A Simulation of Covid-19 Transmission until the Steady State Using Graph Algorithm

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Abstract: This research computes the average days to reach the steady state of COVID-19 infection by repeated simulation of human interactions using a bi-directed graph. It examines the effect of one infected person on a community comprising groups of people who interacts daily with each other such as school, commuter train, family, etc. Randomization is used to determine group structure and a bi-directed graph models the network of frequently interacting people. Once a person is infected, the incubation period is 5 days, and this person possibly infects other people for the next 6 days. A randomization distribution determines whether each person directly linked to an already infected person will be infected, or not. The effective reproduction number of the actual data is used in the study. Finally, this study examines how many days are required to reach the steady state where a new infected person is not observed any more. The study highlights number of days at the infections peak and how many days are required to reach the steady state. Future research would consider multiple starting points, variants, ages, genders, ethnicities, seasons, and regions. Furthermore, comparison with results of AI machine learning will be examined.

Key words: Covid-19, graph algorithm, pandemic simulations, steady state.

1. Introduction

According to [1], the SARS-CoV2 is a type of coronavirus. Coronaviruses include viruses that cause common colds, Severe Acute Respiratory Syndrome (SARS) and the Middle East Respiratory Syndrome (MERS) virus that has been occurring since 2012. It is generally transmitted by droplet or contact infection. The risk of spreading the infection is high even if there are no symptoms such as coughing or sneezing in an enclosed space or when talking with many people in proximity. (WHO reports that a five-minute conversation generally generates about 3,000 droplets, which is about the same as one cough. In the case of the new coronavirus, there is a possibility of transmitting the virus to other people from two days before the onset of symptoms to seven to ten days after the onset of symptoms. Since viral shedding is higher immediately before and after the onset of the disease, asymptomatic carriers (those who have no symptoms but have tested positive) may be able to transmit the virus.

As of 2021, the disease has not been successfully contained globally, and pandemics sometimes occurred due to outbreaks of modified coronaviruses, even in countries where vaccination is well advanced. It is important to know when peak infection might happen so healthcare facilities may be able to get some planning time to take in more patients with serious infection conditions. There is a strong need to model the infection spreading more accurately which can prepare governments to decide lockdowns and for how long [2]-[7].

2. Simulation Method and Usage of the Actual Pandemic Parameters in Japan

Typically, statistical methods are used to simulate the transmission of infectious diseases. For macroscopic prediction of infection, the effective reproduction number is often used, which indicates how many people are infected by one infected person on average. For example, an effective reproduction number > 1.0 indicates that the infection is in the spreading phase and that usually the number of cases and severely ill patients is increasing, and the government and society take various measures to lower the effective reproduction number below 1.0 to lead to the end the infection [8]-[12]. In addition, a multi-agent system (MAS) or a self-organized system is used to solve the human mutual contact or communication caused infection problems that are normally difficult or impossible for an individual agent or a monolithic system [13]-[16].

This paper simulates the infection of high school students. Therefore, each person is represented as a node and each node could be given various characteristics. The adjacent-matrix representation of the graph on page 861 in [1] is adopted to express mutual human interactions by bi-directed graph. C++ [17] is used as the coding language, and the "class structure" of each node is set to the extent and depth of each individual's sociability and the infectivity of each individual. The infectivity of each individual increases when they are sociable and talk a lot, or when they take off their masks and shout relatively loudly, or when they are in contact with many people, and decreases when they prefer to be alone. In addition, each node belongs to multiple groups of various sizes. Each group has its own size and activity characteristics to represent classes, commuting trains, sports clubs, family members, and so on. If the group enrollment is large, or if it is a sports club with unmasked activities, the probability of cluster infection within the group will increase.

The paper uses the actual pandemic parameters in Japan retrieved from reference [18]. The COVID-19 can infect others several days before the onset of obvious symptoms and this characteristic is incorporated in the simulations. The main routes of infection are droplet infection and contact infection. Elderly people are more likely to become seriously ill.

