ANALYTICAL SOLUTION FOR AN IN-HOST VIRAL INFECTION MODEL WITH TIME-INHOMOGENEOUS RATES

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We present the analysis of a time-inhomogeneous Markov chain model based on the *in vivo* viral infection dynamics. The exact solution of a general in-host model with time-dependent rates is obtained by using the Lie-theoretic approach. The results provide both an improvement in numerical efficiency and the potential for analytical solution of other biological processes without clear symmetry.

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1. Introduction

Over the last few decades, in-host mathematical modeling has increasingly been used in attempts to understand the pathogenesis of numerous viruses such as hepatitis B virus (HBV), human immunodeficiency virus type 1 (HIV-1), and human T-cell lymphotropic virus type 1 (HTLV-1) [1–7]. Mathematical models describing the *in vivo* infection process of such viruses are valuable for estimating virion clearance rate, infected cell lifespan, and viral generation time, and for probing the dynamics and mechanism of the virus replication *in vivo* [5, 6]. A simple, while natural, in-host viral model involves the interactions between: *(i)* healthy target cells, *(ii)* infected cells producing viruses, and *(iii)* (matured) free viruses. More realistic aspects such as intracelluar delays, immune responses, and mutation have been incorporated into the models [8–11]. These models have led to a wealth of theoretical research on global stability of the persistence equilibria and infection-free equilibria of the systems, see [5, 8, 9, 11–15] to name but a few. However, due to its coupled nonlinearity, deriving the exact solution of the basic in-host model (even in the non-delay and constant coefficients case) remains a long-standing open research problem.

On the other hand, Markov chain models have proven to be useful in exploring many biological stochastic processes ranging from disease transmission and metapopulation evolution to gene induction [16–20]. From a dynamical system perspective, analysis of such models means to consider the Kolmogorov (master) equations, *i.e.*, a system of linear ODEs, which characterize the evolution of the probability of the process being in a given state at a given time. In this paper, we aim to derive analytical solution for a general viral model with time-dependent rates by using a time-inhomogeneous Markov chain formalism. Here, the proposed Markov chain model describes the *in vivo* infection process, and our battlefield naturally turns to its Kolmogorov equations. However, such a transformation, more often than not, leads to a high-dimensional system not amenable to analytical treatment. One would have to resort to some approximate techniques such as the moment closure method [21, 22].

Here, we circumvent this difficulty by employing the Lie algebraic approach borrowed from Wei and Norman [23]. To use the Wei–Norman method, we need to construct a Lie algebra with a finite dimension. This method has been applied recently to some simple biological population models, such as SIS and SIR epidemics [24–26], for obtaining exact solutions. It is pointed out that, for more complicated biological dynamics, the selection of an appropriate linearly independent basis to form a low-dimensional Lie algebra is a challenging task [21]. In other applications, some restrictive conditions turn out to be necessary. For example, to solve analytically a time-inhomogeneous linear birth–death process with immigration, the immigration rate has to be proportional to the birth rate [27]. In this paper, we manage to generate a Lie algebra of dimension 8 to solve the in-host model, and no restriction is imposed on the involved time-dependent rates.

The rest of the paper is organized as follows. The basic viral dynamics is delineated in Section 2, and the Wei–Norman method is briefly reviewed in Section 3. In Section 4, we show the application of the Lie algebraic approach to the in-host model. Concluding remarks are drawn in Section 5.

