

MATHEMATICAL ANALYSIS OF SPREAD MODELS: FROM THE VIEWPOINTS OF DETERMINISTIC AND RANDOM CASES

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ABSTRACT. This paper models the spread of the pandemic with mathematical analysis to provide predictions for different classes of individuals. We consider the spread by using a branching process and a substitution dynamical system as random and deterministic models, respectively, to approximate the pandemic outbreak. Both approaches are based on the assumption of Markov processing. The deterministic model provides an explicit estimate for the proportion of individuals of a certain type in the particular generation given any initial condition, where a generation means a unit of observation time. The proportion relates to the matrix derived from the Markov setting. In addition, the methodology reveals the efficiency of epidemic control policies, such as vaccine injections or quarantine, by the relative spread rate that is used for the prediction of the number of individuals of a certain type. On the other hand, the stochastic approximation has more of an empirical impact than the deterministic one does. Our investigation explicitly exhibits the spread rate of a certain type with respect to an initial condition of any type. After estimating the average spread rate, the effect of adopting a particular policy can be evaluated. The novelty of this elucidation lies in connecting these two models and introducing the idea of the transition spread model between two topological spread models to capture the change of the spread patterns, which is a real-world phenomenon during the epidemic periods due to changes in the environment or changes in disease control policies. Roughly speaking, the deterministic model is a special case of the stochastic model under some particular probability. Most importantly, with the help of the stochastic model, we establish the transition processing of two deterministic models, which is called a transition model. In other words, any stochastic model is “bounded” by two deterministic models. Moreover, a computable way has been established to predict the long-term spread rate due to the Markov properties of the models and matrix representations for the spread patterns.

1. INTRODUCTION

Periodically, throughout human history, pandemics have spread widely and rapidly all over the world. A contemporary case in point is the coronavirus (COVID-19) outbreak that began in late 2019. To minimize the impact caused by these diseases, developing a mathematical model based

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on real data as a criterion for making informed decisions about preventive initiatives is essential. Among the most frequently investigated mathematical models of epidemics such as COVID-19 is the susceptible-infected-recovered (SIR) model (or similar variants, like SIS and SIRS), calibrated by using flu data and severe acute respiratory syndrome (SARS) data [4, 9, 16, 19, 23]. The investigation focuses on the reproduction number which illustrates whether the epidemic will eventually die out. In other words, this is a long-term prediction of a chaotic system [6, 8, 15, 18].

Instead of focusing on whether the pandemic will die out, short-term prediction of the scope and extent of the pandemic outbreak is also of interest. Some frequently used methodologies are support vector machine, deep learning (such as convolutional neural networks together with long short-term memory), intrinsic mode function, etc. See [1, 5] and the references therein. With the systemic identification of real data, it is possible to predict the spread rate of the pandemic, the probability of individuals becoming infected, and other applications germane to various fields (cf. [2, 7, 13]). Short-term prediction usually depends on how much data can be collected and is therefore difficult to carry out globally. We are interested in developing a model that illustrates the dynamical behavior characterizing the wide spreading of COVID-19 disease around the globe. In other words, we intend to propose a model that captures short-term behavior and is also capable of revealing global tendencies at the same time. For this purpose, beyond the examination of deterministic models, a random system is also significant due to the uncertainty of the transmission of the virus between objects in the real world. Investigating the epidemic spread via two models is the main contribution of this work. Such a discussion reveals the studied subjects in various aspects; thus, it can provide more accurate decision-making (cf. [12, 20] for instance). Despite demonstrating the relation between our two proposed models, we also introduce the transition spread model between two topological spread models to capture the change of the spread patterns, which is a real-world phenomenon during the epidemic periods due to changes in the environment or changes in disease control policies. Another innovation is that a computable way has been established to predict the long-term spread rate due to the Markov properties of the models and matrix representations for the spread patterns.

In this paper, we use a branching process and a substitution dynamical system to model the pandemic's spread, where the spread of disease is assumed to satisfy a Markov process, and thus has a tree structure, as illustrated in Figure 1. More specifically, we divide the objectives into several categories such as those who are capable of spreading the disease, individuals who have received vaccines, mask wearers who also practice social distancing to lower the risk of transmission/infection, etc., and use a Galton-Watson branching process (as our random system) and a substitution system (as our deterministic system) to simulate how the virus is disseminated. Based on the assumption of the spread following a Markov process, we are

able to predict the ratio of the spreading speed. We divide the statuses of individuals during the process of the virus spreading into several classes, such as severely ill, asymptomatic, quarantined, etc. Each individual of the same type could affect his/her surroundings within a fixed time interval by the same pattern. The proposed deterministic model provides an explicit estimate for the proportion of individuals of each type in an arbitrary generation given any initial condition, where a generation represents a unit time. Since the proposed model satisfies Markov processing, the aforementioned proportion can be determined from the matrix obtained by the impact of each type of individual. In addition, our methodology reveals the efficiency of epidemic control policies such as vaccination and quarantine, by the relative spread rate that is used for the prediction of the number of individuals of a certain type. On the other hand, the proposed stochastic model in this paper might be more empirically impactful than the deterministic one, in some ways. Our investigation explicitly demonstrates the spread rate of each type of individual with respect to initial conditions of any type. After estimating the average spread rate, the effect of adopting a particular policy can be evaluated. The novelty of this elucidation lies in connecting these two models. Roughly speaking, the deterministic model is a special case of the stochastic model under some particular probability. Most importantly, with the help of the stochastic model, we establish the transition process of two deterministic models, which is referred to as a transition model. In other words, any stochastic model is “bounded” by two deterministic models. It is worth emphasizing that, once the initial distribution of different types of population and the spread pattern of each type are given, both proposed models can start the simulation simultaneously. Moreover, it is possible to make a hybrid model out of our proposed models to fit real data. Notably, the proposed methodology can be applied to the further study of epidemic models or to ecological systems.

The upcoming sections are devoted to the presentation of our spread model. After unveiling the notations, Section 2 introduces the deterministic and stochastic systems of a Markov process spread model. The deterministic model can be realized as a substitution system. We consider the Galton-Watson branching process as a random system describing the spreading of the disease. The main results and discussion are presented in Section 3. To investigate the spread rate, we can estimate the distribution of a population through the spectral radius of the corresponding mean matrix. We also reveal that the topological spread model is almost surely a particular case of a random spread model by assigning a proper probability distribution to it. Section 4 consists of numerical experiments for the approval of our main theorems. We show that the transition from one random spread model to the other is continuous and monotonic concerning the spread ratio. Conclusions are in Section 5.

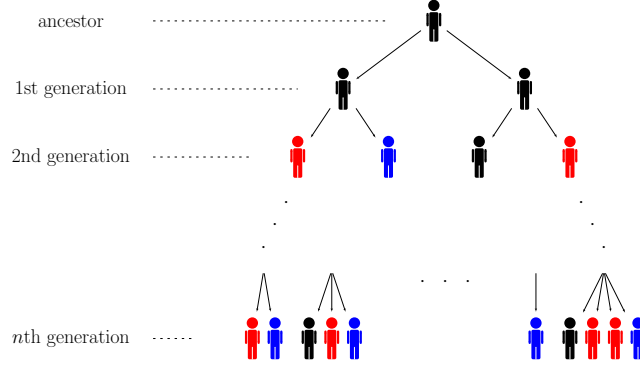


FIGURE 1. An illustration of the spread model; each color represents a particular type of an individual such as severely ill, mildly ill, asymptomatic, during the spreading process.

2. MATERIALS AND METHODS

Throughout this paper, we adopt the following notations.

- $|S|$ denotes the cardinality of the set S .
- $S^k \equiv \{(s_1 s_2 \dots s_k) : s_i \in S, \forall 1 \leq i \leq k\}$ for any set S .
- $S^* \equiv \cup_{k \geq 1} S^k$ for any set S .
- \mathbb{N}_0 is the set of all nonnegative integers.
- $\mathbf{0} = (00 \dots 0)$ and $\mathbf{1} = (11 \dots 1)$ in \mathbb{N}_0^k
- $\mathbf{e}_i = (0 \dots 010 \dots 0) \in \mathbb{N}_0^k$ with the 1 in the i th component.
- Let $\mathbf{u} = [u_i] = (u_1 u_2 \dots u_k)$ and $\mathbf{v} = [v_i] = (v_1 v_2 \dots v_k)$ be k -vectors with $u_i, v_i \in \mathbb{R}$, $i = 1, 2, \dots, k$. Then $\mathbf{u} \leq \mathbf{v}$ means $u_i \leq v_i$ for $i = 1, 2, \dots, k$ while $\mathbf{u} < \mathbf{v}$ means $u_i \leq v_i$ for all i and $u_i < v_i$ for at least one i .
- The absolute value of the vector $\mathbf{x} = [x_i]$ is

$$|\mathbf{x}| = |x_1| + |x_2| + \dots + |x_k|$$

- The sup norm of the vector $\mathbf{x} = [x_i]$ is

$$\|\mathbf{x}\| = \max\{|x_1|, |x_2|, \dots, |x_k|\}$$

- For a vector $\mathbf{x} = [x_i]$ and a $\mathbf{y} = [y_i]$ in \mathbb{N}_0^k ,

$$\mathbf{x}^{\mathbf{y}} = \prod_{i=1}^k x_i^{y_i}$$

- For a matrix $M = [m_{i,j}]$, the sup norm is

$$\|M\| = \max\{|m_{i,j}| : i, j = 1, 2, \dots, k\}$$

The general settings for modelling of the evolution or spreading processes are described as below. It should be noted that we consider those who are infected by a person to be the children of said person. Let $\mathcal{A} = \{a_1, a_2, \dots, a_k\}$ be the *type set*, which is a set of types indicating the status of each individual during the spreading process, e.g., severely ill, mildly ill,

or asymptomatic. Suppose the population is initiated with one individual of type $\alpha = \alpha^{(0)} = a_i \in \mathcal{A}$, and $\alpha_j^{(1)}$ is the type of the j th child of this initial individual, $j = 1, 2, \dots, d_\alpha^{(1)}$, where $d_\alpha^{(1)}$ is the number of children of this initial ancestor of type $\alpha (= a_i)$. Define

