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A LIE ALGEBRA APPROACH TO SUSCEPTIBLE-INFECTED-SUSCEPTIBLE EPIDEMICS

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Abstract. The susceptible-infected-susceptible (SIS) epidemic model can be represented by a continuous-time Markov chain, which is governed by a set of deterministic differential equations (Kolmogorov forward equations). In this paper, a Lie algebra approach is applied to solve an SIS model where infection rate and recovery rate are time-varying. The method presented here has been used widely in chemical and physical sciences but not in epidemic applications due to insufficient symmetries.

1. Introduction

Analytical description of epidemic spreading has a long history and can be traced back to the seminal work of Kermack and McKendrick [11, 3], where only three simple ordinary differential equations are used following the mass action assumption; i.e., the rate of increase in epidemic incidence is proportional to the product of the number of infectious and susceptible individuals. It is also possible to capture the propagation phenomena by mean-field theory [16, 5, 7, 23] or generating function formalism [12, 14, 20] especially when the host population is modeled by a network. Such methods, however, are generally more accurate (and valid in essence) when the population size is relatively large.

Recently, Keeling and Ross [10] proposed a time homogeneous Markov chain model to characterize the stochastic nature of epidemic spreading. The complete ensemble of behavior can be predicted by $N+1$ differential equations for susceptible-infected-susceptible (SIS) dynamics [25] by virtue of the Kolmogorov forward equation [13], which governs the rates of transition between states of the disease. The solution of the system can be expressed by the form of matrix exponentials [10, 18]. Indeed, continuous-time Markovian models are shown to be powerful tools to study stochastic evolutionary processes and have been widely used in other biological and metapopulation models [1, 4, 15, 19].

In this paper, we further investigate the SIS paradigm represented by a time inhomogeneous Markov chain. In this model there is a fixed population of size N, where $S(t)$ and $I(t)$ represent the number of susceptibles and infectives, respectively, in the population at time t, $t \geq 0$, and $S(t) + I(t) = N$. No immunity is conferred

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upon recovery from infection, and recovered individuals return immediately to the susceptible state. Members of the population transmit the infection immediately upon becoming infected. Based on the Lie algebraic method developed in [24], we generate a low-dimensional Lie algebra and solve the Markovian model by deriving matrix exponential solutions. Different from many physical or chemical systems [2, 6], biological or epidemic models often lack of symmetries, which adds difficulty in finding a proper Lie algebra. It is worth noting that Lie algebra solution of some birth-and-death type population models is recently established by House [8].

The rest of the paper is organized as follows. In Section 2, we briefly review the Lie algebraic methodology for continuous-time Markov chains. we then apply it to an SIS epidemic model in Section 3, and conclude the paper in Section 4.

2. Lie algebra solution of time inhomogeneous Markov chains

In algebra theory, a Lie algebra [9] is a vector space V over some field F together with a bilinear map $[\cdot,\cdot] : V \times V \to V$ called the Lie bracket, which satisfies $[X, X] = 0$ and the Jacobi identity

$$[X,[Y,Z]] + [Y,[Z,X]] + [Z,[X,Y]] = 0, \tag{2.1}$$

for all $X, Y, Z \in V$. For $X \in V$, we define an adjoint operator $\mathrm{ad}X$ by

$$(\mathrm{ad}X)Y = [X, Y], \tag{2.2}$$

for $Y \in V$. In doing so, multiple Lie brackets can be expressed in a succinct way; e.g., $(\mathrm{ad}X)^2Y = [X,[X,Y]]$, etc. Every associate algebra gives rise to a Lie algebra V by defining the Lie bracket as a commutator

$$[X, Y] = XY - YX, \tag{2.3}$$

where $X, Y \in V$. In what follows, we will focus on this Lie product. The classical Baker-Campbell-Hausdorff formula can be written in terms of (2.2) as

$$e^X Y e^{-X} = (e^{\mathrm{ad}X})Y, \tag{2.4}$$

where $e^X = \sum_{i=0}^{\infty} X^i/i!$.