2. Description of in-host viral model

In the virus infection process, we consider three basic compartments: the target uninfected cells (X), infected cells (Y), and free viruses (V). Denote the number of cells or virus particles at time t in each compartment by $X(t)$, $Y(t)$, $V(t)$, respectively. We can write down a system of three coupled nonlinear ordinary differential equations (ODEs) for the virus dynamics [2–4, 6] according to the transition diagram (see Fig. 1)

$$\begin{aligned}
\frac{dX(t)}{dt} &= \lambda(t) - d(t)X(t) - \beta(t)X(t)V(t)\,,\\
\frac{dY(t)}{dt} &= \beta(t)X(t)V(t) - a(t)Y(t)\,,\\
\frac{dV(t)}{dt} &= k(t)Y(t) - u(t)V(t)\,,
\end{aligned} \tag{1}$$

where $\lambda(t)$ is the rate at which new target cells are generated from a pool of precursor cells, $d(t)$ is their specific death rate, and $\beta(t)$ is the rate characterizing their infection. Once cells are infected, we assume that they die at rate $a(t)$ either due to viral cytopathicity or the action of immune system, and produce new virus particles at rate $k(t)$ during their life. Finally, virus particles are cleared from the system at rate $u(t)$ per virion due to immune elimination or binding and entry into cells. Other variant models have been considered in the literature, we refer the interested reader to the book [10] for more details.

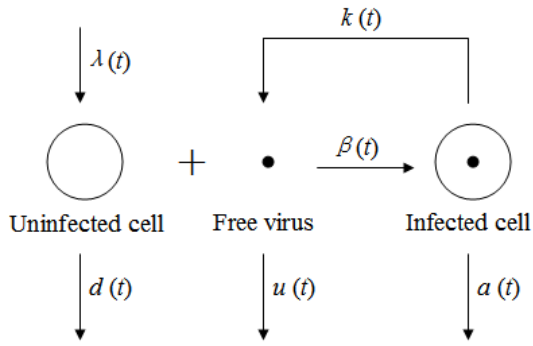

Fig. 1. Illustration of virus infection process.

3. The Wei–Norman method for time-inhomogeneous Markov chains

In this section, we review the Wei–Norman method [23] for solving time-inhomogeneous Markov chains.

A Lie algebra is a vector space $\mathcal{L}$ over some field F together with a bilinear map $[\cdot,\cdot] : \mathcal{L} \times \mathcal{L} \to \mathcal{L}$ called the Lie bracket, which satisfies $[A, A] = 0$ and the Jacobi identity

$$[A,[B,C]] + [B,[C,A]] + [C,[A,B]] = 0\,, \tag{2}$$

for all $A, B, C \in \mathcal{L}$. For $A \in \mathcal{L}$, we define an adjoint operator $\mathrm{ad}A$ by

$$(\mathrm{ad}A)B = [A,B]\,, \tag{3}$$

for $B \in \mathcal{L}$. Thus, $(\mathrm{ad}A)^2 B = [A,[A,B]]$. Every associate algebra gives rise to a Lie algebra $\mathcal{L}$ by defining the Lie bracket as a commutator

$$[A,B] = AB - BA\,, \tag{4}$$

where $A, B \in \mathcal{L}$. In what follows, we will focus on this Lie product. The classical Baker–Campbell–Hausdorff formula can be written as

$$e^A B e^{-A} = \left(e^{\mathrm{ad}A}\right) B\,, \tag{5}$$

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

Given a continuous-time Markov chain, taking values in a finite or countably infinite state space $\mathcal{S}$, its dynamical behavior 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. Using the Kolmogorov forward equation, the probability distribution of the process at time t, $p(t) = (p_i(t), i \in \mathcal{S})$, is given by

$$\frac{dp(t)}{dt} = H(t)p(t)\,, \tag{6}$$

where $H(t) = Q(t)^{\mathrm{T}}$ (here, T represents 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. Using the 'ket' notation $|\cdot\rangle$ [24, 25, 27, 28], the probability vector can alternatively be written as

$$|p(t)\rangle = \sum_{i \in \mathcal{S}} P(i|t)|i\rangle\,, \tag{7}$$

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. It is worth mentioning that $H(t)$ in (6) is time-dependent implying that the process is time inhomogeneous.

