

Study on Pneumonic Plague Based on Double SIR Model

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Keywords: infectious disease. SIR epidemic model. Double transmission. Matlab analysis

Abstract: Plague, also known as black plague, is caused by *Yersinia* bacteria. In order to provide better prevention and control measures for pneumonic plague, I explored the transmission rules of pneumonic plague and established the double SIR model of two-way infection based on the traditional SIR model by adding birth rate, death rate and infection rate between human and mouse and other parameter. In this article, the relationship of infection among different kinds of patients and mice was given and the numerical simulation was carried out on this basis. Finally, the role of the model in the epidemic situation is emphasized, such as providing theoretical significance for the transmission trend of pneumonic plague, and the shortcomings of this paper are also pointed out, such as the lack of data on pneumonic plague and the inability to carry out numerical simulation.

1. Introduction

Plague, also known as the Black Death, is caused by *Yersinia pestis*, an animal-derived bacterium usually found on mammals and their fleas. In the past, if the disease is not treated, the transmission rate and mortality rate are very high, especially pneumonic plague, the fatality rate is almost 100%. Several great plague in the history of the world caused a large number of people to die. The first plague pandemic occurred in the 6th century AD, originating in the Middle East and centered around the near eastern Mediterranean. In 542 AD, it was spread to North Africa and Europe along land and sea trade routes through Port Said in southern Egypt, bringing disaster to almost all the famous countries at that time. The epidemic lasted for 50 to 60 years, and during the peak period, 10,000 people died every day, and the total number of deaths was close to 100 million. The pandemic led to the fall of the Eastern Roman Empire. The second pandemic, which began in the 14th century AD, rose and fell for nearly 300 years, spreading across Eurasia and the northern coast of Africa, especially Europe. Twenty-five million people died in Europe, a quarter of the population at that time. Half of the Italian and British died. At that time, the streets of London were littered with dead, rotting, smelly cats and dogs, which were killed as the cause of the plague. Without cats, however, rats, the true source of the plague, were much more rampant. By August 1665, 2,000 people were dying every week. A month later, 8,000 were dying. It wasn't until a big fire a few months later (known as the Great Fire of London) destroyed most of London's buildings, the rats disappeared, and the plague subsided. The plague pandemic was known historically as the Black Death.

The third pandemic began in the late 19th century (1894). It broke out suddenly and reached its peak in the 1930s, affecting more than 60 countries in Asia, Europe, America and Africa, and killing

more than 10 million people. The speed and extent of the spread of this pandemic far exceeds that of the previous two pandemics.

At early 18th century, the smallpox virus was ravaging Europe, and it was found that the introduction of human vaccination from the East seemed to cure the disease, but there was still a high death rate after vaccination, which attracted the attention of the great mathematician Daniel Bernoulli. When Bernoulli heard about the treatment of smallpox vaccination, he began to think about how to mathematically describe the spread of smallpox and the efficacy of vaccination. At that time, Bernoulli's idea was simple. He divided the population into the infected and the uninfected. The infected could either be cured and turning into uninfected, or die from the disease. Bernoulli's genius was to take into account the age of the person, that is, the time factor, and to build a mathematical equation based on the assumption that the cure rate of the disease was related to age of the studied population. After some calculation, Bernoulli concluded that vaccination, despite the risks, would statistically add about three years to life. Although in today's view, Bernoulli's research is not rigorous, the conclusion is obvious after smallpox inoculation technique in vaccines also almost disappeared, but Bernoulli was the first to try to use the data and the equation to analyze epidemic spread trend, control measures the effectiveness of the mathematician. This kind of scientific thinking was particularly valuable at a time when human beings were completely at the command of infectious diseases, and it is still the fundamental idea of studying infectious diseases with mathematical methods today. More than 100 years later, in the early 20th century, the mathematical modeling of infectious diseases took off, thanks in large part to Scottish army doctor William McKendrick and biochemist William Kermack. McKendrick served in India during a plague epidemic that killed hundreds of thousands of people. But unlike most doctors who study medicine, McKendrick put a lot of thought into mathematical equations, and found that the trend in the number of people infected closely resembled the curves of certain mathematical functions. On his return from India, he teamed up with biochemist William Kermack to analyze data on the number of cases and the number of days they survived, and eventually came up with a landmark model in mathematical epidemiology: the SIR model. Even today, most mathematical studies of infectious diseases have been based on this original SIR model.

