Stochastic Process Modeling of the Infectious Disease Pandemic

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Abstract

Motivation and techniques of stochastic process modeling are discussed as an alternative to the prevailing deterministic SIR-type models of epidemiology in order to account for large statistical variance of infection characteristics observed in the recent COVID-19 pandemic. Analogy to the stochastic performance modeling of computer communication networks can be leveraged.

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1 Motivation and objectives of the research

So-called SIR models have been used as major mathematical tools for quantitative analysis and prediction of the recent world-wide spread of COVID-19 without much success. The SIR-type models are based on a set of simultaneous nonlinear ordinary differential equations in several variables. As such, it would be very difficult, in principle, for theoretically deterministic approaches to account for the large statistical variance in the number of infected people observed in different cities and countries with similar conditions around the world. The deterministic models would, at most, only yield average values for the time-varying characteristics of the disease.

The propagation of an infectious disease is a probabilistic process because contact with infectious persons does not necessarily cause the infection. It cannot be either certain that the vaccination suppresses infection completely. Therefore, deterministic methods do not seem to be appropriate to use for quantitative scaling of the pandemic of infectious diseases. We need to resort to some stochastic process approach for proper dimensioning of the pandemic of infectious diseases.

The late Dr. Hisashi Kobayashi (previously IBM researcher, professor emeritus of Princeton University who passed away in March, 2023) left behind a series of unpublished working papers in which he proposed the birth-and-death-with-immigration (BDI) process model for epidemics and provided new insights that were not available with deterministic models. After his untimely death, the authors of this article were asked by his wife to sort out and bring his work to a wider audience in traditional engineering domains where the stochastic approach has been successfully utilized.

We believe that exploration of novel techniques for epidemic modeling will contribute to society in general as well as to academia with significant impact. In this article, we clarify how the SIR model and the BDI process model are different with respect to the theoretical solution and provide numerical examples as our first exposition of the latter promising approach.

2 SIR model of Kermack-McKendrick

In classical epidemiology of infectious diseases, all individuals in a population with a finite size N are partitioned into three distinct groups. We consider the number of individuals in each group as follows:

$S(t)$ $\triangleq$ Number of individuals who are susceptible to infection at time t,

$I(t)$ $\triangleq$ Number of individuals who are infected (and infectious) at time t,

$R(t)$ $\triangleq$ Number of individuals who have recovered, have died, or have been removed (for example, to a hospital) by time t.

It is assumed that those individuals who join the third group acquire complete immunity so that they never move back to the other groups again. Such a model was first introduced by Kermack and McKendrick in 1927. It is now called the *SIR model*, which has been a major mathematical model for studying recent pandemic of COVID-19.

We have the *conservation law* which holds at all times:

$$S(t) + I(t) + R(t) \equiv N \qquad t \geq 0.$$

Two constant parameters are provided as follows:

$\beta \triangleq$ Mean number of individuals who get infected from $S(t) \cdot I(t)$ persons per unit time (contact rate),

$\gamma \triangleq$ Mean number of individuals who have recovered, died, or been removed per unit time (removal rate).

The infection process is characterized by the number of individuals infected per unit time on average,

$$\mathcal{R}_t \triangleq \frac{\beta S(t)}{\gamma}, \quad (t \geq 0) \quad ; \quad \mathcal{R}_0 \triangleq \frac{\beta S(0)}{\gamma},$$

which are called the *reproduction number* at time t and the *basic reproduction number* (at time 0), respectively. If $\mathcal{R}_t > 1$, $I(t)$ increases, and if $\mathcal{R}_t < 1$, $I(t)$ decreases at time t.

3 A set of simultaneous nonlinear ordinary differential equations

The SIR model is given as the following simultaneous set of first-order (with respect to time t) nonlinear ordinary differential equations:

$$\begin{aligned} \frac{dS(t)}{dt} &= -\beta I(t)S(t), \\ \frac{dI(t)}{dt} &= \beta I(t)S(t) - \gamma I(t), \\ \frac{dR(t)}{dt} &= \gamma I(t), \end{aligned}$$

with the initial conditions: $S(0) = N - 1, I(0) = 1, R(0) = 0$, assuming that there is a single infected individual in the population at time $t = 0$.