In addition, the operator $H(t)$ is assumed to be written as

$$H(t) = \sum_{i=1}^{m} a_i(t) H_i\,, \tag{8}$$

where $a_i(t)$ are real-valued functions, and H_i are linearly independent constant operators generating a Lie algebra $\mathcal{L} = \mathrm{span}\{H_1, \ldots, H_m\}$ by implementing a Lie bracket

$$[H_i, H_j] = H_i H_j - H_j H_i = \sum_{k=1}^{m} \xi_{ij}^k H_k \tag{9}$$

for some real ξ_{ij}^k. The Wei–Norman method looks for a solution of system (6) taking the form of a product of exponentials

$$p(t) = e^{g_1(t)H_1} \dots e^{g_m(t)H_m} p(0) := U(t)p(0)\,, \tag{10}$$

where $g_i(t)$ are real-valued functions and $g_i(0) = 0$ for all $i = 1, 2 \dots, m$.

Substituting (8) and (10) into (6), we obtain

$$\begin{aligned} \frac{dp(t)}{dt} &= \sum_{i=1}^{m} a_i(t) H_i U(t) p(0) \\ &= \sum_{i=1}^{m} \dot{g}_i(t) \left(\prod_{j=1}^{i-1} e^{g_j(t)H_j} \right) H_i \left(\prod_{j=i}^{m} e^{g_j(t)H_j} \right) p(0)\,. \end{aligned} \tag{11}$$

Performing a post-multiplication by the inverse operator U^{-1} and repeatedly applying the Baker–Campbell–Hausdorff formula, we are led to

$$\sum_{i=1}^{m} a_i(t) H_i = \sum_{i=1}^{m} \dot{g}_i(t) \left(\prod_{j=1}^{i-1} e^{g_j(t)\mathrm{ad}H_j} \right) H_i \tag{12}$$

since equation (11) holds for any $p(0)$. Since the operators H_i are chosen to be linearly independent, we can compare the coefficients of each H_i in both sides of (12) to derive a set of ODEs for $g_i(t)$ with initial values $g_i(0) = 0$ (involving ξ_{ij}^k).

4. Lie algebra solution of in-host population dynamics

According to the description in Section 2, the probability vector for the viral model can be written as

$$|p(t)\rangle = \sum_{X,Y,V} P(X, Y, V|t)|X, Y, V\rangle\,, \tag{13}$$

where $P(X, Y, V|t)$ denotes the probability that there are X uninfected target cells, Y infected cells, and V free virus particles at time t. $|X, Y, V\rangle$ is a basis vector, linearly independent of other basis vectors with different cell and virus particle numbers. The state space $\mathcal{S}$ is a countable set.

Let $\hat{\mathcal{O}}$ signify an endomorphism of the vector space spanned by the above basis vectors. The Kolmogorov forward equation governing the in-host dynamics can be written as

$$\frac{d}{dt}|p(t)\rangle = H(t)|p(t)\rangle\,, \tag{14}$$

with the time-evolution operator

$$H(t) = \lambda(t)\hat{E} - d(t)\hat{X} + \beta(t)\left(\hat{X} - \hat{\tau}\right) + k(t)\hat{\rho} - a(t)\hat{Y} - u(t)\hat{V}\,, \qquad (15)$$

where

$$\begin{aligned}
\hat{E}|X,Y,V\rangle &= |X+1,Y,V\rangle\,,\\
\hat{X}|X,Y,V\rangle &= X|X,Y,V\rangle\,,\\
\hat{\tau}|X,Y,V\rangle &= X|X-1,Y+1,V-1\rangle\,,\\
\hat{Y}|X,Y,V\rangle &= Y|X,Y,V\rangle\,,\\
\hat{\rho}|X,Y,V\rangle &= Y|X,Y-1,V+1\rangle\,,\\
\hat{V}|X,Y,V\rangle &= V|X,Y,V\rangle\,. \qquad (16)
\end{aligned}$$

