



ECE - 579A

Data Analysis Report on COVID-19 Dataset (John Hopkins University)

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1. Overview

This is a data analysis report on covid19 dataset from John Hopkins University which gives few insights about the countries - New Zealand, Germany, South Korea and Japan. The report also analyzes few predictive epidemic models which claim to be suitable for epidemics or pandemics like covid19. We have implemented couple of models which are capable of simulating pandemics like covid19, to get the parameters which can tell about the factors like growth rate, reproduction number and control measures. Power Law and Incidence Decay with Exponential Adjustment (IDEA) are the two models which we considered for the covid19 time series dataset to see if these models can fit the pandemic and produce numbers for the above-mentioned factors. Considering the new confirmed cases for both the models, graphs were plotted which show the curves of actual cases and the cases predicted by the model. The report focuses on the models and the parameters they take into consideration for fitting the curve.

2. Covid19 Dataset – John Hopkins University

The dataset contains information about the novel corona virus and the major attributes given in the dataset are related to total infected, cured and deaths caused due to the virus all over the world. The entire dataset spans over 6 months (approx.), starting from 21st January 2020 to 14th July 2020, with utmost 175 observations for every country. The dataset gives a clear idea about the facts like when the first infected, recovered or death case was recorded in a country. John Hopkins University also maintains a separate log of these attributes for the United States which can be helpful to perform exploratory data analysis on U.S.

We mainly focused on New Zealand, Germany, Japan and South Korea by extracting total confirmed cases, date columns of the countries and generated CSV's with confirmed new cases per day which served as input files for our analysis.

3. Modelling

We implemented couple of models which have the parameters like pandemic growth rate, reproduction number and outbreak control measures taken in order to contain the spread of corona virus. The first model that we implemented was based on Power Law. This model can represent the spread of the disease in a country by considering the exponent as growth rate which helps to compare different phases of the corona virus diffusion in different countries. Incidence Decay with Exponential Decay Model - is the model which we analyzed to see the number of many people, on average, does one person with corona virus infect which is termed as Reproduction number. The report explains about the models which claim to simulate the outbreak dynamics and have been tested for accuracy on the countries like New Zealand which almost had no new cases when the analysis was performed. The following sections provide a detailed description about the models.

3.1. Power Law

Power law is defined by the equation as shown below:

$$n(t) = At^\gamma \quad (eq. 1)$$

The above equation can represent the total covid cases curve which gives the value of gamma (γ) for the considered time window. So, we say that with the relative change in γ or the rapidity of the disease, the cumulative number of cases change accordingly. Through the help of power law, we can compare the extent of the disease spread in the countries by comparing the rapidity (γ) for those countries. We can do that by implementing the piece wise approximation for cumulative cases curve and see the change in γ across the period for which data is available. This is exactly what we worked on and the results of it has been discussed in the implementations section of the report.

3.2. Incidence Decay with Exponential Adjustment Model (IDEA)

To know what Incidence Decay with Exponential Adjustment (IDEA) model is about, we need to understand a bit about Farr's law and reproduction number, R_0 . Farr's law of epidemics or Farr's law in short states that the growth and decay of the epidemics follows a bell-shaped curve and takes a symmetrical pattern. However, to understand the strength of infectious disease, we need to know about the measure of spread of the disease which is very well defined by the reproduction number.

Reproduction number basically represents the potential with which the disease can be transmitted. More mathematically, we can define it as the number of secondary infections generated by one primary infection in a susceptible population. If $R_0 > 1$, it means that more than one infection is being caused by the primary infection which suggests the disease is spreading rapidly. On the contrary, if $R_0 < 1$, it suggests that one primary infection is spreading the disease to less than one person which means that the disease will decay and ultimately die out. IDEA model explicitly takes reproduction number as a parameter and estimates the rapidity of the disease. It also considers the second parameter, 'd', which is termed as the control parameter. The control parameter has an abstract sense which considers the preventive measures taken by the country, social distancing, lockdown and many other factors which vary from country to country. By implementing IDEA model, this factor can be represented as a number but cannot be compared with the values of other countries, as the control measures taken are different in different countries and are unknown from the dataset.

According to the IDEA model, the new cases are represented by the following equation:

$$I(t) = \left(\frac{R_0}{(1+d)^t} \right)^t \quad (eq. 2)$$

R_0 : Reproduction number,

d : Control measures,

t : Day for which the cases are being computed.

One of the researchers, John Brownlee, who worked on the measurement of infectiousness of an epidemic defined about the family of curves from which the new observed cases is expressed by:

$$I(t) = e^{-(At^2+Bt+C)} \quad (eq. 3)$$

where t is the time in days and A, B, C are constants. So, he inferred that if $I(t)$ in IDEA model is compared to this expression by which we get,

$$A = \ln(1+d) \quad (eq. 4)$$

$$B = \ln R_0 \quad (eq. 5)$$

$$C = 0$$

Thus, by doing the basic math behind these equations, we can get the values of R_0 and d from it. Extracting R_0 and d for a country is of very crucial importance as it gives a good way to express the spread of the disease as well as how it is being contained by the country. The values of R_0 and d have been extracted and the results can be seen in the implementation part of the report.

4. Implementation of Power Law on Covid19 dataset

Power law distribution was set to fit the covid data for 4 different countries which were mentioned earlier. This was mainly done to compare different countries in terms of the rapidity of spread of the disease which is given by the exponent. In the power law equation, as mentioned above, the power law exponent γ was computed for countries that we took under consideration i.e. New Zealand, South Korea, Japan and Germany. To fit the power law to the covid dataset, we considered total cases, performed the piece-wise approximation for every 10 days and observed the

different γ values. This was helpful to understand the rate of change of rapidity of the disease in different countries over an interval of time. Here we took the overall duration which came out to be 170 days as the we considered the data till 10th July. The observed gamma values of the countries for the entire duration have been represented in the table shown below:

Days	New Zealand	South Korea	Japan	Germany
1 - 10	0	1.728	2.113	2.363
11 - 20	0	1.299	0.4322	0.6922
21 - 30	0	4.666	3.648	0
31 - 40	0	9.912	3.106	13.97
41 - 50	5.318	2.498	4.235	11.10
51 - 60	18.87	0.6604	2.507	12.97
61 - 70	12.57	0.689	5.56	7.451
71 - 80	4.617	0.464	7.428	3.507
81 - 90	0.884	0.176	4.666	1.596
91 - 100	0.263	0.1009	2.294	1.041
101 - 110	0.083	0.1166	0.9	0.5723
111 - 120	0.05	0.209	0.358	0.4139
121 - 130	0	0.429	0.294	0.3159
131 - 140	0	0.5179	0.320	0.2632
141 - 150	0.05	0.534	0.479	0.3087
151 - 160	0.205	0.538	0.7299	0.3998
161 - 170	0.163	0.688	1.805	0.3351

Table.1: Gamma Values for New Zealand, South Korea, Japan and Germany.

The above table represents different gamma values for 4 countries after performing piece wise approximation over a range of 10 days.

Observations : How to interpret the values in above table?

Considering the case of New Zealand, the first covid19 case was recorded after 40 days from 21st January. We have considered the cases of New Zealand from 41st day where the numbers started to increase drastically and implemented power law for every 10 days. From the time span between 41st – 50th days, the gamma value is 5.318 and it grew to 18.87 in range of days 51-60. Graphs for the same are shown below.

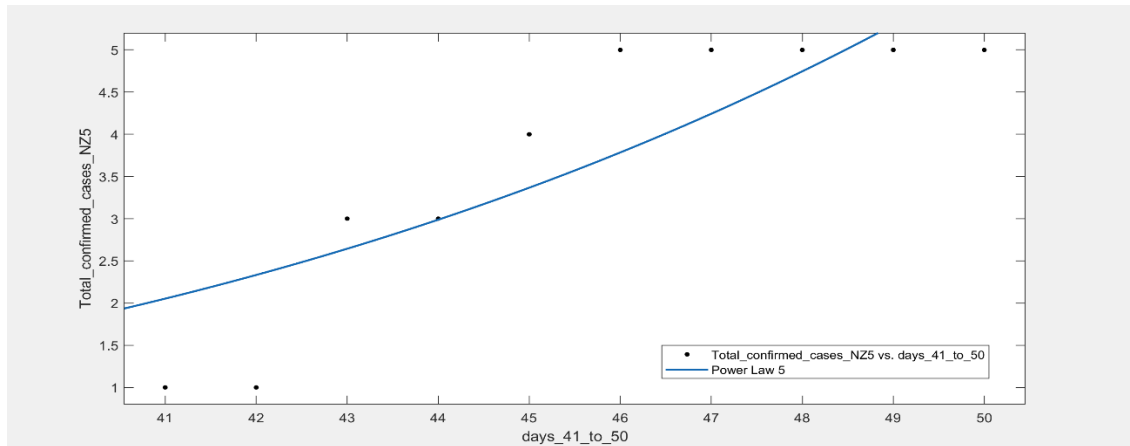


Fig.1 : New Zealand total confirmed cases from 41 to 50 days

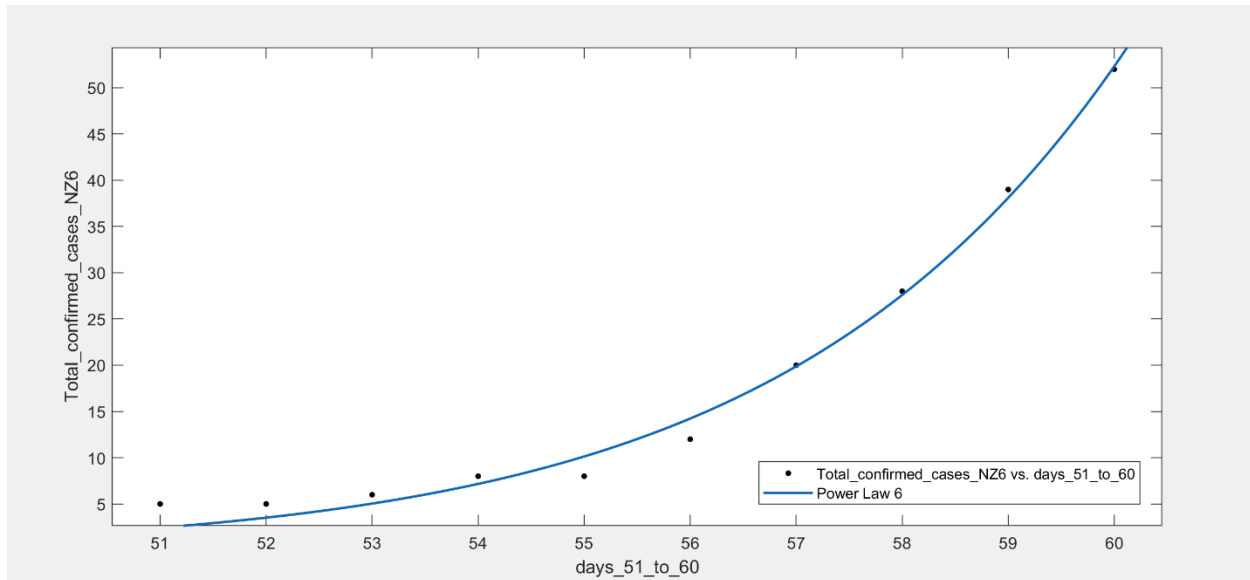


Fig.2 : New Zealand total confirmed cases from 51 to 60 days

From the above graphs, we can see that the total confirmed cases rose from 5 to around 50, which shows an increase of 10 times on 60th day. The gamma value for the above graph came out to be 18.87. Whereas in the next interval i.e. 61-70 days, we can see from the above table that the gamma value dropped down to 12.57. For this interval, let's see the graph for the same.

