

The Comparison For Epidemiological Investigation Of Corona Virus-19 Pandemic

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Abstract— The corona virus is currently in a pandemic. At this point, the most pressing challenge in the health care field is the coronavirus disease (COVID-19) epidemic. “In Korea, the first laboratory confirmed case was confirmed on January 20, 2020[1]”. One way to identify these diseases is building the computational model. And then it needs a way to check whether the model worked or not. In this paper, We explain how to check the model using several programs.

Keywords—Corona Virus Disease 19(Covid-19), Simulation, Epidemiology Compartment Model

I. INTRODUCTION

A novel coronavirus, which is more powerful than “Severe Acute Respiratory Syndrome (SARS) in 2002 and Middle East Respiratory Syndrome (MERS) in 2012 [2]”, occurred in December 2019. As a result, it has been reported that about 900,000 people worldwide have died to date. In order to manage diseases, the Centers for Disease Control and Prevention needs to build a model and use it as an indicator.

There are many ways to make a model. Also, to see if the model is correct, it has to be compared to others. In this paper, We explain how to check the model using several programs. We used the well-known SEI(X)R model as an example to compare programs. In the related work part, we will explain the SIR model that the SEIR model is based on, and in the body of the paper, we will compare the way using two programs, Python and Excel.

II. RELATED WORK

A. SIR Model

The SIR model is a simulation of epidemic disease by dividing into three states: the number of susceptible, infected and recovered. Susceptible is the main abbreviation and expressed as S.

“In case of contact between an infected person and a susceptible person, it is converted into an infectious compartment [3]”. I(Infectious) refers to those capable of

infecting someone. R (Recovered) means people who have recovered from disease

B. Covid-19

Coronavirus-19 is known to have spread to humans by bats in Wuhan, China on December 1, 2019. And it spreads from person to person mainly through direct person-to-person contact. Until September 2020, “the cumulative number of confirmed cases in Korea is about 22,000, and about 18,000 people have been recovered. The total number of deaths was 363 [4]”

III. APPROACH

To compare the methods of implementing the SEI(X)R model, the 3.4 version of Python and the 2016 version of Excel were used.

A. Baseline

TABLE 1. SETTINGS

Sort				
Group	S	E	I	R
Value	51,700,000	0	1	0
Parameter	beta	sigma	Gamma	
Value	2.0	0.25	0.07	
Period	100			

B. The SEI(X)R model implemented in Python 3.4

I used the derivative function ode() provided by Python. Specifically, to simulate, It was based on the total population of Korea, about 5,170,000 people. The initial number of

infectious people was defined as 1, and both E and R were simulated with 0 people. (I.e. $S=N-E-I-R$)

And the corresponding parameters of beta, sigma, and gamma values were defined as 2.0, 0.25, and 0.07, respectively. These values were set arbitrarily. The total duration of the simulation is 100 days. Refer to Table 1

The curve plot derived from simulation in Python is as Figure 1.

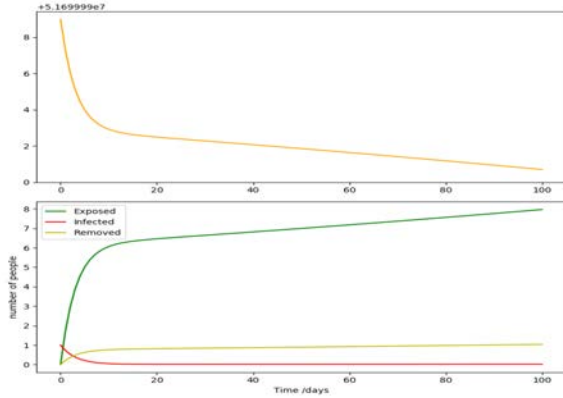


Figure 1. The Curves of SEI(X)R Results in Python 3.4

C. The SEI(X)R model implemented in Excel

I have defined a function that calculates values manually in Excel.

In order to simulate and compare in detail, an experiment was conducted under the same conditions as the SEIR model part using a Python 3.4 program. Refer to Table 1. The curve plot derived from simulation in Excel is as Figure 2.

