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A COMPARISON BETWEEN TWO DIFFERENT STOCHASTIC EPIDEMIC MODELS WITH RESPECT TO THE ENTROPY

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ABSTRACT. In this paper at first a brief history of mathematical models is presented with the aim to clarify the reliability of stochastic models over deterministic models. Next, the necessary background about random variables and stochastic processes, especially Markov chains and the entropy are introduced. After that, entropy of SIR stochastic models is computed and it is proven that an epidemic will disappear after a long time. Entropy of a stochastic mathematical model determines the average uncertainty about the outcome of that random experiment. At the end, we introduce a chain binomial epidemic model and compute its entropy, which is then compared with the DTMC SIR epidemic model to show which one is nearer to reality.

Key words and phrases: DTMC models, Chain binomial models, Markov chain, Epidemiology, Entropy.

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1. INTRODUCTION

The spread of infectious diseases has always been a threatening concern to public health. It has always remained one of the top potential sources of threat to life. It has affected the economic and social developments of societies. Mathematical modelling for infectious diseases has a long history, and great progress has been attained, especially during the 20th century.

To prevent and control infectious diseases, it is important to fully understand their spread mechanisms and transmission dynamics. Hence, we can provide a better strategy to control them. Researches on infectious diseases can be classified as analytical, experimental and theoretical. The study of epidemic dynamics is an important theoretical approach to investigate the transmission dynamics of infectious diseases. Mathematical models have been used to explore these dynamics. The first mathematical model of an infectious disease was presented for smallpox in 1760 [10, 20]. Research on epidemic models, using deterministic mathematical models, began in the 20th century, and a lot of progress have been particularly made in the past 20 years, and mathematicians have presented some models for new diseases like HIV [12, 15].

Most of these models which were introduced by different mathematicians were deterministic [10, 7], but deterministic models have some drawbacks associated with them, which can be responsible for errors in the predicted behaviour of a particular epidemic. For example, Murray et al. suggested a deterministic model to predict the dynamics of rabies prevalence among foxes in England. They predicted the number of infected foxes will increase rapidly until the number of susceptible animals is so low and then the disease was predicted to disappear, but in reality after approximately 2 years there was a sudden reappearance of rabies in foxes [24, 23].

What was the problem? Murray et al. used a continuous approximation for the number of infected foxes. During the years when rabies was seemingly disappeared, there was around one infected, 10^{-18} of a fox per square kilometer, which was responsible for the emergence of a new wave of infection [22, 27].

This example shows that continuous approximation alone does not suffice to determine the dynamics of infectious individuals. Therefore, where the number of infectious or susceptible individuals is small, for example, at the beginning and at the end of an epidemic, or for modelling the spread of infections on networks, deterministic models can be prone to wrong predictions [10, 27]. In 1928 and 1931 Reed-Frost and Greenwood suggested discrete time stochastic models Known as chain binomial epidemic models [13]. Later on, Bartlett studied a continuous time stochastic SIR model [9]. Bailey has studied deterministic and stochastic epidemic models and the estimation of their parameters with more details in his book [8]. Recently, Allen has investigated discrete time Markov chain (DTMC) models and their applications in biology [1]. In this paper, we consider epidemic models based on her ideas.

One of the most important differences between deterministic and stochastic epidemic models is their asymptotic behaviour. For example, in the DTMC SIR model, which is presented in section 4, all the sample paths eventually are absorbed into the disease-free equilibrium, regardless of the magnitude of the basic reproduction number ($\mathcal{R}_0$), while in the deterministic SIR model if $\mathcal{R}_0 > 1$, the model converges to the endemic equilibrium [10]. Moreover, stochastic epidemic models have exclusive advantages associated with them such as, probability of an outbreak, final size distribution of an epidemic, quasi-stationary distribution and expected duration of an epidemic [1, 3, 28, 4, 2, 18, 19]. In this work we have focused on another feature of stochastic models known as the entropy.

The term entropy appeared for the first time in the study of thermodynamics in 1865. In 1948 it was used by Shannon in information theory were entropy (more specifically, Shannon entropy) is a measure for the uncertainty in a random variable that quantifies the expected value of the information contained in a message [26, 11, 5].

The concept of measure theoretic entropy has been introduced in ergodic theory [30]. Also the topological and algebraic versions of the entropy have been defined over special topological spaces, algebraic structures and hyperstructures [14, 21]. The concept of entropy is also employed in other areas of science such as biology, economics, physics and social science [25].

