Derivation analysis of a discrete-time SIS epidemic model with extension of Markov Chain and logistic map.

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1 Abstract

In recent years, the rampant spread of diseases has led to considerable impacts on human society. Limiting such spread requires the formulation of quantitative studies to understand the dynamics of infection and to study the effect of preventative and counteractive action. In 1911, scientists constructed differential equations to study the spread of malaria and found that at a critical mosquito population level the spread of the disease would be limited. This also became the basis for the later dynamics of infectious diseases. This research aims to dynamically analyze the spread of the virus by establishing a mathematical model and assigning specific values to the influencing factors to discuss the relationship between the person who infects others and the infected person. The ultimate goal is that the spread of the disease can be effectively suppressed in a specific proportion of people. Keywords: dynamics of infectious diseases, infected-uninfected relationship.

2 Introduction

Throughout human history, infectious diseases, such as SARS, H5N1, and Ebola, have occurred frequently in various periods. With the emergence of COVID-19 in December 2019, there has been greater emphasis on understanding global epidemics since they have such a detrimental effect on human health and lives. As of July 26, 2023, the World Health Organization (WHO) has reported more than 760 million confirmed cases of COVID-19, with 6.9 million deaths in total (https://covid19.who.int/).

In order to limit the spread of infectious diseases and forecast the evolution of an epidemic outbreak, it is essential to conduct theoretical research and use a mathematical model. Such a model can accurately reveal the spread of infectious diseases among populations. Indeed, in the dynamics of infectious diseases, mathematical models are established based on the characteristics of population migration and transmission mechanisms. By conducting quantitative analysis and numerical calculation of the model, the dissemination process and patterns of infectious diseases can be simulated, providing a decision-making basis for intervention policies such as vaccination [11][14].

3 Literature Review

1766 marks the beginning of mathematical modeling in epidemiology, when D. Bernoulli [2] developed the spread of smallpox using a mathematical model which is also considered the prototype of dynamics models of infectious disease. In 1911, Ross et al. [10] constructed differential equations to study the spread of malaria. A crucial discovery is that if the number of mosquitoes fell below a critical value, malaria would not continue to spread: this formed the earliest concept of basic reproductive numbers. In 1927, Kermack and McKendrick [6] proposed the famous SIR compartmental model and followed this by constructing the SIS compartmental model in 1932. The threshold theorem, one of the key achievements in epidemiology, whereby a noise-containing quantum computer can still accurately simulate an ideal quantum computer when the noise in a single quantum gate is below a specific threshold and the noise satisfies physically specific reasonable assumptions, also derives from the work of Kermack and McKendrick.

In early compartmental models, the population is assumed to be homogeneously mixed, where each individual has a chance to contact any other. In this unrealistic assumption, the effect of local connections is neglected. Recently, complex networks have been used in dynamical epidemic modeling [5] [8] [3]. Indeed, scholars have made various improvements based on the classic compartmental model. In 2001, Pastor et al. [9] established the first dynamic SIS model of complex networks to describe the spread of computer viruses. In 2002, Moreno et al. [7] extended the SIS model to the SIR model in heterogeneous networks. In [1] [13], the authors analyzed discrete-time models in detail. Considering that humans tend to protect themselves by avoiding contact with infectious diseases, Gross et al. [4] extended the SIS epidemic model to adaptive networks in 2006. Some scholars have also investigated the dynamic characteristics and network topology properties of epidemic models [12].

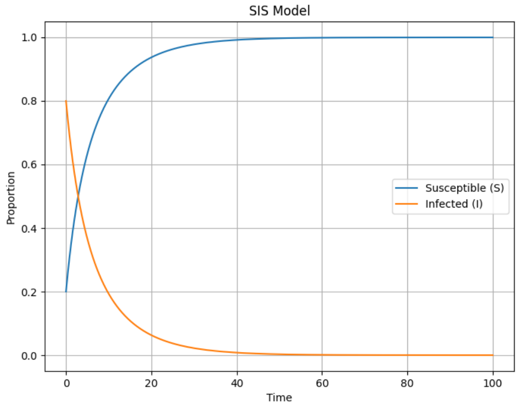
4 Aim

Here, we will consider a SIS (susceptible–infected–susceptible) model in a complex network, where the nodes represent the individuals and the links represent the relationships between the individuals. Firstly, we establish a mathematical model to simulate the relationship between ordinary people and patients, and then compare the images of discrete time and continuous time. As an extension, we use Markov chains to discuss randomness in mathematical models and present the final data through charts. In addition, we use a well-known mathematical method, a logistic map, which is used to study demographic models. This can help us visualize the chaotic phenomena that occur when the rate of change changes through images.

