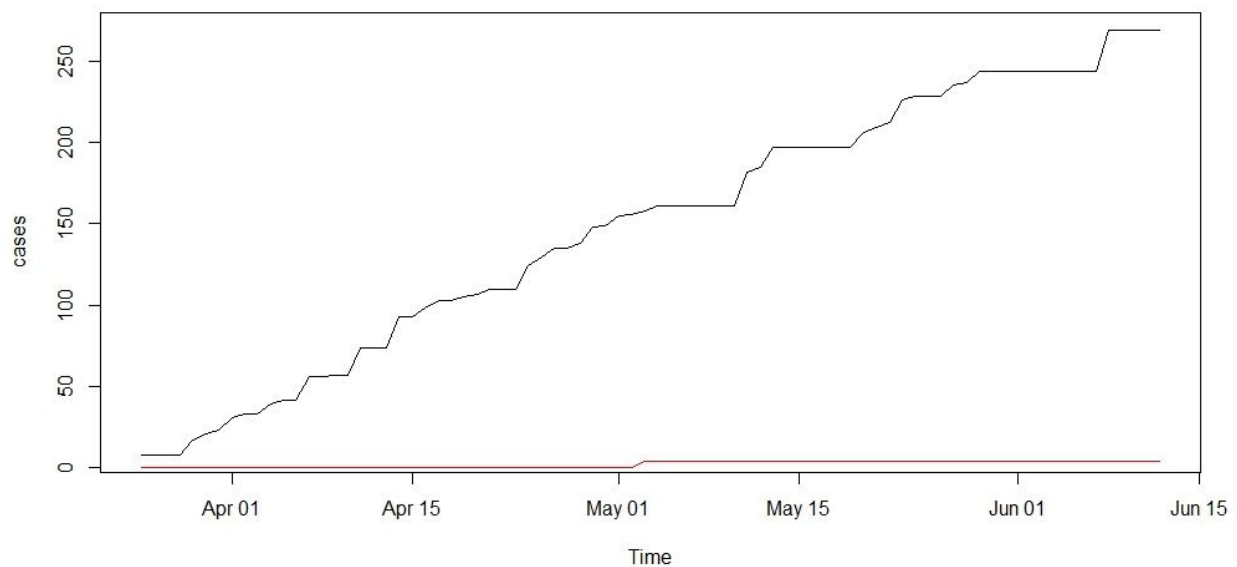
Residual standard error: 0.001962 on 78 degrees of freedom
Multiple R-squared:  0.7594,    Adjusted R-squared:  0.7563
F-statistic: 246.2 on 1 and 78 DF,  p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.kent$date, format = "%m/%d/%y"), mod_deaths3$fitted.values, col="blue", lwd=2)
```

Kent county's deaths relative to the rest of Rhode Island shown on the blue line is about 15 which is much lower than Providence and Bristol. Kent's population is higher than Bristol as Bristol is noted to have 48,479.

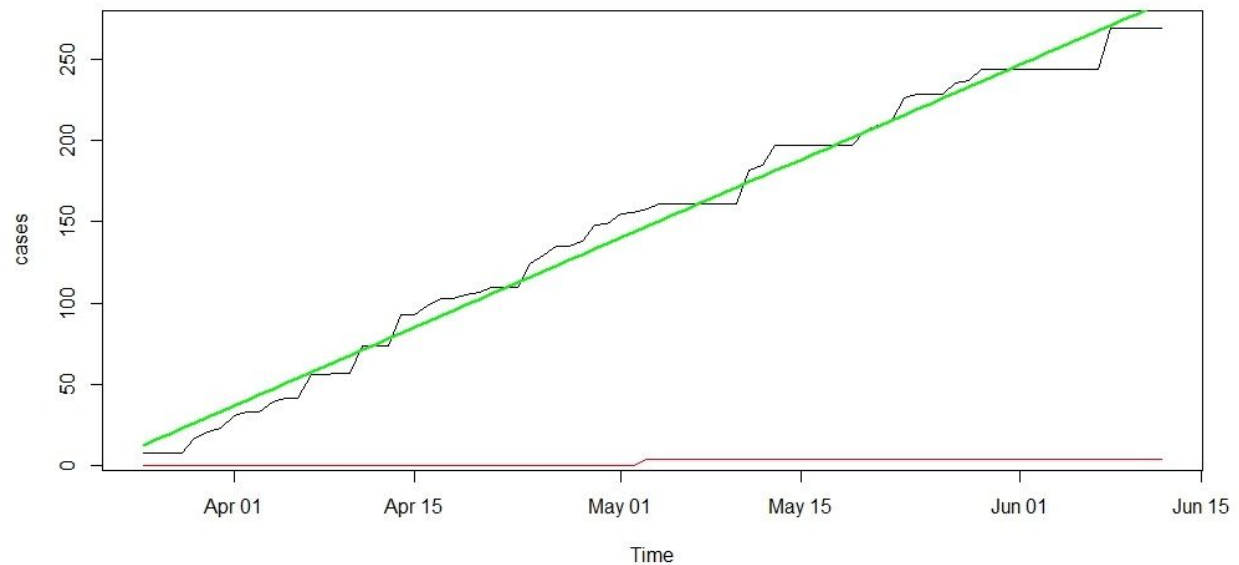
NEWPORT

```
> # Newport County
> Coronavirus_Cases.RI.Newport <- Coronavirus_Cases %>% filter(state == 'Rhode Island', county=='Newport')
> plot(as.Date(Coronavirus_Cases.RI.Newport$date, format="%m/%d/%y"), Coronavirus_Cases.RI.Newport$cases,
type="l", xlab="Time", ylab="cases")
> lines(as.Date(Coronavirus_Cases.RI.Newport$date, format="%m/%d/%y"), Coronavirus_Cases.RI.Newport$deaths, col="red")
> |
```



This illustration shows the Coronavirus Cases in Newport County from April to June with the deaths as the red line. For about every 149 cases, there were 2 deaths on average.

cases	deaths	trend
Min: 8.00	Min: 0.00	Min: 1.0
1st Qu: 88.25	1st Qu: 0.00	1st Qu: 20.75
Median: 159.50	Median: 4.00	Median: 40.50
Mean: 148.60	Mean: 2.05	Mean: 40.50
3rd Qu: 226.50	3rd Qu: 4.00	3rd Qu: 60.25
Max: 269.00	Max: 4.00	Max: 80.00



```
> # Trend for Newport County Cases Absolute
> Coronavirus_Cases.RI.Newport$trend <- 1:80
> mod <- lm(cases ~ trend, data = Coronavirus_Cases.RI.Newport)
> summary(mod)

Call:
lm(formula = cases ~ trend, data = Coronavirus_Cases.RI.Newport)