3. Graph Algorithm Structure Usage of the Actual Pandemic Parameters in Japan

Following [3], it is assumed that the average incubation period is set to be 5 days, and the period of infectious capacity, whether onset or asymptomatic, is set to be 6 days. Furthermore, the simulations expect that the number of days during which the students continue to attend classes at school while retaining the ability to be infected (StayHomeDelay) is 3 days. If symptoms are realized, the student should be isolated at home from then on. After 12 days from the date of infection, any infected student is assumed to be immune and not reinfected. This corresponds to the fact that no high school students have died due to COVID-19 in Tokyo so far.

It is presupposed that a total of 10000 people are considered as the class component of the matrix (class Person[10000]) and that there are 5000 possible groups in a class component of the matrix (class Group[5000]). Each matrix of human class (person) is assigned a flag of off=0/on=1 to indicate the state of infection (person.infected), incubation (person.incubation), onset (person.onset), recovery and immunity (person.recovered) are assigned. The initial date of infection is set to 1, and the total number of infected days (person.infectedDays) is updated every day, and the above status flags change according to the number of infected days. The respective settings are: infected=1 (1<infectedDays), incubation=1 (1<=infectedDays<=5, 5days), onset=1 (6<=infectedDays<=11, 6days), recovered=1 (12<= infectedDays). The number of days of school attendance with the ability to become infected was set as a parameter of StayHomeDelay (3days) as described above, which corresponds to a period of 6<=infectedDays<=8. Table 1 summarizes these COVID-19 infection status.

Table 1. Time Table of COVID-19 Infection Status

	0	1	2	3	4	5	6	7	8	9	10	11	12	13
Infected day	X													
Infection		1	2	3	4	5	6	7	8	9	10	11		
Incubation		1	2	3	4	5								
Onset (infection ability)							1	2	3	4	5	6		
Attend class	🟨	🟨	🟨	🟨	🟨	🟨	1	2	3					
Isolation at Home										🟨	🟨	🟨	🟨	🟨
Recovered													1	2

Person. Activity denotes the strength of each individual's unique infectious capacity. The maximum value is 1.0 if that person does not take various possible measures to prevent infection, such as talking at a distance of 2 m, frequently sterilizing hands, wearing a mask, etc. On the other hand, it becomes small if that person takes various measures to prevent infection to the maximum extent possible. Furthermore, the risk becomes smaller if the various infection prevention measures are taken into account to the maximum extent possible.

Each individual (person) belongs to multiple groups (group), and the total number of groups to which each individual belongs (person. Group Number) is randomly set between 1 and 10, with a maximum of 10, to represent the size of each individual's activity range. For each matrix group class (group), the intensity of infection among the members of the group is set as group. intensity (0~1.0). It will be greater if the ventilation capacity of the activity location is low, or if the activity involves active contact without a mask, such as in a sports club. Infection occurs between members i (person$[i]$) and j (person$[j]$) who belong to group k (group$[k]$), and the probability of its occurrence $p(i,j,k)$ is multiplied by a constant factor Max CrossInfection Ratio to obtain

$$p(i,j,k) = \text{person}[i].\text{activity} \cdot \text{person}[j].\text{activity} \cdot \text{group}[k].\text{intensity} \cdot \text{MaxCrossInfectionRatio} \qquad (1)$$

The constant coefficient used in the cross-infection capability, MaxCrossInfectionRatio, is normalized based on the effective reproduction number to be specified in advance during the initialization of the setup.

It is assumed that the probability of infection is assumed to be the same value in both directions, and as a result, it is assumed that people with a propensity for easily infected behaviors and environments have characteristics that make them easily infected at the same time.

Since each individual person$[i]$ and person$[j]$ belongs to multiple groups, there are n groups of cases where they are together, so the total mutual infection probability is expressed as follows

$$P(i,j) = \sum_{k=1}^{n}[\text{person}[i].\text{activity} \cdot \text{person}[j].\text{activity} \cdot \text{group}[k].\text{intensity} \cdot \text{MaxCrossInfectionRatio}] \qquad (2)$$

10,000 people were randomly assigned to 5000 groups conditional on each person being assigned to at most 10 groups. Person.groupM stores the set of group(s) each person belongs to. Next, group. member stores the set of the IDs of the people assigned to each group. For all groups, we calculated the mutual infection probability $p(i,j,k)$ among group members, and finally obtained the mutual infection probability $P(i,j) = P(j,i)$ between all person[i] and person[j].

