On the average dynamical behaviour of stochastic population models ⋆

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Abstract: The dynamics of highly populated biological systems is often described in terms of ordinary differential equations. The trajectory produced by these equations is continuous and deterministic, and represents the limit behaviour as the system size tends to infinity. Because most biological systems are discrete, stochastic and finite, important phenomena, as oscillations, can be passed over by the limit behaviour. The computation of expected values on the associated embedded Markov process allows one to average functions of interest without resorting to the deterministic limit. In particular, one can average distances and angles with respect to a given reference point. This leads to a description of the process in polar coordinates that determines the dynamical system behaviour around the reference point.

Keywords: Jump Markov process, deterministic limit, average behaviour, stochastic oscillation.

1. INTRODUCTION

The state of biological systems can be expressed naturally by a vector of natural numbers, in which each component of the vector represents the number of elements of a species involved in the system. Depending on the kind of system under consideration, this number of elements can refer to molecules (biochemical system), individuals of a population (ecology system), etc. The state of the system changes when an event, such as a reaction, happens. Inferring the exact occurrence time of events is in most cases impossible or impractical, and hence it is usually assumed that they happen at random. This implies that the system can be modelled as a jump Markov process on the natural numbers, and more precisely as a density dependent Markov process [4]. Because the exact analysis and simulation of a large Markov process is computationally expensive, its dynamics is often studied by considering the deterministic limit. Such a deterministic limit describes the time evolution of the densities of the system populations when the system size tends to infinity. The time evolution of the densities is obtained as a solution of a set of Ordinary Differential Equations (ODE) [5, 9]. This way, the time evolution of a population density is represented by a continuous and deterministic trajectory.

The use of ODEs opens the possibility to take advantage of the rich existing results for dynamical systems described by differential equations [8]. Once the system is studied as an ODE, a straightforward translation of the obtained results to the original discrete stochastic system is usually achieved. One would expect the deterministic limit to be the average behaviour of the Markov process. However, as pointed out in [3, 1, 13], the deterministic limit might fail at capturing important system behaviours such as oscillations, commutations, stochastic resonance, etc. Not surprisingly, the differences between the deterministic limit and the Markov process increase as the system size decreases. As in [13], instead of analysing the deterministic limit and then interpreting the results in the Markov process, we aim at obtaining relevant dynamical information directly from the discrete Markov process. More precisely, we aim at evaluating the average dynamical behaviour of functions of interest on the values of the populations. Instead of computing exactly such an average by means of the Dynkin's formula [14], we propose to approximate it by considering the expected increase of the function yielded by the associated embedded Markov process and the average frequency of events. As shown in the case studies, this approach entails a straightforward and appropriate approximation of the stochastic process. Special attention is paid to the dynamical behaviour around fixed points. In particular, by averaging the increase of the distance and angle to a given fixed point, it is possible to express the evolution in polar coordinates, what can easily uncover oscillating behaviours that might be hidden or underestimated by the deterministic limit. With respect to previous works [10], the average speed of change of affine and quadratic functions provided by the deterministic limit and the Markov process is studied, the dynamics in the vicinity of the fixed points is established and systems with oscillating deterministic limit are considered.

The rest of the paper is organised as follows: Section 2 introduces the notation, formalizes the Markov process and presents a running example. Section 3 shows how to average the change rate of a given function by taking into account the embedded Markov process. Such average is used in Section 4 to estimate the dynamical behaviour of the system around a given reference point. The two case studies presented in Section 5, a prey-predator system and the Brusselator, show that the deterministic limit tends to underestimate the system oscillations. Section 6 concludes the paper.

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2. STOCHASTIC POPULATION MODELS

To define the dynamical system under study, we will use the following parameters and notation:

- $q \in \mathbb{N}$ denotes the number of populations (or species).
- $n \in \mathbb{N}$ denotes the number of events (or reactions).
- $\mathbf{X}(t) \in \mathbb{N}^q_{\geq 0}$ is the state of the system at time t ($X_i(t)$ denotes the number of elements of population i at time t) [1].
- $\nu \in \mathbb{N}^{q\times n}_{\geq 0}$ is the stoichiometry matrix, i.e., ν^j_i is the change produced in population i by event j (ν^j will denote the j^{th} column of ν, i.e., stoichiometry vector of reaction j, and ν_i will denote the i^{th} row of ν).
- $V \in \mathbb{R}_{>0}$ is the size (or volume) of the system.
- $W_j : \mathbb{R}^q_{\geq 0} \times \mathbb{R}_{>0} \to \mathbb{R}_{\geq 0}$ is the transition rate function, i.e, $W_j(\mathbf{X}(t), V)$ is the rate associated to event j for population $\mathbf{X}(t)$ and system size V.

