

# Nearly Completely Decomposable Epidemic-Like Stochastic Processes with Time-Varying Behavior

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## 1. INTRODUCTION

Epidemic-like stochastic processes with time-varying parameters have been introduced to model viral behaviors in communication and social networks, cybersecurity systems, financial markets, and so on [5]. We additionally observe that such stochastic processes can include interactions between local (micro) and global (macro) behaviors within the process, involving migration from one operating regime to another and transitions within each regime. To address this phenomena, we consider herein nearly completely decomposable (NCD) structures [3] in epidemic-like stochastic processes with time-varying behaviors. In doing so, we extend known results for NCD processes to include time-varying parameters and we devise mean-field limits of such epidemic-like processes as regime-switching dynamical systems.

Specifically, in a previous study [5], we explored the connection between a general class of epidemic-like stochastic processes with time-varying parameters that characterizes the type of viral behaviors exhibited in environments such as communication and social networks. We established that, under general assumptions on the time-varying process and under a mean-field scaling with respect to population size  $n$ , the stochastic process converges to a time-varying dynamical system, thus extending the corresponding results in [4] to time-varying processes. In this paper, we first extend our previous work to study the stationary behavior of both the original stochastic process and the mean-field limiting dynamical system, and verify that they, in fact, have similar asymptotic behavior with respect to time. In other words, we establish that the following diagram is commutative.

$$\begin{array}{ccc} X_n(t) & \xrightarrow{t \rightarrow \infty} & X_n \\ n \rightarrow \infty \downarrow & & \downarrow n \rightarrow \infty \\ X(t) & \xrightarrow{t \rightarrow \infty} & X \end{array} \quad \{\mathbf{1}\}$$

Given our above observation on local and global behaviors, we further study a general class of NCD Markov chains (MCs) with time-varying parameters and the corresponding mean-field limiting systems. The classical approach of Courtois consists of approximating the stationary distribution of an NCD MC by a completely decomposable (CD) MC, which characterizes the dynamics within each regime in isolation, together with an auxiliary MC that governs the transitions between regimes [3]. Both the CD MC and the

auxiliary MC are mathematically more tractable than the original NCD MC, and the approximation error is shown to be bounded by the deviation of the transition matrix of the NCD MC from that of the CD MC, which is of order  $O(\epsilon)$ . In this paper, we also streamline the NCD analysis, extending these results to sequences of NCD MCs associated with epidemic-like stochastic processes. This allows us to further approximate such large-scale NCD stochastic processes with time-varying parameters by the corresponding mean-field limiting systems, thus establishing that diagram  $\{\mathbf{1}\}$  above is also commutative with  $\mathbf{X} := (X_n(t), X(t), X_n, X)$  replaced by  $\mathbf{X}_\epsilon := (X_{n,\epsilon}(t), X_\epsilon(t), X_{n,\epsilon}, X_\epsilon)$ .

## 2. MEAN-FIELD LIMIT AND STATIONARY DISTRIBUTION

Following [5], we consider a sequence of Markov processes  $\hat{Z}_n = \{(\hat{X}_n(t), \hat{Y}_n(t)); t \geq 0\}$  indexed by the population size  $n = 1, 2, \dots$  and defined over the probability space  $(\Omega_n, \mathcal{F}_n, \mathbb{P}_n)$ , comprised of state space  $\Omega_n := \{(i, j) : 0 \leq i, j \leq n, i + j = n\}$ ,  $\sigma$ -algebra  $\mathcal{F}_n$  and probability measure  $\mathbb{P}_n$ , with initial probability distribution  $\alpha_n$ . The ordered pair  $(\hat{X}_n(t), \hat{Y}_n(t))$  denotes the non-infected and infected amount of the population at time  $t$ , respectively, where we assume the population of size  $n$  is connected through a complete graph. Let the states  $i \in \{0, 1, 2, \dots, n\}$  represent the number of non-infected members of the population. Then the transition probabilities are given by  $p_{i,i+1} = (n-i)\mu$  and  $p_{i,i-1} = \lambda \frac{i(n-i)}{n}$  for all  $i = 0, 1, \dots, n-1$ . For state  $i = n$ , i.e., everyone is healthy, there is a transition back into the state  $n-1$  with rate  $\nu$ , which guarantees the existence of a stationary distribution.