$$p_\alpha^{(1)} = (\alpha^{(0)}; \alpha_1^{(1)} \cdots \alpha_{d_\alpha^{(1)}}^{(1)}),$$

which is called a *pattern of the 1st generation*, and an illustration of which is provided in Figure 2. A pattern $p_\alpha^{(1)}$ depicts how an individual could affect the surroundings within a fixed interval of time, e.g., $(a_1; a_1 a_1 a_2 a_2 a_2 a_3)$ means an individual of type a_1 will add to the environment two individuals of type a_1 , three of type a_2 , and one of type a_3 within some prescribed time interval. In addition, we denote the *offspring type chart of α in the first generation* by

$$\Pi(p_\alpha^{(1)}) = \alpha_1^{(1)} \cdots \alpha_{d_\alpha^{(1)}}^{(1)}$$

Next, we replace each $\alpha_j^{(1)}$ in $p_\alpha^{(1)}$ by $\Pi(p_{\alpha_j^{(1)}}^{(1)})$, $j = 1, 2, \dots, d_\alpha^{(1)}$ to obtain the pattern of the 2nd generation, i.e.,

$$p_\alpha^{(2)} \equiv \left(\alpha; \Pi(p_{\alpha_1^{(1)}}^{(1)}) \Pi(p_{\alpha_2^{(1)}}^{(1)}) \cdots \Pi(p_{\alpha_{d_\alpha^{(1)}}^{(1)}}^{(1)}) \right) = \left(\alpha^{(0)}; \alpha_1^{(2)} \cdots \alpha_{d_\alpha^{(2)}}^{(2)} \right),$$

where $d_\alpha^{(2)}$ is the total number of offspring in the 2nd generation, and the process is illustrated in Figure 2. In this manner, once $p_\alpha^{(n-1)} = (\alpha; \alpha_1^{(n-1)} \cdots \alpha_{d_\alpha^{(n-1)}}^{(n-1)})$ is defined, we denote the *offspring type chart of α in the $(n-1)$ th generation* by

$$\Pi(p_\alpha^{(n-1)}) = \alpha_1^{(n-1)} \cdots \alpha_{d_\alpha^{(n-1)}}^{(n-1)}.$$

Then, we replace offspring of type $\alpha_j^{(n-1)}$ in $p_\alpha^{(n-1)}$ with $\Pi(p_{\alpha_j^{(n-1)}}^{(1)})$, $j = 1, 2, \dots, d_\alpha^{(n-1)}$

to obtain $p_\alpha^{(n)}$, the pattern of the n th generation and so on. According to the above definition, $p_\alpha^{(n)}$ denotes the outcome of the spreading process after n generations with respect to an initial individual of type α , and this model of spreading has a tree structure intrinsically. For any $\beta \in \mathcal{A}$, denote by $\left| \Pi(p_\alpha^{(n)}) \right|_\beta$ the number j , $j = 1, 2, \dots, d_\alpha^{(n)}$ such that $\alpha_j^{(n)} = \beta$.

2.1. Topological Model. This section deals with the deterministic spreading process. In this case, each element a_i in the type set $\mathcal{A} = \{a_1, a_2, \dots, a_k\}$ is associated with a pattern $p_{a_i}^{(1)}$, for which $\{p_{a_i}^{(1)}\}_{i=1}^k$ is called a *topological spread model*. For a topological spread model, the letters

$$(1) \quad d \equiv \min_{\alpha \in \mathcal{A}} d_\alpha^{(1)}$$

$$(2) \quad D \equiv \max_{\alpha \in \mathcal{A}} d_\alpha^{(1)}$$

are exclusively reserved for these usages. For any topological spread model $\{p_{a_i}^{(1)}\}_{i=1}^k$, the *topological spread rate of β with respect to the root α* is defined

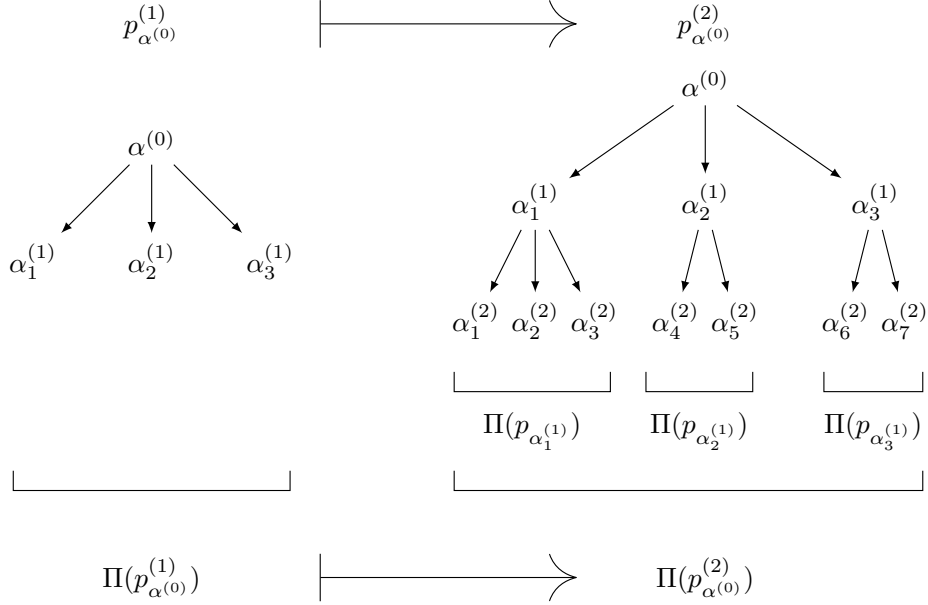


FIGURE 2. Generation of a pattern of length 2 from a pattern of length 1.

as:

$$s_\alpha(\beta) = \lim_{n \rightarrow \infty} s_\alpha^{(n)}(\beta),$$

where $s_\alpha^{(n)}(\beta) = \frac{|\Pi(p_\alpha^{(n)})|_\beta}{d_\alpha^{(n)}}$ is called the n -spread rate of β with respect to the root α , which indicates the proportion of type- β offspring in the n th generation with respect to the initial ancestor α .

For a topological spread model $\{p_{a_i}^{(1)}\}_{i=1}^k$, a substitution ζ on \mathcal{A} to \mathcal{A}^* is defined as

$$\zeta(\alpha) = \Pi(p_\alpha) \text{ for } \alpha \in \mathcal{A}$$

with length $|\zeta(\alpha)| = d_\alpha^{(1)}$. This substitution induces a morphism of the monoid \mathcal{A}^* by putting $\zeta(B) = \zeta(b_0)\zeta(b_1)\cdots\zeta(b_n)$ if $B = b_0\cdots b_n \in \mathcal{A}^*$ and $\zeta(B) = \emptyset$ if $B = \emptyset$. By denoting $\zeta^n = \zeta \circ \zeta^{n-1}$ the n -time iterated map of ζ , it is evident from the construction of $p_\alpha^{(2)}$ that

$$p_\alpha^{(2)} = \left(\alpha; \Pi(p_{\alpha_1}^{(1)}) \cdots \Pi(p_{\alpha_{d_\alpha^{(1)}}}^{(1)}) \right) = \left(\alpha; \Pi(p_\alpha^{(2)}) \right).$$

On the other hand,

$$\begin{aligned}
 \zeta^2(\alpha) &= \zeta \circ \zeta(\alpha) = \zeta(\alpha_1^{(1)} \cdots \alpha_{d_\alpha^{(1)}}^{(1)}) \\
 &= \zeta(\alpha_1^{(1)})\zeta(\alpha_2^{(1)}) \cdots \zeta(\alpha_{d_\alpha^{(1)}}^{(1)}) \\
 &= \Pi(p_{\alpha_1^{(1)}}^{(1)})\Pi(p_{\alpha_2^{(1)}}^{(1)}) \cdots \Pi(p_{\alpha_{d_\alpha^{(1)}}^{(1)}}^{(1)}) \\
 &= \Pi(p_\alpha^{(2)}).
 \end{aligned}$$

Inductively, we have $\zeta^n(\alpha) = \Pi(p_\alpha^{(n)})$ for $n \geq 1$ and therefore the following proposition holds.

Proposition 2.1. *Let $\{p_\alpha^{(1)}\}_{\alpha \in \mathcal{A}}$ be a spread model and ζ be the associated substitution. Then for $n \in \mathbb{N}$, the sets $\{\Pi(p_\alpha^{(n)})\}_{\alpha \in \mathcal{A}}$ and $\{\zeta^n(\alpha)\}_{\alpha \in \mathcal{A}}$ are one-to-one corresponding.*

For the purpose of studying the spread rate $s_\alpha(\beta)$ and the n -spread rate $s_\alpha^{(n)}(\beta)$ for all $\alpha, \beta \in \mathcal{A}$, two additional assumptions are made throughout this section for practical reasons. Firstly, for any ancestor $\alpha \in \mathcal{A}$, $\lim_{n \rightarrow \infty} |\zeta^n(\alpha)| = +\infty$ for all $\alpha \in \mathcal{A}$, i.e., the number of offspring is unbounded in an infinite interval of time. Secondly, for every $\alpha_0 \in \mathcal{A}$ there exists $\zeta(\alpha_0)$ beginning with α_0 . In fact, [21, Proposition 5.1] shows that if $\lim_{n \rightarrow \infty} |\zeta^n(\alpha)| = +\infty$, then there is an equivalent substitution such that this second assumption is satisfied. For a detailed discussion of the spread rate, let B, C be two patterns in \mathcal{A}^* , and let $O_C(B)$ denote the number of occurrences of C in B . In particular, if $\alpha \in \mathcal{A}$, the number $O_\alpha(B)$ is the number of letter α occurring in the pattern B , which forms the (i, j) -th entry of the associated ζ -matrix $M = M_\zeta$, which is a $k \times k$ matrix defined by

$$M = [m_{i,j}] \equiv [O_{a_i}(\zeta(a_j))].$$

Given a $k \times k$ matrix $A = [a_{i,j}]$, we denote by ρ_A the spectral radius of the matrix A . Below are some facts from matrix analysis [11]. A substitution ζ is said to be *irreducible* on \mathcal{A} if for every pair $\alpha, \beta \in \mathcal{A}$, one can find $\ell = \ell(\alpha, \beta)$ such that β occurs in $\zeta^\ell(\alpha)$. A substitution ζ is said to be *primitive* if there exists ℓ such that, for every $\alpha, \beta \in \mathcal{A}$, β occurs in $\zeta^\ell(\alpha)$. Recall that a nonnegative $k \times k$ matrix $M = [m_{i,j}]$ is said to be *irreducible* if, for every i, j , there exists $\ell \geq 1$ such that $m_{ij}^{[\ell]} > 0$, denoted by $M^\ell = [m_{ij}^{[\ell]}]$. M is said to be *primitive* if M^ℓ is positive for some $\ell \geq 1$ (i.e., $m_{ij}^{[\ell]} > 0$ for all $1 \leq i, j \leq k$). Note that ζ is primitive (resp. irreducible) if and only if M_ζ is primitive (resp. irreducible) matrix. It is worth pointing out that under the two assumptions mentioned above, primitivity and irreducibility of a substitution ζ are equivalent properties [21, Proposition 5.5]. In what follows, we always assume ζ is irreducible, and thus the associated ζ -matrix is irreducible, and also primitive.