It is assumed that each transition rate function $W_j(\mathbf{X}(t), V)$ is a differentiable nonnegative function that does not depend on time (for readability we will use $\mathbf{X}$ rather than $\mathbf{X}(t)$). Further, following the notation in [13], it is assumed that $W_j(\mathbf{X}, V)$ satisfies the mass-action law: $W_j(\mathbf{X}, V) = V \cdot w_j(\mathbf{X}/V)$ where $w_j(\mathbf{X}/V)$ is a nonnegative function of real arguments on the system densities. This expression of the mass-action law states that if the densities are kept constant while the system size changes from V to V', then the transition rates change by a factor V'/V. In the following, $W_j(\mathbf{X}(t), V)$ is simplified to $W_j(\mathbf{X})$ for clarity, and densities will be expressed in lowercase, e.g., $\mathbf{x} = \mathbf{X}/V$.

The system is modelled as a jump Markov process in which events are exponentially distributed with rates $W_j(\mathbf{X})$. The occurrence of an event j changes the system state from $\mathbf{X}$ to $\mathbf{X} + \nu^j$. Given that all rates are exponentially distributed, the next event time is also exponentially distributed with rate $R(\mathbf{X}) = \sum_{j=1}^n W_j(\mathbf{X})$, and the probability that the next event is event j is $W_j(\mathbf{X})/R(\mathbf{X})$.

Given a sample path of a jump Markov process, the *embedded process* is the sequence of consecutive states $\{\mathbf{X}^0, \mathbf{X}^1, \mathbf{X}^2, \ldots, \mathbf{X}^k, \ldots\}$ of the path. From a sequence $\{\mathbf{X}^0, \mathbf{X}^1, \mathbf{X}^2, \ldots, \mathbf{X}^k, \ldots\}$, sample paths of the Markov process can be built by producing times for each event with exponentially distributed random variables.

Deterministic limit: Let $F_i(\mathbf{x}) = \sum_{j=1}^n \nu^j_i w_j(\mathbf{x})$ be the vector field for species i, and assume that $\sum_{j=1}^n |\nu^j_i| w_j(\mathbf{x}) < \infty$ and F is Lipschitz continuous, i.e., $\exists M \geq 0$ such that $|F(\mathbf{x}) - F(\mathbf{y})| \leq M|\mathbf{x} - \mathbf{y}|$. Then, the deterministic limit behaviour of the system when V tends to infinity is given by the following ODE [5, 9]: $\frac{dx_i}{dt} = F_i(\mathbf{x}) = \sum_{j=1}^n \nu^j_i w_j(\mathbf{x})$. This ODE can be scaled by V to obtain a deterministic continuous trajectory for a system with size V:

$$\frac{dX_i}{dt} = \sum_{j=1}^{n} \nu^j_i W_j(\mathbf{X}) \qquad (1)$$

Example. Consider an epidemic system [13] consisting of two species: susceptible and infected individuals; and five events: birth, death of a susceptible individual, contagion, recovery, and death of an infected individual. Let $S = X_1$ and $I = X_2$ be the number of susceptible and infected individuals, and $a_b = W_1$, $a_{ds} = W_2$, $a_c = W_3$, $a_r = W_4$ and $a_{di} = W_5$ be the transition rates of events birth, death of a susceptible individual, contagion, recovery, and death of an infected individual respectively. The parameters of the system are: $q = 2$, $n = 5$, $\nu = \begin{pmatrix} 1 & -1 & -1 & 1 & 0 \\ 0 & 0 & 1 & -1 & -1 \end{pmatrix}$, $a_b = \dfrac{S+I}{1 + (b\cdot(S+I))/V}$, $a_{ds} = m_S \cdot S$, $a_c = \beta \cdot S \cdot \dfrac{I}{V}$, $a_r = r \cdot I$, $a_{dI} = m_I \cdot I$, $V = 5 \cdot 10^3$, with $b = 0.4$, $\beta = 10$, $m_S = 0.2$, $m_I = 5$, $r = 3$, and initial populations $S(0) = 4080$ and $I(0) = 500$.

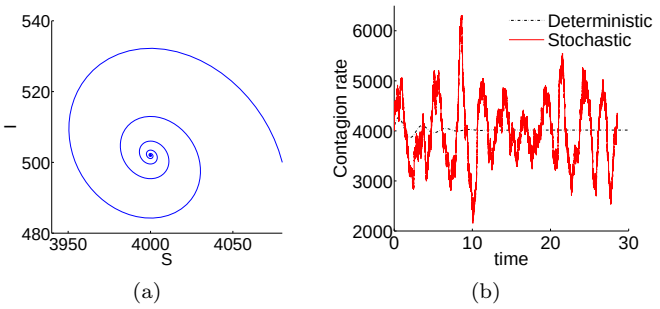


Fig. 1. (a) Trajectory in the phase space of the solution of ODE (1); (b) Contagion rate according to ODE (1) and one stochastic simulation.