In recent years, the entropy theory has been developed to random walks and transformations over general groups [16], and Shanon entropy has been extended to continuous random variables [17]. Moreover, the ordinal patterns, permutation entropy and complexity for stochastic processes referred to as random dynamical systems over totally ordered state spaces have been developed [5, 6].

In a recent paper the entropy which determines the average uncertainty about outcomes of a random experiment has been introduced over the DTMC SIS epidemic models [29]. Thus, one can use this indicator to compare two stochastic models to see which model is more reliable. In this paper a comparison between two stochastic models regard to the entropy has been presented.

In section 2 and 3, some concepts in the probability theory when the state space is finite and the stochastic process is Markov have been reviewed. In section 4, the entropy of DTMC SIR models is computed. In section 5 a chain binomial epidemic model which is similar to SIR models is introduced and its entropy is computed. In the last section a comparison between these two models based on their entropy is presented.

2. PRELIMINARY

Let (Ω, β, μ) be a probability state, and (S, A) be a measurable space. A random variable $X : \Omega \longrightarrow S$ over Ω with state space S, is a measurable function. In this paper S is a finite set. A stochastic process is a family of random variables $X = \{X_t\}_{t\in\tau}$. The joint probability of the random variables $X_0, X_1, ..., X_n$ is shown by the following notation:

$$\mu(\{\omega \in \Omega : X_0(\omega) = x_0, ..., X_n(\omega) = x_n\}) = \text{Prob}\{X_0 = x_0, X_1 = x_1, ..., X_n = x_n\} = p(x_0, x_1, ..., x_n).$$

The stochastic process $X = \{X_n\}_{n\geq 0}$ is called a Markov process or Markov chain if

$$\text{Prob}\{X_n = x_n \mid X_{n-1} = x_{n-1}, ..., X_0 = x_0\} = \text{Prob}\{X_n = x_n \mid X_{n-1} = x_{n-1}\},$$

where $n \geq 1$, and $x_0, x_1, ..., x_n \in S = \{0, 1, 2, ..., N\}$.

The probability mass function associated with the random variable X_n is denoted by $\{p_i(n)\}_{i=0}^{N}$, where

$$p_i(n) = \text{Prob}\{X_n = i\}.$$

The one-step transition probability or only transition probability which is noted as $p_{ji}(n)$, is defined as

$$p_{ji}(n) = \text{Prob}\{X_{n+1} = j \mid X_n = i\}.$$

If the transition probabilities $p_{ji}(n)$ do not depend on n, then X is called time homogeneous or homogeneous.

Let $X = \{X_n\}_{n\geq 0}$ be a homogeneous Markov chain, the matrix $P = (p_{ji})$ is called the transition matrix of X.

Let $X = \{X_n\}_{n\geq 0}$ be a homogeneous Markov chain, the n-step transition probability that is denoted as $p_{ji}^{(n)}$, is defined by

$$p_{ji}^{(n)} = \text{Prob}\{X_n = j \mid X_0 = i\}.$$

The n- step transition matrix is denoted as $P^{(n)} = (p_{ji}^{(n)})$, $P^{(0)} := I_n$, and $P^{(1)} = P$.

There is a relationship between the n- step transition probabilities that is known as Chapman-Kolmogrov equation,

$$p_{ji}^{(n)} = \sum_{k=0}^{N} p_{jk}^{(n-s)} p_{ki}^{(s)}, \qquad 0 < s < n.$$

Thus, $P^{(n)} = P^{(n-s)}P^{(s)}$. Since $P^{(1)} = P$, we have $P^{(n)} = P^n$, for all n.

The vector of probability mass function associated with X_n is denoted by $p(n)$; that is, $p(n) = (p_0(n), ..., p_N(N))^T$, and $\sum_{i=0}^{N} p_i(n) = 1$. The probability distribution associated with X_{n+1} can be found by multiplying the transition matrix P by $p(n)$; that is,

$$p(n+1) = Pp(n),$$

In general, $p(n) = P^n p(0)$, so

$$p(X_n = i) = p_i(n) = \sum_{j=0}^{N} p_{ij}^{(n)} p_j(0).$$

3. STOCHASTIC PROCESSES AND THEIR ENTROPY

Let X be a random variable with sample space (Ω, β, μ) and finite state S. Entropy of X is defined by

$$H(X) = -\sum_{x \in S} p(x) \log[p(x)],$$

where $p(x) = \mu(\{\omega \in \Omega \mid X(\omega) = x\})$.

Let X and Y be two random variables with sample space (Ω, β, μ) but, in general, with various finite state spaces S and $S^{'}$ respectively.