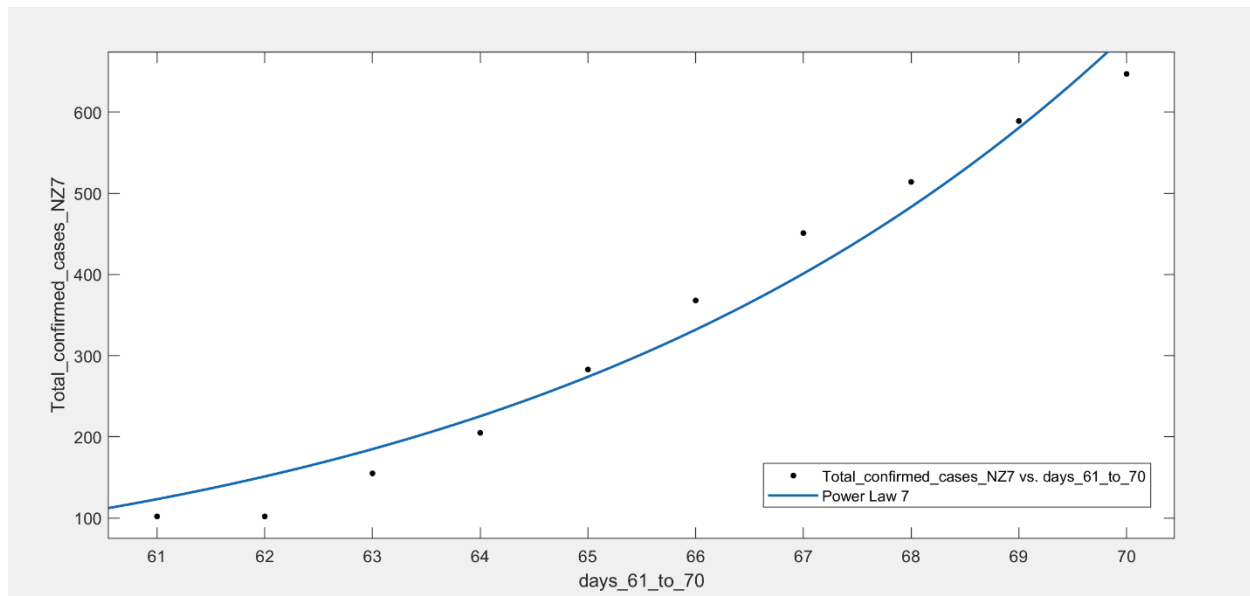


Fig.3 : New Zealand total confirmed cases from 61 to 70 days

The total number of confirmed cases for interval 61-70 goes from 100 to around 600 which is almost 6 times increase in the interval. Hence, we can infer the drop in the gamma value as well because the former increase was 10 times as compared to the latter one which was 6 times. Similarly, we can see that the gamma value for the next interval 71-80 is 4.617 which is again a significant drop. Let's analyse the total cases by looking at the graph for the same.

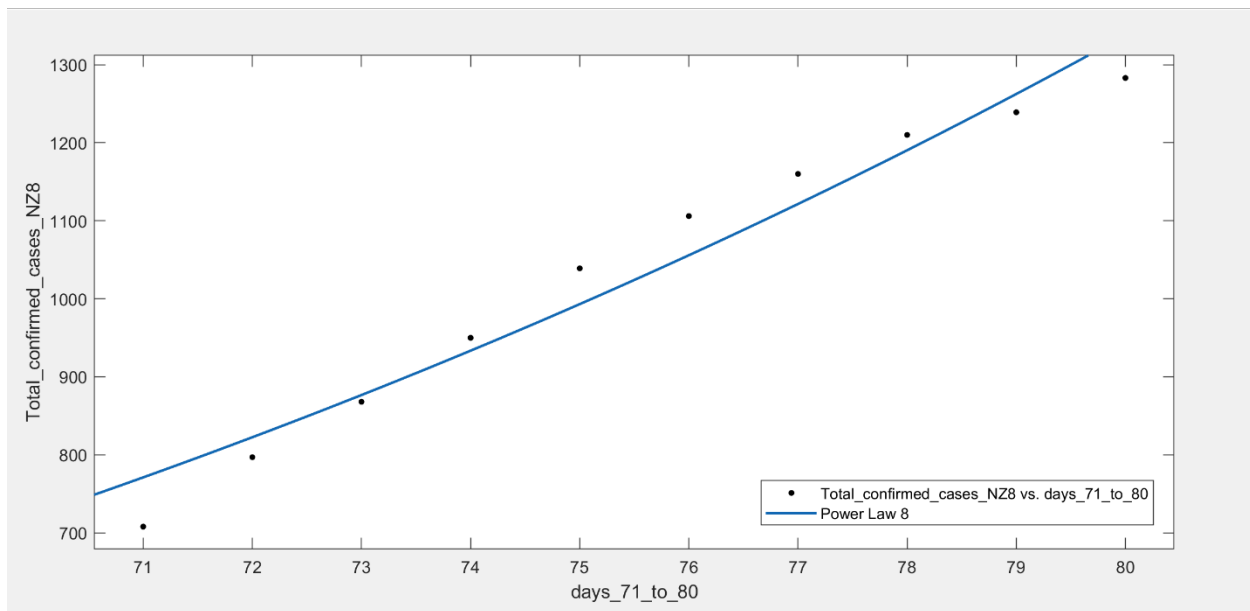


Fig.4 : New Zealand total confirmed cases from 71 to 80 days

The total confirmed cases for the interval 71-80 observed an increase from approximately 750 to 1300 which is almost 2 times increase and hence we can easily infer that the rate of increase of the cases has dropped as compared to the previous 10-day interval i.e. 51-60 and 61-70, hence the gamma value of 4.617. For New Zealand, the gamma value has been decreasing for the subsequent intervals and a gamma value of 0 in the table suggests that the curve has flattened for that 10 days interval. As we can see for the interval 121-130, the gamma value has come down to zero and graph for the same can be seen below.

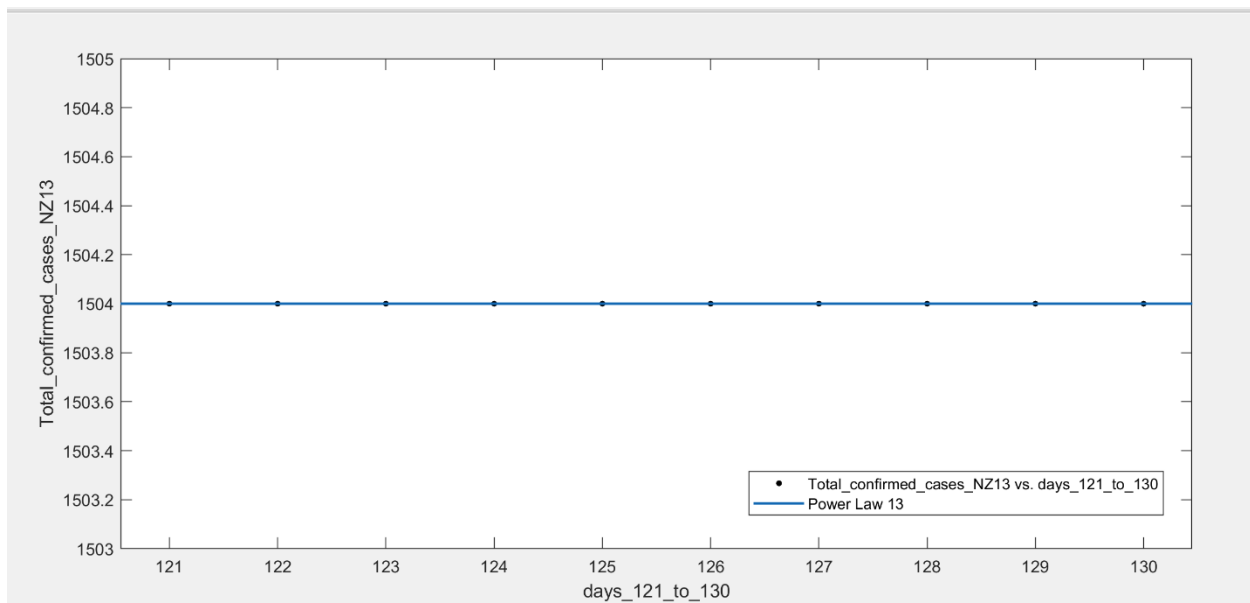


Fig.5 : New Zealand total confirmed cases from 121 to 130 days

Clearly, we can see that the curve has flattened as the gamma value tends to approach zero. Hence the rate of increase and decrease of the gamma value very clearly and concisely demonstrates the spread of the disease for that country. Similarly, we can see for the other countries as well.

For **South Korea**, the curve grew rapidly in the first few 10-day intervals but also it came even more quickly. The gamma value started to grow from 1.728 to 9.912 in the period of first 40 days and then it descended quickly to 2.49 in the next interval and after that it has stayed close to zero i.e. the curve has almost been flattening.

For **Japan**, the growth and descent of the gamma values has been happening on almost the same pace. The maximum gamma value was attained between 70-80 interval when it went till 7.428 and then it has descended in almost the next 40 days. But, in the first week of July, there has been a surge in the number of cases as the gamma value went to 1.805 after going to as low as 0.294.

For **Germany**, the trend saw a huge surge in the interval 30-40 where gamma value went as high as 13.97. It can be noted that for south Korea also, a similar surge in the cases was seen in the same period. The rate of increase has remained for constant for next 25-30 days and after that the cases have been decreasing gradually as the gamma value is decreasing at a medium pace. In the last 50-60 days, the total cases for Germany has been rising slowly and at a constant rate which means that it will slowly approach zero in the next 2 or more months.

[Graphs for all the intervals of 4 countries are given in outputs section of the report.]

5. Implementation of IDEA model

As discussed earlier, IDEA model engrains some crucial parameters that are important in describing the curve of an epidemic. According to Farr's law, any epidemic can be well described by a symmetrical bell-shaped curve. The IDEA model captures all these concepts and gives us a bell-shaped curve that can aptly describe the actual epidemic curve.