4 Numerical examples of the SIR model

The solution to the above set of equations can be obtained by numerical computation. We show two cases. The first case is shown in Figure 1.

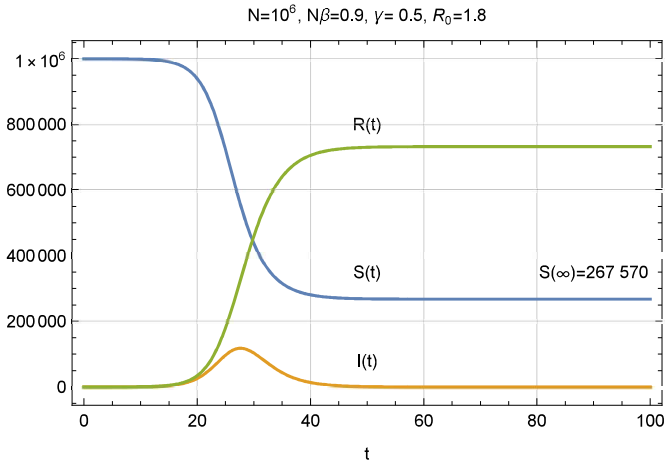

図 1: Behavior of $\{S(t), I(t), R(t)\}$ for the case $N = 1,000,000$, $N\beta = 0.9 < 1$, $\gamma = 0.5$, $\mathcal{R}_0 = 1.8$.

In Figure 1, we observe the following:

(i) $R(t)$ increases monotonically to the limiting value $N - S(\infty)$.

(ii) $S(t)$ decreases monotonically to the limiting value $S(\infty)$.

(iii) $I(t)$, initially 1, first increases, and then decreases to 0.

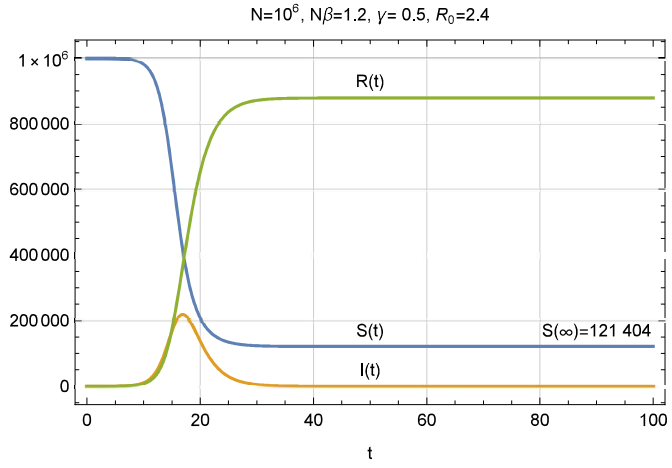

図 2: Behavior of $\{S(t), I(t), R(t)\}$ for the case $N = 1,000,000$, $N\beta = 1.2 > 1$, $\gamma = 0.5$, $\mathcal{R}_0 = 2.4$.

In Figure 2, we observe the following:

(i) With larger $\mathcal{R}_0$, $I(t)$ grows earlier, and its peak is higher than that in Figure 1.

(ii) As more people get infected, and then recover, die, or are removed earlier, there remain fewer susceptible people than in Figure 1.

Given the values of parameters N, β, and γ, the limiting value $S(\infty)$ can be determined as the solution to the nonlinear equation:

$$\frac{S(\infty)}{N-1} = \exp\left[-\frac{\beta}{\gamma}(N - S(\infty))\right].$$

See Hethcote (2000) for an extensive survey of the SIR and other deterministic models.

5 Birth-and-death-with-immigration (stochastic process) model

In a stochastic process model, we do not limit the population size.