The total probability of infection for person[i] can be calculated as follows

$$P(i) = \sum_{j=1}^{N} P(i,j) \qquad (3)$$

The average value of the cross-infection probability $P(i,j)$ of all members of the group in the initial state multiplied by 3 days, the period of possible infection, is theoretically the effective reproduction number.

Therefore, we initially calculated $P(i)$ using MaxCrossInfectionRatio=1.0, and finally normalized using the following formula.

$$\text{MaxCrossInfectionRatio} = \sum_{i=1}^{N}\{(P(i)\cdot \text{EffectiveReproductionNumber})/(N\cdot \text{StayHomeDelay})\} \tag{4}$$

First patients: If the set number of the first patient in the population is very small, for example, one, the infection intensity of this patient person[1].activity is small, the number of groups he belongs to person[1]. groupM is small, and the infection probability $P(1)$ is small, then, although it is a probability calculation in some cases, the patients are moved to home isolation mode before the infection spreads and the infection does not spread at all. Therefore, we set the initial number of patients to be 10 so that the infection would spread stably.

Infection: To determine whether a patient person[*i*] infects an uninfected person person[*j*], if the probability of infection $P(i,j)$ is greater than Rand1, a uniform random number between 0 and 1, then person[*j*] is considered infected.

$$P(i,j)\ >\text{Rand1: person}[j]\text{ is infected} \tag{5}$$

Each day, update everyone's infected/uninfected, incubation, onset, quarantine, and recovery status, and calculate the probability of transmission from infected to uninfected.

4. Discussions and Results

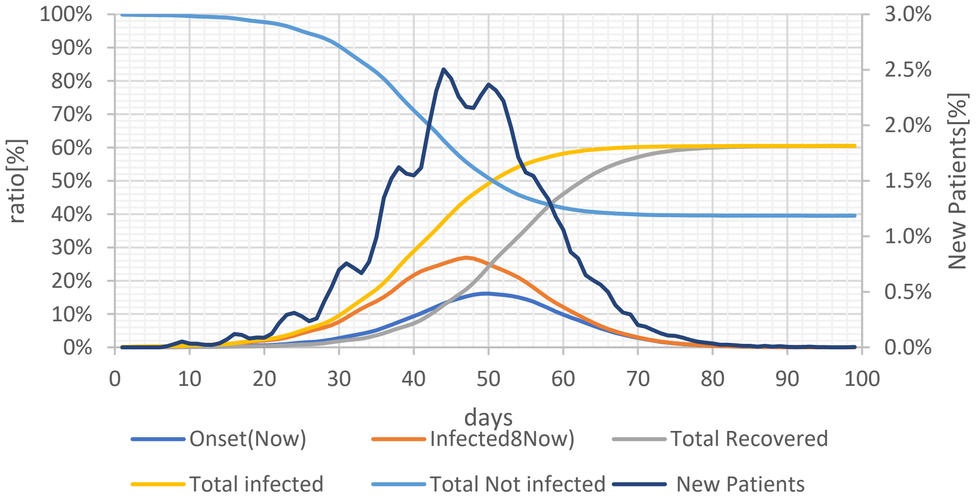

Fig. 1. Time history of ratio of the infection status.

Fig. 1 shows the time history of case 1 and tells that the peak of the epidemic when the number of new cases reached the maximum is 44 days later the new infections is 2.5% at the peak. The day when the number of infected people accumulated to 95% of the final infected people is defined as the convergence day, which is 70 days later, and the total number of infected people was 60%.

Table 2 shows the list of the parameters. We set case 1 as the default case and increased and decreased each parameter to examine the effects of parameters' changes on the results. The changed values from case 1 are highlighted in Table 2.

Table 3 shows the simulation results of the peak infection period, the maximum number of new infections per day, the convergence period, and the final incidence rate for the entire population in each case. Figure 2 shows the ratio of new infections per day in each case.