Proposition 2.2. *Let $A = [a_{i,j}]$ be a $k \times k$ nonnegative matrix written as $A^m = [a_{i,j}^{[m]}]$.*

(i) *We have*

$$(3) \quad \min_{1 \leq i \leq n} \sum_{j=1}^n a_{ij} \leq \rho_A \leq \max_{1 \leq i \leq n} \sum_{j=1}^n a_{ij}.$$

(ii) *If A is a primitive integral matrix, then*

$$(4) \quad \lim_{n \rightarrow \infty} \frac{1}{n} \log a_{ij}^{(n)} = \log \rho_A.$$

(iii) *If A has a positive eigenvector $\mathbf{x} = [x_i]$, then for all $m \geq 1$ and for all $i = 1, \dots, n$, we have*

$$(5) \quad \left(\frac{\min_{1 \leq j \leq k} x_k}{\max_{1 \leq j \leq k} x_k} \right) \rho_A^m \leq \sum_{j=1}^k a_{ij}^{[m]} \leq \left(\frac{\max_{1 \leq j \leq k} x_k}{\min_{1 \leq j \leq k} x_k} \right) \rho_A^m.$$

Let \mathbf{x} be a positive vector, we denote by

$$C_1(\mathbf{x}) = \left(\frac{\max_{1 \leq j \leq k} x_k}{\min_{1 \leq j \leq k} x_k} \right) \text{ and } c_1(\mathbf{x}) = \left(\frac{\min_{1 \leq j \leq k} x_k}{\max_{1 \leq j \leq k} x_k} \right).$$

2.2. Random Model. In order to catch the uncertainty of the spread patterns, we introduce a random spread model in this section by means of branching processes. In this model, $P_\alpha^{(1)}$ becomes a random element representing all the possible outcome patterns, and its distribution will assign to each possible pattern a probability of that pattern happening.

To better describe this random spread model, we start with the introduction of multi-type branching processes in the following.

A k -type Galton-Watson branching process is a mathematical model used to describe the evolution of a population consisting of individuals of k different types, say types a_1, a_2, \dots, a_k .

We assume that each individual of type a_i , $i = 1, 2, \dots, k$, lives a unit of time and, upon death, produces children of all types according to the offspring distribution $\{P^{(i)}(\mathbf{j}) \equiv P^{(i)}(j_1 j_2 \dots j_k)\}_{\mathbf{j} \in \mathbb{N}_0^k}$ and independently of other individuals, where $P^{(i)}(j_1 j_2 \dots j_k)$ is the probability that a type a_i parent produces j_1 children of type a_1 , j_2 children of type a_2 , \dots , j_k children of type a_k . Let $\mathbf{Z}_n = (Z_{n,1} Z_{n,2} \dots Z_{n,k})$ be the population vector in the n th generation, $n = 0, 1, 2, \dots$, where $Z_{n,i}$ is the number of individuals of type a_i in the n th generation.

Note that, from Kolmogorov's consistency theorem, there is a probability space (Ω, \mathcal{F}, P) on which $\{\mathbf{Z}_n(\omega); n \geq 0\}$ are defined and have the distribution determined by the above. In this space Ω , each point represents an entire "family tree", i.e., it specifies the generation number, ancestors, and offspring of each individual (see Athreya and Ney [3]). Different sample points show different possible realizations, see Figure 3.

Let

$$(6) \quad f^{(i)}(s_1 s_2 \dots s_k) \equiv \sum_{j_1, j_2, \dots, j_k \geq 0} P^{(i)}(j_1 j_2 \dots j_k) s_1^{j_1} s_2^{j_2} \dots s_k^{j_k},$$

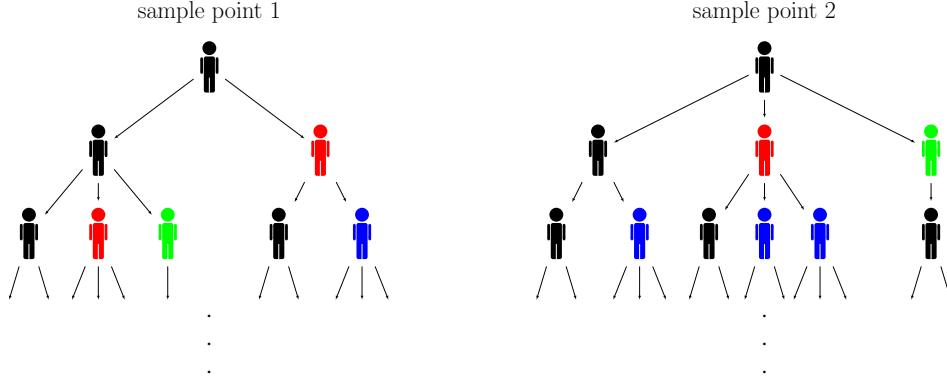


FIGURE 3. Two different sample points of a Galton-Watson branching process.

where $0 \leq s_r \leq 1$, $r = 1, 2, \dots, k$, be the probability generating function of the numbers of various types produced by a type a_i individual.

Let

$$(7) \quad \mathbf{f} \equiv [f^{(i)}] \equiv (f^{(1)} f^{(2)} \dots f^{(k)})$$

be the vector of the generating functions.

Thus, a discrete-time k -type Galton-Watson branching process $\{\mathbf{Z}_n\}_{n \geq 0}$ is a Markov chain on \mathbb{N}_0^k with the transition function

$$(8) \quad P(\mathbf{i}, \mathbf{j}) = P(\mathbf{Z}_{n+1} = \mathbf{j} | \mathbf{Z}_n = \mathbf{i}) \quad \forall \mathbf{i}, \mathbf{j} \in \mathbb{N}_0^k$$

such that, for any \mathbf{i} , $\sum_{\mathbf{j} \in \mathbb{N}_0^k} P(\mathbf{i}, \mathbf{j}) \mathbf{s}^{\mathbf{j}} = (\mathbf{f}(\mathbf{s}))^{\mathbf{i}}$ (see notation (8)).

In particular, if the process is initiated in state \mathbf{e}_i , i.e., there is only one initial ancestor in the 0th generation and this initial ancestor is of type a_i , then we will denote the process $\{\mathbf{Z}_n\}_{n \geq 0}$ by

$$\mathbf{Z}_n^{(i)} = (Z_{n,1}^{(i)} Z_{n,2}^{(i)} \dots Z_{n,k}^{(i)})$$

where, for $j = 1, 2, \dots, k$, $Z_{n,j}^{(i)}$ is the number of type j individuals in the n th generation for a process with $\mathbf{Z}_0 = \mathbf{e}_i$. The probability generating function of $\mathbf{Z}_n^{(i)}$ will be denoted by $\mathbf{f}_n^{(i)}(\mathbf{s})$.

Also, if we let $\xi_{n,r}^{(j)}$ be the vector of offspring of the r th individual of type a_j in the n th generation then, for all r and n , $P(\xi_{n,r}^{(j)} = \cdot) = P^{(j)}(\cdot)$. Thus, the population in the $(n+1)$ th generation can be expressed as

$$(9) \quad \mathbf{Z}_{n+1} = \sum_{j=1}^k \sum_{r=1}^{Z_{n,j}} \xi_{n,r}^{(j)}$$

which is a useful stochastic evolution relation.

We are ready to construct a random spread model using the idea of a k -type Galton-Watson branching process. Based on the setting in Section 2, for a pattern $p_\alpha^{(1)} = (\alpha^{(0)}; \alpha_1^{(1)} \dots \alpha_{d_\alpha^{(1)}}^{(1)})$ the number of the children of the

ancestor α is $d_\alpha^{(1)} = |\xi_{0,1}^{(i)}| = |\mathbf{Z}_1^{(i)}|$, and $p_\alpha^{(1)}$ is called a *random pattern of the 1st generation* to emphasize that it follows from a probability distribution, in contrast to the deterministic topological spread model. Note that this defines a random spread model, which is completely determined by the offspring distributions

$$\{P^{(i)}(\cdot)\}_{i=1}^k$$

of the k -type Galton-Watson branching process $\{\mathbf{Z}_n\}_{n \geq 0} \equiv \{(Z_{n,1}Z_{n,2} \cdots Z_{n,k})\}_{n \geq 0}$, and the random spread model $\{p_{a_i}^{(1)}\}_{i=1}^k$ is called a *random spread model with spread distribution* $\{P^{(i)}(\cdot)\}_{i=1}^k$ and $\{\mathbf{Z}_n\}_{n \geq 0}$ is called the *underlying branching process* of this random spread model.