If X and Y have the joint probability function

$$p(x, y) = \mu(\{\omega \in \Omega \mid X(\omega) = x, Y(\omega) = y\}) = \text{Prob}(X = x, Y = y),$$

where $x \in S$ and $y \in S^{'}$, then the joint entropy of X and Y is defined as follows,

$$H(X, Y) = -\sum_{x \in S} \sum_{y \in S'} p(x, y) \log[p(x, y)].$$

The conditional probability function $p(y \mid x) = \frac{p(x,y)}{p(x)}$ allows us to define the conditional entropy of Y given X which is

$$H(Y \mid X) = -\sum_{x \in S} \sum_{y \in S'} p(x, y) \log[p(y \mid x)].$$

It's clear that $H(X, Y) = H(X) + H(Y \mid X)$ [5, 6, 30, 11].

The (joint) entropy of the random variable vector $X_0^{n-1} = \{X_0, ..., X_{n-1}\}$, where all components have the same state S, is defined by

$$H(X_0, X_1, ..., X_{n-1}) = -\sum_{x_0, x_1, ..., x_{n-1} \in S} p(x_0, x_1, ..., x_{n-1}) \log[p(x_0, x_1, ..., x_{n-1})].$$

Lemma 3.1. *Let the random variables $X_0, ..., X_{n-1}$ be given. Then*

(i) $p(X_0, ..., X_{n-1}) = \prod_{i=0}^{n-1} p(X_i \mid X_{i-1}, ..., X_0)$,

(ii) $H(X_0, ..., X_{n-1}) = \sum_{i=0}^{n-1} H(X_i \mid X_{i-1}, ..., X_0)$,

where $p(X_0 \mid X_{-1}) := p(X_0)$, and $H(X_0 \mid X_{-1}) := H(X_0)$.

Definition 3.1. Entropy of a stochastic process $X = \{X_n\}_{n=0}^{\infty}$ on a probability space (Ω, β, μ) with finite state S is defined by

$$h(X) = \lim_{n\to\infty} \frac{1}{n} H(X_0, ..., X_{n-1}),$$

provided that the limit exists [5, 6, 11].

Lemma 3.2. *If $X = \{X_n\}_{n=0}^{\infty}$ is a homogeneous Markov process, then*

$$H(X_n \mid X_{n-1}, ..., X_0) = H(X_n \mid X_{n-1}).$$

Proof. Here we use 'P' instead of 'Prob' to make our proof shorter.

$$\begin{aligned}
&H(X_n \mid X_{n-1}, ..., X_0) = \\
&\quad - \sum_{x_0,x_1,...,x_n} \mathrm{P}(X_n = x_n, X_{n-1} = x_{n-1}, ..., X_0 = x_0) \log\left[\mathrm{P}(X_n = x_n \mid X_{n-1} = x_{n-1}, ..., X_0 = x_0)\right] \\
&= - \sum_{x_0,x_1,...,x_n} \mathrm{P}(X_{n-1} = x_{n-1}, ..., X_0 = x_0)\mathrm{P}(X_n = x_n \mid X_{n-1} = x_{n-1}) \log[\mathrm{P}(X_n = x_n \mid X_{n-1} = x_{n-1})] \\
&= - \sum_{x_0,x_1,...,x_n} \mathrm{P}(X_{n-1} = x_{n-1})\mathrm{P}(X_{n-2} = x_{n-2}, ..., X_0 = x_0 \mid X_{n-1} = x_{n-1})\mathrm{P}(X_n = x_n \mid X_{n-1} = x_{n-1}) \\
&\qquad \log[\mathrm{P}(X_n = x_n \mid X_{n-1} = x_{n-1})] \\
&= - \sum_{x_{n-1},x_n} \sum_{x_{n-2},...,x_0} \mathrm{P}(X_{n-1} = x_{n-1})\mathrm{P}(X_{n-2} = x_{n-2}, ..., X_0 = x_0 \mid X_{n-1} = x_{n-1}) \\
&\qquad \mathrm{P}(X_n = x_n \mid X_{n-1} = x_{n-1}) \log[\mathrm{P}(X_n = x_n \mid X_{n-1} = x_{n-1})] \\
&= - \sum_{x_{n-1},x_n} \mathrm{P}(X_{n-1} = x_{n-1})\mathrm{P}(X_n = x_n \mid X_{n-1} = x_{n-1}) \log[\mathrm{P}(X_n = x_n \mid X_{n-1} = x_{n-1})] \times \\
&\quad \sum_{x_{n-2},...,x_0} \mathrm{P}(X_{n-2} = x_{n-2}, ..., X_0 = x_0 \mid X_{n-1} = x_{n-1}).
\end{aligned}$$