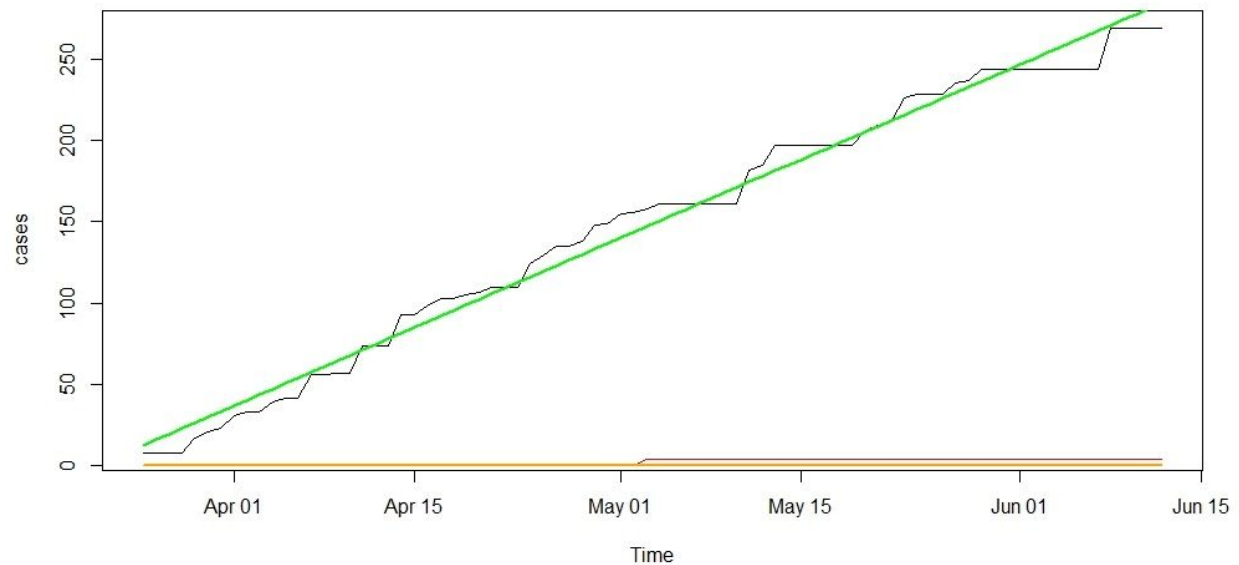
Residuals:
    Min       1Q   Median       3Q      Max
-23.287  -7.515   0.498   7.803  15.718

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  9.27184    2.08646   4.444 2.88e-05 ***
trend        3.44020    0.04475  76.869 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 9.244 on 78 degrees of freedom
Multiple R-squared:  0.987,    Adjusted R-squared:  0.9868
F-statistic: 5909 on 1 and 78 DF,  p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.Newport$date, format = "%m/%d/%y"), mod$fitted.values, col="green",
+       lwd=2)
> |
```

Shown by the green line on the plot, Newport sees 3 cases on a daily basis.



```
> # Trend for Newport County Cases Relative
> mod <- lm(cases/82082 ~ trend, data = Coronavirus_Cases.RI.Newport)
> summary(mod)

Call:
lm(formula = cases/82082 ~ trend, data = Coronavirus_Cases.RI.Newport)

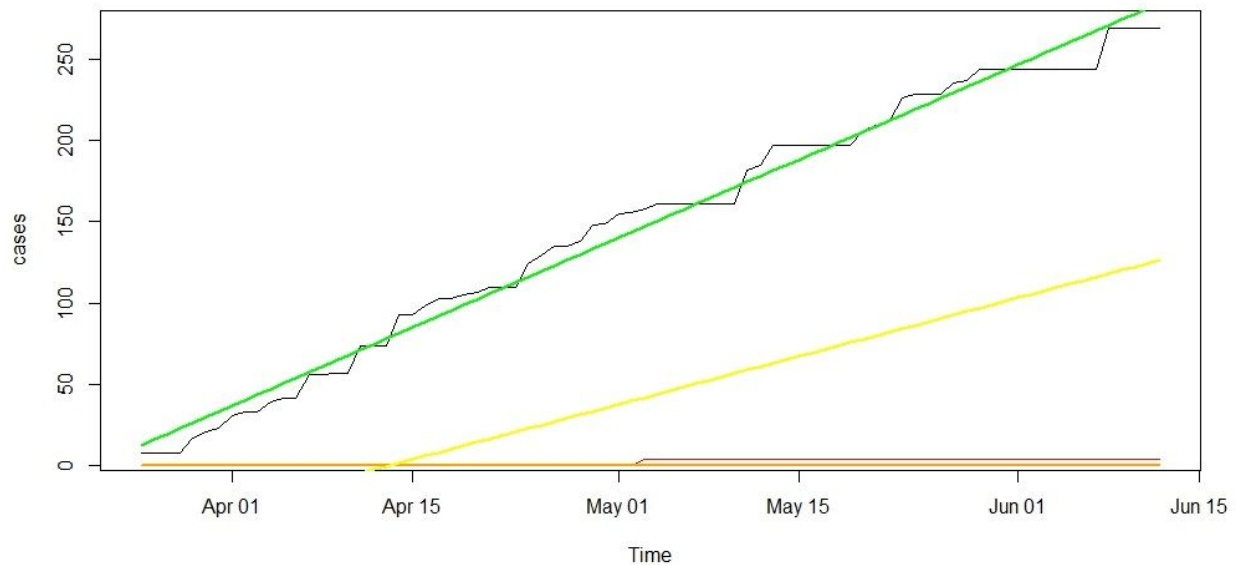
Residuals:
    Min       1Q   Median       3Q      Max
-2.837e-04 -9.155e-05  6.067e-06  9.507e-05  1.915e-04

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.130e-04  2.542e-05   4.444 2.88e-05 ***
trend       4.191e-05  5.452e-07  76.869 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.0001126 on 78 degrees of freedom
Multiple R-squared:  0.987,    Adjusted R-squared:  0.9868
F-statistic: 5909 on 1 and 78 DF,  p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.Newport$date, format = "%m/%d/%y"), mod$fitted.values, col="orange",
+       lwd=2)
> |
```

When looking at the plot, we can see that Newport has less cases relative to the other counties seen on the orange line with the slope given on the trend, 4.



```
> # Trend for Newport County Deaths Absolute
> deaths_Newport <- cumsum(Coronavirus_Cases.RI.Newport$deaths)
> mod <- lm(deaths_Newport ~ trend, data = Coronavirus_Cases.RI.Newport)
> summary(mod)

Call:
lm(formula = deaths_Newport ~ trend, data = Coronavirus_Cases.RI.Newport)

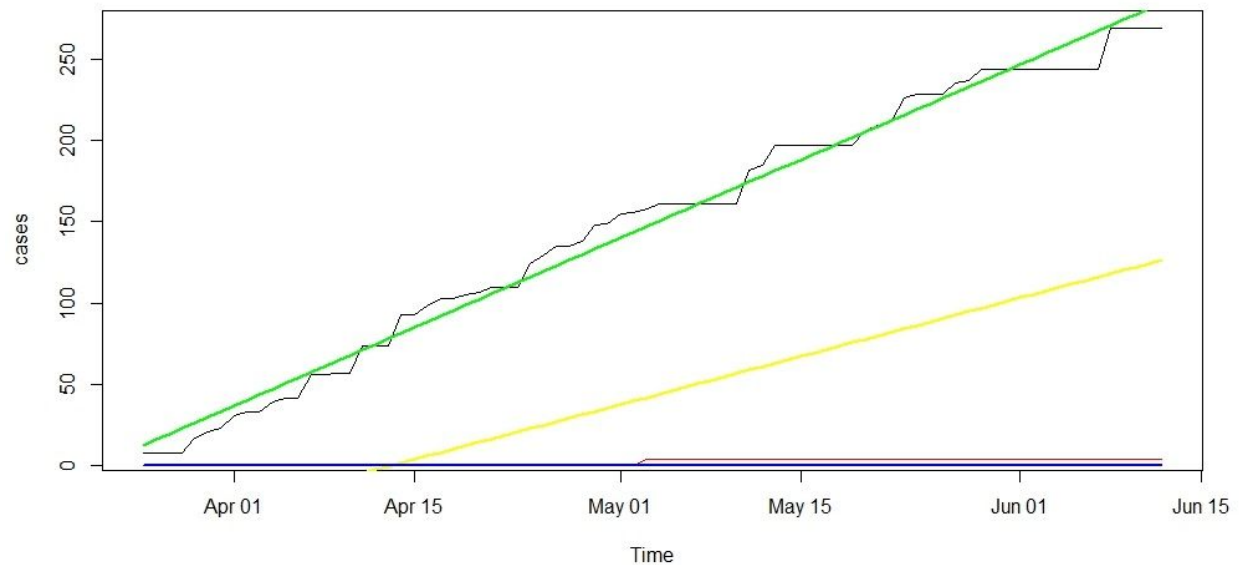
Residuals:
    Min       1Q   Median       3Q      Max
-39.881 -19.556   0.006  19.581  40.393