For $n \in \mathbb{N}$ and $p_\alpha^{(n)}$, a pattern of the n th generation, the offspring type chart of α in n generations is

$$\Pi(p_\alpha^{(n)}) = (\alpha_1^{(n)} \cdots \alpha_{d_\alpha^{(n)}}^{(n)}) \in \mathcal{A}^{d_\alpha^{(n)}}.$$

It is clear that, if $\alpha = a_i$ and $\beta = a_j$, $i, j = 1, 2, \dots, k$, then

$$\left| \Pi(p_\alpha^{(n)}) \right|_\beta = Z_{n,j}^{(i)}.$$

Here, we want to note that both $P_\alpha^{(1)}$ and $\Pi(P_\alpha^{(1)})$ are random elements which provide information about the number of children and the types of all the children of a parent of type α .

When a random spread model $\{p_{a_i}^{(1)}\}_{i=1}^k$ with spread distribution $\{P^{(i)}(\cdot)\}_{i=1}^k$ is given, a natural question that arises is, if a disease has been spreading in some area, what happens to the infection rate in the long run?

Following from Section 2, the n -spread rate of type a_j with respect to an initial ancestor of type a_i is defined as

$$s_{a_i}^{(n)}(a_j) = \frac{\left| \Pi(p_{a_i}^{(n)}) \right|_{a_j}}{d_{a_i}^{(n)}} = \frac{Z_{n,j}^{(i)}}{|\mathbf{Z}_n^{(i)}|}$$

where $\{\mathbf{Z}_n\}_{n \geq 0} \equiv \{(Z_{n,1}Z_{n,2} \cdots Z_{n,k})\}_{n \geq 0}$ is the branching process with offspring distribution $\{P^{(i)}(\cdot)\}_{i=1}^k$. Moreover, what happens to the limit behavior of $s_{a_i}^{(n)}(a_j)$ as $n \rightarrow \infty$? If the limit exists in some sense, then we denote it by $s_{a_i}(a_j)$ and here we call it the *random spread rate of a_j with respect to an initial ancestor of type a_i* .

3. RESULTS AND DISCUSSION

3.1. Topological Model. By virtue of the proposition above, the asymptotic behavior of the spread rate is understood in the way of the following theorem and proposition.

Theorem 3.1 (Spread rate and n -spread rate). *Let $\{p_{a_i}^{(1)}\}_{i=1}^k$ be a spread model, and ζ be the associated substitution with the ζ -matrix M . Suppose $\rho = \rho_M$ is the spectral radius of M , with positive eigenvector $\mathbf{v} = (v_{a_1} v_{a_2} \cdots v_{a_k})$. Then*

- (i) Let $a_i \in \mathcal{A}$. Then, the vector $(s_{a_i}(a_j))_{a_j \in \mathcal{A}}$ is independent of a_i and $(s_{a_i}(a_j))_{a_j \in \mathcal{A}} = \mathbf{v}$, i.e.,

$$\lim_{n \rightarrow \infty} \frac{|\Pi(p_{a_i}^{(n)})|_{a_j}}{d_{a_i}^{(n)}} = \lim_{n \rightarrow \infty} \frac{O_{a_j}(\zeta^n(a_i))}{|\zeta^n(a_i)|} = v_{a_j}.$$

In addition, the speed of convergence is geometric.

- (ii) $c_1(\mathbf{v})\rho^m \leq \sum_{a_j \in \mathcal{A}} s_{a_i}^{(n)}(a_j) \leq C_2(\mathbf{v})\rho^m$.

Proof. See Appendix A.1. □

Theorem 3.2. Suppose $\{p_{a_i}^{(1)}\}_{i=1}^k$ and $\{p_{a_i}^{(1)'}\}_{i=1}^k$ are two spread models with d, D and d', D' being the corresponding minimal and maximal numbers of children of the spread models as defined in (1) and (2), respectively. Let $s_\alpha^{(n)}(\beta)$ and $s_\alpha^{(n)'}(\beta)$ be the n -spread rate of $\{p_{a_i}^{(1)}\}_{i=1}^k$ and $\{p_{a_i}^{(1)'}\}_{i=1}^k$, respectively. Then

- (i) If $D' < d$, then there exist $r < 1$, $C > 0$ such that

$$(10) \quad \frac{\sum_{\alpha \in \mathcal{A}} |\Pi(p_\alpha^{(n)'})|_\beta}{\sum_{\alpha \in \mathcal{A}} |\Pi(p_\alpha^{(n)})|_\beta} \leq Cr^n,$$

for all $\alpha, \beta \in \mathcal{A}$ and $n \in \mathbb{N}$. Here $C = \frac{C_1(\mathbf{v})}{c_1(\mathbf{v}')}$, $r = \frac{\rho'}{\rho}$, where $\rho = \rho_M$ and $\rho' = \rho_{M'}$.

- (ii) If $|\Pi(p_\alpha^{(1)'})|_\beta \leq |\Pi(p_\alpha^{(1)})|_\beta$ and there exists a pair (γ, δ) such that $|\Pi(p_\gamma^{(1)'})|_\delta < |\Pi(p_\gamma^{(1)})|_\delta$, then there exist $r < 1$, $C > 0$ and $N \in \mathbb{N}$ such that

$$(11) \quad \frac{|\Pi(p_\alpha^{(n)'})|_\beta}{|\Pi(p_\alpha^{(n)})|_\beta} \leq Cr^n$$

for all $\alpha, \beta \in \mathcal{A}$ and $n \geq N$.

Proof. See Appendix A.2. □

Remark 3.3. The above-described theorems reveal the following.

- The limit of the n -spread rate $s_{a_i}(a_j)$ of the type a_j exists and is the j th component v_{a_j} of the right eigenvector \mathbf{v} of M (Theorem 3.1). Moreover, it is independent of a_i , i.e., the type of the initial ancestor.
- For a fixed topological spread model, Theorem 3.1 provides an explicit estimate for the proportion of individuals of type β in the n th generation given any initial ancestor α . Such a proportion can be determined from the ζ -matrix.
- Suppose in the spread model $\{p_{a_i}^{(1)}\}_{i=1}^k$ is overall more active than $\{p_{a_i}^{(1)'}\}_{i=1}^k$ in the sense $D' < d$, then Theorem 3.2 (i) asserts that the relative number of descendants of the latter model to the former model is geometrically decreasing. If, in addition $\{p_{a_i}^{(1)}\}_{i=1}^k$ is a more active spread model than $\{p_{a_i}^{(1)'}\}_{i=1}^k$ in each type of children for every

parent, then Theorem 3.2 (ii) shows that the relative number of descendants of type β with respect to the ancestor α also decreases geometrically. These two properties explain the exponential decay in the relative number of infected individuals when essential measures are taken, such as wearing masks or maintaining social distance.

3.2. Random Model. One way to understand the behavior of a random variable is to investigate its mean (i.e., expectation, average). Therefore, to answer the above questions, we first compute the mean matrix.

For a random spread model $\{p_{a_i}^{(1)}\}_{i=1}^k$ with spread distribution $\{P^{(i)}(\cdot)\}_{i=1}^k$ and the underlying branching process $\{\mathbf{Z}_n\}_{n \geq 0}$, let

$$m_{i,j} = E(Z_{1,i}^{(j)}) = E\left(\prod(p_{a_j}^{(1)})\Big|_{a_i}\right)$$

and

$$m_{i,j}^{(n)} = E(Z_{n,i}^{(j)}) = E\left(\prod(p_{a_j}^{(n)})\Big|_{a_i}\right)$$

be the means (averages) of the number of individuals of type a_i in the 1st and n th generations, respectively, as the spread starts with one individual of type a_j . That is, an individual of type a_j will have, on average, $m_{i,j}^{(n)}$ offspring of type a_i in the n th generation. Then, the matrix

$$M \equiv [m_{i,j}]_{k \times k}$$

is called the *offspring mean matrix* of the branching process $\{\mathbf{Z}_n\}_{n \geq 0}$, and $M^{(n)} \equiv [m_{i,j}^{(n)}]_{k \times k}$ is called the *offspring mean matrix in n generations*. By induction, we can prove the following proposition.

Proposition 3.4. *For any $n \in \mathbb{N}$, $M^{(n)} = M^n$, where $M^{(1)} \equiv M$.*

We assume that $0 \leq m_{i,j} < \infty$, for all $i, j = 1, 2, \dots, k$ so that the offspring mean matrix M exists and define the following:

- A random spread model $\{p_{a_i}^{(1)}\}_{i=1}^k$ is said to be *positive regular*, if M is *strictly positive*, i.e., there is an n_0 such that $m_{i,j}^{(n_0)} > 0$ for all $i, j = 1, 2, \dots, k$.
- A random spread model $\{p_{a_i}^{(1)}\}_{i=1}^k$ is said to be *singular*, if for every $i = 1, 2, \dots, k$, there is a unit vector $\mathbf{e}_j \in \mathbb{N}_0^k$ such that $P^{(i)}(\mathbf{e}_j) = 1$.

Proposition 3.5. *Let $\{p_{a_i}^{(1)}\}_{i=1}^k$ be a positive regular and nonsingular random spread model. Then, for every $i = 1, 2, \dots, k$,*

$$d_{a_i}^{(n)} \rightarrow 0 \text{ or } d_{a_i}^{(n)} \rightarrow \infty \quad \text{as } n \rightarrow \infty$$

with probability 1.

The above proposition is known as the Frobenius Theorem and it tells us that in a multi-type branching process, no matter what type the initial ancestor is of, when the population doesn't go extinct, the number of descendants tends to infinity as the time goes to infinity. This property satisfies one of the assumptions for the topological spread model, i.e., $\lim_{n \rightarrow \infty} |\zeta^n(\alpha)| = +\infty$ for all $\alpha \in \mathcal{A}$. For a proof of this proposition, see sections II.6 and II.7 in [10].