It is clear that for every x_{n-1}:

$$\sum_{x_{n-2},...,x_0} \mathrm{P}(X_{n-2} = x_{n-2}, ..., X_0 = x_0 \mid X_{n-1} = x_{n-1}) = 1.$$

Therefore

$$\begin{aligned}
&H(X_n \mid X_{n-1}, ..., X_0) = \\
&\quad - \sum_{x_{n-1},x_n} \mathrm{P}(X_{n-1} = x_{n-1})\mathrm{P}(X_n = x_n | X_{n-1} = x_{n-1}) \log[\mathrm{P}(X_n = x_n \mid X_{n-1} = x_{n-1})] \\
&= - \sum_{x_{n-1},x_n} \mathrm{P}(X_{n-1} = x_{n-1}, X_n = x_n) \log[\mathrm{P}(X_n = x_n \mid X_{n-1} = x_{n-1})] \\
&= H(X_n \mid X_{n-1}).
\end{aligned}$$

∎

Corollary 3.3. *If $X = \{X_n\}_{n=0}^{\infty}$ is a homogeneous Markov chain, then*

$$H(X_0, X_1, ..., X_n) = H(X_0) + H(X_1 \mid X_0) + ... + H(X_n \mid X_{n-1}).$$

Remark 3.1. Let $X = \{X_n\}_{n=0}^{\infty}$ be a homogeneous Markov chain. Then

$$\begin{aligned} H(X_n \mid X_{n-1}) &= -\sum_{j=0}^{N}\sum_{i=0}^{N} \text{Prob}(X_{n-1}=j, X_n=i)\log[\text{Prob}(X_n=i \mid X_{n-1}=j)] \\ &= -\sum_{j=0}^{N}\sum_{i=0}^{N} \text{Prob}(X_{n-1}=j)\text{Prob}(X_n=i \mid X_{n-1}=j)\log(p_{ij}) \\ &= -\sum_{i=0}^{N}\sum_{j=0}^{N} \text{Prob}(X_{n-1}=j)p_{ji}\log(p_{ji}). \end{aligned}$$

The term $h(X_0, ..., X_{n-1}) = \frac{1}{n}H(X_0, ..., X_{n-1})$ is called entropy of order n of X. Therefore, $h(X_0^{n-1}) = h(X_0, ..., X_{n-1})$ is the average uncertainty about n successive outcomes of the random experiment which is modeled by X. For example, let $X = \{X_n\}_{n=0}^{\infty}$ be a discrete- time stochastic process of an epidemic model, so after n- time intervals of length Δt the model outputs n random variables. The expression $h(X_0^{n-1})$ measures average uncertainty and provides an insight on the reliability and accuracy of the model [29].

The value of $h(X_0^{n-1})$ indicates a negative correlation with the accuracy of the model, which means the smaller the value of $h(X_0^{n-1})$, the higher the accuracy of the model is expected to be. Hence, it is deduced that the model with smaller $h(X_0^{n-1})$ is more reliable.

4. DTMC SIR EPIDEMIC MODEL AND ITS ENTROPY

In a SIR epidemic model, individuals are divided into three compartments: Susceptible (individuals who might become infected if exposed), Infectious (individuals who are infected and can transmit the infection), and Removed (individuals who are immune to the infection).

Differential equations that describe the dynamics of an SIR epidemic model are as follows

$$\begin{aligned} \frac{dS}{dt} &= -\beta SI + b(I+R) \\ \frac{dI}{dt} &= \beta SI - (b+\gamma)I \\ \frac{dR}{dt} &= \gamma I - bR, \end{aligned}$$

where $\beta > 0$ is the transmission rate, $\gamma > 0$ is the recovery rate, $b \geq 0$ is the birth rate, and $N = S(t) + I(t) + R(t)$ the total population size is constant, i.e. the birth and death rates are equal, so $\frac{dN}{dt} = 0$ [10].

To formulate a DTMC model, let $S(t)$, $I(t)$ and $R(t)$ denote discrete random variables for the number of susceptible, infected and immune individuals at time t, respectively. The population size is constant, so $R(t) = N - S(t) - I(t)$. Therefore DTMC SIR epidemic model is a bivariate process $\{S(t), I(t)\}_{t=0}^{\infty}$ that $t \in \{0, \Delta t, 2\Delta t, ...\}$ and has a joint probability function given by

$$p_{(s,i)}(t) = \text{Prob}\{S(t)=s, I(t)=i\}.$$

We consider Δt sufficiently small such that at most one change occurs in the states [10, 1]. For $t = n\Delta t$ define

$$p_{(s,i)}(n) := \text{Prob}\{S(t)=s, I(t)=i\}.$$

From now on, this bi-variate stochastic process is denoted by $X = \{X_n\}_{n=0}^{\infty}$.