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -42.505      5.269   -8.067 6.97e-12 ***
trend           2.112      0.113  18.692 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 23.34 on 78 degrees of freedom
Multiple R-squared:  0.8175,    Adjusted R-squared:  0.8152
F-statistic: 349.4 on 1 and 78 DF, p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.Newport$date, format = "%m/%d/%y"), mod$fitted.values, col="yellow",
+       lwd=2)
> |
```

The deaths the county saw per day was 2 as part of the trend analysis highlighted by the yellow line on the plot. For Newport fortunately, the slope of the cases is flatter than the slope for the deaths unlike some of the other counties where it was the opposite.



```
> # Trend for Newport County Deaths Relative
> mod_deaths4 <- lm(deaths_Kent/82082 ~ trend, data = Coronavirus_Cases.RI.Newport)
> summary(mod_deaths4)

Call:
lm(formula = deaths_Kent/82082 ~ trend, data = Coronavirus_Cases.RI.Newport)

Residuals:
    Min       1Q   Median       3Q      Max
-0.0050405 -0.0034375 -0.0006786  0.0030962  0.0090655

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -6.304e-03  8.866e-04  -7.11 4.85e-10 ***
trend        2.984e-04  1.902e-05  15.69 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

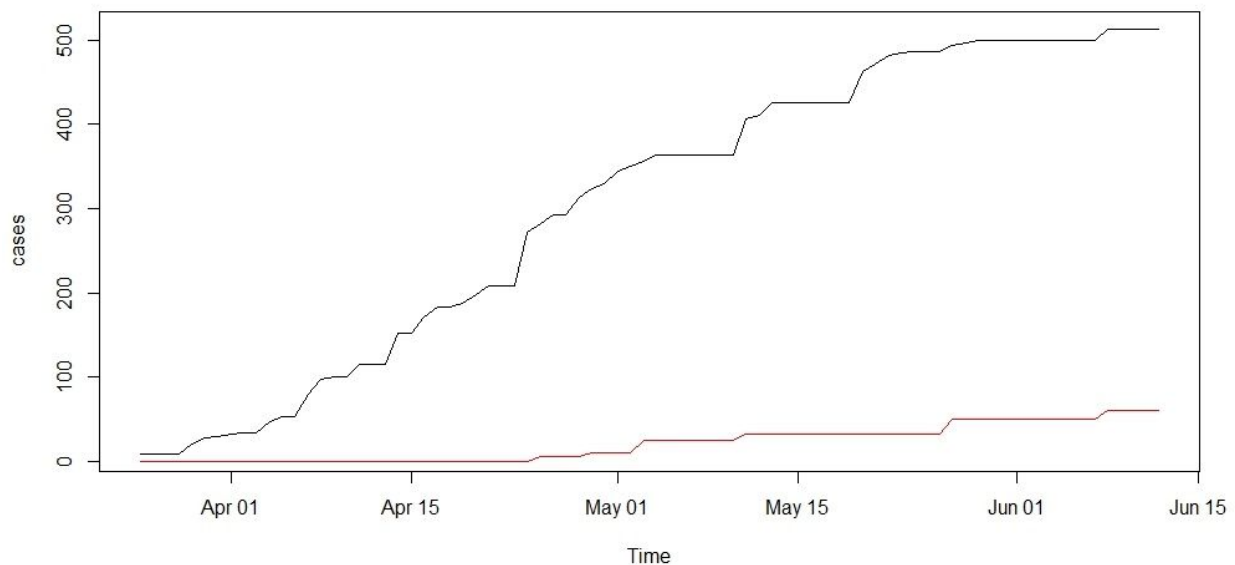
Residual standard error: 0.003928 on 78 degrees of freedom
Multiple R-squared:  0.7594,    Adjusted R-squared:  0.7563
F-statistic: 246.2 on 1 and 78 DF, p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.Newport$date, format = "%m/%d/%y"), mod_deaths4$fitted.values, col
="blue", lwd=2)
> |
```

The deaths proportional to the county's population is about 30 deaths which is higher than Kent despite its relative cases being smaller than Kent's. Nonetheless, the deaths are still lower than the deaths in Bristol and Providence.

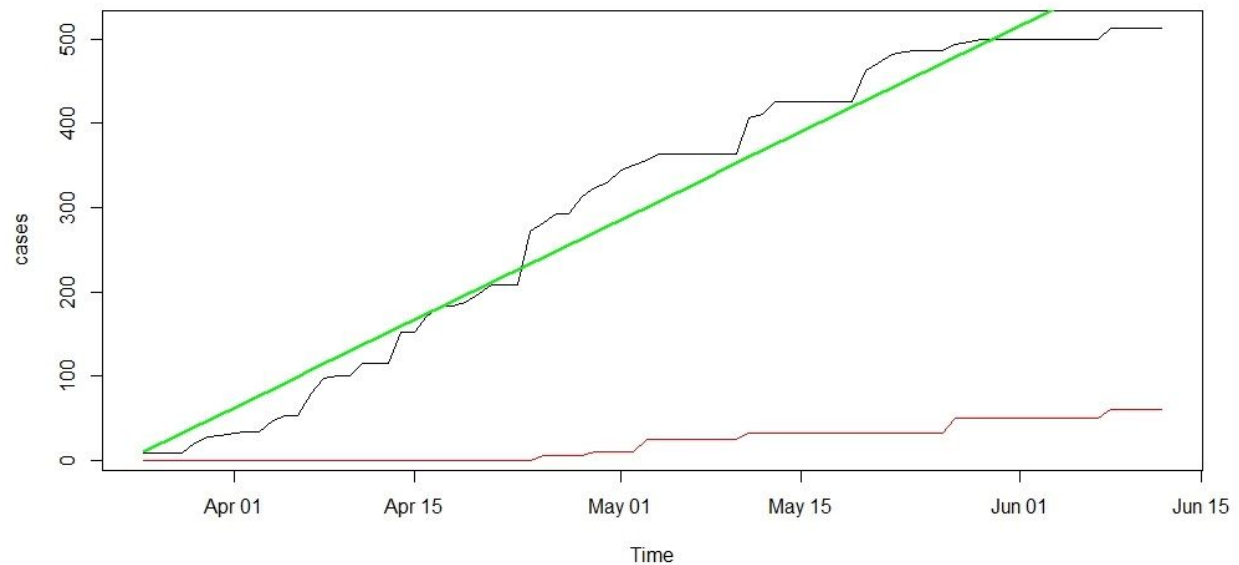
WASHINGTON