Assume we are interested in evaluating the evolution of the contagion rate over time. Figure 1(a) shows the system evolution in the phase space according to ODE (1), the system reaches an equilibrium point at which both species, and hence the contagion rate, keep constant. The dotted line in Figure 1(b) is the time evolution of the contagion rate according to this deterministic view, while the solid line is the time evolution of the contagion rate according to a single stochastic simulation of the Markov process.

Unlike the deterministic evolution, the stochastic simulation exhibits undamped oscillations with approximately constant frequency and amplitude. In fact, the spectral analysis of the stochastic trajectory reveals a peak at frequency 0.33. The following sections explore the deviation induced by ODE (1) with respect to the Markov process when estimating functions over the system trajectory.

3. AVERAGE DYNAMICAL BEHAVIOUR

The ODE (1) represents the limit trajectory of the populations as the system size tends to infinity. Such a limit provides valuable information about the system dynamics. Nevertheless, as the limit is never attained in practice, it must be used with caution when evaluating the time evolution of functions of interest, as the contagion rate in the previous section. We will show that affine functions are appropriately evaluated by the ODE, but more general functions, as quadratic functions, are not.

3.1 Affine functions

Let $f : \mathbb{R}^q_{\geq 0} \to \mathbb{R}$ be an affine function of the type $f(\mathbf{X}) = A\mathbf{X} + b$ (for clarity, we avoid the use of transpose

[1] Notation: A_i denotes the i^{th} component of vector A.

symbols). Let us first evaluate the change rate of f in the deterministic continuous trajectory provided by ODE (1). By the chain rule and (1), the total derivative of $f(\mathbf{X})$ with respect to time is:

$$\begin{aligned}\frac{df}{dt} &= \sum_{i=1}^{q} \frac{\partial f}{\partial X_i}\frac{dX_i}{dt} = \sum_{i=1}^{q} \frac{\partial f}{\partial X_i}\Big(\sum_{j=1}^{n} \nu_i^j W_j(\mathbf{X})\Big) \\ &= \sum_{i=1}^{q} A_i\Big(\sum_{j=1}^{n} \nu_i^j W_j(\mathbf{X})\Big) = A\nu W(\mathbf{X})\end{aligned} \tag{2}$$

where A_i is the i^{th} element of vector A, and $W(\mathbf{X})$ is a vector whose j^{th} element is $W_j(\mathbf{X})$.

In order to estimate the speed of change of function f according to the Markov process, we will consider the expected increase of f produced by the occurrence of an event, and the average frequency of events. At a given state $\mathbf{X}$, the expected [2] increase of function f after the occurrence of an event is the weighted average of the increases of f produced by the different events:

$$\mathbb{E}[\Delta f(\mathbf{X})] = \sum_{j=1}^{n} \frac{W_j(\mathbf{X})}{R(\mathbf{X})}\big(f(\mathbf{X}+\nu^j) - f(\mathbf{X})\big) \tag{3a}$$

$$= \sum_{j=1}^{n} \frac{W_j(\mathbf{X})}{R(\mathbf{X})}\big(A(\mathbf{X}+\nu^j)+b-(A\mathbf{X}+b)\big) \tag{3b}$$

where Δ is the finite difference operator applied to the values of the embedded process. Because at $\mathbf{X}$ the average number of events per time unit, i.e, frequency, is $R(\mathbf{X})$, the average speed of change of f according to the Markov process can be approximated as:

$$\begin{aligned}&R(\mathbf{X})\mathbb{E}[\Delta f(\mathbf{X})] = \sum_{j=1}^{n} W_j(\mathbf{X})\big(A(\mathbf{X}+\nu^j)+b-(A\mathbf{X}+b)\big) \\ &= \sum_{j=1}^{n} W_j(\mathbf{X})\Big(\sum_{i=1}^{q} A_i\nu_i^j\Big) = \sum_{j=1}^{n}\sum_{i=1}^{q} A_i\nu_i^j W_j(\mathbf{X}) = A\nu W(\mathbf{X})\end{aligned} \tag{4}$$

This way, the affine function f is evaluated equally by the ODE and the Markov process (see (2) and (4)). Nevertheless, this is not the case for a more general function f.

3.2 Quadratic functions

Let f be the product of two affine functions $h(\mathbf{X}) = C\mathbf{X} + u$ and $g(\mathbf{X}) = D\mathbf{X} + v$, i.e., $f(\mathbf{X}) = h(\mathbf{X})g(\mathbf{X}) = (C\mathbf{X})(D\mathbf{X}) + C\mathbf{X}v + D\mathbf{X}u + uv$. The sum $C\mathbf{X}v + D\mathbf{X}u + uv$ is an affine function and will be equally evaluated by the ODE and the Markov process, thus, to simplify the presentation we will assume that $u = v = 0$ and hence, $f(\mathbf{X}) = (C\mathbf{X})(D\mathbf{X})$. By using (1), and given that f is a product of functions, the derivative of f is:

