



Final Size Distribution based on a Markov SIRV Epidemic Model for COVID-19 with an Efficient Algorithm

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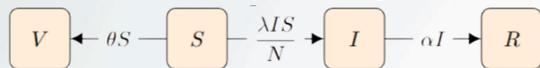
Abstract

The pandemic COVID-19 makes a great impact globally both on human health and on economics. Currently, people are looking forward to the coexistence with the virus instead of reaching the zero-COVID state. In this paper, we use a probability viewpoint to provide a theoretical basis of this decision. To do this, we propose a discrete-time Markov SIRV epidemic model considering the vaccinations and develop an efficient algorithm to compute the final size distribution. Our algorithm requires memory $O(N^2)$ and time complexity $O(N^3)$, where N is the population size. The algorithm requires less memory and less time to compute the desired distribution. Also, we compare the result of the final size with the corresponding deterministic model to see that the ODE model is an approximation of Markov model as N gets larger.

Problem description

Under the current situation of transmission of COVID-19, is it practical to look forward to coexistence with the virus? The final size distribution can answer this question. To calculate the distribution, we need develop an efficient algorithm which does not require large memory and time complexity. Using such algorithm, we can calculate the final size distribution with a large population, which can show numerically that the Markov SIRV model approximates the corresponding deterministic model.

Let S, I, R, V be susceptible, infectious, removed and vaccinated compartments, respectively. We do not consider the demography and assume that there will not be another outbreak, that each infectious case transmits the disease to others following a Poisson process with parameter λ . that when a susceptible is infected, it enters I , that I enters R (dead or recovered) after the exponentially distributed period T with parameter α and that θ is the average ratio of the effective vaccinations in a step. Let N be the total population. Then the process $\{(i(t), s(t))\}$ is a Markov process on the state space $X = \{(i, s) : i + s \leq N\}$. The flow chart is shown as following.



For the continuous-time Markov process, the probabilities of occurrences of an infection and a removal during the time interval $[t, t + \Delta t]$ are given by

$$\mathbb{P}((I(t + \Delta t), S(t + \Delta t)) - (I(t), S(t)) = (1, -1)) = \left(\frac{\lambda I(t)}{N} - \theta\right) S(t) \Delta t + o(\Delta t),$$

$$\mathbb{P}((I(t + \Delta t), S(t + \Delta t)) - (I(t), S(t)) = (-1, 0)) = \alpha I(t) \Delta t + o(\Delta t).$$

We now let $\Delta t = 1$. Then the process $\{i(t), s(t)\}$ is a discrete-time Markov process and we can calculate the transition probabilities as follows.

$$\mathbb{P}((I(t + 1), S(t + 1)) = (i + 1, s - 1) | (I(t), S(t)) = (i, s)) = \frac{\lambda s(1 - \theta)}{\lambda s(1 - \theta) + N\alpha},$$

$$\mathbb{P}((I(t + 1), S(t + 1)) = (i - 1, s) | (I(t), S(t)) = (i, s)) = \frac{N\alpha}{\lambda s(1 - \theta) + N\alpha}.$$

Let $\tau = \inf\{t \geq 0 : I(t) = 0\}$ and

$$P_x(i, s) = \mathbb{P}((I(\tau), S(\tau)) = (0, N - x) | (I(0), S(0)) = (i, s)) \text{ for } x = 0, 1, \dots, N,$$

which gives the probability that the final cumulative infective number is x with initial state (i, s) . Then what we seek is the final size distribution

$$P_x(1, N - 1) \text{ for } x = 1, \dots, N.$$

Result and discussion

Figure 1 shows the idea of our algorithm. The node is denotes $P_s(i, s)$ and the arrows denote the operations in the iteration. The node 14 is what we seek. The columns 0 and 1 are all 0, the nodes 03,04 and 05 are 0 and the node 02 is 1. Notice that when we proceed a column, the memory of previous column is unnecessary. Let $a = (a_0, a_1, a_2, a_3, a_4)$, which saves the values of the nodes 01,11,21,31,41. Next, we proceed to the next column and update a_1, a_2, a_3, a_4 to be 02,12,22,32. Likewise, we then update a_2, a_3, a_4 to be 03,13,23 and proceed successively to the column 4, the newest updated a_4 is exactly the value at the node 14, which is desired. This idea of saving memory is from [2], in which we combine the idea of saving calculation time from [1], to make the computation more efficient.