To start, it is easy to derive the stationary distribution from the balance equations. For  $i = 0, 1, \dots, n-1$ , we have

$$\pi_i = \frac{n^{i+1}}{i!(n-i)} \left(\frac{\mu}{\lambda}\right)^i \pi_0, \quad (1)$$

together with

$$\pi_n = \frac{n^n}{(n-1)!} \left(\frac{\mu}{\lambda}\right)^{n-1} \left(\frac{\mu}{\nu}\right) \pi_0. \quad (2)$$

**Remark.** We know that the distribution is *roughly* a truncated Poisson distribution with rate  $n \frac{\mu}{\lambda}$ . In order to apply Markov's inequality argument, we need to estimate the first two moments. Note that we only need to estimate their order in  $n$ , so we can simply assume that  $\pi_n$  will have the same format as  $\pi_i$ ,  $i = 0, 1, \dots, n-1$ ; later we can include the difference, which will not change our main results.

For the first moment, we have

$$\begin{aligned}\mathbb{E}[X_n] &= \sum_{i=1}^n i\pi_i = \sum_{i=1}^n \frac{n^{i+1}}{(i-1)!(n-i)} \left(\frac{\mu}{\lambda}\right)^i \pi_0 \\ &= n \left(\frac{\mu}{\lambda}\right) \sum_{i=0}^{n-1} \frac{n-i}{(n-i+1)} \pi_i,\end{aligned}$$

from which we can conclude  $\mathbb{E}[X_n] = n\frac{\mu}{\lambda} + o(n)$ . Meanwhile,

$$\begin{aligned}\mathbb{E}[X_n - \mathbb{E}[X_n]]^2 &= \mathbb{E}[X_n^2] - \mathbb{E}[X_n]^2 \\ &= \sum_{i=1}^n i^2 \pi_i - \left(\sum_{i=1}^n i\pi_i\right)^2 = \sum_{i=1}^n \sum_{j=1}^n i(i-j)\pi_j \pi_i,\end{aligned}$$

and thus we have  $\text{Var}[X_n] = O(n)$ . Therefore, for any  $A > 0$ ,

$$\begin{aligned}\mathbb{P}\left[\left|\frac{X_n}{n} - \frac{\mu}{\lambda}\right| > A\right] &= \mathbb{P}\left[\left(X_n - n\frac{\mu}{\lambda}\right)^2 > n^2 A^2\right] \\ &\leq \frac{\mathbb{E}\left[X_n - n\frac{\mu}{\lambda}\right]^2}{n^2 A^2}.\end{aligned}$$

From this derivation we know that the numerator is of order  $O(n)$ , hence the above quantity will converge to zero as  $n \rightarrow \infty$ . This implies that  $\frac{X_n}{n}$  converges weakly to  $\frac{\mu}{\lambda}$  as  $n \rightarrow \infty$ .

To complete our analysis of diagram  $\{\mathbf{1}\}$ , following [5], we show that the sequence of MCs, when scaled by  $n$ , converges to a dynamical system described as follows

$$\frac{dx}{dt} = -\lambda(t)xy + \mu(t)y \quad \text{and} \quad \frac{dy}{dt} = \lambda(t)xy - \mu(t)y.$$

Furthermore, we show that all trajectories of the dynamical system will approach time-varying asymptotic states when  $\lambda(t)$  and  $\mu(t)$  are slowly varying, which includes as a special case  $\frac{\mu(t)}{\lambda(t)} \rightarrow c \in (0, 1)$  as  $t \rightarrow \infty$ . It is easy to see in this special case that the stationary distribution of the inhomogeneous MC  $X_n(t)$  is actually the same as that of a homogeneous MC with  $\lambda(t)$  and  $\mu(t)$  replaced by constants  $\lambda$  and  $\mu$ , such that  $\frac{\mu}{\lambda} = c$ . The above arguments therefore demonstrate that, if we first let the time parameter  $t$  go to infinity and then scale by  $n \rightarrow \infty$ , we will get the same point measure, and thus diagram  $\{\mathbf{1}\}$  is commutative.