$$\begin{aligned}\frac{d\ f}{dt} &= \frac{d\ hg}{dt} = h\frac{dg}{dt} + g\frac{dh}{dt} \\ &= h\sum_{i=1}^{q}\frac{\partial g}{\partial X_i}\frac{dX_i}{dt} + g\sum_{i=1}^{q}\frac{\partial h}{\partial X_i}\frac{dX_i}{dt} \\ &= \sum_{i=1}^{q}\frac{dX_i}{dt}\Big(h\frac{\partial g}{\partial X_i} + g\frac{\partial h}{\partial X_i}\Big) \\ &= \sum_{i=1}^{q}\sum_{j=1}^{n}\nu_i^j W_j(\mathbf{X})(C\mathbf{X}D_i + D\mathbf{X}C_i) \\ &= ((C\mathbf{X})D + (D\mathbf{X})C)\sum_{j=1}^{n}\nu^j W_j(\mathbf{X})\end{aligned} \tag{5}$$

As for affine functions, the average speed of change of f can be approximated by the expected increase of the Markov process, $\mathbb{E}[\Delta f(\mathbf{X})] = \mathbb{E}[\Delta((C\mathbf{X})(D\mathbf{X}))]$, times the average number of events per time unit, $R(\mathbf{X})$. By the product rule of the finite difference operator [3] and given that the vector of expected increases of populations is $\mathbb{E}[\Delta\mathbf{X}] = \sum_{j=1}^{n}\nu^j\frac{W_j(\mathbf{X})}{R(\mathbf{X})}$, the following equality is produced:

$$\begin{aligned}&R(\mathbf{X})\mathbb{E}[\Delta((C\mathbf{X})(D\mathbf{X}))] \\ &= R(\mathbf{X})\mathbb{E}[(C\mathbf{X})\Delta(D\mathbf{X}) + (D\mathbf{X})\Delta(C\mathbf{X}) \\ &\qquad + \Delta(C\mathbf{X})\Delta(D\mathbf{X})] \\ &= R(\mathbf{X})(C\mathbf{X})D\mathbb{E}[\Delta\mathbf{X}] + R(\mathbf{X})(D\mathbf{X})C\mathbb{E}[\Delta\mathbf{X}] \\ &\qquad + R(\mathbf{X})\mathbb{E}[\Delta(C\mathbf{X})\Delta(D\mathbf{X})] \\ &= (C\mathbf{X})D\sum_{j=1}^{n}\nu^j W_j(\mathbf{X}) + (D\mathbf{X})C\sum_{j=1}^{n}\nu^j W_j(\mathbf{X}) \\ &\qquad + R(\mathbf{X})\mathbb{E}[\Delta(C\mathbf{X})\Delta(D\mathbf{X})] \\ &= ((C\mathbf{X})D + (D\mathbf{X})C)\sum_{j=1}^{n}\nu^j W_j(\mathbf{X}) \\ &\qquad + R(\mathbf{X})\mathbb{E}[\Delta(C\mathbf{X})\Delta(D\mathbf{X})]\end{aligned} \tag{6}$$

From (5) and (6), the following equality showing the different speeds of change resulting from the ODE (1) and the Markov process is derived:

$$R(\mathbf{X})\mathbb{E}[\Delta((C\mathbf{X})(D\mathbf{X}))] = \frac{d\ hg}{dt} + R(\mathbf{X})\mathbb{E}[\Delta(C\mathbf{X})\Delta(D\mathbf{X})]$$

Thus, f is, in general, evaluated differently by the ODE that represents the deterministic limit and the Markov process. Quadratic functions as $f(\mathbf{X}) = (C\mathbf{X})(D\mathbf{X}) + C\mathbf{X}v + D\mathbf{X}u + uv$ appear naturally when trying to estimate the evolution of certain reaction rates (as the contagion rate in the previous section), the product of populations that could activate other events, or the squared distance to a given point. For this last case, it can be shown that the deterministic limit underestimates the speed of change of the squared distance with respect to a point a with coordinates $(a_1, \ldots, a_q)$. Let $L_a(\mathbf{X}) = \sum_{i=1}^{q}(X_i - a_i)^2$, then, the speed of change of L_a provided by ODE (1) is:

$$\frac{dL_a}{dt} = \sum_{i=1}^{q}\frac{\partial L_a}{\partial X_i}\frac{dX_i}{dt} = \sum_{i=1}^{q} 2(X_i - a_i)\Big(\sum_{j=1}^{n}\nu_i^j W_j(\mathbf{X})\Big) \tag{7}$$

On the other hand, by the chain rule $\Delta(z^2) = 2z\Delta z + (\Delta z)^2$ and given that the expected increase of population i is $\mathbb{E}[\Delta\mathbf{X}_i] = \sum_{j=1}^{n}\nu_i^j\frac{W_j(\mathbf{X})}{R(\mathbf{X})}$, the speed of change of L_a estimated by the Markov process is:

[2] All the expected values are conditional on the current state. For brevity, $\mathbb{E}[\Delta f(\mathbf{X})]$ denotes the expected increase of f, given $\mathbf{X}$, of the embedded Markov process after the occurrence of an event.