```
> # Washington County
> Coronavirus_Cases.RI.washington <- Coronavirus_Cases %>% filter(state == 'Rhode Island', county=='Washington')
> plot(as.Date(Coronavirus_Cases.RI.washington$date, format="%m/%d/%y"), Coronavirus_Cases.RI.washington$cases, type="l", xlab="Time", ylab="cases")
> lines(as.Date(Coronavirus_Cases.RI.washington$date, format="%m/%d/%y"), Coronavirus_Cases.RI.washington$deaths, col="red")
> |
```



This illustration shows the Coronavirus Cases in Washington County from April to June with the deaths as the red line. For about every 149 cases, there were 2 deaths on average.

cases	deaths	trend
Min: 9.00	Min: 0.00	Min: 1.0
1st Qu: 143.0	1st Qu: 0.00	1st Qu: 20.75
Median: 359.5	Median: 25.00	Median: 40.50
Mean: 304.2	Mean: 21.21	Mean: 40.50
3rd Qu: 485.2	3rd Qu: 32.00	3rd Qu: 60.25
Max: 513.0	Max: 61.00	Max: 80.00



```
> # Trend for Washington County Cases Absolute
> Coronavirus_Cases.RI.washington$trend <- 1:80
> mod <- lm(cases ~ trend, data = Coronavirus_Cases.RI.washington)
> summary(mod)

Call:
lm(formula = cases ~ trend, data = Coronavirus_Cases.RI.washington)

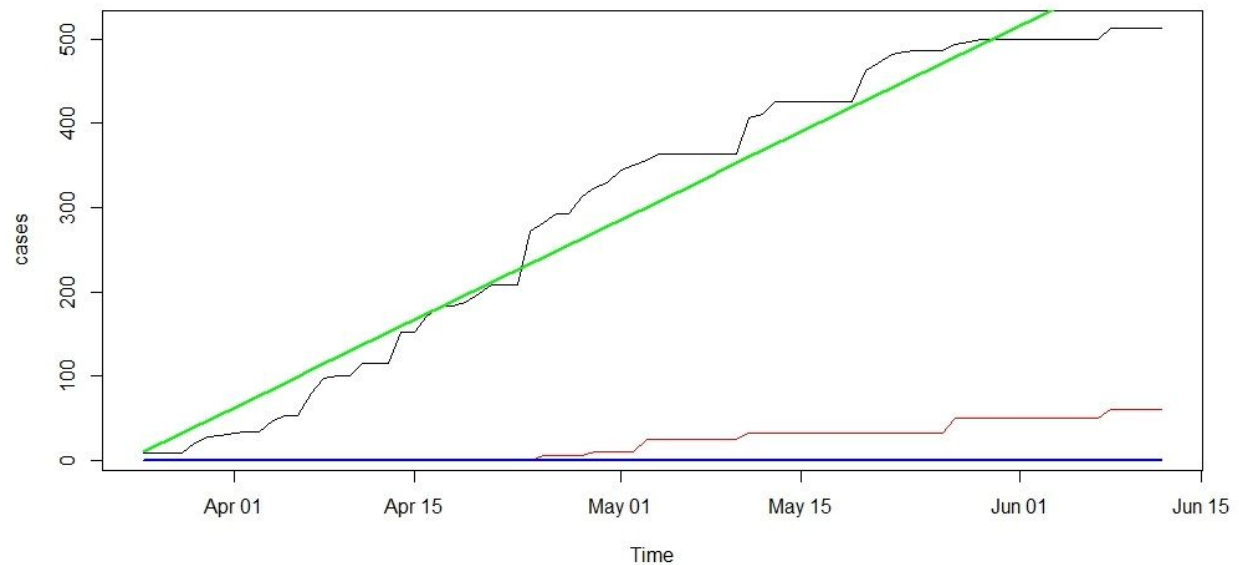
Residuals:
    Min       1Q   Median       3Q      Max
-84.889 -26.429  -2.707   35.409   58.361

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   3.1266     8.3359   0.375   0.709
trend         7.4345     0.1788  41.580 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 36.93 on 78 degrees of freedom
Multiple R-squared:  0.9568,    Adjusted R-squared:  0.9563
F-statistic: 1729 on 1 and 78 DF,  p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.washington$date, format = "%m/%d/%y"), mod$fitted.values, col="green",
+       lwd=2)
> |
```

Washington sees 7 cases per day from April to June plotted through the green line.



```

> # Trend for Washington County Cases Relative
> mod <- lm(cases/125577 ~ trend, data = Coronavirus_Cases.RI.washington)
> summary(mod)

Call:
lm(formula = cases/125577 ~ trend, data = Coronavirus_Cases.RI.washington)

Residuals:
    Min       1Q   Median       3Q      Max
-6.760e-04 -2.105e-04 -2.156e-05  2.820e-04  4.647e-04

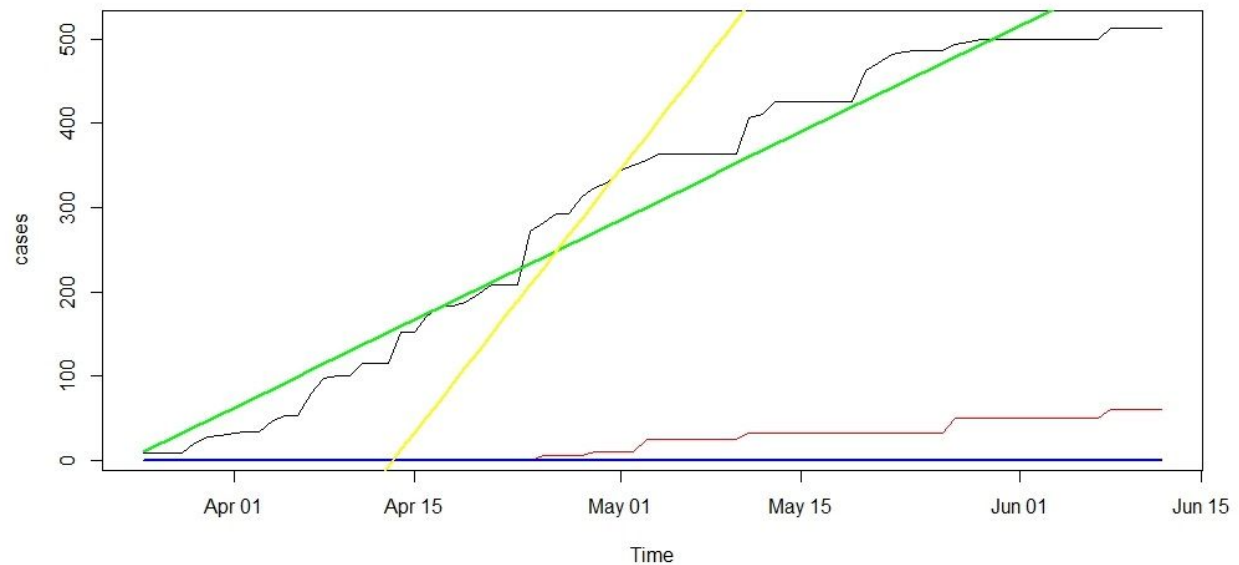
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.490e-05  6.638e-05   0.375   0.709
trend        5.920e-05  1.424e-06  41.580 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.0002941 on 78 degrees of freedom
Multiple R-squared:  0.9568,    Adjusted R-squared:  0.9563
F-statistic: 1729 on 1 and 78 DF, p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.washington$date, format = "%m/%d/%y"), mod$fitted.values, col="blue", lwd=2)
>

```

In relative terms, the county's cases are about 6 which is slightly higher than Newport's cases.