### 3. ANALYSIS OF NCD SYSTEMS

A primary result of Courtois [2] is that the stationary distribution of an NCD MC can be accurately approximated by a system comprising an auxiliary MC and a CD MC. Our first result shows that, under mild conditions, this is true even when we have a sequence of NCD MCs indexed by  $n$ , for which an error bound uniform in  $n$  can also be established. Consequently, in the limit as  $n \rightarrow \infty$ , we obtain an MC whose state space consists of several point measures such that this MC has bounded error in addition to the sequence of NCD MCs. Our ultimate goal will be to establish the commutativity of diagram  $\{\mathbf{1}\}$  with  $\mathbf{X}$  replaced by  $\mathbf{X}_\epsilon$ .

Consider a two-parameter process,  $X_{n,\epsilon}(t)$ , representing the underlying MC that characterizes the discrete system which not only exhibits stochastic epidemic-type behavior within each regime, but also transitions between different regimes. Here,  $n$  is a parameter related to space, often representing the total population of the system under consideration, and  $\epsilon$  represents the relative magnitude of the transition rates between the different regimes. More specifically,

the transition probability matrix for  $X_{n,\epsilon}(t)$  will be denoted as  $Q_{n,\epsilon}$ , where we have

$$Q_{n,\epsilon} = Q_n^* + \epsilon C_n,$$

and

$$Q_n^* = \begin{bmatrix} Q_1^* & & & \\ & Q_2^* & & 0 \\ & & \ddots & \\ & & & Q_M^* \end{bmatrix}.$$

The  $n \times n$  matrix  $Q_m^*$ , for  $m = 1, 2, \dots, M$ , represents the transition probabilities for the states within regime  $m$ , and  $C_n$  represents the transition probabilities between different regimes, whose row sums will be bounded by one. For ease of exposition, we will suppress the index  $n$ , but will address specific details with respect to  $n$  when necessary.

First, define  $\Lambda^*(m) := \text{diag}^*(\lambda_{mi})$  to be the diagonal matrix of the eigenvalues of  $Q_m^*$ , and  $\Lambda^* := \text{diag}(\Lambda^*(m))$ . We then know there exists a non-singular matrix  $H$  such that  $H^{-1}Q^*H = \Lambda^*$ , and thus  $H^{-1}QH = \Lambda^* + \epsilon H^{-1}CH$ . Next, let  $B$  denote the matrix whose rows are the left eigenvectors of  $H^{-1}QH$ . Upon multiplying the above equality by  $B$ , we have  $\Lambda B = B\Lambda^* + \epsilon BH^{-1}CH$ . Observe that, for each  $j = 1, 2, \dots, n$ ,  $\Lambda B e_j = B\Lambda^* e_j + \epsilon BH^{-1}C H e_j$ , especially for each  $j = nm + 1, m = 0, 1, \dots, M - 1$ . Then, from this we can obtain the  $O(\epsilon)$  order for some elements in  $B$ .

#### 3.1 Auxiliary MC

Let  $\pi_i^*$  denote the stationary distribution of  $Q_i^*$ , i.e., solution of  $\pi_i^* = \pi_i^* Q_i^*$ . The state space of the auxiliary MC consists of the set of indices for the blocks, i.e., the number of states is  $M$ . The transition probabilities are defined by  $q_{km} = \sum_{i \in b(k)} \pi_i^* \sum_{j \in b(m)} p_{ij}$  for  $k, m = 1, 2, \dots, M$ , where, for any  $m$ ,  $b(m)$  represents the set that contains all the indices in block  $m$ . Intuitively, this is the aggregation, by weights of  $\pi^*$  (stationary under  $Q^*$ ), of the probability mass of transitions between blocks, which is referred to as the macro-variable system through variable aggregation in [2].