Now the question arises, why do we even need to simulate the curve using IDEA model, what good that will do to us? Well, if we see the power law, it just quantifies the rapidity of a disease in the country. But from IDEA model, we gain two parameters that very closely describes the epidemic i.e. Reproduction number - R_0 and control parameter - d . We can understand the control parameter from the fact that it is inversely proportional to the new cases that arise. In other words, we can say that with the increase in d , the number of new cases decreases. Now ' d ' can be considered as the combination of stringency factors such as lockdown, social distancing, preventive measures taken by the country, border closure and others. So, the main idea was to simulate the curve produced by the IDEA model to the new cases curve and extract out the reproduction number R_0 and d from equation. From the two equations, eq.1 and eq. 2, we easily extract the values of parameters R_0 and d which are very crucial in describing the epidemic. We replicated the above methodology for two countries New Zealand and Germany by considering the new cases of the countries starting from 22nd January to 14th July. We specifically took the bell-shaped parts of the new cases curve, simulated it with curve given by IDEA model and computed the values of R_0 and d . Below are the graphs shown which are considered for implementing IDEA model.

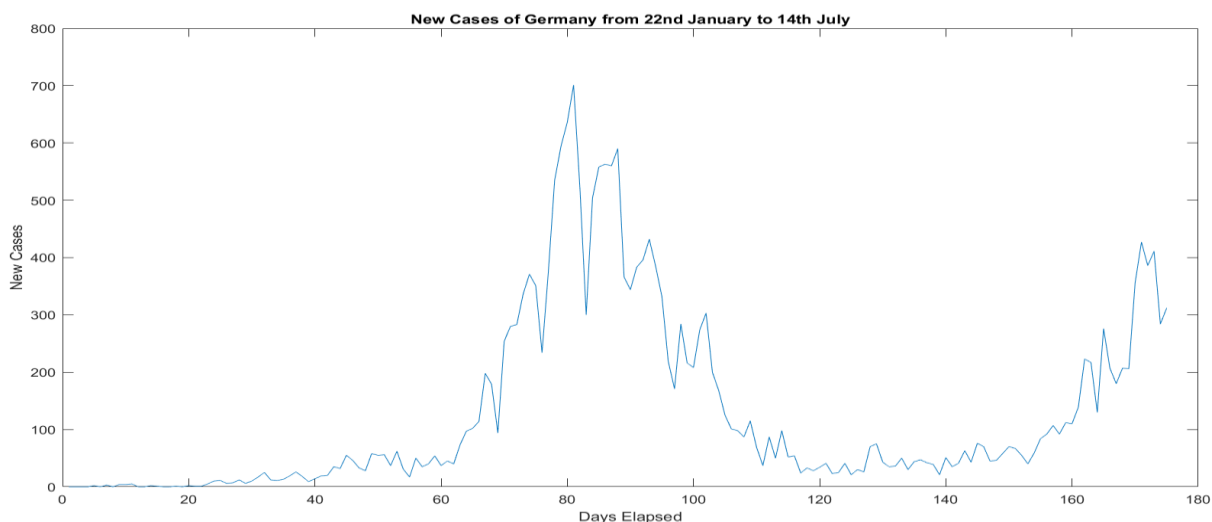


Fig.6 : New Cases of Germany from 22nd Jan to 14th July

Graph showing the first bell-shaped curve of Germany's new cases from 22nd March to 10th May:

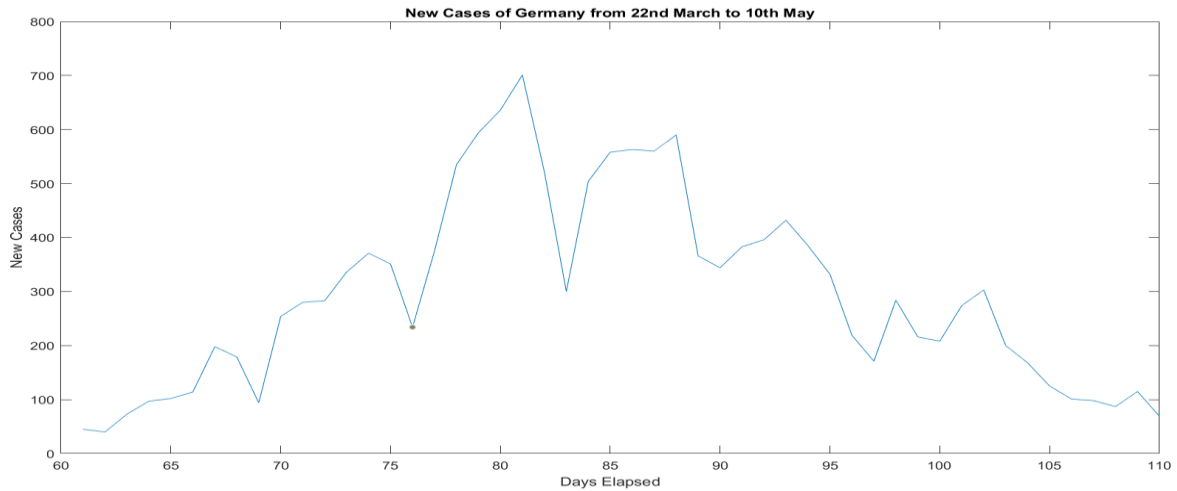


Fig.7 : New Cases of Germany from 22nd March to 10th May

New cases of Germany went down almost flat after 10th May and the numbers started to increase exponentially again from 22nd June. Assuming this second curve also to take the bell-shaped curve when the new cases decrease and flatten out, below is the graph showing the half bell-shaped curve of Germany new cases from 22nd March to 10th May:



Fig.8 : New Cases of Germany from 22nd June to 14th July

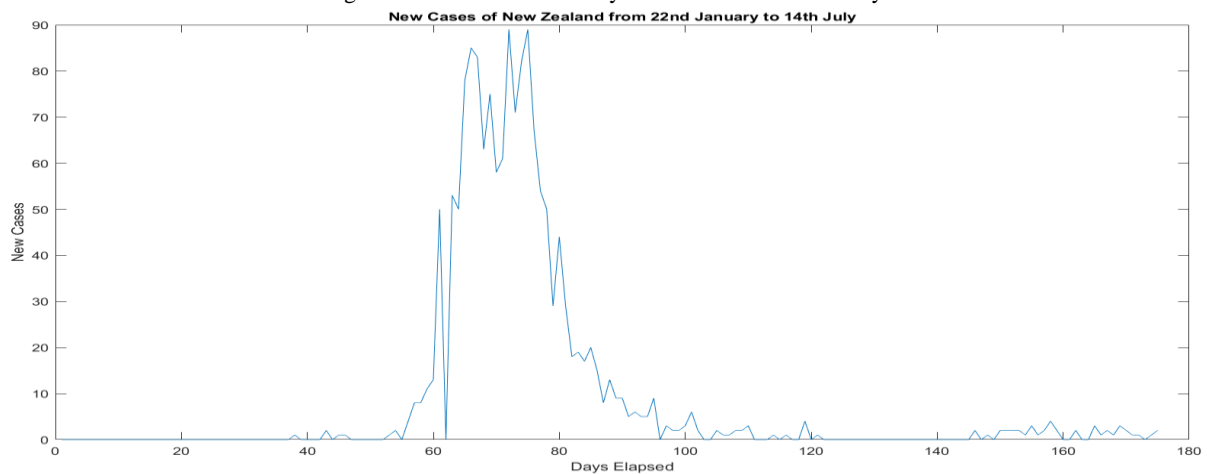


Fig.9 : New Cases of New Zealand from 22nd January to 14th July

Graph showing the bell-shaped curve of New Zealand's new cases from 16th March to 21st April:

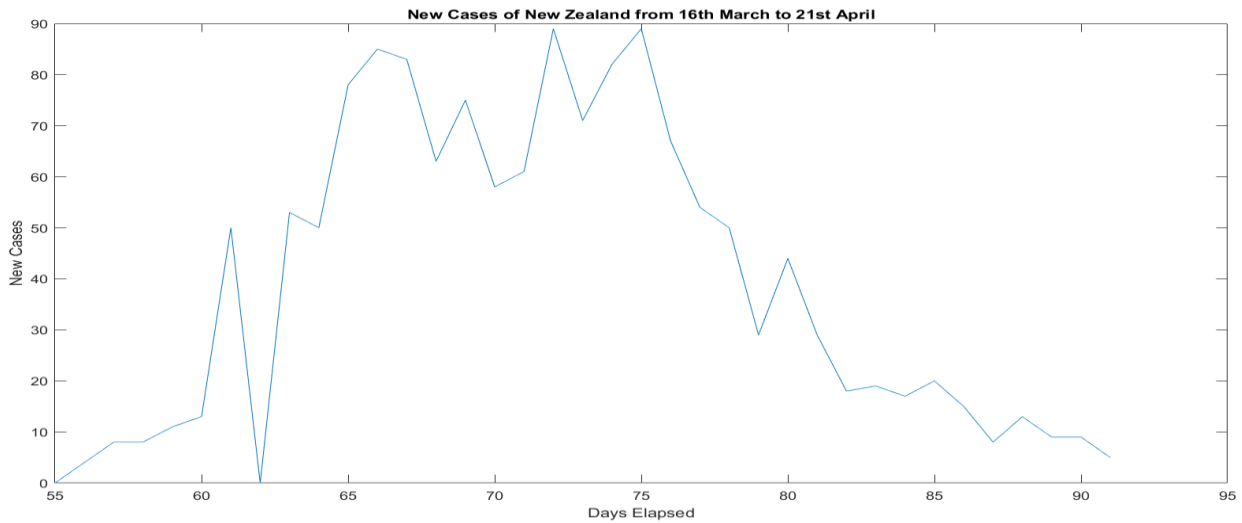


Fig.10 : New Cases of New Zealand from 16th March to 21st April

GERMANY:

For Germany, the new cases curve had a complete bell-shaped curve from 22nd March to 10th May. From 22nd June to 14th July, there was again seen a rise in new cases which could be regarded as the rising exponential part of the bell-shaped curve. Hence, we simulated these two parts of the Germany's new cases curve and computed the values of constants A and B which are shown below:

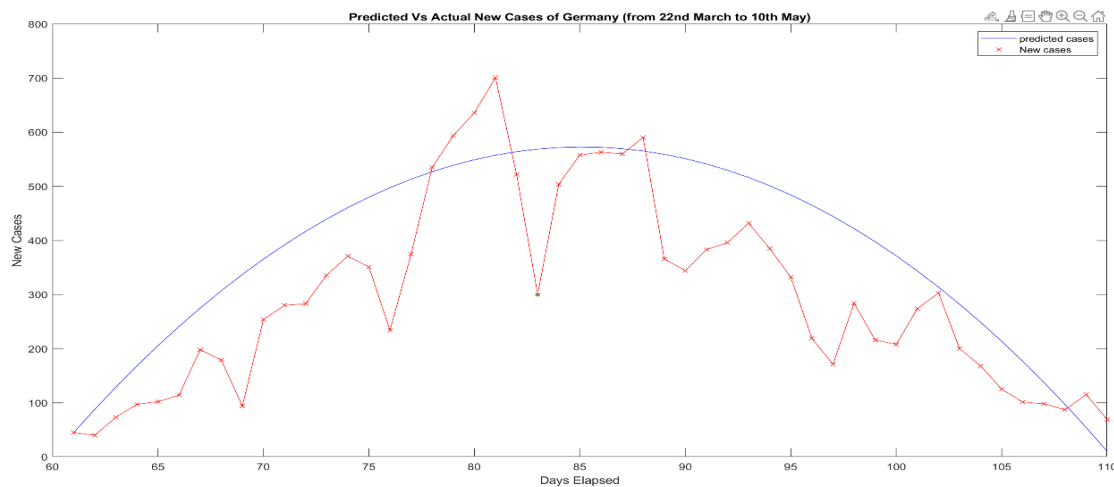


Fig.11 : Predicted new cases using IDEA vs Actual new cases of Germany from 22nd March to 10th May

The above graph corresponds to the first bell shaped part of the new cases curve from 22nd March to 10th May. First, we computed the A and B values for the period. We got the following values:

$$A = 0.0303$$

$$B = 1.521$$

Further we extracted out the values of R_0 and d from the values of A and B using eq.4 and eq.5. We obtain the following values for the above A and B:

$$R_0 = 4.576$$

$$d = 0.0307$$

Observations: Hence, we can see that the reproduction number came out to be around 4.6 (approx.) which means that during this period one primary infector was able to transmit the infection further to 4.6 people and that gives us a clear idea how deadly the disease proved to be for that country. Also, the value of d came out to be 0.0307. Since we are unclear about the units of d , hence we can't say much on the value of this parameter which proves out to be the drawback of the model.

Now let's have a look at the second time period of Germany where the new cases curve started to rise again. In other words, we can say that it represents the rising exponential part of the bell-shaped curve. We computed the values of A and B for this curve which represents the data from 22nd June to 14th July which is represents the latest data we have. Below shown is the curve for the second part of the data:

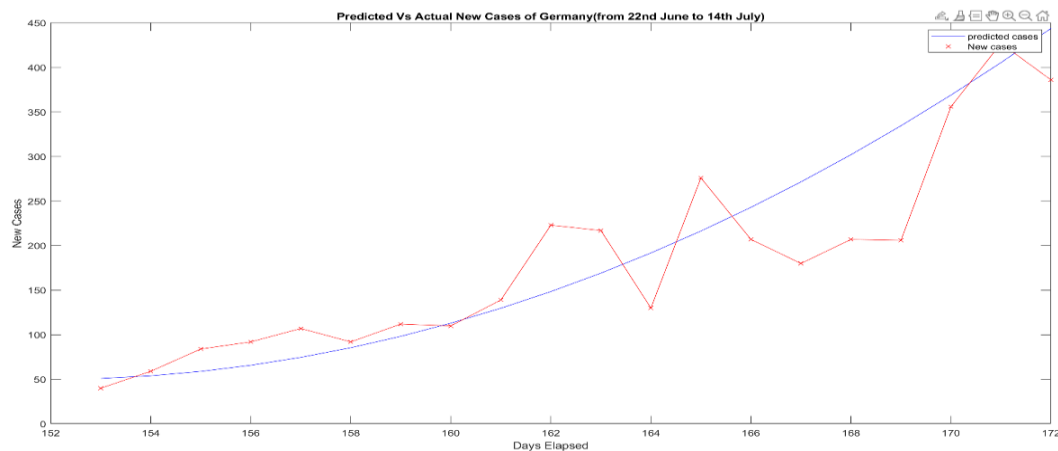


Fig.12 : Predicted new cases using IDEA vs Actual new cases of Germany from 22nd June to 14th July

So, from 22nd June a rise was seen in the number of new cases till 14th July, and we simulated the IDEA model curve to the same and computed the following values for A and B :

$$A = -0.4923$$

$$B = 0$$

So, we further extracted the values of R_0 and d which came out to be the following:

$$R_0 = 1.0$$

$$d = -0.389$$

Observations: The value R_0 suggests that one primary infector in this period is infecting exactly 1 secondary infection which is not as deadly as the previous value of R_0 which was 4.5 times this value. Again, since we are not much clear about the value of d so we can't say much on that again. Now let's have a look at the New Zealand's scenario.

NEW ZEALAND:

For New Zealand, the new cases had a bell-shaped curve between 16th March to 21st April. Hence, we simulated the new cases curve for New Zealand between the above-mentioned period and computed the values of constants A and B by equating the equations mentioned in the introduction part. Below is shown the graph for simulated curve vs the actual new cases curve.

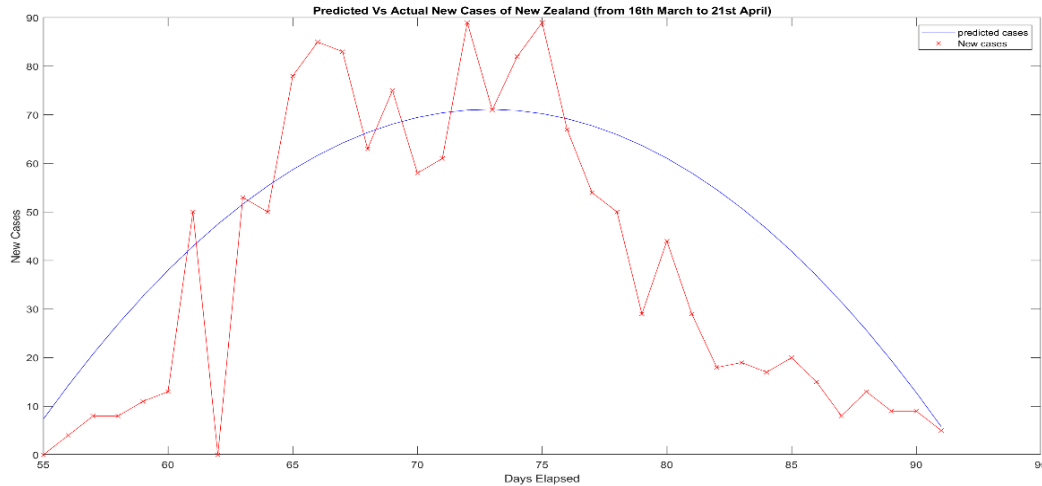


Fig.13 : Predicted new cases using IDEA vs Actual new cases of New Zealand from 16th March to 21st April
The above graph represents the period between 16th March to 21st April. The value of constants as computed in accordance with the IDEA model are:

$$A = 0.0199$$

$$B = 0.7529$$

Further we extracted the values of R_0 and d . Below are shown the value for the same:

$$R_0 = 2.123$$

$$d = 0.2009$$

Observations: The value of R_0 came out to be 2.123 which means the one person/infecter was transmitting the infection to approx. 2 other people which is again a very deadly number for any country. But if we compare these numbers to that of Germany, the R_0 for New Zealand is almost half to that of Germany and hence we can say that the spread of the disease in Germany was much deadlier than New Zealand.

Though we cannot make any specific deductions from the value of ' d ' for each country, in comparison, control parameter is much higher for New Zealand than for Germany. In other words, we can say that the stringency measure for New Zealand was much higher than that of Germany and hence, New Zealand managed to flatten the curve much earlier which are some very important insights from the model.

Summing up the entire work done using IDEA model in the below table:

Countries	Observation Period	A	B	R_0	d
Germany	22 nd March – 10 th May	0.0303	1.521	4.576	0.0307
	22 nd June – 14 th July	-0.4923	0.0	1.0	-0.389
New Zealand	16 th March – 21 st April	0.0199	0.7529	2.123	0.2009

Table.2: Gamma Values for New Zealand, South Korea, Japan and Germany.

6. Conclusion

Implementing the power law gave an insight on the rapidity of the spread of the disease. Further, it was useful to compare the rate of the change of the rapidity of the disease by doing the piece wise approximation over the newly observed cases. The drawback of the power law is that it can not completely and succinctly express the outbreak of the disease as it just gives an idea of how the infection was spreading. Moving on to the IDEA model, it gave two parameters in return, reproduction number and control parameter. Reproduction number came out to be an extremely useful parameter that can very well describe the outbreak of the disease. Control parameter, on the other hand, gave more of an abstract view of how the disease was being controlled, but being unitless, we couldn't extract out the fruitful insights out of it. In a nutshell, this report speaks about how the covid situation of countries which can be compared by simulating the new cases being recorded per day.

7. Code and Outputs

MATLAB Code for IDEA model implemented on New Zealand:

```
clear all;
syms A;
syms B;
syms t;

nz = readtable("CSVs\NZ_AAEDM.csv",'PreserveVariableNames',true)
nz_conf = nz{:,2};
nz_recv = nz{:,3};
nz_newcases = [0];

for i = 2:size(nz_recv,1)
    nc = nz_conf(i)-nz_conf(i-1);
    if nc<0
        nc=0;
    end
    nz_newcases = [nz_newcases; nc];
end

plot(nz_newcases)

ylabel('New Cases')
xlabel('Days Elapsed')
title('New Cases of New Zealand from 22nd January to 14th July')

[A_sol1,B_sol1,nz_newcases1] = generate_a_b(nz_newcases,55,91,A,B,t);

time = [1:size(nz_newcases1,1)];
days1 = time+54;

plot(days1,nz_newcases1)
ylabel('New Cases')
xlabel('Days Elapsed')
title('New Cases of New Zealand from 16th March to 21st April')

A_1 = A_sol1(32,1);
B_1 = B_sol1(32,1);
p = vpa(B_1).*time - vpa(A_1).*time.^2;
p = 10*p;

P1 = double(p);
plot(days1,P1,'color',[0 0 1])
hold on
scatter(days1,nz_newcases1,'rx')
hold on
plot(days1,nz_newcases1,'color',[1 0 0])
legend('predicted cases','New cases')
ylabel('New Cases')
xlabel('Days Elapsed')
title('Predicted Vs Actual New Cases of New Zealand (from 16th March to 21st April)')
hold off
```

```

function val = error_rate(predicted,confirmed)
    val = sqrt(mean((predicted-confirmed).^2));
end

function [A_sol,B_sol,country_newcases] = generate_a_b(country_newcases,days_from,days_to,A,B,t)
country_newcases = country_newcases(days_from:days_to,:);
I = B*t-A*t^2;
T = [1:length(country_newcases)];
eqn = subs(I,T.');
x = [eqn-vpa(log(country_newcases)) == 0];
y = [];
for i = 1:length(x)
    y = [y solve([x(3) x(i)],[A,B])];
end
A_sol = zeros(length(y),1);
B_sol = zeros(length(y),1);
for i = 1:length(y)
    A_sol(i,1) = y(1,i).A;
    B_sol(i,1) = y(1,i).B;
end
a = isnan(A_sol);
ind_a = find(a == 1);
b = isinf(A_sol);
ind_b = find(b == 1);
c = [ind_a;ind_b];
d = [1:size(A_sol)];
e = setdiff(d,c);
A_sol = A_sol(e,:);
B_sol = B_sol(e,:);
end

