



Stochastic models on the transmission of novel COVID-19

Bimal Kumar Mishra¹

Received: 5 October 2020 / Revised: 6 July 2021 / Accepted: 24 August 2021 / Published online: 6 September 2021

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Abstract New diseases have always been part of humanity's world, and some of them had created severe threat to human kind and challenge to the researchers and medical practitioners. The deadly novel coronavirus SARS-CoV-2 (severe acute respiratory syndrome- coronavirus -2) said to be COVID-19, the name given by WHO on February 11, 2020, is presently the most disastrous infectious disease. In the present paper our basic objective is to assess the risk of spreading the disease in human population and is measured in terms of probability. The proposed stochastic models help us to understand the probability of infection to n number of customers when these customers have spent time t in any system, say, shopping mall or public transportation or restaurant. Stochastic models are developed with arrival rate of the customers towards the system to be considered as a Poisson distribution and service time following an exponential distribution. A special case of cardiac centre is considered in this paper, where the risk of COVID-19 is highly contagion, with limited number of beds and doctors.

Keywords Poisson distribution · Exponential distribution · COVID-19 · Stochastic model

1 Introduction

The highly infectious disease of the twenty-first century, coronavirus disease (COVID-19), has affected nearly all corners of the globe. After declaring severe acute respiratory syndrome corona virus 2 (SARS-CoV-2), also said to be COVID-19, as pandemic by World Health Organization (WHO) on February 11, 2020., WHO had reported 27,688,740 confirmed cases of COVID-19, including 899,315 deaths with 201,115 new cases in 216 countries as of 10:28 am CEST, 10th September 2020 (<https://covid19.who.int>, . xxxx).

Mathematical models on infectious diseases provide predictions about the evolution of the number of infected, recovered, and deceased patients. The critical parameters of the infectious disease model, that is, infectivity contact rate, recovery rate, and death rate play a vital role in the predictions accuracy, along with the reproduction number which depends on these rates are crucial in helping governments to take appropriate measures to combat the epidemic and flatten the curve (Bimal Kumar Mishra 2020). Sometimes it becomes very difficult to model an infectious disease when partial and inaccurate information is available. He et al. (He et al. 2020) developed a stochastic model to understand the transmitting behavior of COVID-19 in human population. Hoertel et al. (Hoertel et al. 2020) developed a stochastic agent-based model of coronavirus disease with various intervention strategies. Maheshwari et al. (Maheshwari et al. 2020) stressed on the role of Big Data Analytics in the present COVID-19 transmission. Chen et al. (Chen et al. 2021) in his work addresses on the very interesting and relevant query “Can customer arrival rates be modelled by sine waves?” Olivares and Staffetti (Olivares and Staffetti 2021) studied the uncertainty

✉ Bimal Kumar Mishra
principalmcc@vbu.ac.in

¹ Markham College of Commerce, Hazaribag, India

quantification and sensitivity analysis of a mathematical model of the SARS-CoV-2 virus transmission dynamics with a mass vaccination strategy. Moore et al. (Moore et al. 2021) used the epidemiological data from the UK together with estimates of vaccine efficacy to predict the possible long-term dynamics of SARS-CoV-2 under the planned vaccine rollout. Mishra et al. (Mishra et al. 2021) developed the SEQIQR model to understand the transmission of the corona virus with an emphasis on home isolation and hospital quarantine. Li et al. (Li 2020) developed a model to assess the effect of mass influenza vaccination on the spread of COVID-19 and other respiratory pathogens in the case of a coincidence of the outbreak with the influenza season. Batistela et al. (SIRSi 2020) studied SIRSi-Vaccine dynamical model for the Covid-19 pandemic. Fanelli, and Piazza developed a SIRD compartmental model by dividing the human population in susceptible, infected, recovered and death classes. They simulated the model for mainland China, Italy and France using real data and also forecast the spread of COVID-19 in these three countries (Fanelli and Piazza 2020). Ndairou et al. (Ndairou et al. 2020) developed a mathematical model with eight compartments. The inclusion of super spreaders class makes it different from other COVID-19 based models. Matheus et al. (Ribeiro 2020) evaluated autoregressive integrated moving average (ARIMA), cubist regression (CUBIST), random forest (RF), ridge regression (RIDGE), support vector regression (SVR), and stacking-ensemble learning in the task of time series forecasting with one, three, and six-days ahead the COVID-19 cumulative confirmed cases in ten Brazilian states with a high daily incidence. Tagliazucchi et al. (Tagliazucchi et al. 2020) build increasingly complex and realistic models, ranging from simple homogeneous models used to estimate local reproduction numbers, to fully coupled inhomogeneous (deterministic or stochastic) models incorporating mobility estimates from cell phone location data.