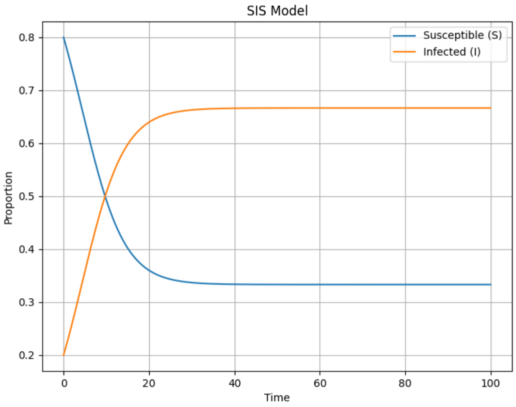
5 SIS model

In this research, our group members used the Susceptible-Infected-Susceptible (SIS) approach to show epidemics in networks. In this model, a person only can be in a susceptible(S) state or an infected(I) state. A susceptible person has little immunity and is more likely to be infected after contact with an infected person. When an infected person gets the disease they may be cured by medical treatment later, but they will never get immunity against this disease.

Now, we need to define some concepts by using some alphabetical letters to make them shorter and clearer to read. λ is the number of effective contacts per patient per day μ is the proportion of patients who recover in the total number of patients. N is the total number of people S refers to the proportion of susceptible individuals in the total population and i refers to the proportion of infected individuals in the total population. σ refers to λ/μ. In this model, we assume that all people are alive and the total population N is a constant, which means nobody will immigrate or emigrate to or from from this place. Here are two figures which show two different value of σ.



$\sigma \le 1$



$\sigma \ge 1$

The process below is a mathematical deduction written by our group to prove the graph above.

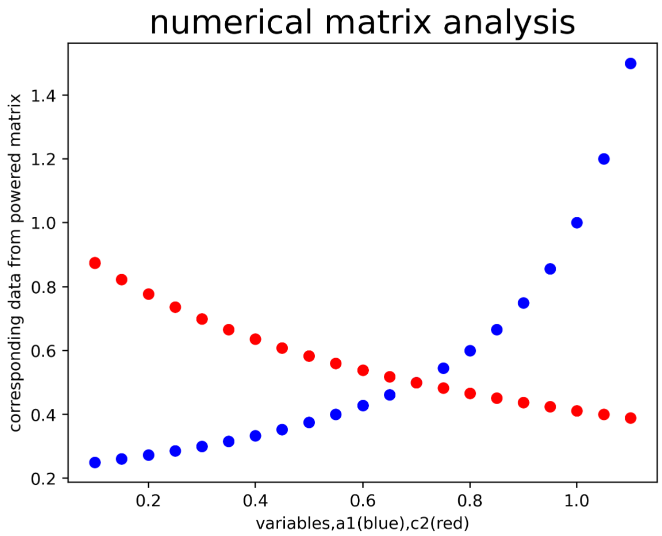
$$\frac{di}{dt} = \lambda is - \mu i$$
$$because \;\; s + i = 1,$$
$$= \lambda i(1-i) - \mu i$$
$$= \lambda i - \lambda i^2 - \mu i$$
$$= (\lambda - \mu)i - \lambda i^2$$
$$i^{-2}i' - (\lambda-\mu)i^{-1} = -\lambda$$
$$let \;\; i^{-1} = u,$$
$$i^{-2} * i' = -\frac{du}{dt}$$
$$-\frac{du}{dt} - (\lambda-\mu)u = -\lambda$$
$$\frac{du}{dt} + (\lambda-\mu)u = \lambda$$
$$According\,to\,First\,Order\,Linear\,Differential\,Equation,$$
$$u = e^{-\int(\lambda-\mu)dt}[\int \lambda e^{\int(\lambda-\mu)dt}dt + c]$$
$$u = e^{-(\lambda-\mu)t}[\frac{\lambda}{\lambda-\mu}e^{(\lambda-\mu)t} + c]$$
$$u = \frac{\lambda}{\lambda-\mu} + ce^{-(\lambda-\mu)t}$$
$$i^{-1} = \frac{\lambda}{\lambda-\mu} + ce^{-(\lambda-\mu)t}$$