Proposition 3.6. *Let $\{p_{a_i}^{(1)}\}_{i=1}^k$ be a positive regular and nonsingular random spread model, then there is a $\rho > 0$ such that ρ is an eigenvalue of the offspring mean matrix M with both algebraic and geometric multiplicity one and $|\lambda| < \rho$ for any other eigenvalue λ of M .*

The readers may refer to [14, Appendix 2, Page 542] for more details about Proposition 3.6.

From now on, we assume that the spectral radius ρ_M of the offspring mean matrix M for the random spread model is greater than 1. This assumption ensures that the population has a chance to survive, i.e. $d_{a_i}^{(n)} \rightarrow \infty$ for some i .

Theorem 3.7. *(Average spread rate and average n -spread rate). Let $\{p_{a_i}^{(1)}\}_{i=1}^k$ be a positive regular and nonsingular random spread model. Let $\rho = \rho_M$ be the maximal eigenvalue of M and let $\mathbf{u} = [u_i]$ and $\mathbf{v} = [v_i]$ be the left and right eigenvector of M associated with ρ such that $\mathbf{v} \cdot \mathbf{1} = 1$ and $\mathbf{u} \cdot \mathbf{v} = 1$. Then,*

(i) *for any $i, j = 1, 2, \dots, k$,*

$$\lim_{n \rightarrow \infty} \frac{m_{i,j}^{(n)}}{\rho^n} = v_i u_j.$$

(ii) *For every $i = 1, 2, \dots, k$, there exists a random variable W_i such that for every $j = 1, 2, \dots, k$,*

$$\lim_{n \rightarrow \infty} \frac{|\Pi(p_{a_i}^{(n)})|_{a_j}}{\rho^n} = u_j W_i$$

with probability 1.

(iii) *For any $i = 1, 2, \dots, k$, on the event of nonextinction, i.e., on the event $\{d_{a_i}^{(n)} \rightarrow \infty\}$,*

$$s_{a_i}(a_j) \equiv \lim_{n \rightarrow \infty} s_{a_i}^{(n)}(a_j) = \lim_{n \rightarrow \infty} \frac{|\Pi(p_{a_i}^{(n)})|_{a_j}}{d_{a_i}^{(n)}} = v_j$$

with probability 1.

Proof. It follows from Theorem 1 on Page 192 in [3]. □

Remark 3.8. The above theorem tells us the following:

- The average growth rate of the spread is geometric.
- The number of individuals of type a_j in the n th generation grows like ρ^n and is proportional to the j th component of the left eigenvector \mathbf{u} of the offspring mean matrix M associated with the maximal eigenvalue ρ .
- The limit of the n -spread rate $s_{a_i}(a_j)$ of the type a_j exists and is the j th component v_j of the right eigenvector \mathbf{v} of M which is independent of a_i , the type of the initial ancestor.

Now, as defined in (1) and (2), we have

$$D = \max_{\alpha \in \mathcal{A}} E(d_\alpha^{(1)}) = \max_{1 \leq i \leq k} E|\mathbf{Z}_1^{(i)}| = \max_{1 \leq i \leq k} E\left(\sum_{j=1}^k Z_{1,j}^{(i)}\right) = \max_{1 \leq i \leq k} \sum_{j=1}^k m_{j,i}$$

and

$$d = \min_{\alpha \in \mathcal{A}} E(d_\alpha^{(1)}) = \min_{1 \leq i \leq k} E|\mathbf{Z}_1^{(i)}| = \min_{1 \leq i \leq k} E\left(\sum_{j=1}^k Z_{1,j}^{(i)}\right) = \min_{1 \leq i \leq k} \sum_{j=1}^k m_{j,i}$$

as the maximal and minimal column sums of the offspring mean matrix M .

For a random phenomenon, it is difficult to predict exactly which outcome among many possible ones will happen, even though its probability distribution is known. In this case, the average (expectation, mean) is often a good estimate for it. The next theorem provides a strategy to compare two random spread models in an average sense.

Theorem 3.9. *Suppose $\{p_{a_i}^{(1)}\}_{i=1}^k$ and $\{p_{a_i}^{(1)'}\}_{i=1}^k$ are two positive regular and nonsingular random spread models with n -spread rates $s_\alpha^{(n)}(\beta)$ and $s_\alpha^{(n)'}(\beta)$, respectively.*

(i) *If $D' < d$, then there exist $r < 1$, $C > 0$ such that*

$$\frac{E\left(\sum_{\alpha \in \mathcal{A}} \left| \prod(p_\alpha^{(n)'}) \right|_\beta\right)}{E\left(\sum_{\alpha \in \mathcal{A}} \left| \prod(p_\alpha^{(n)}) \right|_\beta\right)} \leq Cr^n$$

for all $\alpha, \beta \in \mathcal{A}$ and for all $n \in \mathbb{N}$. Here, $C = \frac{C_1(\mathbf{v})}{c_1(\mathbf{v}'')}$, where

$$C_1(\mathbf{v}) = \left(\frac{\max_{1 \leq i \leq k} v_i}{\min_{1 \leq i \leq k} v_i}\right) \text{ and } c_1(\mathbf{v}'') = \left(\frac{\min_{1 \leq i \leq k} v_i}{\max_{1 \leq i \leq k} v_i}\right),$$

and $r = \frac{\rho'}{\rho}$, where $\rho = \rho_M$ and $\rho' = \rho_{M'}$ are the Perron-Frobenius eigenvalues of the offspring mean matrices M and M' for the models $\{p_{a_i}^{(1)}\}_{i=1}^k$ and $\{p_{a_i}^{(1)'}\}_{i=1}^k$, respectively.

(ii) *If $m'_{i,j} \leq m_{i,j}$ for all $i, j = 1, 2, \dots, k$ and there exists a pair (i_0, j_0) such that $m'_{i_0, j_0} < m_{i_0, j_0}$, then there exist $r < 1$ and $C > 0$ and $N \in \mathbb{N}$ such that*

$$\frac{E\left(\left| \prod(p_\alpha^{(n)'}) \right|_\beta\right)}{E\left(\left| \prod(p_\alpha^{(n)}) \right|_\beta\right)} \leq Cr^n$$

for all $\alpha, \beta \in \mathcal{A}$ and for all $n \geq N$.

Proof. After taking the expectation on the random variables, the proofs in the deterministic case can be applied to prove the results for the random spread models. \square

3.3. Connection between the Topological Spread Model and Random Spread Model. This subsection is devoted to the discussion of the relation between random spread models and topological spread models. Since a topological spread model is defined by deterministic patterns of the 1st generation, the following proposition follows naturally.

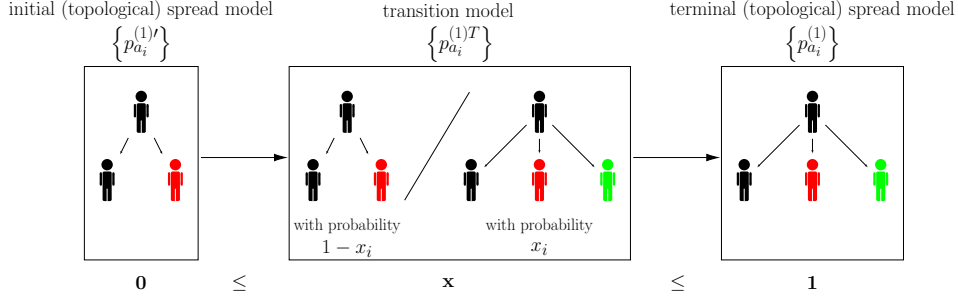


FIGURE 4. An illustration of a transition model.

The next proposition tells us that every topological spread model is almost surely a special case of a random spread model by assigning a proper probability distribution to it.

Proposition 3.10. *Let $\{p_{a_i}^{(1)}\}_{i=1}^k$ be a random spread model with spread distribution $\{P^{(i)}(\cdot)\}_{i=1}^k$. If, for every $i = 1, 2, \dots, k$, there is a vector $\mathbf{j}^{(i)} \in \mathbb{N}_0^k$ such that $P^{(i)}(\mathbf{j}^{(i)}) = 1$, then $\{p_{a_i}^{(1)}\}_{i=1}^k$ is a topological spread model with probability 1.*

Proof. See Appendix A.3. □

One essential part of the work involved in disease control is to develop a strategy to change the spread pattern to reduce the number of infected cases or the infection rate. During an effective control process, we often can see the spread pattern is gradually changed to another pattern. To represent what happens in this transition phase, we now introduce a special type of random spread model. Given two topological spread models $\{p_{a_i}^{(1)}\}_{i=1}^k$ and $\{p_{a_i}^{(1)'}\}_{i=1}^k$, a random spread model, denoted by $\{p_{a_i}^{(1)T}\}_{i=1}^k$, is called a *transition model* to the *terminal model* $\{p_{a_i}^{(1)}\}_{i=1}^k$ from the *initial model* $\{p_{a_i}^{(1)'}\}_{i=1}^k$, if there exists a vector $\mathbf{0} \leq \mathbf{x} = (x_1 x_2 \cdots x_k) \leq \mathbf{1}$ such that, for each $i = 1, 2, \dots, k$,

$$P^{(i)}\left(\left|\prod (p_{a_i}^{(1)})\right|_{a_1}, \left|\prod (p_{a_i}^{(1)})\right|_{a_2}, \dots, \left|\prod (p_{a_i}^{(1)})\right|_{a_k}\right) = x_i$$

and

$$P^{(i)}\left(\left|\prod (p_{a_i}^{(1)'})\right|_{a_1}, \left|\prod (p_{a_i}^{(1)'})\right|_{a_2}, \dots, \left|\prod (p_{a_i}^{(1)'})\right|_{a_k}\right) = 1 - x_i$$

where $\{P^{(i)}(\cdot)\}_{i=1}^k$ is the underlying spread distribution of $\{p_{a_i}^{(1)T}\}_{i=1}^k$.