According to the Wei–Norman method reviewed in Section 3, it is applicable only if the operators H_i in (8) generate a finite dimensional Lie algebra. Now, we introduce two more operators $\hat{\sigma}$ and $\hat{I}_d$, defined as

$$\hat{\sigma}|X,Y,V\rangle = X|X-1,Y,V\rangle \qquad \text{and} \qquad \hat{I}_d|X,Y,V\rangle = |X,Y,V\rangle\,, \qquad (17)$$

so that the Lie algebra $\mathcal{L} = \text{span}\{\hat{E},\hat{X},\hat{\tau},\hat{Y},\hat{\rho},\hat{V},\hat{\sigma},\hat{I}_d\}$ is closed under the action of the Lie bracket. In Table I, we show the complete set of Lie brackets. The eight operators defined above are all linear operators acting on basis vectors. They are interpreted as follows: $\hat{E}$ increases the uninfected target cell population by one; $\hat{X}$ returns the number of uninfected target cells; $\hat{\tau}$ returns the number of uninfected cells, reduces the uninfected cell population and the virus population by one, and increases the infected cell population by one; $\hat{Y}$ returns the number of infected cells; $\hat{\rho}$ returns

TABLE I

Values of $[\hat{\mathcal{O}}_1, \hat{\mathcal{O}}_2]$ for the viral model.

$\hat{\mathcal{O}}_1$	$\left[\hat{\mathcal{O}}_1,\hat{E}\right]$	$\left[\hat{\mathcal{O}}_1,\hat{X}\right]$	$\left[\hat{\mathcal{O}}_1,\hat{\tau}\right]$	$\left[\hat{\mathcal{O}}_1,\hat{Y}\right]$	$\left[\hat{\mathcal{O}}_1,\hat{\rho}\right]$	$\left[\hat{\mathcal{O}}_1,\hat{V}\right]$	$\left[\hat{\mathcal{O}}_1,\hat{\sigma}\right]$	$\left[\hat{\mathcal{O}}_1,\hat{I}_d\right]$
$\hat{E}$	0	$-\hat{E}$	0	0	0	0	$-\hat{I}_d$	0
$\hat{X}$	$\hat{E}$	0	$-\hat{\tau}$	0	0	0	$-\hat{\sigma}$	0
$\hat{\tau}$	0	$\hat{\tau}$	0	$-\hat{\tau}$	$-\hat{\sigma}$	$\hat{\tau}$	0	0
$\hat{Y}$	0	0	$\hat{\tau}$	0	$-\hat{\rho}$	0	0	0
$\hat{\rho}$	0	0	$\hat{\sigma}$	$\hat{\rho}$	0	$-\hat{\rho}$	0	0
$\hat{V}$	0	0	$-\hat{\tau}$	0	$\hat{\rho}$	0	0	0
$\hat{\sigma}$	$\hat{I}_d$	$\hat{\sigma}$	0	0	0	0	0	0
$\hat{I}_d$	0	0	0	0	0	0	0	0

the number of infected cells, depletes these by one, and increases the virus population by one; $\hat{V}$ returns the number of free viruses; $\hat{\sigma}$ returns the number of uninfected cells and depletes these by one; $\hat{I}_d$ is the identity operator which returns the number one.

The remaining task is to apply the Wei–Norman method to equation (14). In other words, we need to look for a solution of the form

$$|p(t)\rangle = e^{g_1(t)\hat{I}_d} e^{g_2(t)\hat{\sigma}} e^{g_3(t)\hat{E}} e^{g_4(t)\hat{X}} e^{g_5(t)\hat{\tau}} e^{g_6(t)\hat{\rho}} e^{g_7(t)\hat{Y}} e^{g_8(t)\hat{V}} |p(0)\rangle \,. \tag{18}$$