$i = [\frac{\lambda}{\lambda-\mu} + ce^{-(\lambda-\mu)t}]^{-1}$
$let\ i(0) = b,$
$b = [\frac{\lambda}{\lambda-\mu} + c]^{-1}$
$c = \frac{1}{b} - \frac{\lambda}{\lambda-\mu}$
$i = [\frac{\lambda}{\lambda-\mu} + (\frac{1}{b} - \frac{\lambda}{\lambda-\mu})e^{-(\lambda-\mu)t}]^{-1}$
$i = [\frac{1}{1-\frac{1}{\sigma}} + (\frac{1}{i_0} - \frac{1}{1-\frac{1}{\sigma}}e^{\lambda(1-\frac{1}{\sigma})t}]^{-1}$

When σ tends to infinity, the result of i tends to a certain limit but when tends to 0, the result of i tends to 0, which means that all the people are recovered and will not be reinfected because the population of infected is 0.

6 Markov chain

A Markov chain is used to understand stochastic processes in probability theory and mathematical statistics. The Markov property is when a Stochastic process takes into account the present state and all past states, and the conditional probability distribution of its future state only depends on the current state. For example, if we want to predict future weather through Markov properties, then tomorrow's weather can only be predicted based on today's weather. We can also apply the Markov property to the SIS model, indicating that the number of infected and susceptible people on the next day is only related to the number of people on the previous day. In this way, we can list a matrix to express the probability of transition between states S and I. After multiple operations of multiplication, the infected and susceptible population will converge on a fixed proportion. Based on the results obtained, we can draw a graph and finally come to a conclusion.

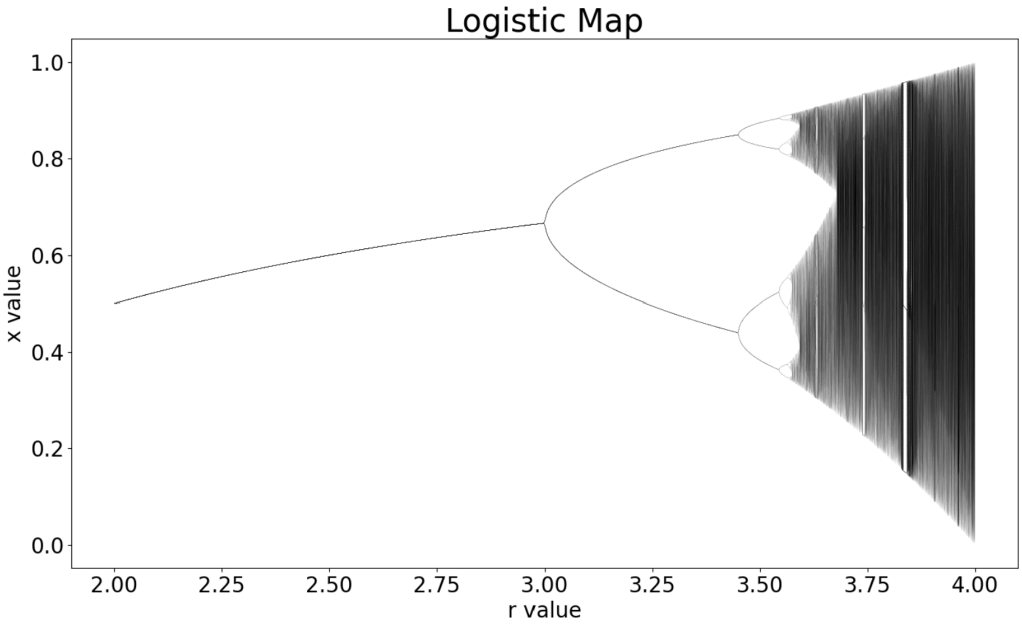


7 Logistic Map

A logistic map is a quadratic polynomial map, which is a classic example of chaotic phenomena generated by simple nonlinear equations. This mapping is famous due to a paper published by biologist Robert May in 1976 which covered a demographic model. The mathematical expression can be written as