Proposition 3.11. *If the random spread model $\{p_{a_i}^{(1)T}\}_{i=1}^k$ is a transition model to the terminal topological spread model $\{p_{a_i}^{(1)}\}_{i=1}^k$ from the initial topological spread model $\{p_{a_i}^{(1)'}\}_{i=1}^k$, then*

- (i) *If $\mathbf{x} = \mathbf{1}$, then $\{p_{a_i}^{(1)T}\}_{i=1}^k = \{p_{a_i}^{(1)}\}_{i=1}^k$ with probability 1.*
- (ii) *If $\mathbf{x} = \mathbf{0}$, then $\{p_{a_i}^{(1)T}\}_{i=1}^k = \{p_{a_i}^{(1)'}\}_{i=1}^k$ with probability 1.*

Proof. The proof is straightforward by the previous proposition. □

Now, for any $\mathbf{0} \leq \mathbf{x} = (x_1 x_2 \cdots x_k) \leq \mathbf{1}$, we let the random spread model $\{p_{a_i}^{(1)T}(\mathbf{x})\}_{i=1}^k$ be a transition model to the terminal spread model $\{p_{a_i}^{(1)}\}_{i=1}^k$ from the initial spread model $\{p_{a_i}^{(1)'}\}_{i=1}^k$ such that

$$P_{\mathbf{x}}^{(i)}\left(\left|\prod (p_{a_i}^{(1)})\right|_{a_1}, \left|\prod (p_{a_i}^{(1)})\right|_{a_2}, \cdots, \left|\prod (p_{a_i}^{(1)})\right|_{a_1}\right) = x_i$$

and

$$P_{\mathbf{x}}^{(i)}\left(\left|\prod (p_{a_i}^{(1)'})\right|_{a_1}, \left|\prod (p_{a_i}^{(1)'})\right|_{a_2}, \cdots, \left|\prod (p_{a_i}^{(1)'})\right|_{a_1}\right) = 1 - x_i,$$

where $\{P_{\mathbf{x}}^{(i)}(\cdot)\}_{i=1}^k$ is the underlying spread distribution of $\{p_{a_i}^{(1)T}(\mathbf{x})\}_{i=1}^k$.

Furthermore, let M and M' be the ζ -matrices of the topological spread models $\{p_{a_i}^{(1)}\}_{i=1}^k$ and $\{p_{a_i}^{(1)'}\}_{i=1}^k$ with the spectral radii (maximal eigenvalues) ρ_M and $\rho_{M'}$, and let $M_T(\mathbf{x})$ be the offspring mean matrix of the underlying branching process $\{\mathbf{Z}_n\}_{n \geq 0}$ for $\{p_{a_i}^{(1)T}(\mathbf{x})\}_{i=1}^k$ with the spectral radius $\rho_T(\mathbf{x})$. We also call ρ_M , $\rho_{M'}$ and $\rho_T(\mathbf{x})$ the *terminal*, *initial* and *transition spectral radii*, respectively.

Theorem 3.12. *Under the sup norm for the matrices and vectors, we have*

- (i) *If $\mathbf{x} \rightarrow \mathbf{1}$, then $\rho_T(\mathbf{x}) \rightarrow \rho_M$.*
- (ii) *If $\mathbf{x} \rightarrow \mathbf{0}$, then $\rho_T(\mathbf{x}) \rightarrow \rho_{M'}$.*

Proof. See Appendix A.4. □

Remark 3.13. The theorem says that, as the vector $\mathbf{x} \rightarrow \mathbf{1}$, i.e., the transition model has a higher and higher chance to perform the pattern in the terminal spread model $\{p_{a_i}^{(1)}\}_{i=1}^k$, the transition spectral radius $\rho_T(\mathbf{x})$ converges to the terminal spectral radius ρ_M of $\{p_{a_i}^{(1)}\}_{i=1}^k$. That is, the average growth rate of the spread of the transition model tends to the growth rate of the spread of the terminal model $\{p_{a_i}^{(1)}\}_{i=1}^k$.

Moreover, the proof of the above theorem provided in Appendix A.4 can be adopted to show the following corollary.

Corollary 3.14. *The map $\mathbf{x} \rightarrow \rho_T(\mathbf{x})$ is continuous.*

4. NUMERICAL EXAMPLES

For the topological spread model, the following example provides an estimate for both spread rates by means of Theorem 3.1 and Theorem 3.2.

Example 4.1. Let $\mathcal{A} = \{a_1, a_2, a_3\}$ be the type set of a topological spread model $\{p_{a_i}^{(1)}\}_{i=1}^k$.

- (i) If

$$\begin{aligned} p_{a_1}^{(1)} &= (a_1; a_1 a_1 a_2 a_2 a_3), \\ p_{a_2}^{(1)} &= (a_2; a_1 a_2 a_2 a_3 a_3), \\ p_{a_3}^{(1)} &= (a_3; a_2 a_2 a_3 a_3 a_3), \end{aligned}$$

note that $D = d = 5$.

Then the associated substitution ζ is defined as

$$\begin{aligned}\zeta(a_1) &= a_1 a_1 a_2 a_2 a_3, \\ \zeta(a_2) &= a_1 a_2 a_2 a_3 a_3, \\ \zeta(a_3) &= a_2 a_2 a_3 a_3 a_3.\end{aligned}$$

The ζ -matrix is

$$M = \begin{bmatrix} 2 & 1 & 0 \\ 2 & 2 & 2 \\ 1 & 2 & 3 \end{bmatrix}.$$

One can easily check that $\rho_M = 5$, and it follows from Theorem 3.1 that we have $s_\alpha(a_1) = \frac{2}{15} \approx 0.133$, $s_\alpha(a_2) = \frac{2}{5} = 0.4$ and $s_\alpha(a_3) = \frac{7}{15} \approx 0.467$.

(ii) If

$$\begin{aligned}p_{a_1}^{(1)'} &= (a_1; a_1 a_1 a_2 a_2), \\ p_{a_2}^{(1)'} &= (a_2; a_1 a_2 a_3 a_3), \\ p_{a_3}^{(1)'} &= (a_3; a_2 a_3 a_3 a_3),\end{aligned}$$

note that $D' = d' = 4$. The associated ζ' -matrix is

$$M' = \begin{bmatrix} 2 & 1 & 0 \\ 2 & 1 & 1 \\ 0 & 2 & 3 \end{bmatrix}.$$

Since $D' = 4 < d = 5$, Theorem 3.2 is applied to show that

$$\frac{\sum_{i=1}^3 |\Pi(p_{a_i}^{(n)'})|_{a_1}}{\sum_{i=1}^3 |\Pi(p_{a_i}^{(n)})|_{a_1}} \leq \frac{C_1(\mathbf{v}')}{c_1(\mathbf{v})} \left(\frac{4}{5}\right)^n = 14 \left(\frac{4}{5}\right)^n = 14(0.8)^n.$$

For example,

$$\frac{\sum_{i=1}^3 |\Pi(p_{a_i}^{(20)'})|_{a_1}}{\sum_{i=1}^3 |\Pi(p_{a_i}^{(20)})|_{a_1}} \leq 14 \times \left(\frac{4}{5}\right)^{20} \approx 0.16141.$$

(iii) Since $M' < M$, Theorem 3.2 is applied to show that there exists a $C > 0$, and $N \in \mathbb{N}$ such that $\forall 1 \leq i, j \leq 3$,

$$\frac{|\Pi(p_{a_i}^{(n)'})|_{a_j}}{|\Pi(p_{a_i}^{(n)})|_{a_j}} \leq C \left(\frac{4}{5}\right)^n = C(0.8)^n \text{ for } n \geq N.$$

Aside from the topological spread model, the following example demonstrates the estimation of the spread rate of the random spread model.

Example 4.2. Let $\{p_{a_i}\}_{i=1}^3$ be a random spread model.

(i) If the random spread model is given as follows:

$$p_{a_1} = \begin{cases} (a_1; a_1 a_1 a_1 a_2 a_2 a_2 a_3), & \text{with probability } \frac{1}{3} \\ (a_1; a_1 a_2 a_2 a_3), & \text{with probability } \frac{1}{3} \\ (a_1; a_1 a_1 a_2 a_2 a_3), & \text{with probability } \frac{1}{3} \end{cases}$$

$$p_{a_2} = \begin{cases} (a_2; a_1 a_2 a_2 a_2 a_3), & \text{with probability } \frac{1}{3} \\ (a_2; a_1 a_2 a_3), & \text{with probability } \frac{1}{3} \\ (a_2; a_2 a_2 a_3), & \text{with probability } \frac{1}{3} \end{cases}$$

$$p_{a_3} = \begin{cases} (a_3; a_1 a_1 a_2 a_2 a_3 a_3), & \text{with probability } \frac{1}{3} \\ (a_3; a_2 a_2 a_3), & \text{with probability } \frac{1}{3} \\ (a_3; a_1 a_2 a_2 a_3), & \text{with probability } \frac{1}{3} \end{cases}$$

then

$$m_{1,1} = 3 \cdot \frac{1}{3} + 1 \cdot \frac{1}{3} + 2 \cdot \frac{1}{3} = \frac{6}{3} = 2$$

$$m_{2,1} = 3 \cdot \frac{1}{3} + 2 \cdot \frac{1}{3} + 2 \cdot \frac{1}{3} = \frac{7}{3},$$

and, similarly, we can find that

$$m_{3,1} = \frac{4}{3}, m_{1,2} = \frac{2}{3}, m_{2,2} = 2, m_{3,2} = 1, m_{1,3} = 1, m_{2,3} = 2, m_{3,3} = \frac{4}{3}.$$

Hence, the offspring mean matrix is

$$M = \begin{bmatrix} 2 & \frac{2}{3} & 1 \\ \frac{7}{3} & 2 & 2 \\ \frac{4}{3} & 1 & \frac{4}{3} \end{bmatrix}.$$

We have the sums of columns 1, 2 and 3, which are $\frac{17}{3}$, $\frac{11}{3}$ and $\frac{13}{3}$, so that $D = \frac{17}{3}$ and $d = \frac{11}{3}$. The Perron-Frobenius eigenvalue is

$$\rho_M \approx 4.34848$$

and the corresponding normalized right eigenvector is

$$\mathbf{v} = (0.25 \ 0.48 \ 0.27).$$

Therefore, the spread rates are

$$s_{a_i}(a_1) = 0.25 \quad s_{a_i}(a_2) = 0.48 \quad s_{a_i}(a_3) = 0.27$$

for all $i = 1, 2, 3$.