Thanks to (12) and the action of exponential operators shown in Table II, we are led to the following linear relation

$$\begin{aligned}
&\lambda(t)\hat{E} - (d(t) - \beta(t))\,\hat{X} - \beta(t)\hat{\tau} + k(t)\hat{\rho} - a(t)\hat{Y} - u(t)\hat{V} \\
&= \dot{g}_1(t)\hat{I}_d + \dot{g}_2(t)\hat{\sigma} + \dot{g}_3(t)\left(\hat{E} + g_2(t)\hat{I}_d\right) \\
&+\dot{g}_4(t)\left(\hat{X} + g_2(t)\hat{\sigma} - g_3(t)\hat{E} - g_2(t)g_3(t)\hat{I}_d\right) + \dot{g}_5(t)e^{-g_4(t)}\hat{\tau} \\
&+\dot{g}_6(t)\left(\hat{\rho} - g_5(t)e^{-g_4(t)}\hat{\sigma} + g_3(t)g_5(t)e^{-g_4(t)}\hat{I}_d\right) \\
&+\dot{g}_7(t)\left(\hat{Y} - g_5(t)e^{-g_4(t)}\hat{\tau} + g_6(t)\hat{\rho} - g_5(t)g_6(t)e^{-g_4(t)}\hat{\sigma}\right. \\
&\left.+g_3(t)g_5(t)g_6(t)e^{-g_4(t)}\hat{I}_d\right) \\
&+\dot{g}_8(t)\left(\hat{V} + g_5(t)e^{-g_4(t)}\hat{\tau} - g_6(t)\hat{\rho} + g_5(t)g_6(t)e^{-g_4(t)}\hat{\sigma}\right. \\
&\left.-g_3(t)g_5(t)g_6(t)e^{-g_4(t)}\hat{I}_d\right) \,.
\end{aligned} \tag{19}$$

TABLE II

Values of $e^{g(\mathrm{ad}\hat{\mathcal{O}}_1)}\hat{\mathcal{O}}_2$ with a scalar g for the viral model.

$\hat{\mathcal{O}}_1$	$e^{g(\mathrm{ad}\hat{\mathcal{O}}_1)}\hat{E}$	$e^{g(\mathrm{ad}\hat{\mathcal{O}}_1)}\hat{X}$	$e^{g(\mathrm{ad}\hat{\mathcal{O}}_1)}\hat{\tau}$	$e^{g(\mathrm{ad}\hat{\mathcal{O}}_1)}\hat{Y}$	$e^{g(\mathrm{ad}\hat{\mathcal{O}}_1)}\hat{\rho}$	$e^{g(\mathrm{ad}\hat{\mathcal{O}}_1)}\hat{V}$	$e^{g(\mathrm{ad}\hat{\mathcal{O}}_1)}\hat{\sigma}$	$e^{g(\mathrm{ad}\hat{\mathcal{O}}_1)}\hat{I}_d$
$\hat{E}$	$\hat{E}$	$\hat{X} - g\hat{E}$	$\hat{\tau}$	$\hat{Y}$	$\hat{\rho}$	$\hat{V}$	$\hat{\sigma} - g\hat{I}_d$	$\hat{I}_d$
$\hat{X}$	$e^{g}\hat{E}$	$\hat{X}$	$e^{-g}\hat{\tau}$	$\hat{Y}$	$\hat{\rho}$	$\hat{V}$	$e^{-g}\hat{\sigma}$	$\hat{I}_d$
$\hat{\tau}$	$\hat{E}$	$\hat{X} + g\hat{\tau}$	$\hat{\tau}$	$\hat{Y} - g\hat{\tau}$	$\hat{\rho} - g\hat{\sigma}$	$\hat{V} + g\hat{\tau}$	$\hat{\sigma}$	$\hat{I}_d$
$\hat{Y}$	$\hat{E}$	$\hat{X}$	$e^{g}\hat{\tau}$	$\hat{Y}$	$e^{-g}\hat{\rho}$	$\hat{V}$	$\hat{\sigma}$	$\hat{I}_d$
$\hat{\rho}$	$\hat{E}$	$\hat{X}$	$\hat{\tau} + g\hat{\sigma}$	$\hat{Y} + g\hat{\rho}$	$\hat{\rho}$	$\hat{V} - g\hat{\rho}$	$\hat{\sigma}$	$\hat{I}_d$
$\hat{V}$	$\hat{E}$	$\hat{X}$	$e^{-g}\hat{\tau}$	$\hat{Y}$	$e^{g}\hat{\rho}$	$\hat{V}$	$\hat{\sigma}$	$\hat{I}_d$
$\hat{\sigma}$	$\hat{E} + g\hat{I}_d$	$\hat{X} + g\hat{\sigma}$	$\hat{\tau}$	$\hat{Y}$	$\hat{\rho}$	$\hat{V}$	$\hat{\sigma}$	$\hat{I}_d$
$\hat{I}_d$	$\hat{E}$	$\hat{X}$	$\hat{\tau}$	$\hat{Y}$	$\hat{\rho}$	$\hat{V}$	$\hat{\sigma}$	$\hat{I}_d$