$$x_{n+1} = rx_n(1 - x_n)$$

and by discussing the rate of change r and repeatedly calculating it, we can obtain different stable values of the infected to uninfected population ratio. After r exceeds 3.6, the stable value will no longer appear regularly and chaotic phenomena will occur, as shown in the following image.



Author Contributions

Conceptualization: W.M, C.Y, W.Y, Z.J and Z.S; summarization: W.M; significance investigation: W.M, W.Y; literature review: W.Y; research aims: W.M, Z.J; SIS model research: C.Y, Z.S; proposal analysis, edition: Z.J. All authors have read and agreed to the published version of the manuscript.

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Research Guidelines

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Informed Consent Statement

Not Applicable.

Data Availability

Please contact the corresponding author(s) for all reasonable requests for access to the data.

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Conflicts of Interest

The authors declare no conflict of interest.

Intellectual Property

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References

[1] Linda JS Allen. Some discrete-time si, sir, and sis epidemic models. *Mathematical biosciences*, 124(1):83–105, 1994. 2

[2] Daniel Bernoulli and Dominique Chapelle. Essai d'une nouvelle analyse de la mortalité causée par la petite vérole, et des avantages de l'inoculation pour la prévenir. 2023. 2

[3] Stefano Boccaletti, Vito Latora, Yamir Moreno, Martin Chavez, and D-U Hwang. Complex networks: Structure and dynamics. *Physics reports*, 424(4-5):175–308, 2006. 2

[4] Thilo Gross, Carlos J Dommar D' Lima, and Bernd Blasius. Epidemic dynamics on an adaptive network. *Physical review letters*, 96(20):208701, 2006. 2

[5] Hans Heesterbeek, Roy M Anderson, Viggo Andreasen, Shweta Bansal, Daniela De Angelis, Chris Dye, Ken TD Eames, W John Edmunds, Simon DW Frost, Sebastian Funk, et al. Modeling infectious disease dynamics in the complex landscape of global health. *Science*, 347(6227):aaa4339, 2015. 2

[6] William Ogilvy Kermack and Anderson G McKendrick. A contribution to the mathematical theory of epidemics. *Proceedings of the Royal Society of London. Series A, Containing papers of a mathematical and physical character*, 115(772):700–721, 1927. 2

[7] Yamir Moreno, Romualdo Pastor-Satorras, and Alessandro Vespignani. Epidemic outbreaks in complex heterogeneous networks. *The European Physical Journal B-Condensed Matter and Complex Systems*, 26:521–529, 2002. 2

[8] Mark EJ Newman. The structure and function of complex networks. *SIAM review*, 45(2):167–256, 2003. 2

[9] Romualdo Pastor-Satorras and Alessandro Vespignani. Epidemic spreading in scale-free networks. *Physical review letters*, 86(14):3200, 2001. 2

[10] Ronald Ross. *The prevention of malaria*. John Murray, 1911. 2

[11] Boris Shulgin, Lewi Stone, and Zvia Agur. Pulse vaccination strategy in the sir epidemic model. *Bulletin of mathematical biology*, 60(6):1123–1148, 1998. 2

[12] Xinhe Wang, Zhen Wang, and Hao Shen. Dynamical analysis of a discrete-time sis epidemic model on complex networks. *Applied Mathematics Letters*, 94:292–299, 2019. 2

[13] Yang Wang, Deepayan Chakrabarti, Chenxi Wang, and Christos Faloutsos. Epidemic spreading in real networks: An eigenvalue viewpoint. In *22nd International Symposium on Reliable Distributed Systems, 2003. Proceedings.*, pages 25–34. IEEE, 2003. 2

[14] Gul Zaman, Yong Han Kang, and Il Hyo Jung. Stability analysis and optimal vaccination of an sir epidemic model. *BioSystems*, 93(3):240–249, 2008. 2