```
> # Trend for Washington County Deaths Absolute
> deaths_washington <- cumsum(Coronavirus_Cases.RI.washington$deaths)
> mod <- lm(deaths_washington ~ trend, data = Coronavirus_Cases.RI.washington)
> summary(mod)

Call:
lm(formula = deaths_washington ~ trend, data = Coronavirus_Cases.RI.washington)

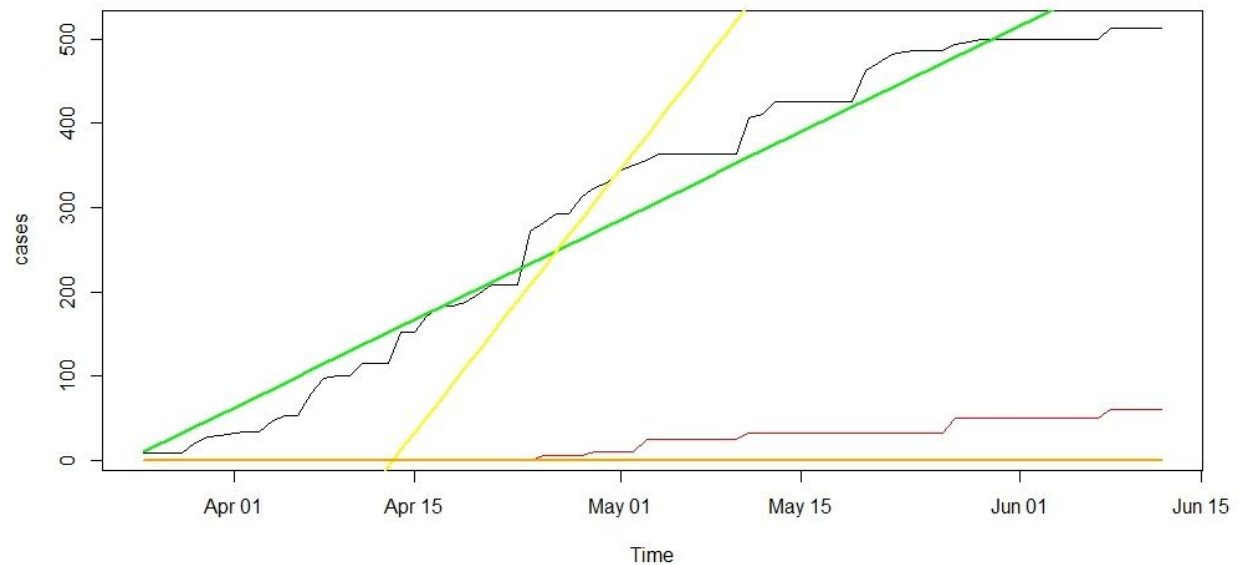
Residuals:
    Min       1Q   Median       3Q      Max
-297.18 -205.18  -53.47   186.25   529.38

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -398.114    52.107   -7.64 4.67e-11 ***
trend         19.572     1.118   17.51 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 230.8 on 78 degrees of freedom
Multiple R-squared:  0.7972,    Adjusted R-squared:  0.7946
F-statistic: 306.6 on 1 and 78 DF,  p-value: < 2.2e-16

> lines(as.Date(Coronavirus_Cases.RI.washington$date, format = "%m/%d/%y"), mod$fitted.values, col="yellow", lwd=2)
> |
```

The deaths are about 20 deaths after conducting the trend analysis. The deaths are more than twice the cases as shown by the steepness of the slope as opposed to the slope of the cases.



```
> # Trend for Washington County Deaths Relative
> mod_deaths5 <- lm(deaths_washington/125577 ~ trend, data = Coronavirus_Cases.RI.washington)
> summary(mod_deaths5)

Call:
lm(formula = deaths_washington/125577 ~ trend, data = Coronavirus_Cases.RI.washington)

Residuals:
    Min       1Q   Median       3Q      Max
-0.0023665 -0.0016339 -0.0004258  0.0014832  0.0042156

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.0031703  0.0004149   -7.64 4.67e-11 ***
trend         0.0001559  0.0000089   17.51 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.001838 on 78 degrees of freedom
Multiple R-squared:  0.7972,    Adjusted R-squared:  0.7946
F-statistic: 306.6 on 1 and 78 DF,  p-value: < 2.2e-16

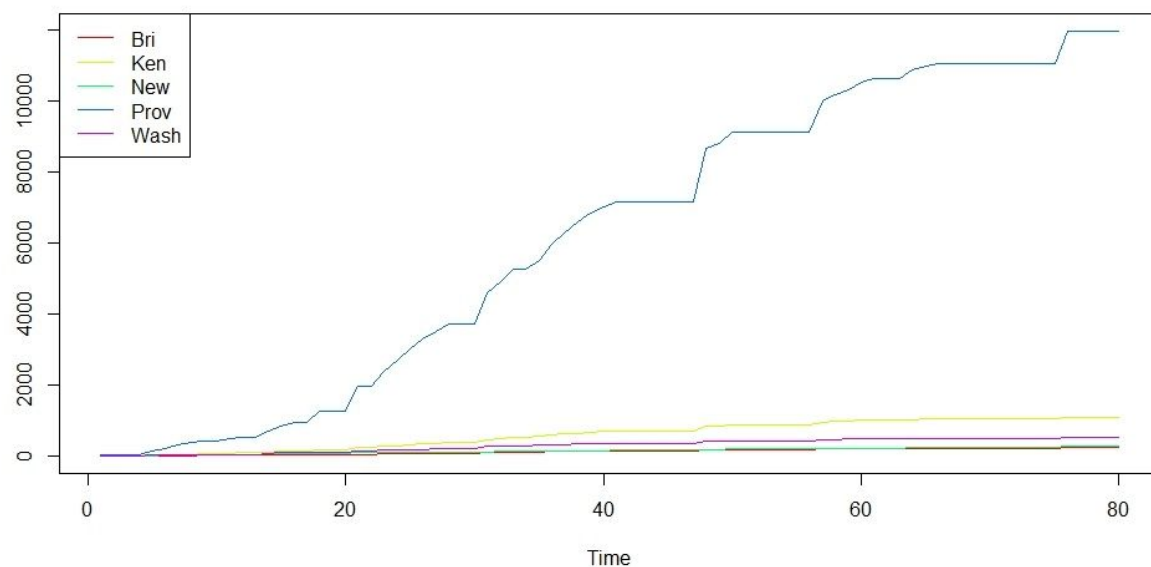
> lines(as.Date(Coronavirus_Cases.RI.washington$date, format = "%m/%d/%y"), mod_deaths5$fitted.values, col="orange", lwd=2)
> |
```

When taking the accumulated deaths and dividing by the county's population and doing the trend analysis, we find that the deaths are relatively about 16. It's slightly higher than Kent but lower than the rest of the counties.