Solving the set of ODEs derived from (19) for each basis operator in $\mathcal{L}$ gives

$$
\begin{aligned}
g_1(t) &= \int_0^t \lambda(s)e^{-\Psi(s)} \\
&\quad \times \left[\int_0^s k(w)e^{\Lambda(w)-\Gamma(w)} \left(\int_0^w \beta(z)e^{\Psi(z)+\Gamma(z)-\Lambda(z)}dz\right) dw\right] ds \\
&\quad + \int_0^t k(s) \left(\int_0^s \lambda(w)e^{-\Psi(w)}dw\right) e^{\Lambda(s)-\Gamma(s)} \\
&\quad \times \left(\int_0^s \beta(w)e^{\Psi(w)+\Gamma(w)-\Lambda(w)}dw\right) ds\,, \\
g_2(t) &= -e^{-\Psi(t)} \int_0^t k(s)e^{\Lambda(s)-\Gamma(s)} \left(\int_0^s \beta(w)e^{\Psi(w)+\Gamma(w)-\Lambda(w)}dw\right) ds\,, \\
g_3(t) &= e^{\Psi(t)} \int_0^t \lambda(s)e^{-\Psi(s)}ds\,, \\
g_4(t) &= \Psi(t)\,, \\
g_5(t) &= -e^{\Lambda(t)-\Gamma(t)} \int_0^t \beta(s)e^{\Psi(s)+\Gamma(s)-\Lambda(s)}ds\,, \\
g_6(t) &= e^{\Gamma(t)-\Lambda(t)} \int_0^t k(s)e^{\Lambda(s)-\Gamma(s)}ds\,, \\
g_7(t) &= -\Gamma(t)\,, \\
g_8(t) &= -\Lambda(t)\,,
\end{aligned} \tag{20}
$$

where $\Gamma(t) := \int_0^t a(s)ds$, $\Lambda(t) := \int_0^t u(s)ds$, and $\Psi(t) := \int_0^t(\beta(s) - d(s))ds$.

Example. To check the result, we consider a scenario examining the effects of drug treatment on HIV-1 viral load [6, 7]. Assume that the system is at quasi steady state before drug treatment and that the uninfected cell number X remains at approximately its steady-state value X_0. After treatment, we assume that no new infections occurs. Therefore, to see the effect of treatment, we set $|p(0)\rangle = |X_0, Y_0, V_0\rangle$, $\lambda(t) = d(t) = \beta(t) = 0$, $k(t)/c = a(t) \equiv a$, and $u(t) \equiv u$ for some $c > 0$. Note that c can be interpreted as the total number of virus particles produced from one

cell. Denote by $|\mathcal{V}(t)\rangle = \sum_{X,Y,V} V|X,Y,V\rangle$. It follows from (20) that $V(t) = \langle \mathcal{V}(t)|p(t)\rangle = V_0 e^{-ut} + \frac{caY_0}{u-a}(e^{-at} - e^{-ut})$ is the number of mature free viruses in the system at time t, and that the number of infected cells varies as $Y(t) = Y_0 e^{-at}$. These are in line with the analytical results obtained in [6, 7].