```

MATLAB Code for IDEA model implemented on Germany:

```

clear all;
syms A;
syms B;
syms t;

germany = readtable("CSVs\Germany_AAEDM.csv",'PreserveVariableNames',true);
germany_conf = germany{:,2};
germany_recv = germany{:,3};
germany_newcases = [0];

for i = 2:size(germany,1)
    germany_newcases = [germany_newcases; germany_conf(i)-germany_conf(i-1)];
end

plot(germany_newcases)
ylabel('New Cases')

```

```

xlabel('Days Elapsed')
title('New Cases of Germany from 22nd January to 14th July')

[A_sol1,B_sol1,germany_newcases1] = generate_a_b(germany_newcases,61,110,A,B,t);
I = B*t-A*t^2;
T = [1:length(germany_newcases1)];
eqn = subs(I,T.);
x = [eqn-vpa(log(germany_newcases1)) == 0];
y = [];
for i = 1:length(x)
    y = [y solve([x(3) x(i)],[A,B])];
end
A_sol1 = zeros(length(y),1);
B_sol1 = zeros(length(y),1);
for i = 1:length(y)
    A_sol1(i,1) = y(1,i).A;
    B_sol1(i,1) = y(1,i).B;
end
% A_sol1
% B_sol1

time = [1:size(A_sol1,1)];
days1 = time+60;

plot(days1,germany_newcases1)
ylabel('New Cases')
xlabel('Days Elapsed')
title('New Cases of Germany from 22nd March to 10th May')

A_1 = A_sol1(47,1);
B_1 = B_sol1(47,1);
p = vpa(B_1).*time - vpa(A_1).*time.^2;
p = 30*p;

P1 = double(p);
plot(days1,P1,'color',[0 0 1])
hold on
scatter(days1,germany_newcases1,'rx')
plot(days1,germany_newcases1,'color',[1 0 0])
legend('predicted cases','New cases')
ylabel('New Cases')
xlabel('Days Elapsed')
title('Predicted Vs Actual New Cases of Germany (from 22nd March to 10th May)')
hold off

[A_sol2,B_sol2,germany_newcases2] = generate_a_b(germany_newcases,153,172,A,B,t);
I = B*t-A*t^2;
T = [1:length(germany_newcases2)];
eqn = subs(I,T.);
x = [eqn-vpa(log(germany_newcases2)) == 0];
y = [];

```

```

for i = 1:length(x)
    y = [y solve([x(3) x(i)],[A,B])];
end
A_sol1 = zeros(length(y),1);
B_sol1 = zeros(length(y),1);
for i = 1:length(y)
    A_sol1(i,1) = y(1,i).A;
    B_sol1(i,1) = y(1,i).B;
end
% A_sol2
% B_sol2

time = [1:size(A_sol2,1)];
days2 = time + 152;

plot(days2,germany_newcases2)
ylabel('New Cases')
xlabel('Days Elapsed')
title('New Cases of Germany from 22nd June to 14th July')

A_1 = A_sol2(3,1);
B_1 = B_sol2(3,1);
p = vpa(B_1).*time - vpa(A_1).*time.^2;
p = 2*p+50;

P1 = double(p);
plot(days2,P1,'color',[0 0 1])
hold on
scatter(days2,germany_newcases2,'rx')

plot(days2,germany_newcases2,'color',[1 0 0])
legend('predicted cases','New cases')
ylabel('New Cases')
xlabel('Days Elapsed')
title('Predicted Vs Actual New Cases of Germany(from 22nd June to 14th July)')
hold off

function val = error_rate(predicted,confirmed)
    val = sqrt(mean((predicted-confirmed).^2));
end

function [A_sol,B_sol,country_newcases] = generate_a_b(country_newcases,days_from,days_to,A,B,t)
country_newcases = country_newcases(days_from:days_to,:);
I = B*t-A*t^2;
T = [1:length(country_newcases)];
eqn = subs(I,T.);
x = [eqn-vpa(log(country_newcases)) == 0];
y = [];
for i = 1:length(x)
    y = [y solve([x(3) x(i)],[A,B])];
end
A_sol = zeros(length(y),1);