```

> # Time series for the counties cases
> Bristol_cases <-subset(Rhode_Island,Rhode_Island$county=="Bristol")
> Kent_cases<-subset(Rhode_Island,Rhode_Island$county=="Kent")
> Newport_cases <-subset(Rhode_Island,Rhode_Island$county=="Newport")
> Providence_cases <-subset(Rhode_Island,Rhode_Island$county=="Providence")
> Washington_cases <-subset(Rhode_Island,Rhode_Island$county=="Washington")
> ts.plot(data.frame(Bristol_cases=Bristol$cases,
+                   Kent_cases=Kent$cases,Newport_cases=Newport$cases,
+                   Providence_cases=Providence$cases,
+                   Washington_cases=Washington$cases), gpars=list(col=rainbow(5)))
> legend("topleft", legend=c("Bri","Ken","New",
+                           ,"Prov","wash"),col=rainbow(5), lty=1)
> |

```

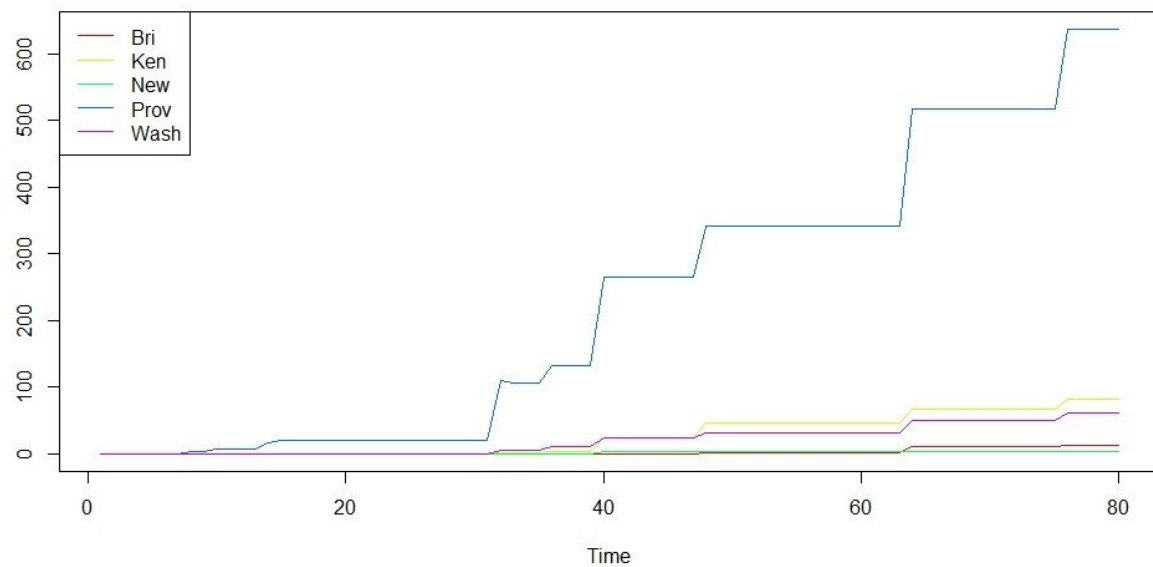


This is the time series plot comparing the cases among the 5 counties. The comparison is done in absolute terms and not taking into account it's respective populations. Providence had the most cases being 179 while Bristol had the lowest cases, being 3, slightly less than Newport.

```

> # Time series for the counties deaths
> Bristol<-subset(Rhode_Island,Rhode_Island$county=="Bristol")
> Kent<-subset(Rhode_Island,Rhode_Island$county=="Kent")
> Newport<-subset(Rhode_Island,Rhode_Island$county=="Newport")
> Providence<-subset(Rhode_Island,Rhode_Island$county=="Providence")
> Washington<-subset(Rhode_Island,Rhode_Island$county=="Washington")
> ts.plot(data.frame(Bristol=Bristol$deaths,
+                   Kent=Kent$deaths,Newport=Newport$deaths,
+                   Providence=Providence$deaths,
+                   Washington=Washington$deaths), gpars=list(col=rainbow(5)))
> legend("topleft", legend=c("Bri","Ken","New",
+                           ,"Prov","Wash"),col=rainbow(5), lty=1)
> |

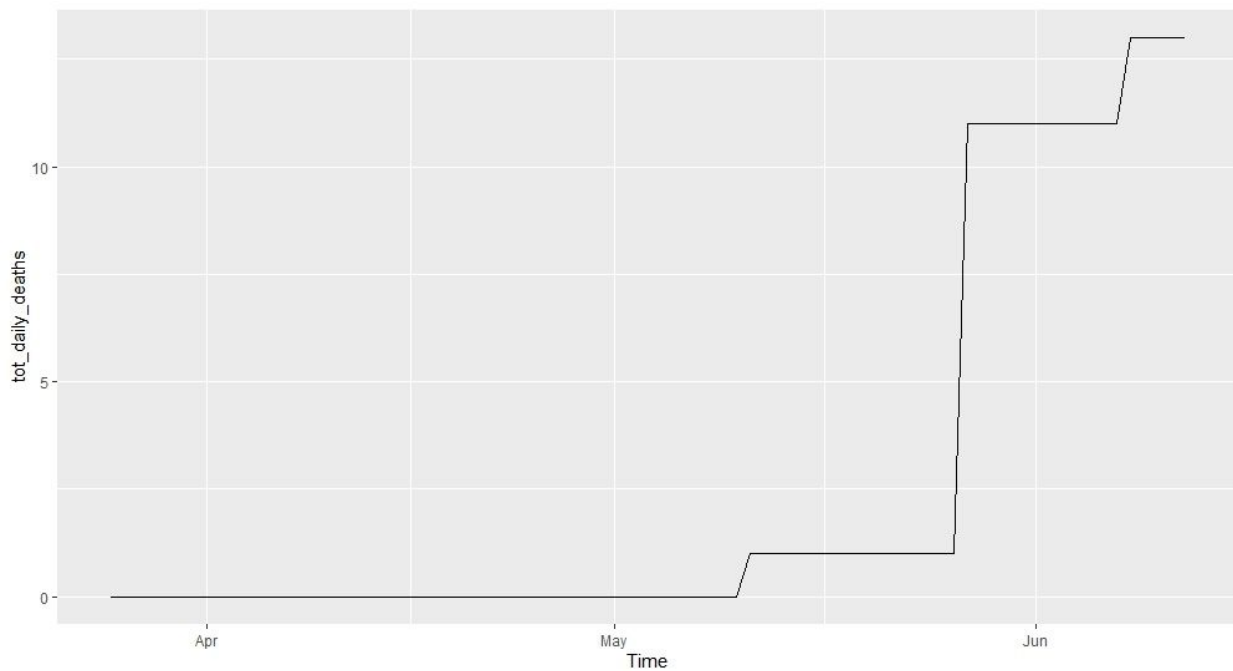
```



Similar to the previous plot, this is the time series plot compares the deaths among the 5 counties. Providence has the most deaths, being 215 while Newport had the least deaths, being 2.

CUMULATIVE DEATHS OF THE 5 COUNTIES