The type of processes we consider here are continuous-time Markov chains [10, 13], taking values in a finite or countably infinite state space $\mathcal{S}$. The dynamical behavior of the Markov chain is specified by a matrix $Q(t) = (q_{ij}(t), i, j \in \mathcal{S})$, where $q_{ij}(t)$ is the rate of transition from state i to state j, for $j \neq i$, and $-q_{ii}(t) = q_i(t) = \sum_{j\neq i} q_{ij}(t)$ is the total rate at which we move out of state i at time t. In light of the Kolmogorov forward equation (also called the ensemble or master equation), the probability distribution of the process at time t, $p(t) = (p_i(t), i \in \mathcal{S})$, is given by

$$\frac{\mathrm{d}p(t)}{\mathrm{d}t} = H(t)p(t), \tag{2.5}$$

where $H(t) = Q(t)^T$ (T means transpose), and $p(t)$ is a column probability vector with component $p_i(t)$ representing the probability of finding the system in state i at time t. Making use of the Dirac notation for vectors (kets $|\cdot\rangle$), the probability vector can alternatively be written as

$$|p(t)\rangle = \sum_{i\in\mathcal{S}} P(i|t)|i\rangle, \tag{2.6}$$

where $P(i|t)$ is the probability that the Markov chain in question taking the value of i at time t, and $|i\rangle$ is a basis vector, linearly independent of any other basis vector

with different value. Note that $H(t)$ in (2.5) is time-dependent implying that the process is time inhomogeneous.

The Lie algebraic method introduced in [24] requires a decomposition of the operator $H(t)$ as

$$H(t) = \sum_{i=1}^{m} a_i(t) H_i, \tag{2.7}$$

such that $a_i(t)$ are real-valued functions, and H_i are linearly independent constant operators generating a Lie algebra $V = \operatorname{span}\{H_1, \cdots, H_m\}$ by implementing a Lie bracket

$$[H_i, H_j] = H_i H_j - H_j H_i = \sum_{k=1}^{m} \xi_{ijk} H_k \tag{2.8}$$

for some real ξ_{ijk}. The solution of system (2.5) can be uncoupled into a product of exponentials [24]

$$p(t) = e^{g_1(t)H_1} \cdots e^{g_m(t)H_m} p(0) = U(t)p(0), \tag{2.9}$$

where $g_i(t)$ are real-valued functions and $g_i(0) = 0$.

Substituting (2.7) and (2.9) into (2.5), we obtain

$$\begin{aligned} \frac{\mathrm{d}p(t)}{\mathrm{d}t} &= \sum_{i=1}^{m} a_i(t) H_i U(t) p(0) \\ &= \sum_{i=1}^{m} \dot{g}_i(t) \Big(\prod_{j=1}^{i-1} e^{g_j(t)H_j} \Big) H_i \Big(\prod_{j=i}^{m} e^{g_j(t)H_j} \Big) p(0). \end{aligned} \tag{2.10}$$

On multiplying $U(t)^{-1}$ on both sides of (2.10), we have

$$\begin{aligned} &\sum_{i=1}^{m} a_i(t) H_i \Big(\prod_{j=1}^{m} e^{g_j(t)\mathrm{ad}H_j} \Big) p(0) \\ &= \sum_{i=1}^{m} a_i(t) H_i U(t) p(0) U(t)^{-1} \\ &= \sum_{i=1}^{m} \dot{g}_i(t) \Big(\prod_{j=1}^{i-1} e^{g_j(t)H_j} \Big) H_i \Big(\prod_{j=i}^{m} e^{g_j(t)H_j} \Big) p(0) U(t)^{-1} \\ &= \sum_{i=1}^{m} \dot{g}_i(t) \Big(\prod_{j=1}^{i-1} e^{g_j(t)\mathrm{ad}H_j} \Big) H_i \Big(\prod_{j=1}^{m} e^{g_j(t)\mathrm{ad}H_j} \Big) p(0). \end{aligned} \tag{2.11}$$

Since $p(0)$ is arbitrary, we conclude that

$$\sum_{i=1}^{m} a_i(t) H_i = \sum_{i=1}^{m} \dot{g}_i(t) \Big(\prod_{j=1}^{i-1} e^{g_j(t)\mathrm{ad}H_j} \Big) H_i. \tag{2.12}$$

From (2.12) we derive a linear relation between $a_i(t)$ and $\dot{g}_i(t)$ with initial values $g_i(0) = 0$ (involving ξ_{ijk}), as the operators H_i are linearly independent.

The calculation of $p(t)$ is achieved in $O(1)$ through (2.12) rather than $O(t)$ by means of incremental direct integrations. Therefore, the computation complexity can be dramatically reduced. The matrix exponential form (2.9) would be useful if the derivative of the solution with respect to some model parameter is required in subsequent calculations [24, 26].

3. An example: SIS epidemic spreading

The susceptible-infected-susceptible (SIS) epidemiological model [25] is an accurate yet simple representation of endemic infections. It is often used as a paradigm for many sexually transmitted infections and computer virus propagations [3, 21, 22]. The model describes the evolution of an infection in a fixed population, where N individuals in the population are divided into two subclasses: the susceptible pool, of size S, and the infected (and infectious) class, of size I, with $S + I = N$. Susceptible individuals become infected at a rate $\beta(t)$ by contagion from infected individuals, and infected individuals, in turn, recover (and once again become susceptible) at a rate $\gamma(t)$.