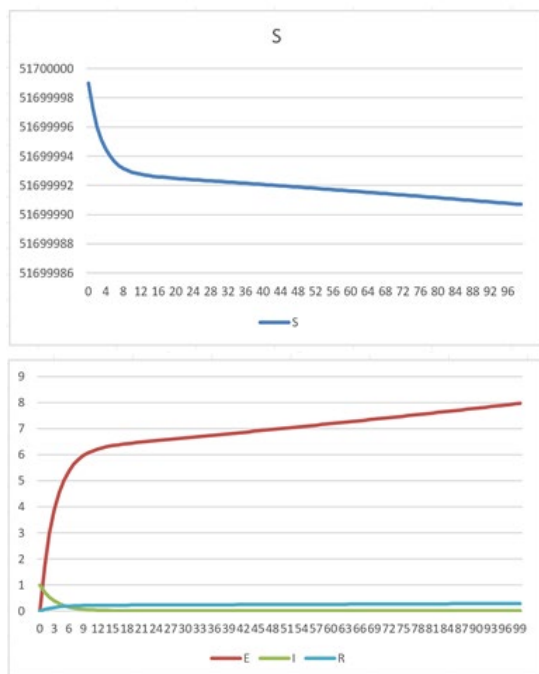


Figure 2. The Curves of SEI(X)R Results in Excel

The curves of Figure 1 and Figure 2 seem to match, but you can see that the values are actually slightly different.

D. The SEI(X)R model using self-implemented function in Python3.4

In another attempt, without using the differential function provided by Python, we implemented it using the self-produced function from Python. The results are as follows.

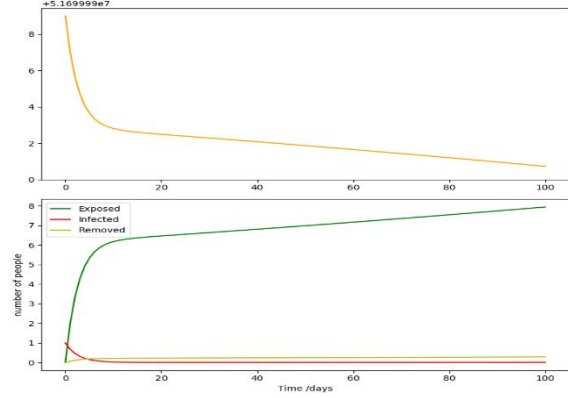


Figure 3. The Curves of SEI(X)R Results Self-Implemented Function in Python 3.4

E. The Original SEIR model

$$\begin{aligned} \frac{dS}{dt} &= aN - uS - \frac{dS}{dt} \\ \frac{dE}{dt} &= -(u+a)E + \frac{dS}{dt} \\ \frac{dI}{dt} &= aE - (r+u)I \\ \frac{dR}{dt} &= rI - uR \end{aligned}$$

Figure 4. The Equations of SEIR [3]

The above figure represents the SEIR equation. These four states proceed to $S \rightarrow E \rightarrow I \rightarrow R$ in the event of $R > 0$.

Here, R means the Reproduction number.

In this study, I compared these three methods in programs.

Since these values are not important, they were set by randomly initializing. The values in Table 1 represent random initial values for simulation.

The people in Korea suffered a great crisis from the Gwanghwamun assembly and the club incident as well as the Shincheonji worship incident.

In Korea, It is likely to continue to face these crises in the future. As a basic stage for disease research, I hope that these studies can be helpful as the foundation

IV. CONCLUSIONS

We have compared how to study epidemic disease with two programs.

The results of the study were the same as in Figure 1 and Figure. 2 and Figure 3. However, when looking at the results of actual values, the median values were slightly different.

In the actual computation process, this seems to be due to the algorithmic nature of the ode() function provided by Python 3.4. But the results of the curve in pictures were fine. As the next study, we plan to build a system for epidemic disease research. We will interact with these two programs to create a real model and so on.

REFERENCES

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WooHyun Park is now a Doctor Student at Sungkyunkwan University in South Korea. His research interests lie in artificial intelligence and Game.