(ii) We consider another random spread model:

$$p_{a_1}^{(1)'} = \begin{cases} (a_1; a_1 a_1), & \text{with probability } \frac{1}{4} \\ (a_1; a_1 a_2), & \text{with probability } \frac{1}{2} \\ (a_1; a_2 a_3), & \text{with probability } \frac{1}{4} \end{cases}$$

$$p_{a_2}^{(1)'} = \begin{cases} (a_2; a_1), & \text{with probability } \frac{1}{3} \\ (a_2; a_2), & \text{with probability } \frac{1}{3} \\ (a_2; a_3), & \text{with probability } \frac{1}{3} \end{cases}$$

$$p_{a_3}^{(1)'} = \begin{cases} (a_3; a_1 a_2 a_3), & \text{with probability } \frac{1}{4} \\ (a_3; a_2 a_2 a_3), & \text{with probability } \frac{1}{2} \\ (a_3; a_1 a_2 a_2 a_3), & \text{with probability } \frac{1}{4} \end{cases}$$

then $m_{1,1} = 1$, $m_{2,1} = \frac{3}{4}$, $m_{3,1} = \frac{1}{4}$, $m_{1,2} = \frac{1}{3}$, $m_{2,2} = \frac{1}{3}$, $m_{3,2} = \frac{1}{3}$, $m_{1,3} = \frac{1}{2}$, $m_{2,3} = \frac{7}{4}$, $m_{3,3} = 1$ and hence the offspring mean matrix is

$$M' = \begin{bmatrix} 1 & \frac{1}{3} & \frac{1}{4} \\ \frac{3}{4} & \frac{1}{3} & \frac{7}{4} \\ \frac{1}{4} & \frac{1}{3} & 1 \end{bmatrix}.$$

We have the sums of columns 1, 2 and 3, which are 2, 1 and $\frac{13}{4}$, so that $D' = \frac{13}{4} < d = \frac{11}{3}$ and $d' = 1$. Note that $D' < d$. The Perron-Frobenius eigenvalue is

$$\rho_{M'} \approx 1.87991$$

and the corresponding normalized right eigenvector is

$$\mathbf{v}' = (0.31 \ 0.44 \ 0.25).$$

Therefore, the spread rates are

$$s_{a_i}(a_1) = 0.31 \quad s_{a_i}(a_2) = 0.44 \quad s_{a_i}(a_3) = 0.25$$

for all $i = 1, 2, 3$.

Since $D' < d$, we have

$$\begin{aligned} \frac{E\left(\sum_{i=1}^3 | \Pi(p_{a_i}^{(n')}) |_{a_j}\right)}{E\left(\sum_{i=1}^3 | \Pi(p_{a_i}^{(n)}) |_{a_j}\right)} &\leq \frac{C_1(\mathbf{v}')}{c_1(\mathbf{v})} \left(\frac{\rho_{M'}}{\rho_M}\right)^n \\ &\approx \frac{0.44/0.25}{0.25/0.48} \left(\frac{1.87991}{4.34848}\right)^n \approx 3.38 \cdot (0.43)^n. \end{aligned}$$

Moreover, since $M' < M$, we also have $C > 0$ and $N \in \mathbb{N}$, such that for any $i, j = 1, 2, 3$ and any $n \geq N$,

$$\frac{E\left(| \Pi(p_{a_i}^{(n)}) |_{a_j}\right)}{E\left(| \Pi(p_{a_i}^{(n')}) |_{a_j}\right)} \leq C(0.43)^n.$$

Remark 4.3. The above two examples demonstrate the process of how we apply the theorems with numerical data. This leads us to make the following remarks:

- The first part in both examples shows how we construct the ζ -matrix for a topological spread model and the offspring mean matrix for a random spread model once the initial spread patterns are given. As long as the matrices are constructed, we can compute their spectral radii (maximal eigenvalues) and the corresponding left- and right-eigenvectors. Therefore, the (average) spread rates can be determined.
- In the second part of each example, two different models are compared. With the given initial spread patterns, we first compute (D, d) and (D', d') . D and D' are the maximal column sums of the corresponding ζ - or the offspring mean matrices while d and d' are the minimal column sums. D and D' also mean the maximal (average) numbers of descendants (or people being infected) of individuals in the population under the given initial spread patterns. Similarly, d and d' represent the minimal (average) numbers of descendants. In the examples, we have $D' < d$ and then our theorems tell us that the relative number of descendants of the model $\{p_{a_i}^{(1')}\}_{i=1}^k$ to the model

$\{p_{a_i}^{(1)k}\}_{i=1}^k$ is geometrically decreasing with rate $\frac{\rho_{M'}}{\rho_M}$. In addition, to figure out the ratio of descendants of a certain type initiated by an individual of any given type, we can further compare the corresponding entries in M and M' .

In the following, we give some examples of transition models to exhibit an interesting phenomenon.

Example 4.4. Let $\{p_{a_i}^{(1)T}\}_{i=1}^2$ be a transition model with the associated vector $\mathbf{x} = (x_1, x_2)$ defined as follows:

$$p_{a_1}^{(1)T} = \begin{cases} (a_1; a_1 a_1 a_1 a_2 a_2), & \text{with probability } x_1 \\ (a_1; a_1 a_1 a_2 a_2 a_2), & \text{with probability } 1 - x_1, \end{cases}$$

$$p_{a_2}^{(1)T} = \begin{cases} (a_2; a_1 a_2 a_2 a_2 a_2 a_2), & \text{with probability } x_2 \\ (a_2; a_1 a_2 a_2 a_2 a_2), & \text{with probability } 1 - x_2. \end{cases}$$

According to Proposition 3.10 and Proposition 3.11, if (x_1, x_2) is at the corners $(1, 1)$ and $(0, 0)$, it defines the terminal and initial topological spread models, respectively. It should be noted that each choice of the pair (x_1, x_2) , $0 \leq x_1, x_2 \leq 1$, defines a specific transition model to the terminal topological model from the initial one. For the transition model, the offspring mean matrix is

$$M = \begin{bmatrix} 2 + x_1 & 1 \\ 3 - x_1 & 4 + x_2 \end{bmatrix}$$

and we can see that the offspring mean matrices with $(x_1, x_2) = (0, 0)$ and $(1, 1)$ coincide with the corresponding ζ -matrices for the above two topological spread models. For example, when $x_1 = x_2 = 0$, the offspring mean matrix coincides with the ζ -matrix of the topological spread model $\{(a_1; a_1 a_1 a_2 a_2 a_2), (a_2; a_1 a_2 a_2 a_2 a_2)\}$, which is given as

$$M = \begin{bmatrix} 2 & 1 \\ 3 & 4 \end{bmatrix}.$$

In addition to Table 1, the plots of the spectral radii and of the spread rates for the transition model with various (x_1, x_2) are provided in Figure 5. Not only is this figure consistent with Table 1, but the spectral radius is continuous with respect to the vector (x_1, x_2) as a result of Corollary 3.14. In particular, when (x_1, x_2) tends to $\mathbf{1}$, the spectral radius $\rho_T(\mathbf{x})$ tends to ρ_M as implied by Theorem 3.12.

On the other hand, due to the continuity of the spectral radius of the transition model, an inverse problem can be studied and answered. That is, we are able to find a suitable pair (x_1, x_2) which allows us to construct the transition model with a designated spectral radius. This idea can be applied to the following: when the current (initial) topological spread pattern is figured out and the future (terminal) topological pattern is specified, we can determine the probabilities (x_1, x_2) and control the distribution of the transition model to reduce or increase the spread rate of certain type to a specific spread rate, which depends on the spectral radius. This usually

x_1	x_2	ρ	$s(a_1)$	$s(a_2)$
0.0	0.0	5.000	0.250	0.750
0.2	0.1	5.074	0.258	0.742
0.1	0.1	5.075	0.252	0.748
0.3	0.2	5.148	0.260	0.740
0.3	0.4	5.300	0.250	0.750
0.5	0.5	5.371	0.258	0.742
0.7	0.6	5.440	0.267	0.733
0.7	0.8	5.595	0.257	0.743
0.9	0.9	5.661	0.266	0.734
1.0	1.0	5.732	0.268	0.732

TABLE 1. Spectral radius and spread rate of the transition model in Example 4.4 with respect to (x_1, x_2) .

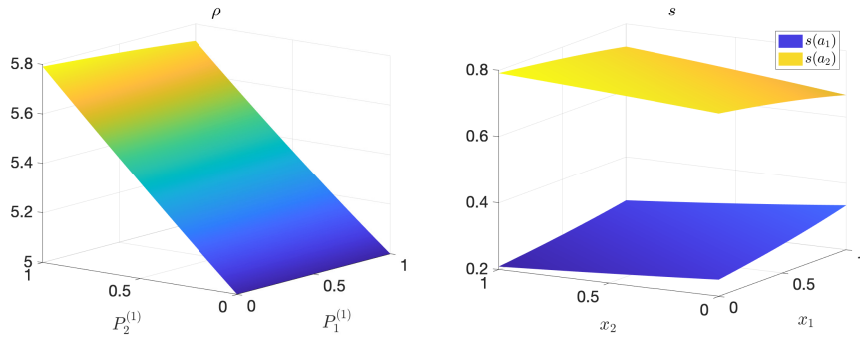


FIGURE 5. Effect of the number of a certain type of children on the spread rate.

can be done by adopting some strategies such as a quarantine, lockdown or mask-wearing policy during the epidemic prevention period.

5. CONCLUSION

Due to the fact that many spread patterns of infectious viruses show tree structures, we propose two mathematical models from the topological and random aspects to maintain these unique features and study the long-term behaviors of the spreads of disease after the initial infectious pattern has been found. This paper is an interdisciplinary study involving substitution dynamical systems and the theory of branching processes. One key point of our proposed models is that a computable way has been established to predict the long-term spread rate due to the Markov properties of the models and matrix representations for the spread patterns. We also introduce the transition spread model between two topological spread models to capture the change of the spread patterns, which is a real-world phenomenon during the epidemic periods due to changes in the environment or changes in disease control policies. As an application, our work can draw a comparison

between two spread models with different initial spread patterns, and this idea can be used for decision-making.