The above description of the SIS model leads to a Markovian process [10] whose probability vector can be written as

$$|p(t)\rangle = \sum_{S,I} P(S, I|t)|S, I\rangle, \tag{3.1}$$

where $P(S, I|t)$ denotes the probability that there are S susceptible individuals and I infected ones at time t. $|S, I\rangle$ is a basis vector, linearly independent of other basis vectors with different susceptible and infected numbers. The state space $\mathcal{S}$ consists of $N + 1$ elements.

The Kolmogorov equation governing this process can be written as

$$\frac{\mathrm{d}}{\mathrm{d}t}|p(t)\rangle = H(t)|p(t)\rangle, \tag{3.2}$$

with

$$H(t) = \gamma(t)(\hat{\rho} - \hat{I}) + \beta(t)(\hat{\sigma} - \hat{S}), \tag{3.3}$$

where

$$\begin{aligned} \hat{S}|S, I\rangle &= S|S, I\rangle \\ \hat{I}|S, I\rangle &= I|S, I\rangle \\ \hat{\rho}|S, I\rangle &= I|S + 1, I - 1\rangle \\ \hat{\sigma}|S, I\rangle &= S|S - 1, I + 1\rangle \end{aligned} \tag{3.4}$$

and all these operators are linear operators (note that a similar collection is derived for SIR model in [8]). Table 1 shows the complete set of Lie brackets, under which the algebra $V = \mathrm{span}\{\hat{S}, \hat{I}, \hat{\rho}, \hat{\sigma}\}$ is closed.

$\hat{X}$	$[\hat{X}, \hat{S}]$	$[\hat{X}, \hat{I}]$	$[\hat{X}, \hat{\rho}]$	$[\hat{X}, \hat{\sigma}]$
$\hat{S}$	0	0	$\hat{\rho}$	$-\hat{\sigma}$
$\hat{I}$	0	0	$-\hat{\rho}$	$\hat{\sigma}$
$\hat{\rho}$	$-\hat{\rho}$	$\hat{\rho}$	0	$\hat{S} - \hat{I}$
$\hat{\sigma}$	$\hat{\sigma}$	$-\hat{\sigma}$	$\hat{I}$	0

Table 1. Values of $[\hat{X}, \hat{Y}]$ for SIS model.

We need to look for a solution of the form

$$|p(t)\rangle = e^{g_1(t)\hat{S}} e^{g_2(t)\hat{I}} e^{g_3(t)\hat{\sigma}} e^{g_4(t)\hat{\rho}} |p(0)\rangle. \tag{3.5}$$

$\hat{X}$	$e^{g(\mathrm{ad}\hat{X})}\hat{S}$	$e^{g(\mathrm{ad}\hat{X})}\hat{I}$	$e^{g(\mathrm{ad}\hat{X})}\hat{\rho}$	$e^{g(\mathrm{ad}\hat{X})}\hat{\sigma}$
$\hat{S}$	$\hat{S}$	$\hat{I}$	$e^{g}\hat{\rho}$	$e^{-g}\hat{\sigma}$
$\hat{I}$	$\hat{S}$	$\hat{I}$	$e^{-g}\hat{\rho}$	$e^{g}\hat{\sigma}$
$\hat{\rho}$	$\hat{S}-g\hat{\rho}$	$\hat{I}+g\hat{\rho}$	$\hat{\rho}$	$\hat{\sigma}+g\hat{S}-g\hat{I}-g^2\hat{\rho}$
$\hat{\sigma}$	$\hat{S}+g\hat{\sigma}$	$\hat{I}-g\hat{\sigma}$	$\hat{\rho}+g\hat{I}-\frac{g^2}{2}\hat{\sigma}$	$\hat{\sigma}$

TABLE 2. Values of $e^{g(\mathrm{ad}\hat{X})}\hat{Y}$ with a scalar g for SIS model.