[3] The product rule of the finite difference operator states: $\Delta(hg) = h\Delta g + g\Delta h + \Delta h\Delta g$

$$
\begin{aligned}
R(\mathbf{X})\mathbb{E}[\Delta L_a(\mathbf{X})] &= R(\mathbf{X})\mathbb{E}[\Delta \sum_{i=1}^{q}(X_i - a_i)^2] \\
&= R(\mathbf{X})\sum_{i=1}^{q}\mathbb{E}[\Delta(X_i - a_i)^2] \\
&= R(\mathbf{X})\sum_{i=1}^{q}\mathbb{E}[2(X_i - a_i)\Delta X_i + (\Delta X_i)^2] \\
&= R(\mathbf{X})\sum_{i=1}^{q}2(X_i - a_i)\mathbb{E}[\Delta X_i] + R(\mathbf{X})\sum_{i=1}^{q}\mathbb{E}[(\Delta X_i)^2] \\
&= \sum_{i=1}^{q}2(X_i - a_i)\Big(\sum_{j=1}^{n}\nu_i^j W_j(\mathbf{X})\Big) + R(\mathbf{X})\sum_{i=1}^{q}\mathbb{E}[(\Delta X_i)^2]
\end{aligned}
\tag{8}
$$

From (7) and (8), the following equality is obtained:

$$
R(\mathbf{X})\mathbb{E}[\Delta L_a(\mathbf{X})] = \frac{dL_a}{dt} + R(\mathbf{X})\sum_{i=1}^{q}\mathbb{E}[(\Delta X_i)^2] \tag{9}
$$

hence, given that $\sum_{i=1}^{q}\mathbb{E}[(\Delta X_i)^2] \geq 0$, the Markov process estimates that the system moves away faster from (or approaches slower) point a as long as events happen, i.e., as long as $R(\mathbf{X}) > 0$. In particular, if a is a fixed point it holds that $\frac{dL_a(a)}{dt} = 0$, i.e., the effect of all the events cancels out, and hence, the trajectory given by the deterministic limit stays constant at a. However, according to the Markov process events will keep on occurring if a is not an extinction point, and hence, the system can move away from a at an average speed of $R(\mathbf{X})\sum_{i=1}^{q}\mathbb{E}[(\Delta X_i)^2]$ and describe a different trajectory.

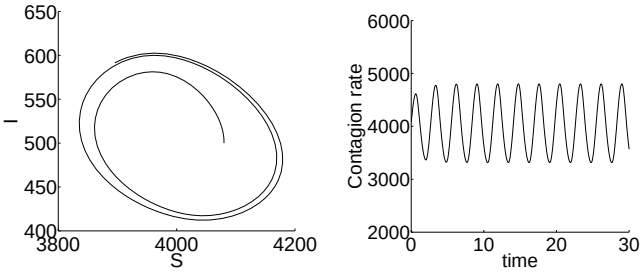
Notice that as V increases and tends to infinity while the concentrations are kept constant, the trajectory of the Jump Markov process will converge to that of the deterministic limit [5, 9]. Nevertheless, in many systems of interest, the value of V cannot be taken as infinity and just considering the deterministic limit can overlook important properties of the system dynamics.

By reasoning in a similar way as in the above mathematical developments, next section will make use of the expected value of the embedded process to provide a different view (polar instead of cartesian) of the system evolution. Such a view is the result of estimating the distance and angle of the state of the system to a given reference point.

4. BEHAVIOUR AROUND A REFERENCE POINT

The trajectory yielded by ODE (1) in the phase space at a time τ is tangent to the weighted average of the column vectors of ν according to their transition rates. In other words, the future positions of the system are computed according to the weighted average of the cartesian coordinates of the vectors ν^j. An alternative way to study the evolution of a process with size V is to compute the future positions of the system according to the weighted average of other, non cartesian, coordinate system.

As derived from equation (3a), the average speed of change of a given function f, which can represent a given coordinate in a coordinate system, according to the Markov process is:



(a) (b)

Fig. 2. (a) Trajectory in the phase space of the solution of ODE (11) for the epidemic system in Section 2; (b) Contagion rate according to ODE (11).

$$
\begin{aligned}
R(\mathbf{X})\mathbb{E}[(\Delta f(\mathbf{X})] &= R(\mathbf{X})\sum_{j=1}^{n}\frac{W_j(\mathbf{X})}{R(\mathbf{X})}(f(\mathbf{X}+\nu^j) - f(\mathbf{X})) \\
&= \sum_{j=1}^{n}W_j(\mathbf{X})f(\mathbf{X}+\nu^j) - R(\mathbf{X})f(\mathbf{X})
\end{aligned}
\tag{10}
$$

Next subsection uses (10) to propose an ODE that expresses the system evolution in polar coordinates by capturing the speed of change of the distance and angle with respect to a given reference point. In the following, we will focus on systems having two species, i.e., $q = 2$.