```

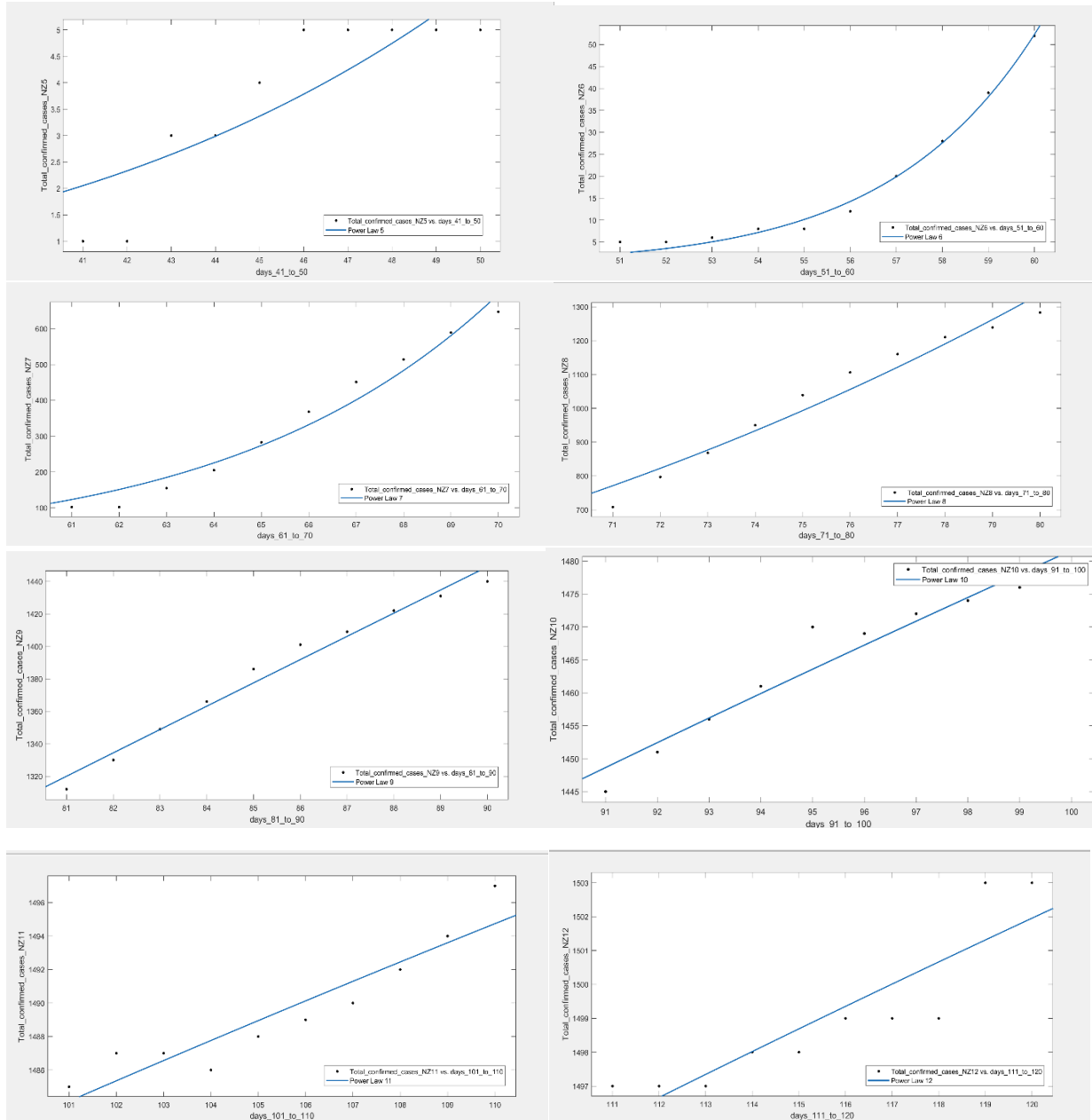


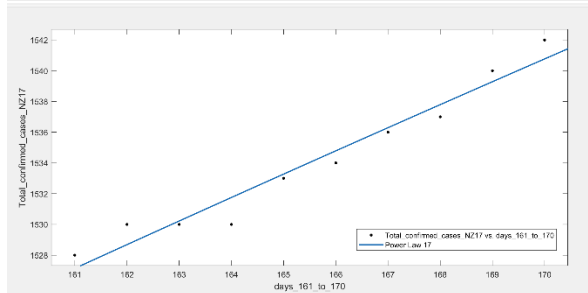
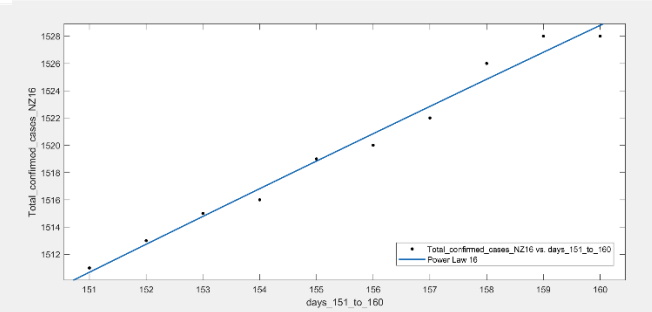
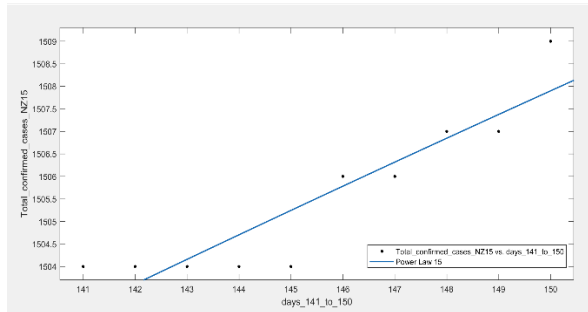
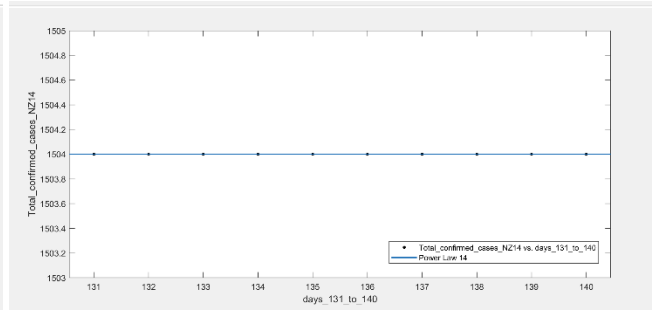
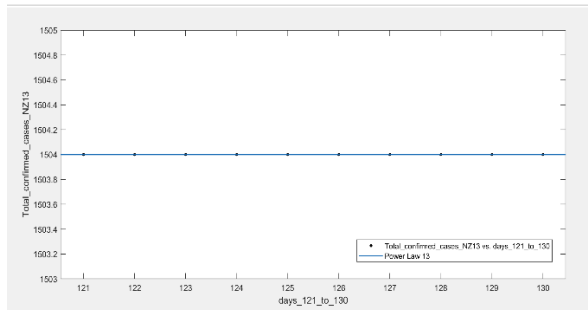
```

B_sol = zeros(length(y),1);
for i = 1:length(y)
    A_sol(i,1) = y(1,i).A;
    B_sol(i,1) = y(1,i).B;
end
end

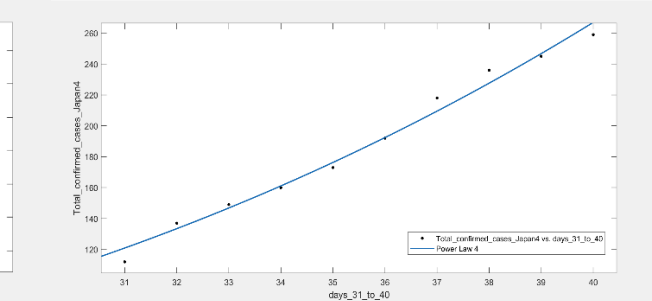
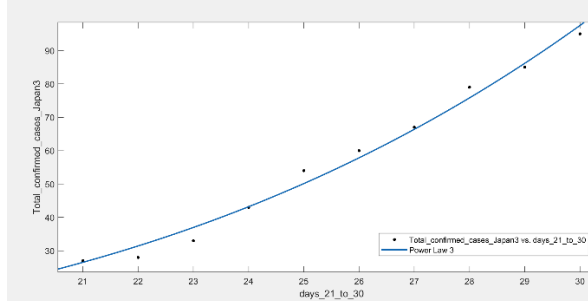
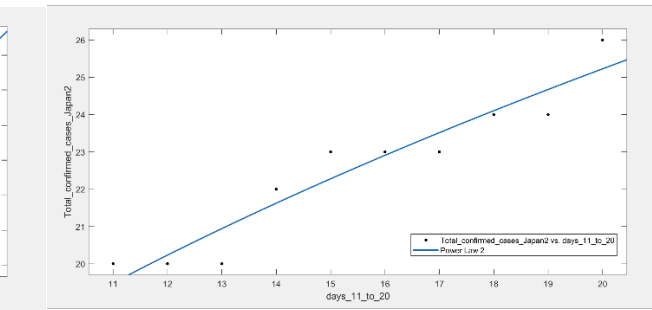
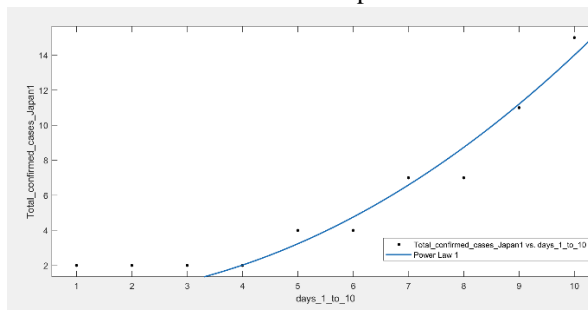
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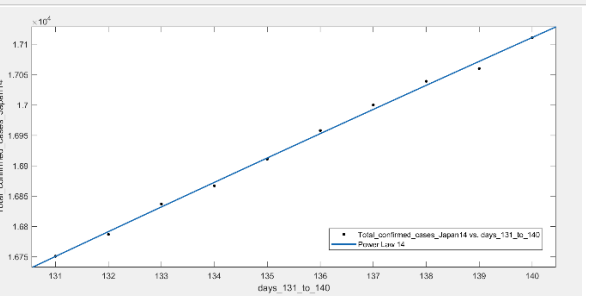
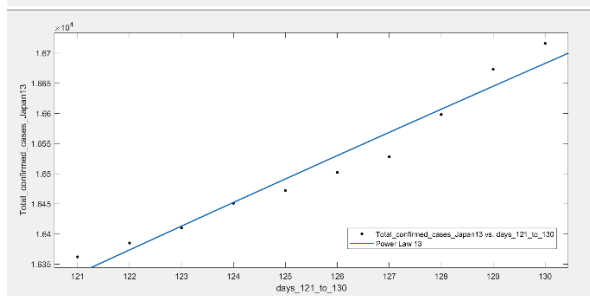
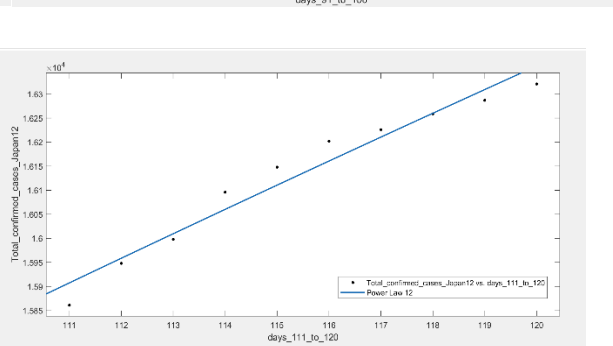
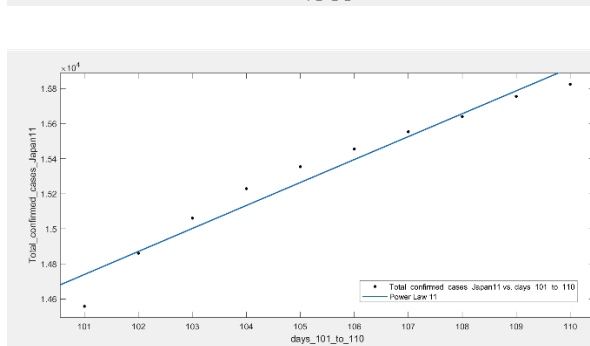
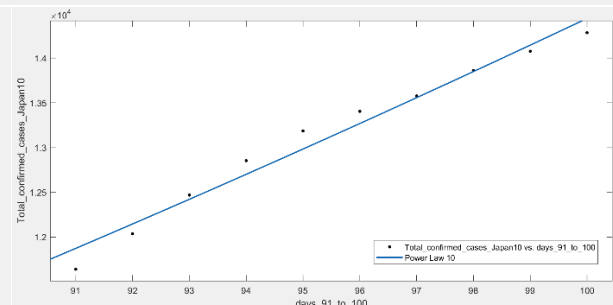
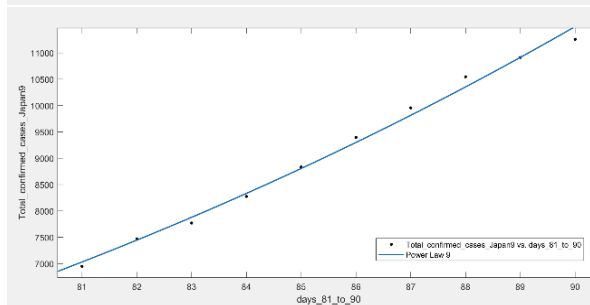
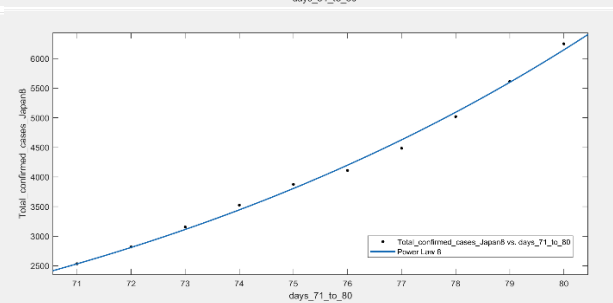
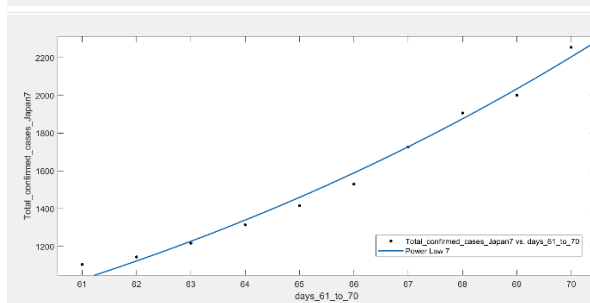
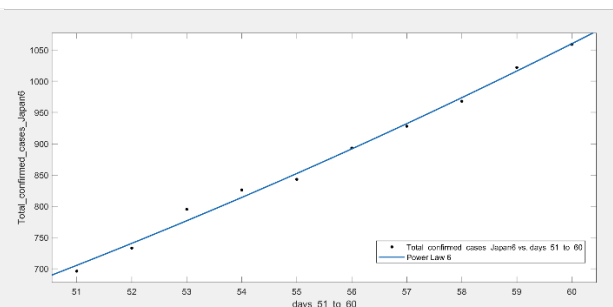