(1) Birth-and-death-with-immigration (BDI) process

Three constant parameters of the model:

- λ (birth rate) : number of individuals infected from others per unit time
- μ (death rate) : number of individuals who become non-infectious per unit time
- ν (immigration rate) : number of infected persons who enter from outside per unit time

(2) A continuous-time Markov process $\{I(t), R(t); t \geq 0\}$

$$\begin{aligned} I(t) &\triangleq \text{number of infected individuals at time } t, \quad I(0) = I_0 \\ R(t) &\triangleq \text{number of individuals who have recovered,} \\ &\quad \text{died, or been removed by time } t, \quad R(0) = 0 \end{aligned}$$

(3) Joint Probability Mass Function (PMF)

$$P_{m,n}(t) \triangleq P\{R(t) = m, I(t) = n\}, \quad m, n = 0, 1, 2, \ldots$$

(4) Chapman-Kolmogorov equations

$$\begin{aligned} P_{m,n}(t + \Delta t) &= P_{m,n}^{R,I}(t)\{1 - [n(\lambda + \mu) + \nu]\Delta t\} + P_{m-1,n+1}(t)(n+1)\mu\Delta t \\ &+ P_{m,n-1}(t)[(n-1)\lambda + \nu]\Delta t + o(\Delta t), \quad m, n = 0, 1, 2, \ldots \end{aligned}$$

(5) Forward Kolmogorov differential equations

$$\begin{aligned} \frac{dP_{m,n}(t)}{dt} &= -[n(\lambda + \mu) + \nu]P_{m,n}(t) + (n+1)\mu P_{m-1,n+1}(t) \\ &+ [(n-1)\lambda + \nu]P_{m,n-1}(t), \quad m, n = 0, 1, 2, \ldots \end{aligned}$$

(6) Joint Probability Generating Function (PGF)

$$G(y,z;t) \triangleq E\left[y^{R(t)}z^{I(t)}\right] = \sum_{m=0}^{\infty}\sum_{n=0}^{\infty}\Pr\{R(t)=m, I(t)=n\}y^m z^n$$

satisfies a planar Partial Differential Equation (PDE)

$$\frac{\partial G(y,z;t)}{\partial t} - [\lambda z(z-1) - \mu(z-y)]\frac{\partial G(y,z;t)}{\partial z} = -\nu(z-1)G(y,z;t),$$

which can be solved by Lagrange's method (Betz, et al., 1954).

6 Lagrange's method for the planar PDE

The corresponding set of auxiliary differential equations defining the normal at a point on the solution surface is given by

$$\frac{dt}{1} = -\frac{dz}{\lambda z(z-1) - \mu(z-y)} = -\frac{dG(y,z;t)}{\nu(z-1)G(y,z;t)}. \qquad (*)$$

From the quadratic equation

$$\lambda z(z-1) - \mu(z-y) = \lambda(z - z_1(y))(z - z_2(y)) = 0,$$

we have

$$z_1(y) \triangleq \frac{\lambda+\mu+\sqrt{D(y)}}{2\lambda} \quad ; \quad z_2(y) \triangleq \frac{\lambda+\mu-\sqrt{D(y)}}{2\lambda}.$$

With the determinant $D(y) \triangleq (\lambda+\mu)^2 - 4\lambda\mu y$, we have

$$z_1(1) = 1, \quad z_2(1) = \frac{\mu}{\lambda}, \quad \sqrt{D(1)} = |\lambda - \mu| = |a|, \quad \text{where} \;\; a \triangleq \lambda - \mu.$$

From the leftmost and middle terms of $(*)$, we get

$$\frac{z - z_1(y)}{z - z_2(y)} e^{\sqrt{D(y)}\, t} = C_1.$$

From the middle and rightmost terms of $(*)$, we get

$$G(y,z;t) H(z; z_1(y), z_2(y))^{\frac{r}{z_1(y) - z_2(y)}} = C_2,$$

where C_1 and C_2 are integration constants, and

$$H(z; z_1(y), z_2(y)) \triangleq \frac{(z - z_1(y))^{1-z_1(y)}}{(z - z_2(y))^{1-z_2(y)}}.$$

We assume a functional relation $C_2 = f(C_1)$.
From the initial condition $R(0) = 0$ and $I(0) = I_0$ at $t = 0$, we get

$$G(y,z;0) = z^{I_0} = H(z; z_1(y), z_2(y))^{\frac{r}{z_2(y) - z_1(y)}} f\left(\frac{z - z_1(y)}{z - z_2(y)}\right), \quad \text{where} \;\; r \triangleq \frac{\nu}{\lambda}.$$