```
> #Cumulative deaths
> Bristol_deaths <- Coronavirus_Cases.Rhode_Island %>% filter(county == 'Bristol') %>% group_by(date) %>% summarise(tot_daily_deaths = sum(deaths))
> ggplot(Bristol_deaths, aes(x = as.Date(date, format = "%m/%d/%Y"), y = tot_daily_deaths)) + geom_line() + xlab("Time")
> summary(Bristol_deaths)
  date          tot_daily_deaths
Length:80
Class :character
Mode  :character
Min.   : 0.000
1st Qu.: 0.000
Median : 0.000
Mean   : 2.663
3rd Qu.: 1.000
Max.   :13.000
```

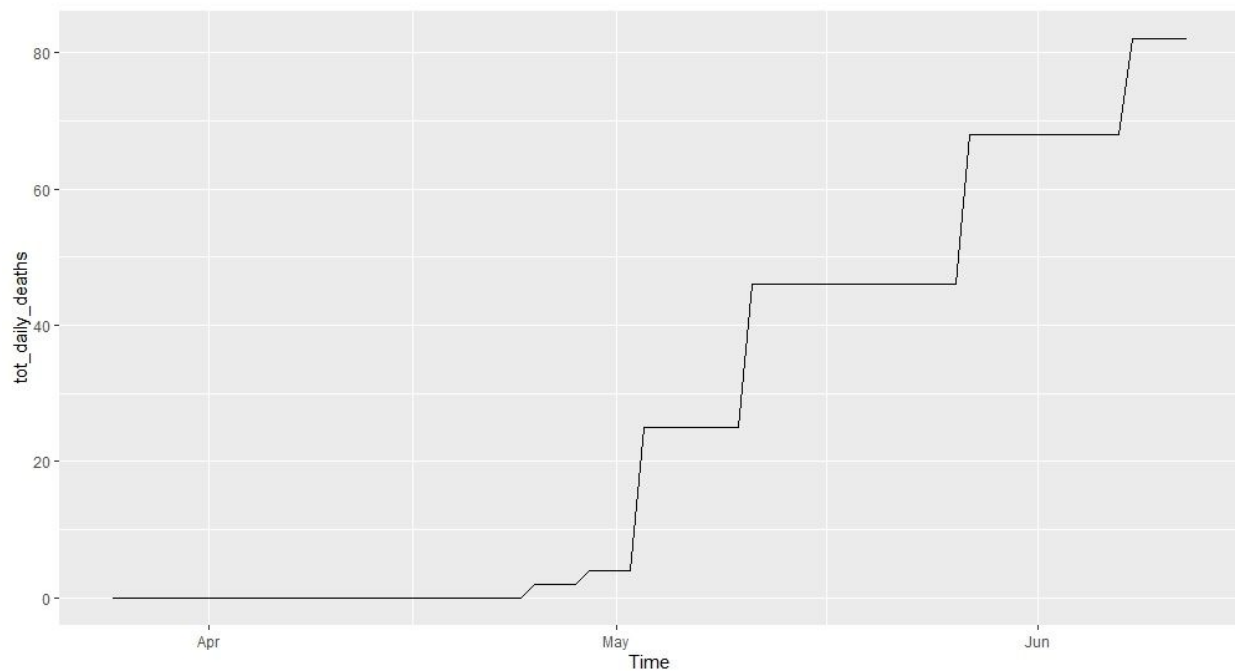


Bristol did not see deaths until early to mid May and it would continue to increase going into June.

```

> Kent_deaths <- Coronavirus_Cases.Rhode_Island %>% filter(county == 'Kent') %>% group_by(date) %>% summarise
(tot_daily_deaths = sum(deaths))
> ggplot(Kent_deaths, aes(x = as.Date(date, format = "%m/%d/%Y"), y = tot_daily_deaths)) + geom_line() + xlab
("Time")
> summary(Kent_deaths)
      date      tot_daily_deaths
Length:80      Min.   : 0.00
Class :character 1st Qu.: 0.00
Mode  :character Median :25.00
                Mean  :27.32
                3rd Qu.:46.00
                Max.  :82.00

```

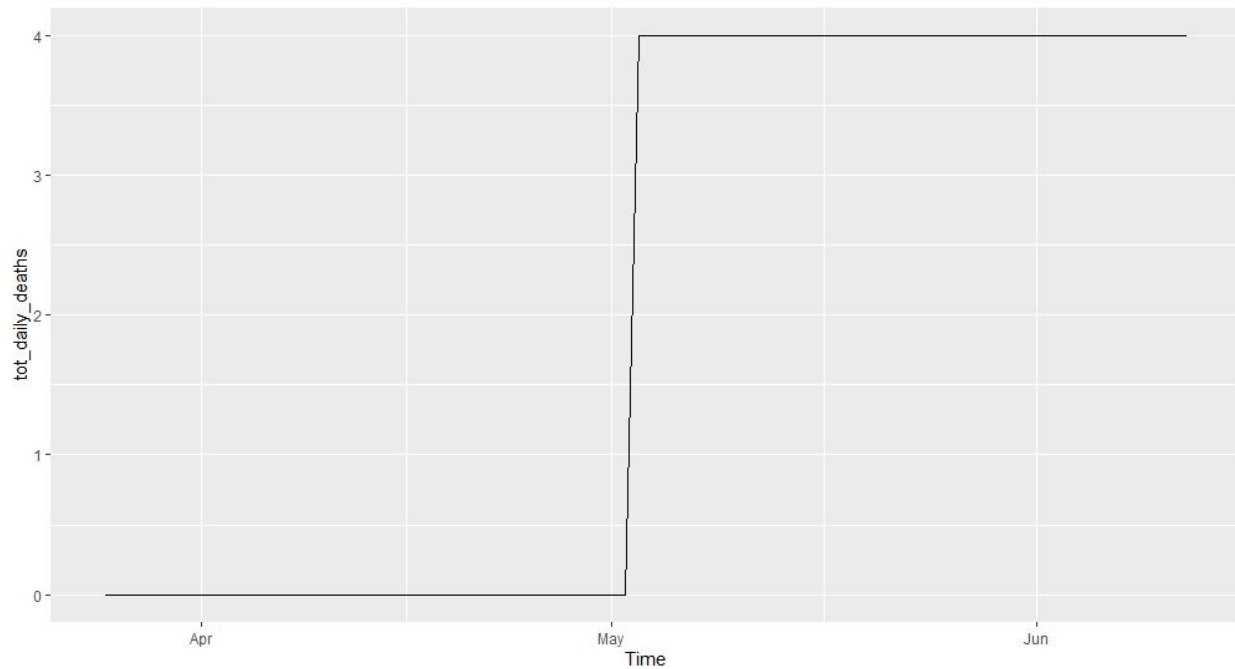


It looks like Kent County started seeing deaths before May. It looks like a pattern for the month of May in a staircase like fashion. The deaths would increase and remain constant for a period of time before increasing again and repeating the cycle.