Lemma 4.1. *The stochastic process $X = \{X_n\}_{n=0}^{\infty}$ is a homogeneous Markov chain.*

The transition probabilities are denoted as follows:

$$p_{(s',i'),(s,i)}(\Delta t) = \text{Prob}\{X_{n+1} = (s',i') | X_n = (s,i)\}.$$

Hence,

$$p_{(s+k,i+j),(s,i)}(\Delta t) = \begin{cases} \beta i s \Delta t & (k,j) = (-1,1) \\ \gamma i \Delta t & (k,j) = (0,-1) \\ b i \Delta t & (k,j) = (1,-1) \\ b(N-s-i)\Delta t & (k,j) = (1,0) \\ 1 - \beta i s \Delta t - [\gamma i + b(N-s)]\Delta t & (k,j) = (0,0) \\ 0 & \text{otherwise} \end{cases}.$$

The time step Δt should be chosen sufficiently small such that each of the transition probabilities be equal or smaller than 1. In order to define the transition probability, we consider an order on the states (s,i) that $(s,i) < (s',i') \Leftrightarrow s < s'$ or $s = s', i < i'$. According to this order, the transition matrix P is a $(N+1)^2 \times (N+1)^2$ matrix, and $p(n) = P^n p(0)$, where $p^{(n)}_{(s,i),(s',i')} = (p^n)_{(s,i),(s',i')}$, and

$$p(n)_{(s,i)} = \sum_{s'=0}^{N} \sum_{i'=0}^{N} p^{(n)}_{(s,i),(s',i')}\, p_{(s',i')}(0).$$

Theorem 4.2. *Let $X = \{X_n\}_{n=0}^{\infty}$ be the stochastic process of the SIR epidemic model and $X_0 = (s_0, k_0)$, s_0 and k_0 are the initial size of susceptible and infected individuals respectively, then $h(X_0, X_1, ..., X_n)$ is the sum of $(s_0,k_0)^{th}$ column entries of the following matrix*

$$H_n = H(P)\left(\frac{0 + I + P + ... + P^{n-1}}{n+1}\right),$$

where P is the transition matrix and

$$H(P) = \left(-p_{(s,i)(s',i')} \log\, p_{(s,i)(s',i')}\right)_{(N+1)^2 \times (N+1)^2},$$

and $0log0 := 0$.

Proof. By corollary 3.3,

$$h(X_0, ..., X_n) = \frac{1}{n+1} H(X_0, ..., X_n) = \frac{H(X_0) + H(X_1 \mid X_0) + ... + H(X_n \mid X_{n-1})}{n+1}.$$

Since $X_0 = (s,k)$ is fixed, it is clear that $H(X_0) = 0$. Thus

$$h(X_0, ..., X_n) = \frac{H(X_1 \mid X_0) + ... + H(X_n \mid X_{n-1})}{n+1}.$$

According to Remark 3.1,

$$H(X_n \mid X_{n-1}) = \sum_{(s',i')} \sum_{(s,i)} \text{Prob}(X_{n-1} = (s',i'))\, p_{(s,i),(s',i')} \log\left(\frac{1}{p_{(s,i),(s',i')}}\right).$$