Recently due to some reason or how, when several countries of the world after lockdown has adopted unlock down policy with certain restrictions, the rate of transmission of COVID-19 has increased several manifolds. The policy for reopening shopping malls, public transportation, restaurants etc., even after certain preventive measures, has opened the door of high transmission rate of the disease. When partial and inaccurate information is available, researchers look forward for the prediction of chaotic dynamical system, that is, developing stochastic models to understand the probability of infection to n number of customers when they have spent time t in any system, say, shopping mall or public transportation or restaurant.

2 The stochastic model

In this section, we develop a stochastic model on the transmitting behavior of severe acute respiratory syndrome corona virus 2 (SARS-CoV-2), said to be COVID-19. Our basic objective is to assess the risk of spreading the disease and is measured in terms of probability. The infection is at the highest level when two individuals are within 2 m of each other, when one of them is having symptom or infected by COVID-19. We are interested in knowing the probability of number of newly infected COVID-19 individuals in any system (say, shopping mall or public transportation or restaurant) when infected individuals have spent time t in that system.

2.1 Model I: the pre-infection and post infection process

When an individual or group of individuals enter into the system (shopping mall or traveling in a public transport or restaurant) having the symptoms of COVID-19 or infected by COVID-19 is said to be in a “pre-infection stage” of the mass population and the “post infection stage” means “an individual or group of individuals being infected” by the infected individual(s) who are departing from the system after spending a substantial amount of time in the system (say around 3 to 4 h) and were at a close proximity (may be less than 2 m) with uninfected individuals. We do assume that the infected individual(s) arriving to the system is a random variable and follows Poisson distribution. The departure time of an infected individual(s) from the system is a random variable and follows an exponential distribution. This process is defined by the following axioms:

Axiom 1: Given $N(t) = n$, that is, given that there are n individuals in the system at time t , the conditional probability distribution of the time (reckoned from the instant t) until the next infected arrives is exponential with parameter λ_n ($n = 0, 1, 2, \dots$).

Axiom 2: Given $N(t) = n$, the conditional probability distribution of the time (reckoned from the instant t) until the next infected leaves the system is exponentially distributed with parameter μ_n ($n = 1, 2, \dots$), $\mu_0 = 0$.

Axiom 3: The arrival and departure of the infected individuals in the system occur independently for a given population size n .

Let Δt denote a small increment in the time t .

- (i) P [no arrival of infected individual in a small interval $(t, t + \Delta t) | N(t) = n] = \int_{\Delta t}^{\infty} \lambda_n e^{-\lambda_n t} dt, = e^{-\lambda_n \Delta t} = 1 - \lambda_n \Delta t + o(\Delta t)$, (using axiom 1)

- (ii) P [two or more infected individuals in the interval $(t, t + \Delta t] | N(t) = n] = o(\Delta t)$, due to axiom 3.
- (iii) P [arrival of exactly one infected in the interval $(t, t + \Delta t] | N(t) = n] = [1 - [1 - \lambda_n \Delta t + o(\Delta t)] + o(\Delta t)] = \lambda_n \Delta t + o(\Delta t)$, by using (i) and (ii)
- (iv) P [exactly one infected individual leaving the system in an interval $(t, t + \Delta t] | N(t) = n] = \mu_n \Delta t + o(\Delta t)$
- (v) P [no infected arriving the system and no infected leaving the system in $(t, t + \Delta t] | N(t) = n] = 1 - \Delta t(\lambda_n + \mu_n) + o(\Delta t)$

This follows from the fact that in a small interval $(t, t + \Delta t]$, we have the following three mutually exclusive and exhaustive events:

1. Exactly one infected arrives the system and no infected leaves the system.
2. Exactly one infected leaves the system and no infected arrives the system.
3. No infected arriving or no infected departing from the system.