In Fig. 2 and Fig. 3, we show the variation of $V(t)$ and $Y(t)$ for $a < u$ and $a > u$, respectively, with different values of c. $V(t)$ is higher for larger c, indicating the larger number of virus particles generated. We observe from Fig. 3 that the curves of $V(t)$ for $c = 1$ and 2 will first increase and then decrease exponentially. This discrepancy is due to the second term in the expression of $V(t)$ above, which compensates the decay if $a > u$, namely, $d(\frac{\exp(-at)-\exp(-ut)}{u-a})/dt > 0$.

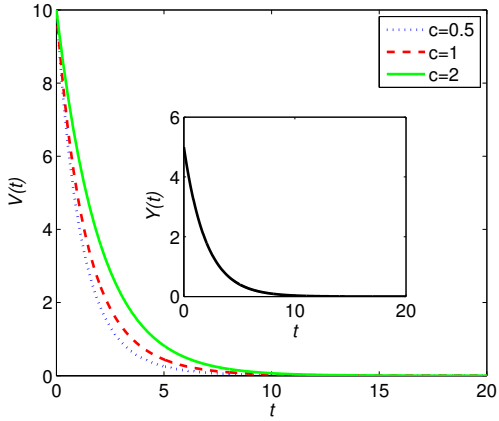

Fig. 2. Viral dynamics for $V_0 = 10$, $Y_0 = 5$, $a = 0.5$, $u = 1$.

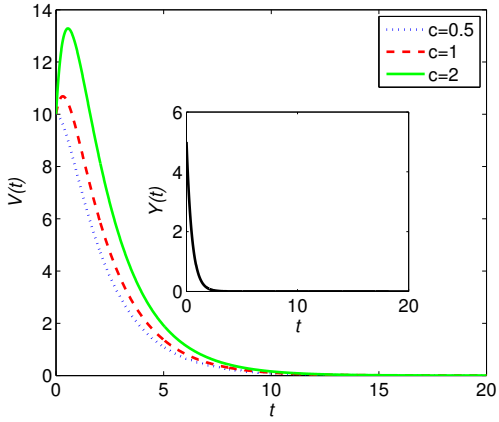

Fig. 3. Viral dynamics for $V_0 = 10$, $Y_0 = 5$, $a = 2$, $u = 0.5$.

5. Conclusion

In this paper, we have investigated the solution of viral infection dynamics *in vivo* (1) through a time-inhomogeneous Markov chain characterization. Based on the Kolmogorov equation and the Wei–Norman method, the analytical solution for the in-host model is obtained in terms of matrix exponentials. The computational efficiency is another benefit of the Wei–Norman method since $p(t)$ can be calculated in $O(1)$ operations through (12) rather than $O(t)$ by means of incremental direct integrations.

A variant of system (1) in biology consists of replacing the first equation by

$$\frac{dX(t)}{dt} = \lambda - dX(t) + rX(t)\left(1 - \frac{X(t)}{K}\right) - \beta X(t)V(t)\,,$$

where the newly added logistic term represents the rate cells increase through mitosis [9]. It is known that such addition gives rise to Hopf bifurcations and periodic orbits. When it comes to algebraic approach, new operators describing the quadratic X^2 would be essential. We may have another moderate goal, namely to solve the system (1) with an additional immune cells (such as Cytotoxic T-cells) dynamics described by an ODE involving Y [9]. A simple trick employed in [29] may be useful in creating a Lie algebra in this case.

However, as pointed out in [24], lack of symmetry in generic biological or ecological models largely precludes the construction of an appropriate Lie algebra as compared with many physical processes. It is hoped that the method offered in this study could lead to further progress in pursue of exact solution of more realistic biological population dynamics.

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