It is clear that

$$\text{Prob}(X_{n-1} = (s',i')) = p^{(n-1)}_{(s',i'),(s_0,k_0)},$$

so

$$
\begin{aligned}
&h(X_0,...,X_n)\\
&=\sum_{(s',i')}\sum_{(s,i)}\frac{\text{Prob}(X_0=(s',i'))+...+\text{Prob}(X_{n-1}=(s',i'))}{n+1}p_{(s,i),(s',i')}\log\left(\frac{1}{p_{(s,i),(s',i')}}\right)\\
&=\sum_{(s',i')}\sum_{(s,i)}\frac{p^{(0)}_{(s',i'),(s_0,k_0)}+...+p^{(n-1)}_{(s',i'),(s_0,k_0)}}{n+1}p_{(s,i),(s',i')}\log\left(\frac{1}{p_{(s,i),(s',i')}}\right)\\
&=\sum_{(s',i')}\sum_{(s,i)}\frac{p^{(0)}_{(s',i'),(s_0,k_0)}+...+p^{(n-1)}_{(s',i'),(s_0,k_0)}}{n+1}(H(p))_{(s,i),(s',i')}\\
&=\sum_{(s',i')}\sum_{(s,i)}\frac{I_{(s',i'),(s_0,k_0)}+P_{(s',i'),(s_0,k_0)}+...+(P^{n-1})_{(s',i'),(s_0,k_0)}}{n+1}(H(p))_{(s,i)(s',i')}\\
&=\sum_{(s,i)}\frac{(H(p))_{(s,i),(s_0,k_0)}+H(p)P)_{(s,i),(s_0,k_0)}+...+(H(p)P^{n-1})_{(s,i),(s_0,k_0)}}{n+1}\\
&=\sum_{(s,i)}\left(\frac{H(p)+H(p)P+...+H(p)P^{n-1}}{n+1}\right)_{(s,i),(s_0,k_0)}.
\end{aligned}
$$

Thus, $h(X_0,...,X_n)$ is the sum of $(s_0,k_0)^{th}$ column entries of the following matrix

$$\frac{(H(p)+H(p)P+...+H(p)P^{n-1})}{n+1}=H(p)\left(\frac{0+I+P+...+P^{n-1}}{n+1}\right).$$

∎

In the DTMC SIR epidemic model, the state $(s,i)=(N,0)$ is recurrent and the others are transient, therefore the matrix P^n converges to a $(N+1)^2\times(N+1)^2$ matrix that all entries are zero, but the $(N^2+N+1)^{th}$ row entries are 1. Therefore

$$\lim_{n\to\infty}H_n=0.$$

Hence, $h(X)=0$. We can say as time increases this model becomes closer to reality. This model predicts that after a long time, disease will disappear, so this prediction is true because $h(X)=0$.

When we are using stochastic processes, it is important to determine the average uncertainty about n consecutive outcomes in model.

In the next example, $h(X_0^n)$ for the DTMC SIR epidemic model has been computed.

Example 4.1. Put $N=10$, $\Delta t=0.1$, $\beta=0.01$, $\gamma=0.5$, $I(0)=2$, $b=0$ and $S(0)=8$ the entropy table is

Table 4.1: Entropy of DTMC SIR model

n	*20*	*60*	*100*	*200*	*300*
$h(X_0^n)$	*0.2755*	*0.1545*	*0.0996*	*0.0507*	*0.0338*

5. CHAIN BINOMIAL EPIDEMIC MODEL

Let S_n be a discrete random variable for the number of susceptible individuals at time $n\Delta t$. Δt represents the infectious period, and I_n represents new infected individuals.

There is no birth and death, so the number of susceptible individuals is decreasing over time. Therefore, $S_{n+1} + I_{n+1} = S_n$ and $S_n, I_n \in \{0, 1, ..., s_0\}$, where $S_0 = s_0$.

Let α be the probability of a contact between a susceptible and an infected individual, and β be the probability that the susceptible individual is infected after contact. Let $P_{I(t)}$ be the probability that a susceptible individual does not become infected at time t. In the Greenwood model we assume that $P_{I(t)}$ is constant ($p = 1 - \alpha\beta$), and in the Reed-Frost model we assume that $P_{I(t)} = p^{I(t)}$ [1, 10], but it is clear that α is a function of infected individuals ($I(t)$).

Hence, if at time t there are $I(t)$ infected individuals and $N(t)$ is the population size at time t, then

$$P_{I(t)} = 1 - \frac{I(t)}{N(t)}\beta.$$

In this model, we assume that $\Delta t = \frac{1}{\gamma}$, where γ is the recovery rate, and the model is a bi-variate Markov chain.

This process is denoted by $\{S_n, I_n\} = \{(S, I)_n\}$ for $n = 0, 1, 2, ...$ I_n represents infected individuals at time $n\Delta t$. Thus, during the time interval n to $n + 1$,

$$P_{i_n} = 1 - \frac{i_n}{N}\beta.$$

The transition probability $P_{(s,i)_{n+1},(s,i)_n}$ is a binomial probability, and

$$P_{(s,i)_{n+1},(s,i)_n} = \begin{pmatrix} S_n \\ S_{n+1} \end{pmatrix} P_{i_n}^{S_{n+1}} (1 - P_{i_n})^{S_n - S_{n+1}}. \tag{5.1}$$

This model like the DTMC SIR epidemic model is a bi-variate process. In this model, we order the states (s, i) as previous, and this bi-variate stochastic process is denoted by $X = \{X_n\}_{n=0}^{\infty}$.