4.1 Averaging distances and angles

The speed of change of the distance, ρ, and angle, ϕ, of the system state, $\mathbf{X}$, with respect to a given point $a = (a_x, a_y)$ can be obtained by considering two functions, one for the distance, $f_\rho(\mathbf{X}) = \sqrt{(X - a_x)^2 + (Y - a_y)^2}$, and one for the angle, $f_\phi(\mathbf{X}) = \text{atan}(Y - a_y, X - a_x)$, where (X, Y) are the cartesian coordinates of $\mathbf{X}$, and $\text{atan}(y, x) : \mathbb{R}\times\mathbb{R} \to \mathbb{R}$ is the arctangent of a point with cartesian coordinates (x, y) that takes into account the quadrant.

We will assume that the range of $\text{atan}(y, x)$ is $(-\pi, \pi]$ and that $\text{atan}(0, 0) = 0$. In order to avoid discontinuities in the angle when it is close to π, i.e, when the state switches between the second and third quadrant, we will not consider just the angle returned by atan, but the overall angular distance run by the trajectory (this is achieved by function g in (11)). Equation (10) can be used to compute the average speed of change of $f_\rho(\mathbf{X})$ and $f_\phi(\mathbf{X})$, what allows us to describe the time evolution of the system in polar coordinates (ρ, ϕ) by means of the following ODE:

$$
\begin{aligned}
\frac{d\rho}{dt} &= R(\mathbf{X})\mathbb{E}[\Delta f_\rho(\mathbf{X})] \\
&= \sum_{j=1}^{n}W_j(\mathbf{X})f_\rho(\mathbf{X}+\nu^j) - R(\mathbf{X})f_\rho(\mathbf{X}) \\
\frac{d\phi}{dt} &= R(\mathbf{X})\mathbb{E}[\Delta f_\phi(\mathbf{X})] \\
&= \sum_{j=1}^{n}W_j(\mathbf{X})\left(f_\phi(\mathbf{X}+\nu^j) + g(\mathbf{X}, \nu^j, a)\right) - R(\mathbf{X})f_\phi(\mathbf{X})
\end{aligned}
\tag{11}
$$

where $g(\mathbf{X}, \nu^j, a)$ is defined as:

$$g(\mathbf{X},\nu^j,a)=\begin{cases}+2\pi & \text{if } f_\phi(\mathbf{X})>\pi/2 \text{ and } f_\phi(\mathbf{X}+\nu^j)<-\pi/2\\ -2\pi & \text{if } f_\phi(\mathbf{X})<-\pi/2 \text{ and } f_\phi(\mathbf{X}+\nu^j)>\pi/2\\ 0 & \text{otherwise}\end{cases}$$

The first(second) case of the above expresion avoids the discontinuity of the angle returned by atan when the trajectory moves from the second to the third quadrant(from the third to the second quadrant). Since functions $R(\mathbf{X})$, $W_j(\mathbf{X})$, $f_\rho(\mathbf{X})$ and $f_\phi(\mathbf{X})$ are defined on populations expressed in cartesian coordinates, it is necessary to transform (ρ,ϕ) to cartesian coordinates to evaluate the right-hand side of (11).

In contrast to the trajectory in Figure 1(a) for the epidemic system, Figure 2(a) shows a limit cycle trajectory that is produced by ODE (11). The initial state is $(4080, 500)$ and the reference point a is the fixed point $(4000, 502)$. Figure 2(b) is the time evolution of the contagion rate evaluated on the trajectory produced by ODE (11), the amplitude of this signal is 743 and the frequency 0.35 (recall that the spectral analysis of the stochastic simulation found a peak at 0.33). Thus, ODE (11) uncovers the stochastic oscillations shown in Figure 1(b) and is consistent with the sustained oscillations reported in [13].

5. CASE STUDIES

This section presents the trajectories that the cartesian ODE (1) and the polar ODE (11) yield for two case studies: a prey-predator model and the Brusselator [6].

5.1 A predator-prey model

Let us consider a prey-predator model in which the number of preys is denoted by $X_1 = X$, and the number of predators by $X_2 = Y$. Let the stoichiometry matrix be $\nu = \left(\begin{smallmatrix}1 & -1 & 0 & 0\\ 0 & 0 & 1 & -1\end{smallmatrix}\right)$, and the transition rates be $W_1(\mathbf{X}) = \alpha X$, $W_2(\mathbf{X}) = \beta XY/V$, $W_3(\mathbf{X}) = \delta XY/V$, $W_4(\mathbf{X}) = \gamma Y$ where $\alpha = 10$, $\beta = 0.01$, $\gamma = 100$, $\delta = 0.02$ and $V = 1$.