Employing (2.12) and the action of exponential operators shown in Table 2, we obtain

$$\begin{aligned}&\gamma(t)\hat{\rho}-\gamma(t)\hat{I}+\beta(t)\hat{\sigma}-\beta(t)\hat{S}\\&=\dot{g}_1(t)\hat{S}+\dot{g}_2(t)\hat{I}+\dot{g}_3(t)e^{g_2}e^{-g_1}\hat{\sigma}+\dot{g}_4(t)\Big(e^{-g_2}e^{g_1}\hat{\rho}+g_3\hat{I}-\frac{g_3^2}{2}e^{g_2}e^{-g_1}\hat{\sigma}\Big).\end{aligned}\tag{3.6}$$

Equating terms in (3.6) in front of the same basis matrices yields

$$\begin{aligned}g_1(t)&=-\mathrm{B}(t),\\g_4(t)&=\int_0^t\gamma(u)e^{g_2(u)+\mathrm{B}(u)}\mathrm{d}u,\end{aligned}\tag{3.7}$$

where $\mathrm{B}(t)=\int_0^t\beta(u)\mathrm{d}u$; $g_2(t)$ and $g_3(t)$ are determined by the initial value problem

$$\begin{aligned}\dot{g}_2(t)&=-\gamma(t)-g_3(t)\gamma(t)e^{g_2(t)+\mathrm{B}(t)},\\\dot{g}_3(t)&=\beta(t)e^{-\mathrm{B}(t)-g_2(t)}+\frac{\gamma(t)}{2}e^{g_2(t)+\mathrm{B}(t)}g_3(t)^2,\\g_2(0)&=g_3(0)=0.\end{aligned}\tag{3.8}$$

The function g_3 satisfies a Riccati equation, which may be solved by standard reduction techniques or numerical integration; see e.g. [17]. Let $|\mathcal{I}(t)\rangle=\sum_{S,I}I|S,I\rangle$, and then $I(t)=\langle\mathcal{I}(t)|p(t)\rangle$ is the number of infected individuals in the population at time t. In Fig. 1 we illustrate $I(t)$ with respect to different choices of $\beta(t)$ and $\gamma(t)$ in a population of size $N=100$.

When $\gamma=0$, the model reduces to a simple susceptible-infected (SI) epidemics, where individuals, once infected, are infected (and infectious) forever. In this case, the solution of (3.6) can be obtained as

$$\begin{aligned}g_1(t)&=-\mathrm{B}(t),\\g_3(t)&=\int_0^t e^{-\mathrm{B}(u)}\beta(u)\mathrm{d}u,\\g_2(t)&=g_4(t)=0,\end{aligned}\tag{3.9}$$

where $\mathrm{B}(t)=\int_0^t\beta(u)\mathrm{d}u$. Note that this can be derived similarly from the SIR model addressed in [8]. The consistency confirms that our result is valid.

Conclusion. In this paper, we showed that it is possible to solve susceptible-infected-susceptible (SIS) model via a Lie algebra methodology. Lie algebra solution of differential equations has found host of useful applications in physical systems, where wealthy symmetries exist. Due to insufficient symmetry, this method is not widely used in biological or social systems. For future work, more complex

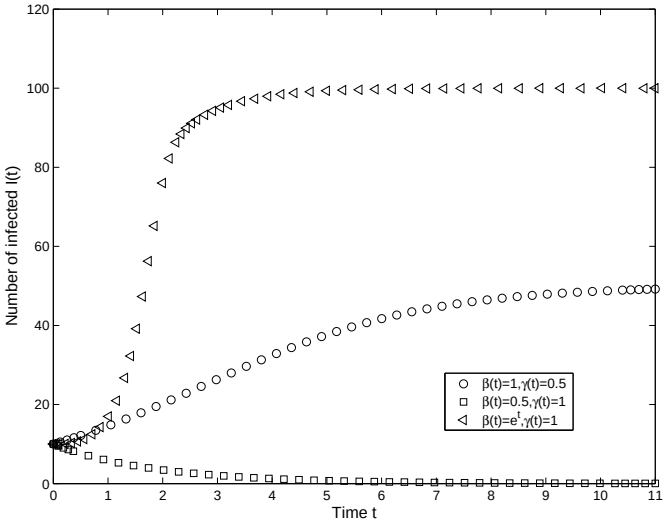

FIGURE 1. Dynamics of the SIS model with $N = 100$ and $|p(0)\rangle = |0.9 \cdot N, 0.1 \cdot N\rangle$. $I(t) = \langle \mathcal{I}(t)|p(t)\rangle$ are plotted with respect to $\beta(t) = 1, \gamma(t) = 0.5$ (circles), $\beta(t) = 0.5, \gamma(t) = 1$ (squares), and $\beta(t) = e^t, \gamma(t) = 1$ (triangles), where $|p(t)\rangle$ are obtained from (3.5).

and realistic epidemiological mechanisms, such as susceptible-exposed-infectious-recovered (SEIR) model, are worthy of further research.

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