Transition matrix for this model is a $(s_0 + 1)^2 \times (s_0 + 1)^2$, upper triangle matrix that is given by

$$\begin{array}{c} (0,0) \\ (0,1) \\ \vdots \\ (0,s_0) \\ (1,0) \\ \vdots \\ (1,s_0) \\ \vdots \\ (s_0,0) \\ \vdots \\ (s_0,s_0) \end{array} \begin{pmatrix} 1 & 1 & \dots & 1 & 0 & \dots & 0 & \dots & 0 & \dots & 0 \\ 0 & 0 & \dots & 0 & 0 & \dots & 1 - P_{s_0} & \dots & 0 & \dots & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & \dots & 0 & 0 & \dots & 0 & \dots & 0 & \dots & (1 - P_{s_0})^{s_0} \\ 0 & 0 & \dots & 0 & 1 & \dots & P_{s_0} & \dots & 0 & \dots & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & \dots & 0 & 0 & \dots & 0 & \dots & 0 & \dots & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & \dots & 0 & 0 & \dots & 0 & \dots & 1 & \dots & P_{s_0}^{s_0} \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & \dots & 0 & 0 & \dots & 0 & \dots & 0 & \dots & 0 \end{pmatrix}.$$

Since it is possible that $i_0 > s_0$, at first for computing the entropy the start time $t = 0$ will be ignored. One can prove the following theorem like Theorem 4.2.

Theorem 5.1. *let $X = \{X_n\}_{n=1}^{\infty}$ be the stochastic process of this model and $X_1 = (s_1, i_1)$, then $h(X_1, ..., X_{n+1})$ is the sum of $(s_1, i_1)^{th}$ column entries of the following matrix*

$$H_n(s_1) = H(P)\left(\frac{0 + I + P + ... + P^{n-1}}{n+1}\right).$$

Corollary 5.2. *Let $X = \{X_n\}_{n=0}^{\infty}$ be the stochastic process of the model and $X_0 = (s_0, i_0)$, then*

$$h(X_0, X_1, ..., X_{n+1}) = \frac{H(X_1) + (n+1)\sum_{s_1=0}^{s_0} \text{Prob}(S_1 = s_1)H_n(s_1)}{n+2}.$$

Proof. Since $X_0 = (s_0, i_0)$, $H(X_0) = 0$, then

$$\begin{aligned} H(X_0, ..., X_{n+1}) &= H(X_1, X_2, ..., X_{n+1}) \\ &= H(X_1) + H(X_2, ..., X_{n+1} \mid X_1) \\ &= H(X_1) + \sum_{x_1} \text{Prob}(X_1 = x_1)H(X_2, ..., X_{n+1} \mid X_1 = x_1) \\ &= H(X_1) + \sum_{s_1=0}^{s_0} \text{Prob}(S_1 = s_1)H(X_2, ..., X_{n+1} \mid X_1 = (s_1, i_1)) \\ &= H(X_1) + \sum_{s_1=0}^{s_0} \text{Prob}(S_1 = s_1)(n+1)H_n(s_1). \end{aligned}$$

Therefore

$$h(X_0, X_1, ..., X_{n+1}) = \frac{H(X_1) + (n+1)\sum_{s_1=0}^{s_0} \text{Prob}(S_1 = s_1)H_n(s_1)}{n+2}.$$

∎

Remark 5.1. $H(X_1) = -\sum_{s_1=0}^{s_0} \text{Prob}(S_1 = s_1)\log[\text{Prob}(S_1 = s_1)]$ because $i_1 = s_0 - s_1$, and

$$P(S_1 = s_1) = P_{(s_1, s_0 - s_1),(s_0, i_0)} = \begin{pmatrix} s_0 \\ s_1 \end{pmatrix} P_{i_0}^{s_1}(1 - P_{i_0})^{s_0 - s_1}.$$

In the next example, $h(X_0^n)$ for this chain binomial model has been computed.

Example 5.1. The population size is $N = 12$, the infectious period is $\Delta t = 2$, $\beta = 0.01$, $\gamma = 0.5$, $b = 0$, $S(0) = 10$ and $I(0) = 2$. The entropy table is

Table 5.1: Entropy of chain binomial model

n	*1*	*3*	*5*	*10*	*15*
$h(X_0^n)$	*0.0284*	*0.0171*	*0.0122*	*0.0071*	*0.0051*

In Example 5.1 we consider $N = 12$ and $S(0) = 10$ to make the total number of states (the dimension of the transition matrix) in the chain binomial model equal to the corresponding DTMC SIR model. Now comparing the entropy of these two model can help us to understand which one is more reliable. In the next section a comparison between these two models is presented.