#### 3.2 Error Analysis

Suppose  $\tilde{\pi}$  is the stationary distribution of the auxiliary MC with  $M$  states. We further have as above that  $\pi_i^*$  is the stationary distribution conditional on being in regime  $i$ . Let  $\pi$  denote the stationary distribution of the original NCD MC. Then the quantity  $\tilde{\pi}_m \pi_{i,j}^*$  will be used as an approximation of  $\pi_{i,j}$ , namely the stationary probability for state  $j$  in regime  $i$  of the original NCD MC.

For the (transposed) stationary vector, we know that

$$\pi^t = B(1)H^{-1}$$

where  $B(1)$  denotes the first row of the matrix  $B$ , i.e., the left eigenvector of the matrix  $H^{-1}QH$  corresponding to the eigenvalue 1. Recall that  $\pi$  can be viewed as the left eigenvector of  $Q$  corresponding to the eigenvalue of 1, and  $\beta(1)$  represents the the left eigenvector of  $H^{-1}QH$  corresponding to the same eigenvalue.

From the fact that  $H^{-1}$  is a block matrix, we can rewrite the above into the following block form

$$\pi_m^t = B(1)_m H_m^{-1}, m = 1, 2, \dots, M,$$

where  $B(1)_m$  denotes the  $m$ -th block of the (transposed) vector  $B(1)$ . For all vectors and matrices with subscript  $m$ ,

we refer to the  $m$ -th block of the vectors and matrices.

Next, we have

$$\pi_m^t = B(1)_m H_m^{-1} = B(1)_m I_{i_m, t} H_m^{-1} + B(1)_m I_{i_m, h} H_m^{-1}.$$

Note that  $i_m$  is the cardinality of  $b(m)$ , and  $I_{i_m}$  denotes the identity matrix of dimension  $i_m \times i_m$ . Let  $I_{i_m, h}$  denote the matrix whose first row and first column element is 1 with all others 0, and  $I_{i_m, t}$  the difference between  $I_{i_m}$  and  $I_{i_m, h}$ .

We therefore obtain

$$\pi_m^t - \tilde{\pi}_m \pi_i^* = B(1)_m I_{i_m, t} H_m^{-1} + [B_m I_{i_m, h} H_m^{-1} - \tilde{\pi}_m \pi_i^*], \quad (3)$$

for which we have the following main result.

**THEOREM 3.1.** *The approximation error is of linear order of the NCD parameter  $\epsilon$ , namely*

$$\pi_m^t - \tilde{\pi}_m \pi_i^* = O(\epsilon). \quad (4)$$

We now establish Theorem 3.1 by showing that both terms on the right hand side of Eq. (3) are  $O(\epsilon)$ .

### 3.2.1 $O(\epsilon)$ estimation of the first term

Once again, the basic identity is given by  $\Lambda B = B\Lambda^* + \epsilon B H^{-1} C H$ . For convenience, let us denote the set  $F \subseteq \{1, 2, \dots, n\}$  containing all the indices that are the first of each block, i.e.,  $F := \{\sum_{k=0}^m i_k + 1, m = 0, 1, \dots, m-1\}$ . Let  $E$  be the matrix containing  $e_j, j \in F$ . We then have

$$\Lambda B E - B\Lambda^* E = \epsilon B H^{-1} C H, \quad (5)$$

and thus all the elements in the matrix  $\Lambda B E - B\Lambda^* E$  are  $O(\epsilon)$ . It follows that in each block the off-diagonal elements on the first row and column will be  $O(\epsilon)$ , and hence these  $B$  elements will be  $O(\epsilon)$ . At this point, we require that there exist a nonzero uniform lower bound for the spectral gaps of the sequence of MCs, indexed by  $n$ . Meanwhile, Meise [6] shows that such lower bounds can be connected to a supremum of a family of expected hitting times. It is easy to verify for the epidemic model, under mild conditions on  $\lambda(t)$  and  $\mu(t)$ , that the supremum of this family of expected hitting time can be uniformly bounded, which implies that a uniform lower bound of the spectral gap exists. With this fact, we can conclude that every nonzero element in  $B(1)_m I_{i_m, t}$  will be  $O(\epsilon)$ , and so is the first term in (3).