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APPENDIX A. PROOF OF THEOREMS

A.1. Proof of Theorem 3.1.

Proof. It follows from [21, Proposition 5.8] that $\lim_{n \rightarrow \infty} \frac{O_{a_j}(\zeta^n(a_i))}{|\zeta^n(a_i)|} = v_{a_j}$ for all $a_i, a_j \in \mathcal{A}$, which is a positive vector, independent of a_i and $\sum_{\alpha \in \mathcal{A}} v_\alpha =$

1. In addition, the speed of convergence is geometric. Combining these with Proposition 2.1, we obtain result (i). Since \mathbf{v} is positive, the result (ii) follows from Proposition 2.2 (iii). This completes the proof. \square

A.2. Proof of Theorem 3.2.

Proof. (i) Let ζ and ζ' be the associated substitutions of $\{p_{a_i}^{(1)}\}_{i=1}^k$ and $\{p_{a_i}^{(1)'}\}_{i=1}^k$ respectively. Denote by $M = M_\zeta = [m_{i,j}]$ ($M' = M_{\zeta'} = [m'_{i,j}]$) the ζ -matrix (ζ' -matrix). Since $D' < d$, it follows from (3) and the definitions of D' and d , that we have

$$\begin{aligned} \rho' &\leq \max_{\alpha \in \mathcal{A}} \sum_{\beta \in \mathcal{A}} m'_{\beta,\alpha} = \max_{\alpha \in \mathcal{A}} d_\alpha^{(1)'} = D' \\ &< d = \min_{\alpha \in \mathcal{A}} d_\alpha^{(1)} = \min_{\alpha \in \mathcal{A}} \sum_{\beta \in \mathcal{A}} m_{\beta,\alpha} \leq \rho. \end{aligned}$$

Therefore, $\frac{\rho'}{\rho} < 1$. Let \mathbf{v} and \mathbf{v}' be the eigenvectors of M and M' corresponding to the eigenvalues ρ and ρ' , respectively. Since both M and M' are both primitive integral matrices, \mathbf{v} and \mathbf{v}' are both positive vectors. It follows from (5) that

$$\begin{aligned} \sum_{\alpha \in \mathcal{A}} |\Pi(p_\alpha^{(n)'})|_\beta &= \sum_{\alpha \in \mathcal{A}} m'^{[n]}_{\beta,\alpha} \leq C_1(\mathbf{v}') (\rho')^n \\ &\leq \frac{C_1(\mathbf{v}')}{c_1(\mathbf{v}')} \left(\frac{\rho'}{\rho}\right)^n c_1(\mathbf{v}') \rho^n \\ &\leq \frac{C_1(\mathbf{v}')}{c_1(\mathbf{v}')} \left(\frac{\rho'}{\rho}\right)^n \sum_{\alpha \in \mathcal{A}} m_{\beta,\alpha}^{[n]} \\ &= \frac{C_1(\mathbf{v}')}{c_1(\mathbf{v}')} \left(\frac{\rho'}{\rho}\right)^n \sum_{\alpha \in \mathcal{A}} |\Pi(p_\alpha^{(n)})|_\beta. \end{aligned}$$

Thus, the inequality (10) follows by taking $C \equiv \frac{C_1(\mathbf{v}')}{c_1(\mathbf{v}')}$ and $r \equiv \frac{\rho'}{\rho} < 1$.

(ii) Note that the assumption of $|\Pi(p_\alpha^{(1)'})|_\beta \leq |\Pi(p_\alpha^{(1)})|_\beta$ implies that $M \leq M'$, and the assumption of $|\Pi(p_\gamma^{(1)'})|_\delta < |\Pi(p_\gamma^{(1)})|_\delta$ shows that $m'_{\delta,\gamma} < m_{\delta,\gamma}$. Since M and M' are both primitive matrices, Theorem 4.4.7 of [17] is applied to show that we have $\rho' < \rho$. It also follows from (4) that there exist $N \in \mathbb{N}$, C_1 and $C_2 > 0$ such that for $n \geq N$ and $\forall \alpha, \beta \in \mathcal{A}$,

$$m'^{[n]}_{\beta,\alpha} \leq C_2 (\rho')^n \text{ and } C_3 \rho^n \leq m_{\beta,\alpha}^{[n]}.$$

Therefore

$$\begin{aligned} |\Pi(p_\alpha^{(n)'})|_\beta &\equiv m'^{[n]}_{\beta,\alpha} \leq C_2 (\rho')^n \leq C_2 C_3 \rho^n C_3^{-1} \left(\frac{\rho'}{\rho}\right)^n \\ &\leq C_2 C_3^{-1} \left(\frac{\rho'}{\rho}\right)^n m_{\beta,\alpha}^{[n]} = |\Pi(p_\alpha^{(n)})|_\beta. \end{aligned}$$

Thus, the inequality (11) follows by taking $C \equiv C_2 C_3^{-1}$ and $r \equiv \frac{\rho'}{\rho} < 1$. This completes the proof. \square

A.3. Proof of Theorem 3.10.

Proof. For each $i = 1, 2, \dots, k$, let $\mathbf{Z}^{(i)}$ be the k -type Galton-Watson branching process (initiated with an individual of type a_i) with offspring distribution $\{P^{(i)}(\mathbf{j})\}_{\mathbf{j}^{(i)} \in \mathbb{N}_0^k}$ and let Ω_i be the event that $\mathbf{Z}_1^{(i)} = \mathbf{j}^{(i)}$. By the assumptions, $P(\Omega_i) = 1$ for all $i = 1, 2, \dots, k$. Let $\Omega_0 = \bigcap_{i=1}^k \Omega_i$, then $P(\Omega_0) = 1$. On Ω_0 , the pattern $p_{a_i}^{(1)}$ is deterministic for every $i = 1, 2, \dots, k$, and the proof is complete. \square

A.4. Proof of Theorem 3.12. To prove the theorem, we need the following two lemmas.

Lemma A.1. *Let λ be an eigenvalue of A of algebraic multiplicity m . Then for any sufficient small $\epsilon > 0$, there is a $\delta > 0$ such that if $\|E\| < \delta$, then there are exactly m eigenvalues $\lambda_1, \dots, \lambda_m$ of $A + E$ with $|\lambda_i - \lambda| \leq \epsilon$ for all $i = 1, 2, \dots, m$.*

The proof of Lemma A.1 can be found in [22, Page 167].

Lemma A.2. *Let A be an $n \times n$ matrix with the spectral radius ρ_A . For any $r > \rho_A$, there is a $\delta > 0$ such that $\rho_{A+E} \leq r$, for any $n \times n$ matrix E with $\|E\| < \delta$.*

Proof. Let $r > \rho_A$ be given, then we have that for any λ with $|\lambda| \geq r > \rho_A$, the matrix $\lambda I - A$ is invertible. Since $\sup_{|\lambda| \geq r} \|(\lambda I - A)^{-1}\| < \infty$, we let

$$\delta = \frac{1}{\sup_{|\lambda| \geq r} \|(\lambda I - A)^{-1}\|}$$

and, if $\|E\| < \delta$, then

$$\|(\lambda I - A)^{-1}E\| \leq \|(\lambda I - A)^{-1}\| \|E\| < 1$$

and hence $I - (\lambda I - A)^{-1}E$ is invertible. Thus,

$$\lambda I - (A + E) = (\lambda I - A)[I - (\lambda I - A)^{-1}E]$$

is also invertible for any λ with $|\lambda| > r$. So, $r \geq \rho_{A+E}$. \square

Now, we are ready to prove Theorem 3.12.

Proof. Let $M = [m_{i,j}]_{k \times k}$, $M' = [m'_{i,j}]_{k \times k}$ and $M_T(\mathbf{x}) = [m_{i,j}(\mathbf{x})]_{k \times k}$. For any given $\mathbf{x} = (x_1 x_2 \dots x_k)$ with $\mathbf{0} \leq \mathbf{x} \leq \mathbf{1}$, then we have, for all $i, j = 1, 2, \dots, k$,

$$m_{i,j}(\mathbf{x}) = x_j m_{i,j} + (1 - x_j) m'_{i,j}$$

and hence $M_T(\mathbf{x}) = M + E(\mathbf{x})$, where the (i, j) -entry of E is $(1 - x_j)(m'_{i,j} - m_{i,j})$, and, as $\mathbf{x} \rightarrow \mathbf{1}$,

$$\|E(\mathbf{x})\| \leq \left[\max_{1 \leq i \leq k} (1 - x_i) \right] \left[\max_{1 \leq i, j \leq k} m'_{i,j} - \min_{1 \leq i, j \leq k} m_{i,j} \right] \rightarrow 0.$$

Now, note that $M = M_T(\mathbf{1})$ with probability 1 and its spectral radius ρ_M is simple, so for any $\epsilon > 0$, by the convergence of $\|E(\mathbf{x})\|$ as $\mathbf{x} \rightarrow \mathbf{1}$ and Lemmas A.1 and A.2, there is a $\delta > 0$ such that for any \mathbf{x} with $\|\mathbf{x} - \mathbf{1}\| < \delta$, we have $\rho_T(\mathbf{x}) \leq \rho_M + \epsilon$ and there exists exactly one eigenvalue $\lambda(\mathbf{x})$ of $M_T(\mathbf{x})$ such that $|\lambda(\mathbf{x}) - \rho_M| < \epsilon$. Therefore,

$$\rho_M - \epsilon < \lambda(\mathbf{x}) \leq \rho_T(\mathbf{x}) \leq \rho_M + \epsilon$$

which implies $\rho_T(\mathbf{x}) \rightarrow \rho_M$ as $\mathbf{x} \rightarrow \mathbf{1}$. (ii) can be proved along similar lines. \square

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