6. DISCUSSION

Analysis of the entropy is an important approach in the study of dynamical systems, in particular when the study aims to explore relative comparison of two mathematical models. In this paper the entropy of two stochastic epidemic models is introduced. In example 4.1, for the DTMC SIR epidemic model we computed the entropy at time step n, which is illustrated by $h(X_0^n)$. Also in example 5.1 the entropy at time step n for the chain binomial model has been computed.

Using Table 4.1 and Table 5.1 we have plotted Figure 1 which shows how the entropy of these two model will change with respect to the time.

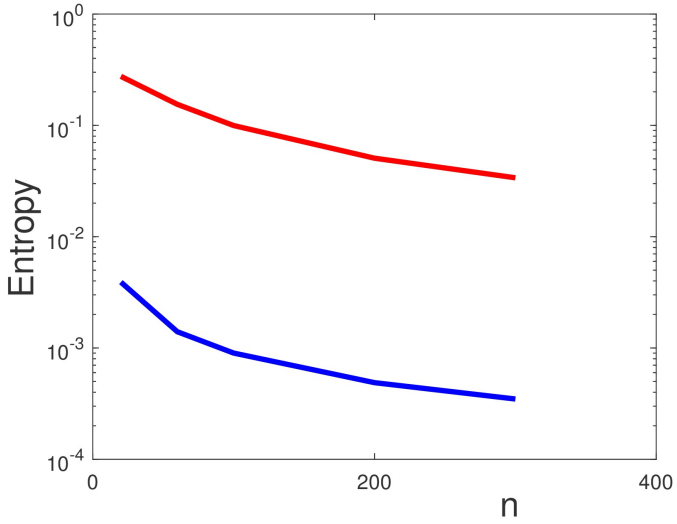

Figure 1: Red curve shows the entropy of the DTMC SIR model, and Blue curve indicates the entropy of the chain binomial epidemic model.

Figure 1 indicates that the chain binomial model is more efficient than the DTMC SIR model. Hence, in this case with the given parameters, the prediction of the future of this epidemic by chain binomial model is more accurate than the DTMC SIR model. It is clear just based on these two examples we could not derive a general conclusion. However, as you know chain binomial models were developed to help in understanding the spread of a disease within a small population [10], and our numerical results are in agreement that the chain binomial epidemic models are more accurate than DTMC SIR models. Hence, when we want to study the spread of a disease in a society, at first we can compare our models with the method that is proposed in this paper to have an idea which model is closer to reality.

As follows, we show how the entropy of this chain binomial model changes by changing the transmission rate (β).

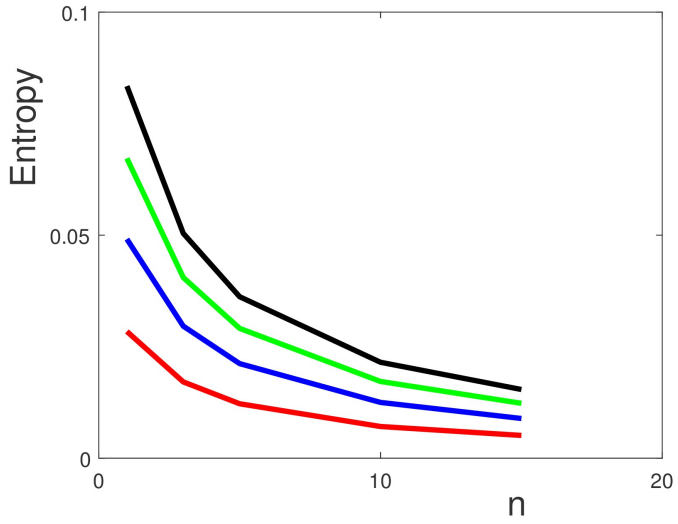

Figure 2: Black: $\beta = 0.01$, *Green:* $\beta = 0.02$, *Blue:* $\beta = 0.03$ *and Red:* $\beta = 0.04$.

Figure 2 illustrates, with the given parameters, by decreasing β the entropy of this model will decrease. Thus, the prediction of future is easier and it is more accurate over time.

There are some further directions in which this work can be extended. Since the proof of Theorem 4.2 is general, one can extend it to all DTMC models, and use it as a tool to compare them. The way that one can define the transition probabilities is not unique [1]. Therefore, it could be an interesting idea to study how changing them can change the entropy.

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