We denote these events by A, B, and C. Thus (iii), (iv) and (v) can be written as:

$$P(A|N(t) = n) = \lambda_n \Delta t + o(\Delta t)$$

$$P(B|N(t) = n) = \mu_n \Delta t + o(\Delta t)$$

$$P(C|N(t) = n) = 1 - \Delta t(\lambda_n + \mu_n) + o(\Delta t)$$

Let $P_n(t)$ denote the probability that there are n number of infected individuals in the system at any time t, that is,

$$P_n(t) = P[N(t) = n]$$

$$\begin{aligned} \text{Now, } P_n(t + \Delta t) &= P(N(t) = n \text{ and } \text{Cor}N(t) \\ &= n + 1 \text{ and } \text{Bor}N(t) = n - 1 \text{ and } A) + o(\Delta t) \\ &= [1 - \Delta t(\lambda_n + \mu_n)]P_n(t) + P_{n+1}(t)\mu_{n+1}\Delta t \\ &\quad + P_{n-1}(t)\lambda_{n-1}\Delta t + o(\Delta t) \end{aligned}$$

Thus we have,

$$\begin{aligned} \lim_{\Delta t \rightarrow 0} \frac{P_n(t) - P'_n(t)}{\Delta t} &= P'_n(t) \\ &= -(\lambda_n + \mu_n)P_n(t) + \mu_{n+1}P_{n+1}(t) \\ &\quad + \lambda_{n-1}P_{n-1}(t) \end{aligned} \tag{1}$$

For $n = 0, P_{n-1}(t) = 0$, and $\mu_0 = 0$, hence we have,

$$P'_0(t) = -\lambda_0 P_0(t) + \mu_1 P_1(t) \tag{2}$$

If at the start of the system, that is, at time zero, the system has i individuals, the initial conditions are

$$P_i(0) = 1, P_n(0) = 0, \text{ for } n \neq i \tag{3}$$

Further since $P_n(t), n = 0, 1, 2, \dots$ is the

probability distribution of the state n at time t, we must have,

$$\sum_{n=0}^{\infty} P_n(t) = 1, P_n(t) \geq 0, \forall n \text{ and } t \tag{4}$$

The existence and uniqueness of solutions of (1) to (4) have been well studied by Feller, McGregor, and Karlin (Breiman 1957).

It has been proved that the system (1) to (4) has a unique solution for all t if the series

$$\sum_{k=1}^{\infty} \prod_{i=1}^k \frac{\mu_i}{\lambda_i} = \infty \tag{5}$$

If in addition, the series

$$\sum_{k=1}^{\infty} \prod_{i=1}^k \frac{\lambda_{i-1}}{\mu_i} \text{ is convergent} \tag{6}$$

Then for all k, the limits

$$P_k = \lim_{t \rightarrow \infty} P_k(t) \text{ exist} \tag{7}$$

and are independent of the initial condition (3) (Hoertel et al. 2020).

We set, $\lim_{t \rightarrow \infty} P'_n(t) = 0$ and $\lim_{t \rightarrow \infty} P_k(t) = P_k$ in Eqs. (1), (2), and (4), and obtain

$$-(\lambda_n + \mu_n)P_n + \lambda_{n-1}P_{n-1} + \mu_{n+1}P_{n+1} = 0, n \geq 1 \tag{8}$$

$$-\lambda_0 P_0 + \mu_1 P_1 = 0 \tag{9}$$

$$\sum_{n=0}^{\infty} P_n = 1 \tag{10}$$

From Eqs. (8) and (9), we have,

$$P_n = C_n P_0 \tag{11}$$

where

$$C_n = \frac{\lambda_0 \lambda_1 \lambda_2 \dots \lambda_{n-1}}{\mu_0 \mu_1 \mu_2 \dots \mu_n}, n = 1, 2, \dots, C_0 = 1 \tag{12}$$

Using mathematical induction, it can be shown that (11) is true for all n.

Substituting (11) in (1), we have, $P_0(\sum_{n=0}^{\infty} C_n) = 1$, where $C_0 = 1$.

Thus, we have,

$$P_0 = \left(\sum_{n=0}^{\infty} C_n \right)^{-1} \tag{13}$$

provided that the series $\sum_{n=0}^{\infty} C_n$ is convergent. Thus the convergence of the series is a necessary condition for the steady-state (Gross and Harris xxxx).

We summarize some of the critical variables involved in estimating the events happening in the system (shopping mall, restaurant, public transport) with the help of (11):

- a. Average number of individuals in the system,

$$L = \sum_{n=0}^{\infty} nP_n \quad (14)$$

- b. Average length of time an individual spends in the system,

$$W = \frac{L}{\lambda} \quad (15)$$

where, $\bar{\lambda} = \sum_{n=0}^{\infty} \lambda_n P_n$

These two variables will help us to understand the spread of the disease in n number of individuals at any time t .