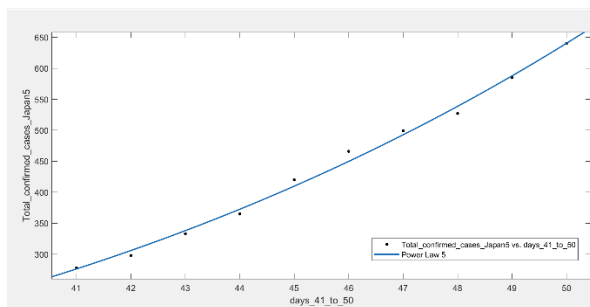
Power Law Model Results for New Zealand:

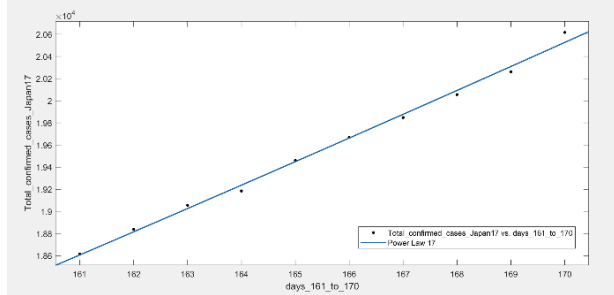
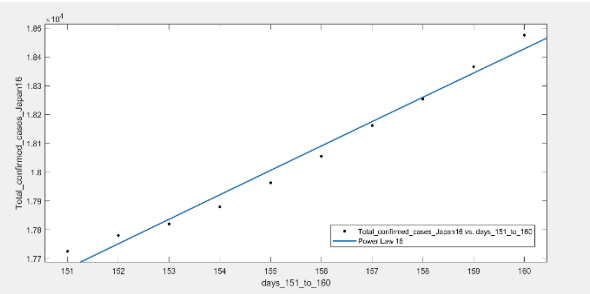
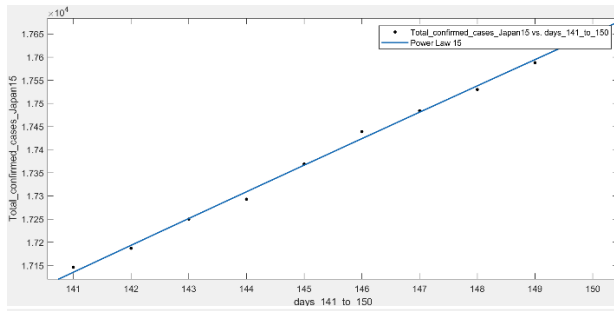




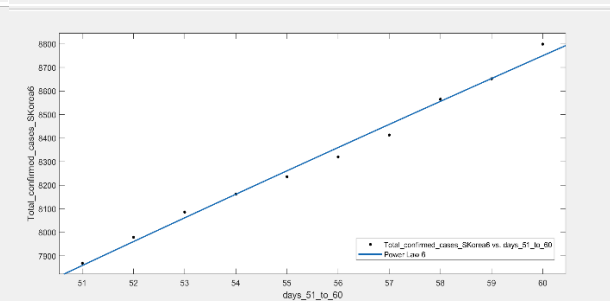
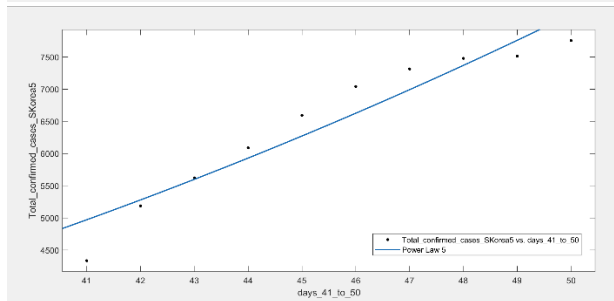
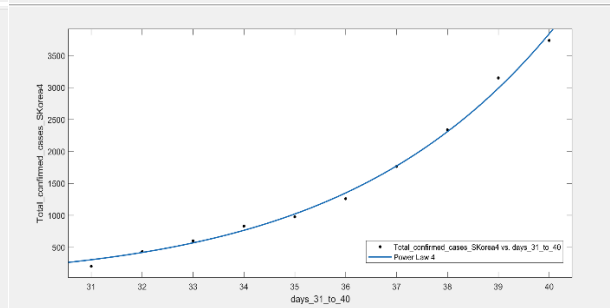
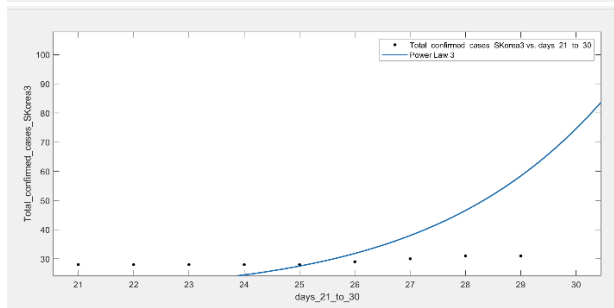
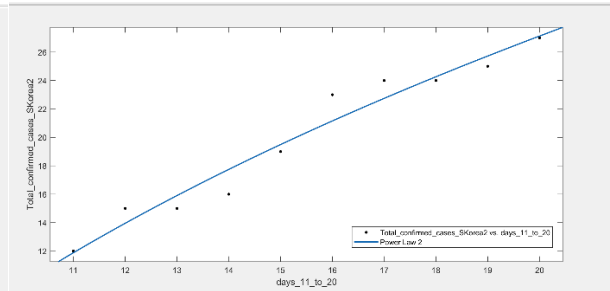
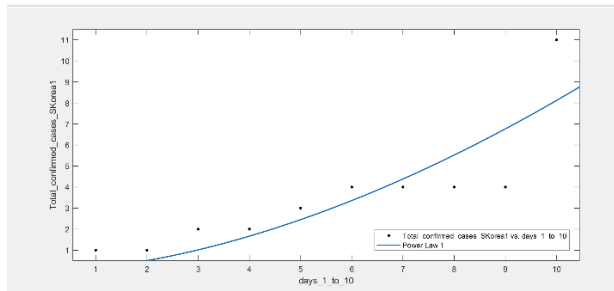
Power Law Model Results for Japan

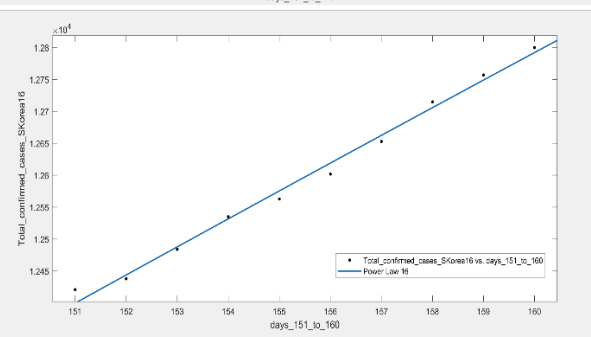
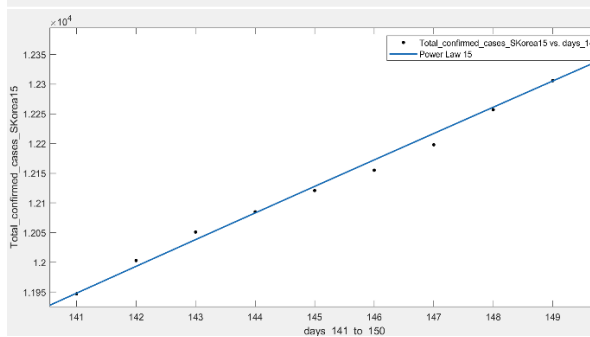
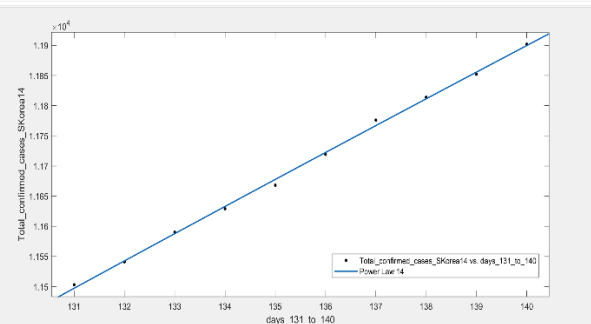
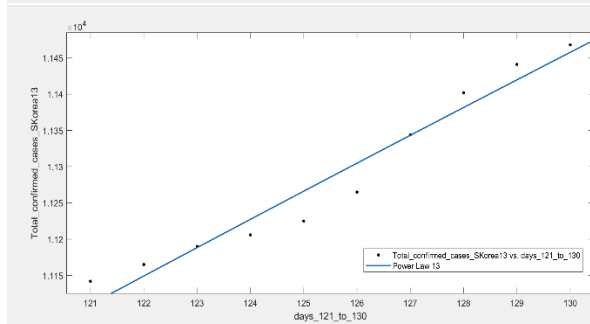
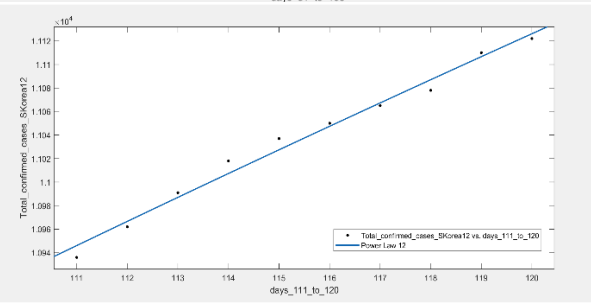
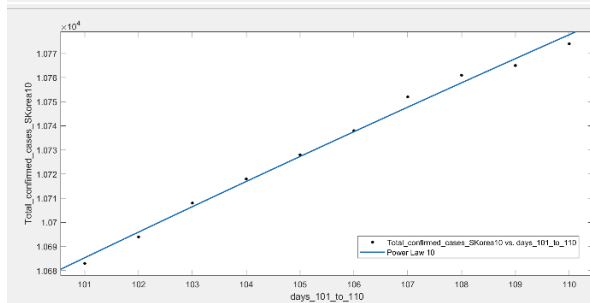
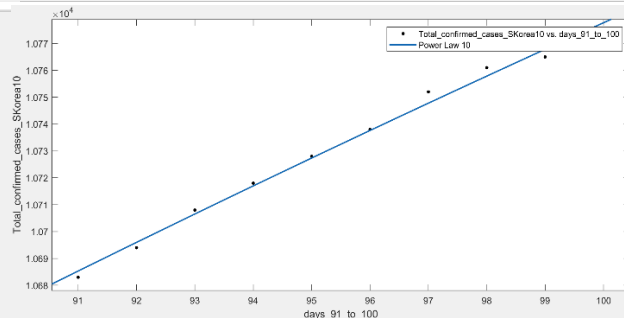
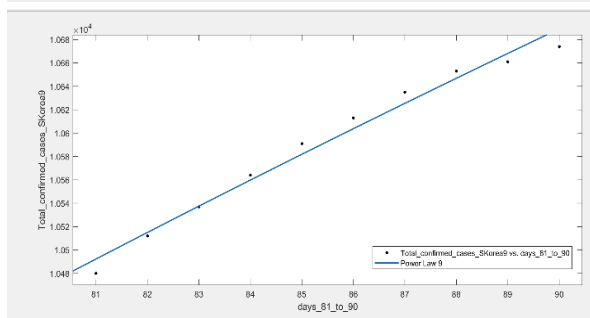
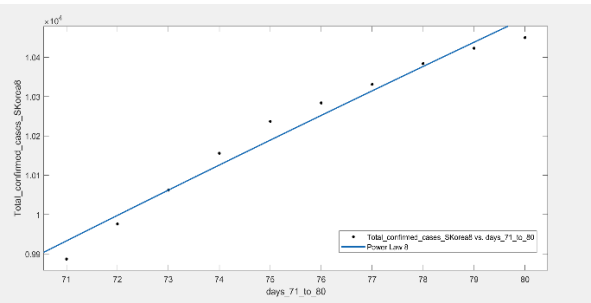
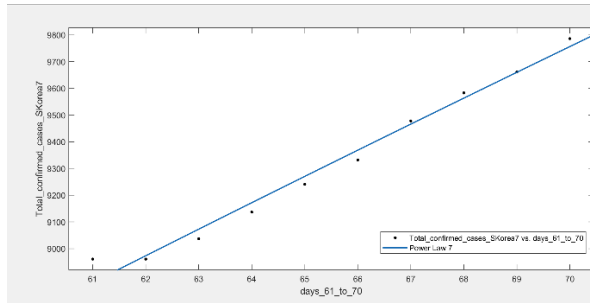


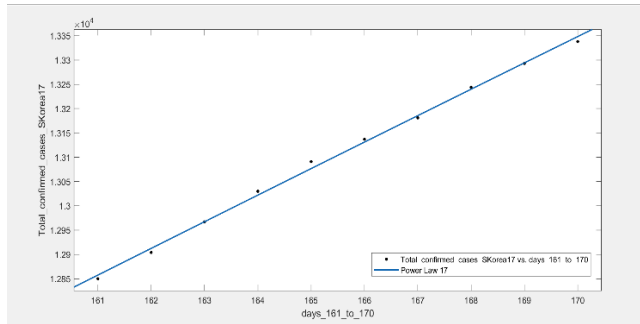




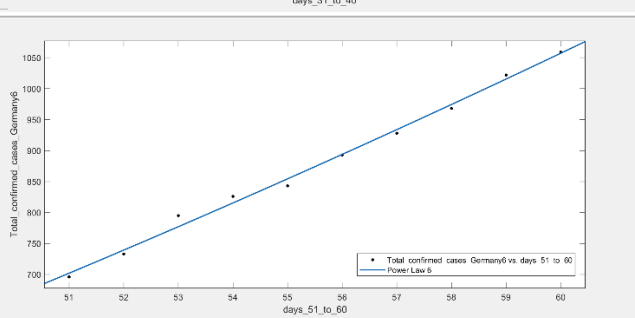