The ODE (1) for this model are the well-known Lotka-Volterra equations [2]: $\frac{dX}{dt} = X(\alpha - \beta Y)$; $\frac{dY}{dt} = -Y(\gamma - \delta X)$. The non-extinction fixed point is $(\gamma/\delta, \alpha/\beta)$. The polar coordinates will take this fixed point as origin.

Let us use (8) to compute the average speed of change of the squared distance, $L_a(\mathbf{X}) = (X - \gamma/\delta)^2 + (Y - \alpha/\beta)^2$, to the fixed point $a = \big(\gamma/\delta, \alpha/\beta\big)$ at each point (X, Y). For the given system parameters, it holds:

$$\begin{aligned}R(\mathbf{X})\sum_{i=1}^{q}\mathbb{E}[(\Delta X_i)^2] &= R(\mathbf{X})\big(\mathbb{E}[(\Delta X)^2]+\mathbb{E}[(\Delta Y)^2]\big)\\ &= R(\mathbf{X})\left(\sum_{j=1}^{n}(\nu_1^j)^2\frac{W_j(\mathbf{X})}{R(\mathbf{X})}+\sum_{j=1}^{n}(\nu_2^j)^2\frac{W_j(\mathbf{X})}{R(\mathbf{X})}\right)\\ &= \big((1\cdot W_1(\mathbf{X})+1\cdot W_2(\mathbf{X}))+(1\cdot W_3(\mathbf{X})+1\cdot W_4(\mathbf{X}))\big)\\ &= \alpha X+\beta XY/V+\delta XY/V+\gamma Y\end{aligned}$$

and

$$\begin{aligned}\sum_{i=1}^{q}2(X_i-a_i)\Big(\sum_{j=1}^{n}\nu_i^j W_j(\mathbf{X})\Big) &= 2\left(X-\frac{\gamma}{\delta}\right)(\alpha X-\beta XY/V)\\ &\quad+2\left(Y-\frac{\alpha}{\beta}\right)(\delta XY/V-\gamma Y)\end{aligned}$$

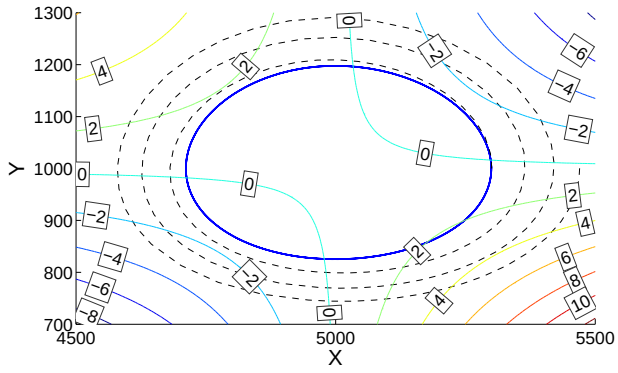


Fig. 3. Trajectories of ODE (1) and ODE (11) for a simple predator-prey system.

Then, according to (8), the average speed of change of L_a becomes:

$$\begin{aligned}R(\mathbf{X})\mathbb{E}[\Delta L_a(\mathbf{X})] &= 2\left(X-\frac{\gamma}{\delta}\right)(\alpha X-\beta XY/V)\\ &\quad+2\left(Y-\frac{\alpha}{\beta}\right)(\delta XY/V-\gamma Y)\\ &\quad+\alpha X+\beta XY/V+\delta XY/V+\gamma Y\end{aligned}$$

Let the initial populations of the system be $(5300, 1000)$. The isolines shown in Figure 3 correspond to the values of $R(\mathbf{X})\mathbb{E}[\Delta L_a(\mathbf{X})]$ divided by 10^6. It can be observed that the system tends to move away from the fixed point $\left(\frac{\gamma}{\delta}, \frac{\alpha}{\beta}\right) = (5000, 1000)$ since all the values of $R(\mathbf{X})\mathbb{E}[\Delta L_a(\mathbf{X})]$ around that point are positive.

The trajectory for the Lotka-Volterra equations, i.e., ODE (1), is the inner (solid) trajectory in Figure 3. The trajectory given by ODE (11) during 0.6 time units is the outer (dotted) trajectory. While the cartesian ODE produces a closed trajectory whose amplitude depends on the initial populations, the trajectory provided by the polar ODE moves away from the fixed point, what is consistent with the *resonant stochastic amplification* and the tendency to extinction pointed out in [12] and [15].