2.2 Case study: cardiac nursing home—risk of COVID-19 contagion (model II)

The coronavirus is infecting indiscriminately via droplets in the air or on surfaces, transmitted by coughing, sneezing or talking in close proximity. If a person gets coronavirus, the first thing it attacks is the lungs, setting of an inflammatory response that can stress the cardiovascular system of the body. First, the oxygen levels in the body will naturally fall when infected with a respiratory disease and then, the inflammatory nature of COVID-19 will cause a drop in blood pressure. Naturally the heart will have to beat and pump harder in both scenarios in order to supply oxygen to the body. This can become serious in cases with cardiovascular issues. Other groups susceptible to lower lung function include those patients who have undergone an organ transplant, those receiving chemotherapy, those with concomitant leukaemia or lymphoma suffering heart diseases are theoretically at the highest risk of contracting coronavirus on heart patients and succumbing to the same. The elderly are most susceptible and this is even more so in the case of elderly people with cardiovascular disease. Dr. Ashish observed that patients with serious heart problems like heart failure, dilated cardiomyopathy; to name a few, are at highest risk (<https://aakashhealthcare.com>, coronavirus-heart-patients. xxxx).

Cardiac nursing home or doctor's clinic with specialization in cardiology having limited number of beds (m) and limited number of doctors (s), ($m \geq s$) are becoming the centre of hotspot of COVID-19. Patients from an infinite population arrive towards the clinic or nursing home, from now onwards said to be system, for their treatment and may or may not be suffering from COVID-19. Our objective is to find the probability of n number of coronavirus patients, denoted by P_n , in these m number of patients at any instant of time. This P_n will further help us

to estimate (i) how many coronavirus patients there are in the system, and (ii) the length of time the coronavirus patients spend in the system.

Assumptions:

1. The interarrival times of the patients to the system are independent exponential variates with parameters λ .
2. The service time for each doctor is exponential with parameter μ .
3. The individual service times are mutually independent among the doctors as well as patients.
4. Population size is infinite, but the system cannot hold more than m patients.
5. The system has s number of doctors, working in parallel.
6. $m \geq s$

In (11) of Model I, substituting

$$\lambda_0 = \lambda_1 = \lambda_2 = \dots = \lambda_{m-1} = \lambda; \lambda_n = 0 \text{ for } n \geq m$$

$$\mu_n = n\mu, \text{ if } n < s, \text{ and } \mu_n = s\mu, \text{ if } n \geq s \quad (16)$$

We have,

$$C_n = \begin{cases} \frac{\rho^n}{n!}, \text{ for } n = 0, 1, 2, \dots, s-1 \\ \frac{\rho^n}{s!s^{n-s}}, \text{ for } n = s, s+1, \dots, m \end{cases}; C_n = 0 \text{ for } n = m+1, m+2, \dots \quad (17)$$

where, $\rho = \frac{\lambda}{\mu}$ said to be traffic intensity.

Thus from (17) and (11), we have,

$$P_n = \begin{cases} \frac{\rho^n P_0}{n!}, \text{ for } n = 0, 1, 2, \dots, s-1 \\ \frac{\rho^n P_0}{s!s^{n-s}}, \text{ for } n = s, s+1, \dots, m \end{cases}; P_n = 0 \text{ for } n = m+1, m+2, \dots \quad (18)$$

Using the fact that $\sum_{n=0}^{\infty} P_n = 1$, we get,

$$P_0 = 1 / \left[1 + \rho^s \left\{ \frac{1 - (\frac{\rho}{s})^{m-s+1}}{s!(1 - \frac{\rho}{s})} \right\} + \sum_{n=1}^{s-1} \frac{\rho^n}{n!} \right], \frac{\rho}{s} \neq 1 \quad (19)$$

3 Conclusion

The novel coronavirus disease COVID-19 which has come out with different variants and a great threat to human population across the globe has attracted researchers to develop models for minimizing the spread of the disease in the human population. The proposed stochastic models in this paper are to assess the risk of spreading the disease in the human population. Certain axioms and hypothesis are well considered during the pre-infection and post-infection process of COVID-19 in the human population. We have obtained the probability of number of newly infected COVID-19 individuals in any system (say,

shopping mall or public transportation or restaurant), when infected individuals have spent time t in that system, and it will help us to estimate (i) how many coronavirus patients there are in the system, and (ii) the length of time the coronavirus patients spend in the system. The study of these parameters will definitely throw managerial insights in space and crowd management, keeping into mind the physical distancing. Cardiac centers which is quiet contagious in the present pandemic scenario is considered, with limited number of beds and doctors as a case study, where we have also obtained the probability of number of newly infected COVID-19 individuals in the centre.

Acknowledgements The author is thankful to the anonymous referees whose suggestions have substantially improved the quality of the paper.

Funding No funding from any of the agencies.

Declarations

Conflicts of interest The author declared that there is no conflict of interest.

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