### 3.2.2 $O(\epsilon)$ estimation of the second term

Since  $I = E + (I - E)$ , we have

$$\Lambda B E - B\Lambda^* E - \epsilon B E H^{-1} C H E = \epsilon B (I - E) H^{-1} C H E. \quad (6)$$

From the above analysis, each term in  $B I_E'$  is  $O(\epsilon)$ , and hence the right hand side of Eq. (6) is  $O(\epsilon^2)$ . The left hand side is basically  $P - I$ , where  $P$  is the transition matrix for the auxiliary MC. The desired result can be obtained after we add  $\tilde{\pi}(P - I)$  to the left hand side of the equation, which would not change the equation, since  $\tilde{\pi}(P - I) = 0$ . Observe that  $H C$  is basically a vector whose elements are all ones, which is due to the fact that on each block this is simply the first right eigenvector, and thus an all-ones vector due to stochasticity. Therefore,  $\epsilon E H^{-1} C H$  actually recovers the dynamics of the auxiliary MC.

- By the above arguments, the left hand side of Eq. (6) can be actually written as  $B(1)[P - \lambda(1)I_M]$ .

- Then Eq. (6) yields that  $\text{Det}(P - \lambda(1)I_M) = O(\epsilon)$ , and thus there exists an eigenvalue  $\mu(L)$  of  $P$  such that  $|\lambda(1) - \mu(L)| = O(\epsilon)$ . Combining this with the fact (by definition) that  $U(L)[P - \mu(L)I_M] = 0$ , we have  $[B(1) - U(L)][P - \mu(L)I_M] = O(\epsilon^2)$ .
- Since  $P$  is about  $\epsilon$  away from identity, all elements of  $P - \mu(1)I_N$  are on the order of  $\epsilon$ .

**Remark.** While we will only study the class of epidemic-like systems in what follows, the error analysis presented here applies to general NCD MCs.

## 3.3 Complete the Diagram

Recall that  $X_{n, \epsilon}$  represents the stationary distribution of  $X_{n, \epsilon}(t)$ , or the limit as  $t \rightarrow \infty$ . Let  $Y_{n, \epsilon}$  denote the stationary distribution for the CD MC and auxiliary MC. The above arguments confirm that the total variation distance between the two sequences of measures are of order  $O(\epsilon)$ , i.e.,  $d_{TV}(X_{n, \epsilon}, Y_{n, \epsilon}) = O(\epsilon)$ , uniformly in  $n$ . Next, consider  $\bar{X}_\epsilon = \frac{1}{n} X_{n, \epsilon}$  and  $\bar{Y}_\epsilon = \frac{1}{n} Y_{n, \epsilon}$ . We further conclude that  $d_{TV}(\bar{X}_\epsilon, \bar{Y}_\epsilon) = O(\epsilon)$ . Meanwhile, from our analysis in Section 2, we know that  $\bar{Y}_\epsilon$  will be an MC between point measures, which provides a nice interpretation of the original stochastic process.

Let us now take the other route in the alternative version of diagram  $\{1\}$ . First, consider the process  $\bar{X}_\epsilon(t) = \frac{1}{n} X_{n, \epsilon}(t)$  and  $\bar{Y}_\epsilon(t) = \frac{1}{n} Y_{n, \epsilon}(t)$ . From the analysis in [5], we know that  $\bar{Y}_\epsilon(t)$  is a regime-switching dynamical system, a special case of the broader class of hybrid dynamical systems that have many applications in modeling biological and chemical systems [1]<sup>1</sup>. We can also apply the analysis of the dynamical system in [5] to conclude that the equilibrium state of  $\bar{Y}_\epsilon(t)$  will be those point measures in combination. Hence, we conclude that diagram  $\{1\}$  with  $\mathbf{X}$  replaced by  $\mathbf{X}_\epsilon$  is also commutative.

## 4. REFERENCES

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<sup>1</sup>Even simple regime-switching dynamical systems can exhibit complicated dynamics. For instance, a simple 2-dimensional dynamical system with a continuous piecewise-linear vector field and driven by a periodic signal, can exhibit chaotic behavior [7].