Table 2. The Simulation Parameter of 9 Cases

Simulation parameter	simulation case								
Parameter	1	2	3	4	5	6	7	8	9
Population	10000	10000	10000	10000	10000	10000	10000	10000	10000
StayHomeDelay	3	3	3	3	3	3	3	2	4
groupsNumber	5000	2500	10000	5000	5000	5000	5000	5000	5000
maxGroupsNumber	10	10	10	20	5	10	10	10	10
EffectiveReproductionNumber	1.8	1.8	1.8	1.8	1.8	1.0	3.0	1.8	1.8

Table 3. The Simulation Results of 9 Cases

Simulation parameter	simulation case								
Results	1	2	3	4	5	6	7	8	9
max epidemic period[day]	44	44	51	44	57	82	36	63	45
max new patients ratio[%]	2.5%	2.8%	2.2%	2.9%	1.7%	0.8%	5.0%	1.4%	3.4%
stable period[day]	70	69	74	66	87	124	53	88	63
total infected ratio[%]	60%	61%	59%	61%	55%	37%	73%	45%	68%

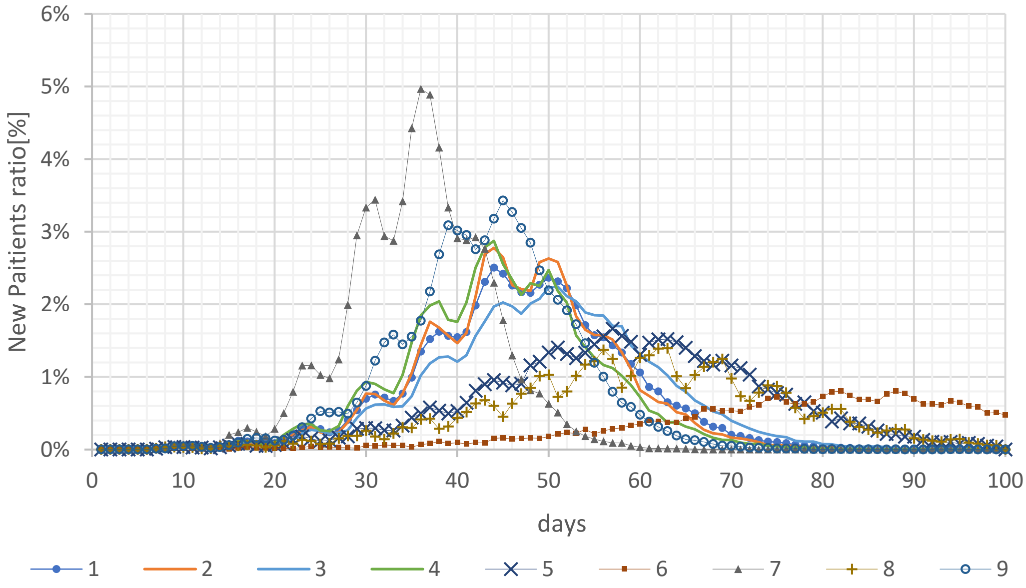

Fig. 2. Time history of the new patients of 9 cases.

The results show that some assessments can be deducted about COVID-19's peak timing and height.

1) Not effective: Reducing the number of whole groups can slightly delay peak timing and lower the height, but it is negligible. Smaller meetings are not effective in preventing infection.
2) Effective: Reducing the number of groups a person belongs to, reducing the average effective

reproduction number, and reducing the attending class period while having infection ability are effective.

In the case No.6, we started with an effective reproduction number of 1.0 for all the initial 10,000 individuals, and we saw an increase in infection, although weaker than in the other cases. This is due to the intensive reproduction of the infection among people who have a relatively higher ability to infect and to be infected.

5. Suggest Future Research, Enhancements

Future research would consider multiple starting points, variants, ages, genders, ethnicities, regions, seasons, and vaccine level. These variables can be easily incorporated into our model through the change of the parameter values. This paper dealt with the 10,000 people due to the author's notebook computer's capacity. More people can be examined with a more powerful computer. Furthermore, comparison with results of AI machine learning will be examined.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Toshinari Baba is the single author. Therefore, he did everything such as constructing a model, analyzing the data, and writing the paper.

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Toshinari Baba was born in Tokyo, Japan. He is the New International School of Japan in Tokyo. His teacher, Mr. Hubbs, used computer technology effectively to motivate students in Walter Hayes Elementary School in Palo Alto, CA and that's the start of his programming journey. He continued to learn programming at Ex-Gram instructed by Dr. Hirayama. He has been studying C++ under the guidance of Mr. Ganesan in Bay Area. He wants to contribute as a software engineer to realize the world where we all can reach our potentials.