Changing the variable from z to w by

$$w \triangleq \frac{z - z_1(y)}{z - z_2(y)} \quad ; \quad z = \frac{z_1(y) - z_2(y)w}{1 - w},$$

we determine

$$\begin{aligned} f(w) &\triangleq \left(\frac{z_1(y) - z_2(y)w}{1 - w}\right)^{I_0} H(z; z_1(y), z_2(y))^{\frac{r}{z_1(y) - z_2(y)}} \\ &= \left(\frac{z_1(y) - z_2(y)w}{1 - w}\right)^{I_0} \left[(z_1(y) - z_2(y))^{z_2(y) - z_1(y)} (1 - w)^{z_1(y) - z_2(y)} w^{1 - z_1(y)}\right]^{\frac{r}{z_1(y) - z_2(y)}} \\ &= \left(\frac{z_1(y) - z_2(y)w}{1 - w}\right)^{I_0} \left(\frac{1 - w}{z_1(y) - z_2(y)}\right)^{r} w^{\frac{r(1 - z_1(y))}{z_1(y) - z_2(y)}}. \end{aligned}$$

(1) Product-form solution:

$$G(y, z; t) = G^{\mathrm{BD}:I_0}(y, z; t) \cdot G^{\mathrm{BDI}:0}(y, z; t),$$

where

$$G^{\mathrm{BD}:I_0}(y, z; t) = \left(\frac{z_1(y)(z - z_2(y)) - z_2(y)(z - z_1(y))e^{\sqrt{D(y)}\, t}}{z - z_2(y) - (z - z_1(y))e^{\sqrt{D(y)}\, t}}\right)^{I_0},$$

$$G^{\mathrm{BDI}:0}(y, z; t) = \left(\frac{z_1(y) - z_2(y)}{z - z_2(y) - (z - z_1(y))e^{\sqrt{D(y)}\, t}}\right)^{r} e^{\nu(1 - z_1(y))t}.$$

This product-form solution implies that the process $\mathrm{BDI}:I_0$ consists of the superposition of two independent processes $\mathrm{BD}:I_0$ and $\mathrm{BDI}:0$.

(2) Marginal distribution of $I(t)$

$$\begin{aligned} E\left[z^{I(t)}\right] &= G(1, z; t) = \left(\frac{\lambda z - \mu - \mu(z - 1)e^{at}}{\lambda z - \mu - \lambda(z - 1)e^{at}}\right)^{I_0} \\ &\cdot \left(\frac{a}{\lambda z - \mu + \lambda(z - 1)e^{at}}\right)^{r}. \end{aligned}$$

$$\text{Mean}: \quad E[I(t)] = I_0 e^{at} + \frac{\nu}{a}(e^{at} - 1),$$

$$\text{Variance}: \quad \mathrm{Var}[I(t)] = I_0 \frac{\lambda + \mu}{a} e^{at}(e^{at} - 1) + \frac{\nu}{a^2}(\lambda e^{at} - 1)(e^{at} - 1).$$

(3) Marginal distribution of $R(t)$

$$E\left[y^{R(t)}\right] = G(y,1;t) = G^{\text{BD:}I_0}(y,1;t)\cdot G^{\text{BDI:0}}(y,1;t),$$

where

$$G^{\text{BD:}I_0}(y,1;t) = \left(\frac{z_1(y)(1-z_2(y)) - z_2(y)(1-z_1(y))e^{\sqrt{D(y)}\,t}}{1-z_2(y)-(1-z_1(y))e^{\sqrt{D(y)}\,t}}\right)^{I_0},$$

$$G^{\text{BDI:0}}(y,1;t) = \left(\frac{z_1(y)-z_2(y)}{1-z_2(y)-(1-z_1(y))e^{\sqrt{D(y)}\,t}}\right)^{r} e^{\nu(1-z_1(y))t}.$$

$$\text{Mean}: \quad E[R(t)] = \frac{\mu}{a}\left[I_0(e^{at}-1)+\frac{\nu}{a}(e^{at}+at-1)\right],$$

$$\begin{aligned}\text{Variance}: \quad \text{Var}[R(t)] &= I_0\left[\frac{2\lambda\mu^2}{a^2}\left(\frac{e^{2at}-1}{a}-2te^{at}\right)-\frac{\mu^2}{a^2}(e^{at}-1)^2+\frac{\mu}{a}(e^{at}-1)\right]\\ &+\frac{\nu}{\lambda}\left[\frac{(\lambda\mu)^2}{a^4}(-5+(1-4at)e^{at}+e^{2at})+\frac{\lambda\mu}{a^2}(e^{at}-1)\right]+\frac{\mu\nu t}{a}\left(1+\frac{2\lambda\mu}{a^2}\right).\end{aligned}$$