```

> Newport_deaths <- Coronavirus_Cases.Rhode_Island %>% filter(county == 'Newport') %>% group_by(date) %>%
  summarise(tot_daily_deaths = sum(deaths))
> ggplot(Newport_deaths, aes(x = as.Date(date, format = "%m/%d/%Y"), y = tot_daily_deaths)) + geom_line()
+ xlab("Time")
> summary(Newport_deaths)
      date      tot_daily_deaths
Length:80      Min.      :0.00
Class :character 1st Qu.:0.00
Mode  :character Median :4.00
              Mean  :2.05
              3rd Qu.:4.00
              Max.  :4.00

```

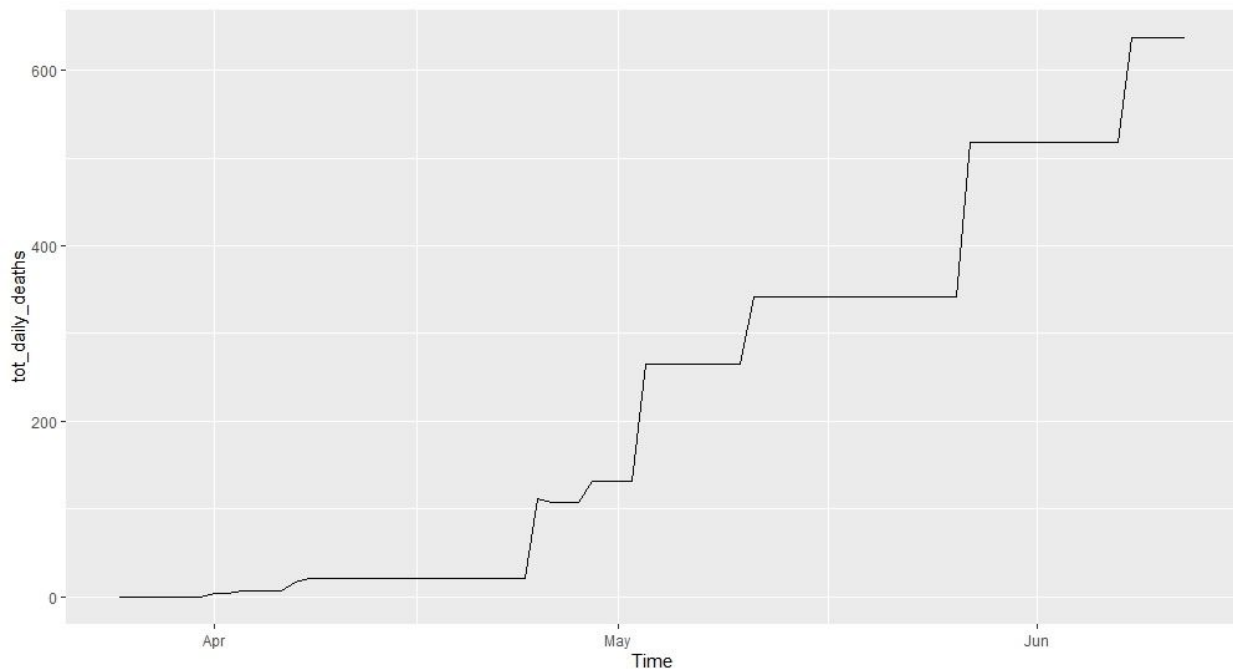


Up until the beginning of May, there were no deaths. The plot shows the deaths going from 0 to 4 and the curve stays flat the whole month of May and going into June.


```

> Providence_deaths <- Coronavirus_Cases.Rhode_Island %>% filter(county == 'Providence') %>% group_by(date) %>% summarise(tot_daily_deaths = sum(deaths))
> ggplot(Providence_deaths, aes(x = as.Date(date, format = "%m/%d/%Y"), y = tot_daily_deaths)) + geom_line() + xlab("Time")
> summary(Providence_deaths)
      date      tot_daily_deaths
Length:80      Min.   : 0.0
Class :character 1st Qu.: 20.0
Mode  :character Median :265.0
                Mean  :229.3
                3rd Qu.:342.0
                Max.   :637.0

```

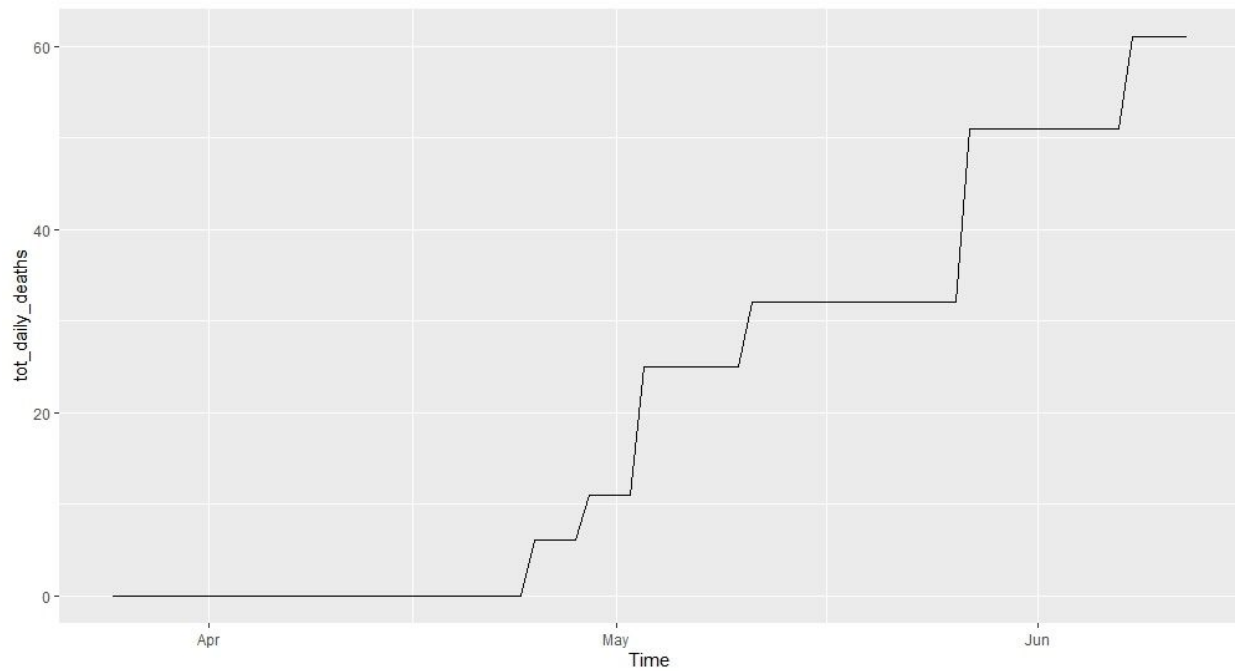


Unlike the other counties, Providence saw deaths early at the beginning of April which would make sense as the 1st cases arrived in Providence. When looking at the beginning of May to mid-May, it seems like the rate of deaths slows down. We do see towards the end of May, the rate of the cumulative deaths increases, being more than the previous time periods. The rate does slow down during the beginning of June as the curve flattens going into June.

```

MAX.      :657.0
> washington_deaths <- Coronavirus_Cases.Rhode_Island %>% filter(county == 'washington') %>% group_by(date) %>% summarise(tot_daily_deaths = sum(deaths))
> ggplot(washington_deaths, aes(x = as.Date(date, format = "%m/%d/%Y"), y = tot_daily_deaths)) + geom_line() + xlab("Time")
> summary(washington_deaths)
  date      tot_daily_deaths
Length:80      Min.      : 0.00
Class :character 1st Qu.:  0.00
Mode  :character Median :25.00
                Mean  :21.21
                3rd Qu.:32.00
                Max.   :61.00

```



Washington county would see no deaths until shortly before May. The rate of the cumulative deaths increases significantly going into May and end of May before slowing down going into June.

CONCLUSION

Since the spring, I have struggled to determine a dataset suitable for my research involving time series until I decided to do the COVID-19 dataset. It was also since the spring, I have been on state orders, now Title 32 through the Air National Guard helping with the COVID-19 relief efforts. While it was time consuming along with finishing up my last semester, it encouraged me to know more about the disease to better understand it as well as improve my approach to it and the capstone provided the perfect opportunity.

Researching on this dataset as well as conducting the data analysis on it has been a rewarding experience for me. From before the beginning of the summer to now, I have struggled yet nonetheless persisted through the trials and tribulations I faced on a daily basis. I have learned to utilize R more efficiently when it comes to regression, visualization, and time series in a way that I feel I would be able to apply to other topics. It's a testament to saying that my growth has been monumental.

After going through the analysis on R, I would say that there should be more emphasis on the relativity of the cases and deaths rather than the absolute. People should take into account the population. Oftentimes, I hear repeatedly that cases are going down or vice versa as well as dismissing the death rate when taking into account the whole country. It's a complacent mindset that has led to the deaths continually rising. It should be considered if we hear about the need to contain the spread. It's noted that some of the bigger counties were doing better than the smaller counties when taking into account the respective population. With that being said, we need to assess the percentages and that comes with changing our approach.

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