5.2 The Brusselator

The Brusselator is a theoretical model proposed by Prigogine and collaborators [7] for a type of autocatalytic reaction. The model consists of four reactions: $r_1 : A \to X$, $r_2 : 2X + Y \to 3Y$, $r_3 : B + X \to Y + D$, $r_4 : X \to E$. The net reaction is $A+B \to D+E$ and the intermediate species are X and Y. As in previous works [11], the populations of A and B will be kept constant to values a and b respectively, and the focus will be on the evolution of $X = X_1$ and $Y = X_2$. Under this assumption the stoichiometry matrix is $\nu = \left(\begin{smallmatrix}1 & 1 & -1 & -1\\ 0 & -1 & 1 & 0\end{smallmatrix}\right)$, and the transition rates are $W_1(\mathbf{X}) = a$, $W_2(\mathbf{X}) = X^2Y/V^2$, $W_3(\mathbf{X}) = bX/V$, $W_4(\mathbf{X}) = X$. The ODE (1) for this model is: $\frac{dX}{dt} = a + X^2Y/V^2 - bX/V - X$; $\frac{dY}{dt} = bX/V - X^2Y/V^2$ which has a fixed point at $(a, \frac{b}{a}V)$. This fixed point becomes unstable and ODE (1) exhibits a limit cycle when $b > V + a^2/V$.

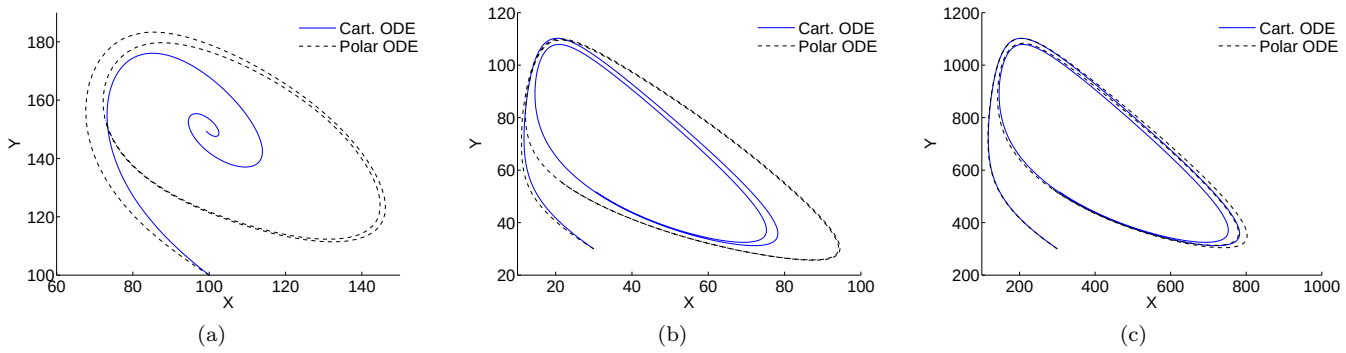


Fig. 4. Phase space trajectories of the cartesian ODE (1) and polar ODE (11) for the Brusselator.

The trajectories in the phase space in Figure 4(a) correspond to parameters $a = 100$, $b = 150$, $V = 100$, $X(0) = Y(0) = 100$. It can be observed that while the cartesian ODE (1) tends to the fixed point $q = (100, 150)$, the polar ODE (11), which takes q as reference point, presents sustained oscillations that are also exhibited by the jump Markov process.

Figure 4 shows the trajectories of two models with same initial concentrations for all the species $a = 1V$, $b = 2.5V$, $X(0) = Y(0) = 1V$, and different system sizes, $V = 30$ and $V = 300$ for Figure 4(b) and Figure 4(c) respectively. As expected, the cartesian ODE shows a limit cycle and scales with V. Although the polar ODE also enters a limit cycle for both sizes, it does not scale with V and gets closer to the trajectory of the cartesian ODE for higher values of V. In fact, in the limit $V \to \infty$ the Markov process will converge to the cartesian ODE [5, 9], and then, the estimation of distances and angles will be the same both by the cartesian ODE and the proposed polar ODE, what results in the same system trajectory.

6. CONCLUSIONS

The time evolution of biological systems modelled by jump Markov processes tends to a deterministic limit as the system size tends to infinity. Such a deterministic limit is obtained as a solution of a system of ordinary differential equations (ODE), and hence, the obtained trajectory is continuous and deterministic. Because real systems are inherently discrete and stochastic, and their size is finite, they never attain the mentioned limit. In fact, if only the deterministic limit is used to analyze the system dynamics, relevant features, as sustained oscillations, can be overlooked.

An alternative approach to study the dynamics is to consider directly the jump Markov process. The combined use of the expected value of the associated embedded Markov process and the transition rates can be employed to estimate the average speed change of a function of interest. This speed of change is, in general, different to the speed of change provided by the deterministic limit. Among the functions that can be estimated, we have focused on the distance and angle with respect to a given reference point. These two functions are the basis to define an ODE in polar coordinates. Such an ODE provides additional dynamical information and can be straightforwardly used to infer the average system behaviour around the reference point.

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