(4) Covariance of $I(t)$ and $R(t)$

$$\begin{aligned}\text{Cov}[I(t),R(t)] &= \left.\frac{\partial^2 \log G(y,z;t)}{\partial y\partial z}\right|_{y=z=1}\\ &= \frac{I_0}{a/\lambda}\left[-\frac{\mu}{a}(1+e^{at})-2\mu te^{at}\right]\\ &- \frac{I_0}{(a/\lambda)^2}\left[\left\{-\frac{2\mu}{a}+\frac{\mu^2}{\lambda a}(1-e^{at})\right\}\left(1-\frac{\mu}{\lambda}e^{at}\right)+\frac{\mu}{a}(1-e^{2at})\right]\\ &- \frac{\lambda\mu\nu}{a^3}\left(1+2ate^{at}-e^{2at}\right).\end{aligned}$$

Similar analysis is possible for the BDI process model when $\lambda(t)$, $\mu(t)$, and $\nu(t)$ are arbitrary functions of time t.

7 Numerical examples of the stochastic process model

We plot the mean $E[I(t)]$ and $E[R(t)]$, the variance $\mathrm{Var}[I(t)]$ and $\mathrm{Var}[R((t)]$, and the covariance $\mathrm{Cov}[I(t), R(t)]$ by assuming the following parameter values:

$$\lambda = 0.5, \quad \mu = 0.2, \quad (a \triangleq \lambda - \mu = 0.3), \quad \nu = 0.2, \quad I_0 = 1.$$

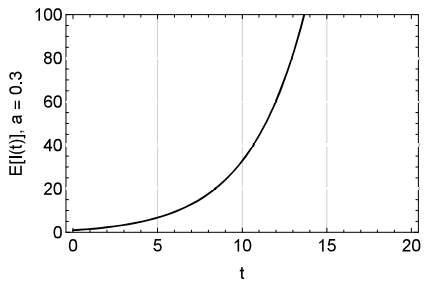

Fig. 3 $E[I(t)]$

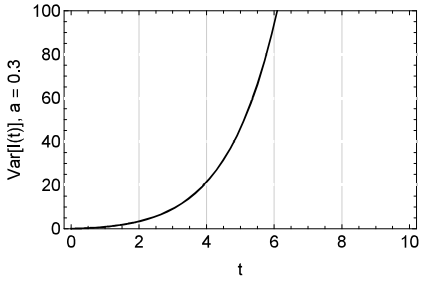

Fig. 4 $\mathrm{Var}[I(t)]$

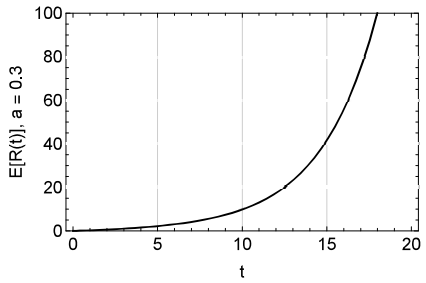

Fig. 5 $E[R(t)]$

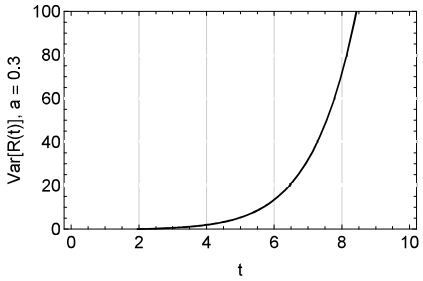

Fig. 6 $\mathrm{Var}[R(t)]$

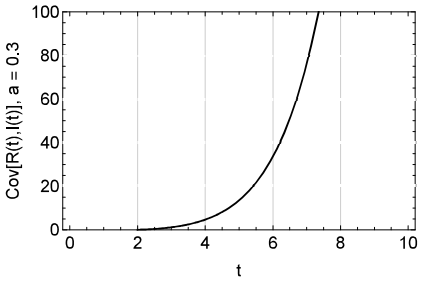

Fig. 7 $\mathrm{Cov}[I(t), R(t)]$

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