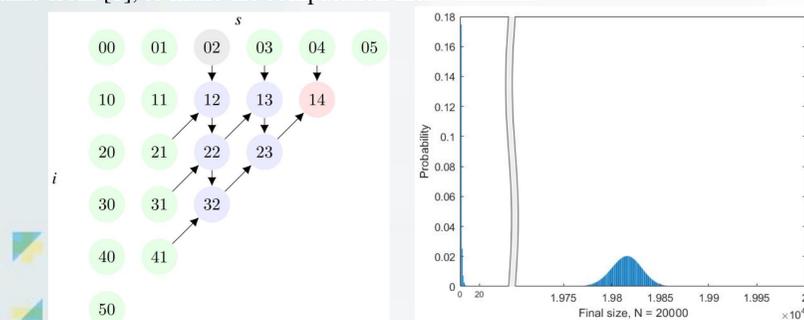


Figure 1.

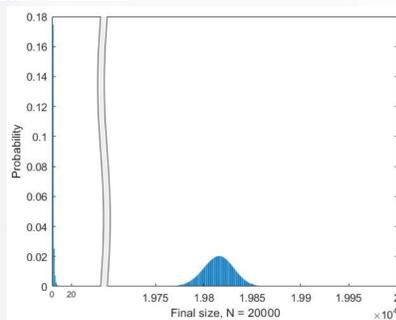


Figure 2.

Figure 2 is the result of final size distribution when $N = 20000$, $\lambda = 1.95$, $\alpha = 0.4$ and $\theta = 0.03$. The distribution is bimodal.

We approximate the final epidemic value R_∞ from the corresponding deterministic ODE model in Table 1.

Population size N	3000	5000	10000	20000
$\mathbb{E}(x) / N$	0.7811	0.7812	0.7812	0.7812
R_∞ / N	0.8246	0.8179	0.7993	0.7821
$ \mathbb{E}(x) / N - R_\infty / N $	4.35%	3.67%	1.81%	0.09%

Table 1.

We compare the efficiency of our algorithm and Algorithm 1 in [1] in Table 2.

Algorithm	Our algorithm	Algorithm 1 in [1]
Required memory	$O(N^2)$	$O(N^3)$
Time complexity	$O(N^3)$	$O(N^4)$
CPU time (sec) when $N = 100$	0.012	2.896
CPU time (sec) when $N = 500$	0.136	1842.124
CPU time (sec) when $N = 1000$	0.684	29325.387

Table 2.

The basic reproduction number is defined to be

$$\mathcal{R}_0 = \frac{\lambda}{\alpha}$$

and the effective reproduction number follows to be $\mathcal{R}_e = \frac{\lambda(1 - \theta)}{\alpha}$ due to the immunity from vaccinations.

In the Markov SIRV model, the extinction probability is derived to be the minimum among 1 and $1 / \mathcal{R}_e$, which is the reciprocal of the effective reproduction number. This has an important connection with the final size distribution. Under our setting of parameters, we can calculate the extinction probability as 0.2115.

We draw the bar chart of the cumulative probability of final size with a large population in Figure 3 to observe that the plateau value in the chart is approximately the value of the extinction probability.

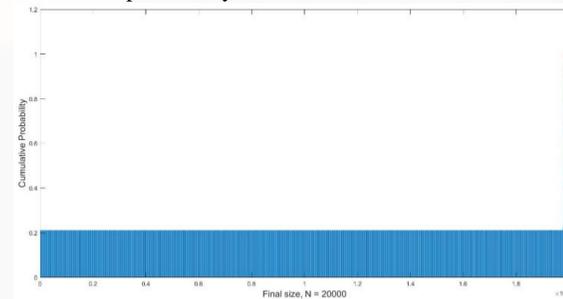


Figure 3.

Conclusions

Our algorithm requires memory $O(N^2)$ and time complexity $O(N^3)$, where N is the population size. For the correspondence to the results from the deterministic model described by ODEs, it is both explained mathematically and observed numerically that the deterministic model is an approximation of the Markov SIRV model for large N . The numerical result based on the data from the USA shows that the second peak of the distribution occurs with around 99% of the population and the extinction probability of COVID-19 is as low as 21.15% so that it is not easy to reach the zero-COVID state under the current situation.

References

- [1] Z. G. İşlier, R. Güllü, and W. Hörmann, An exact and implementable computation of the final outbreak size distribution under Erlang distributed infectious period, *Mathematical Biosciences*, 325 (2020), p. 108363.
- [2] A. J. Black and J. V. Ross, Computation of epidemic final size distributions, *Journal of theoretical biology*, 367 (2015), pp. 159–165.
- [3] P. E. Greenwood and L. F. Gordillo, Stochastic epidemic modeling, in *Mathematical and statistical estimation approaches in epidemiology*, Springer, 2009, pp. 31–52.