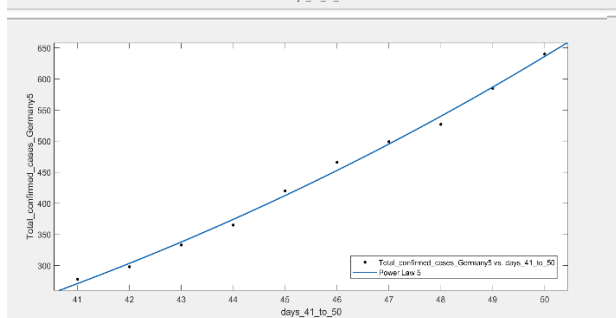
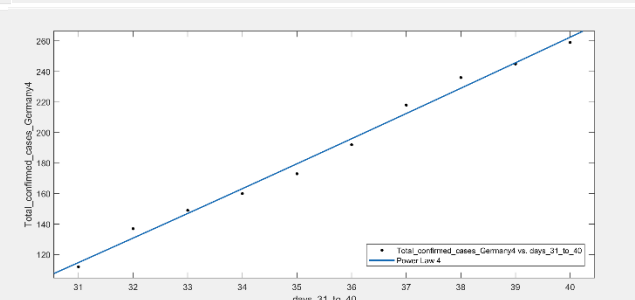
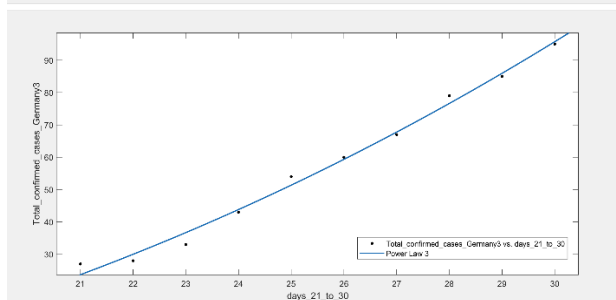
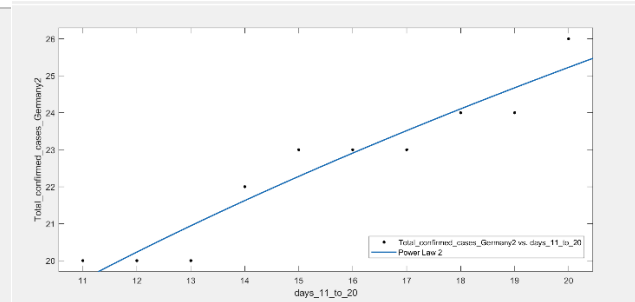
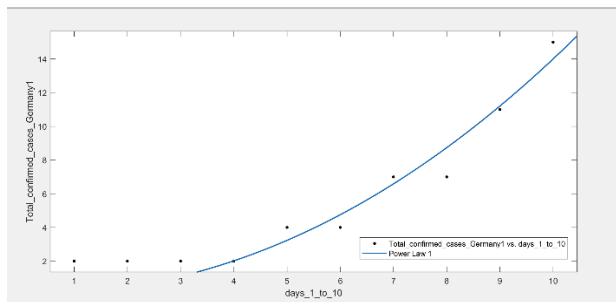
Power Law Model Results for South Korea

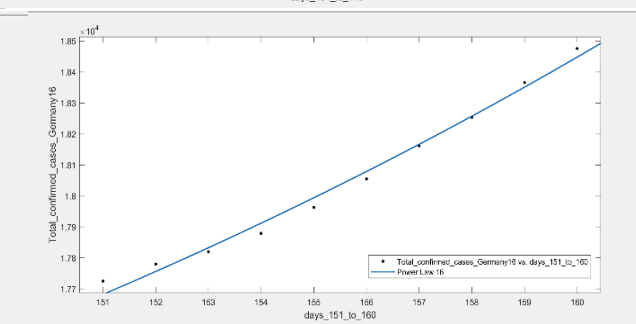
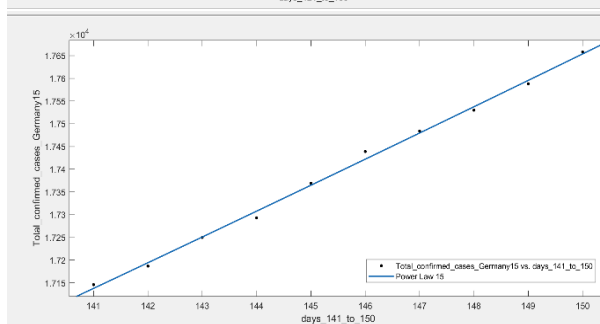
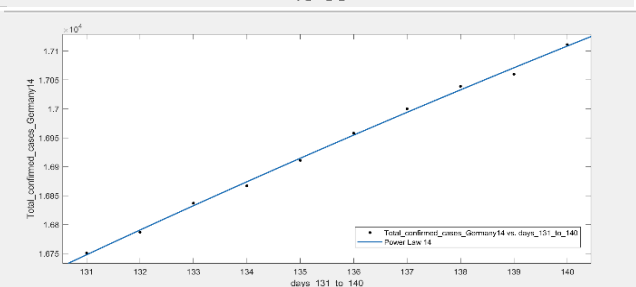
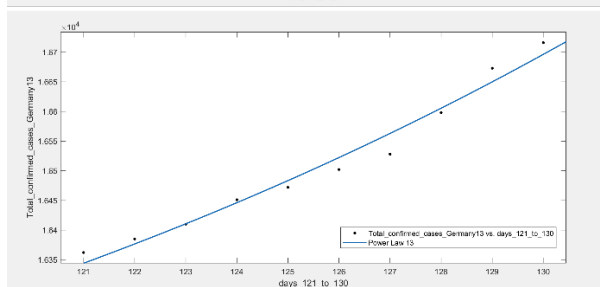
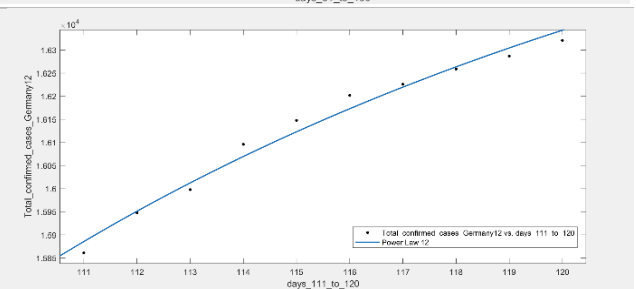
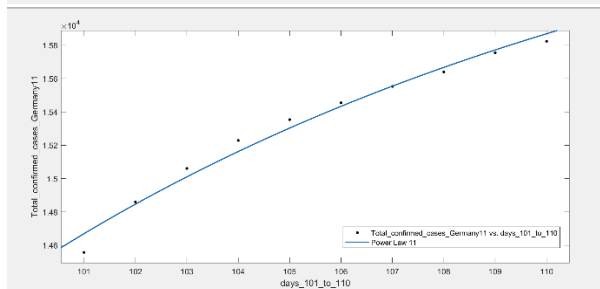
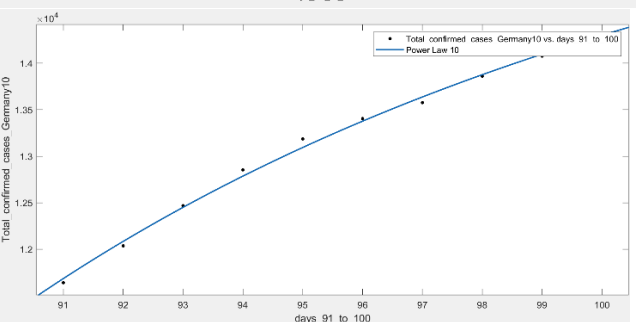
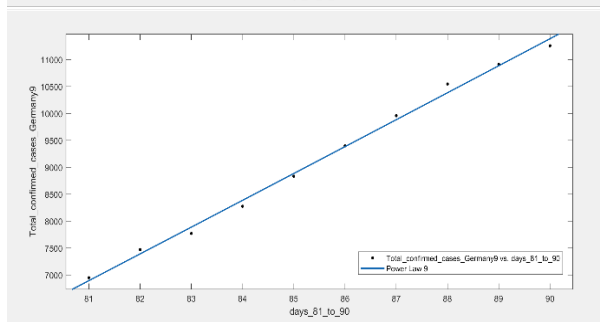
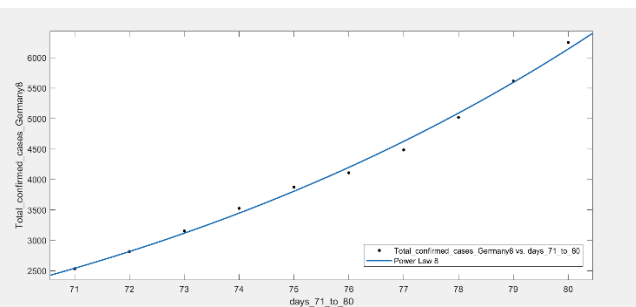
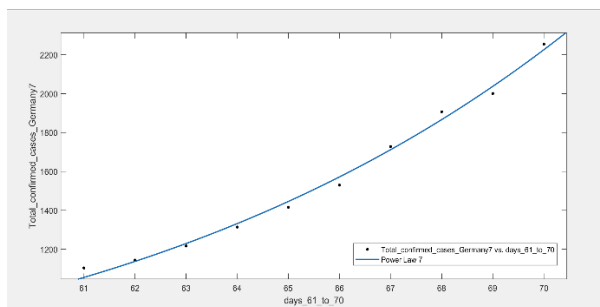






Power Law Model Results for Germany:





8. References

- [1]. Relatedness of Incidence Decay with Exponential Adjustment, “Farr’s Law” and Compartmental Difference equation SIR models.
- [2]. Search for the trend of Covid 19 infection following Farr’s law, IDEA model and Power law.