In 1910, the plague first spread to China, causing a devastating disaster in the northeast, ranking the first among different kinds of infectious diseases. On November 16, 2019, a person from the Bayantalasum Quarry in Xilinguole League, Inner Mongolia Autonomous Region had repeated fever during treatment at Huade County Hospital in Ulan Chabu City. After consultation with experts, he was diagnosed as a confirmed case of bubonic plague. In this article, I have performed stability analysis and numerical simulation on the model to reveal the spread of the plague. The development trends are predicted, providing researchers with a theoretical basis for the plague epidemic, so as to seek reliable prevention and control strategies.

2. Literature Review

Research on infectious diseases has a long history, dating back to 1760. D. Bemoulh studied the transmission of smallpox W by establishing a mathematical model, which was the first case of studying the transmission of infectious diseases using mathematical models. About 150 years later, it was not until the early 20th century that the deterministic mathematical model for the study of infectious diseases emerged. In 1906, Hamier studied the repeated epidemics of measles by establishing a discrete time mathematical model. In 1911, Ross established a mathematical differential equation for infectious diseases in order to explore the dynamic transmission behavior of scar disease between mosquitoes and human beings. Until 1927, when Kmrnrk and MrKeidirik established the model of the infectious diseases of the famous SIR storehouse room, from 1665 to 1666 have been explored in London black death and the spread of the law of the plague, Mumbai in

1906 which is infectious disease model in the foundation which is the most classic models, their subsequent again in expanding SIS bin model was set up in 1932, put forward the determine whether infectious diseases epidemic threshold value theorem. The stochastic model of infectious diseases was first established by McKendrick[1] in 1927 and the subsequent stochastic model of infectious diseases began to be widely studied and developed rapidly. In 20th century, infectious diseases research development is rapid, releasing a large number of infectious disease model works. In 1998, Shulgin and Stone established an SIR determination model with the same birth rate and death rate based on the SIR model of seasonal changes.

In 2003, there is an outbreak of SARS in Beijing, China. Shi[2] constructed a discrete stochastic model of the dynamics of SARS transmission based on the tracking of the chain of infection of each patient, through which the process, characteristics and control factors of the evolution of the epidemic over time in a specific area could be understood. Under the same model parameters, the calculation of a large number of stochastic models helps people to estimate the best and worst cases and formulate countermeasures. Shi used data published by the Ministry of Health of the Chinese government at the time, including daily reports of confirmed and probable cases of SARS patients since April 21, 2003. Shi ultimately concluded that the impact of random uncertainties in the early stages of the epidemic was particularly significant. For example, under the same parameters, the results of different models randomly generated in the simulation of the SARS epidemic in Beijing can vary greatly, and the cumulative number of patients in the extreme model can differ by 20 times.

Pneumonic plague is listed as a leading "critical biological agent" by the Centers for Disease Control, but there has been little research on the subject. In December 2006, Massin[3], Legrand, Valleron and Flahault first developed a mathematical chamber model to describe the geographical and temporal transmission of pneumonic plague epidemics after use as a biological weapon, taking into account the average duration of incubation and transmission periods. Massin, Legrand, Valleron and Flahault developed a deterministic chamber model to study the geographical and temporal transmission of pneumonic plague after aerosol release. Massin, Legrand, Valleron and Flahault then carried out univariate and multivariate analyses to assess the key parameters for controlling the outbreak in France and concluded that a reference scenario of 1000 index cases in Paris would have resulted in 2500 deaths if intervention had been introduced 10 days after the attacks. And the findings suggest that rapid initiation of interventions has the greatest impact on the eventual size of the outbreak, followed by the wearing of masks, preventive treatment of contacts, and isolation. Massin, Legrand, Valleron and Flahault found that limiting mixing between areas had little effect on reducing casualties, although it did limit casualties to one area.

Since the first case was confirmed in Mexico in March 2009, the pandemic has spread around the world. As of March 31, 2010, China has reported more than 127,000 confirmed cases of H1N1, with 800 deaths. In June 2011, Yang[4], Li and Zhu started from the classic SIR model and established a differential equation model suitable for A (H1N1) influenza after considering factors such as isolation, immune capacity after cure, migration and prevention and control factors. Then Yang, Li and Zhu used the Jacobian matrix to analyze the stability. In addition, considering the characteristics of "poor" data information, after simplifying the model, numerical simulation is carried out by combining the estimated data parameters of June 13, 2009 solstice and November 15, 2009. Finally, Yang, Li and Zhu analyzed the results and suggested that the spread of H1N1 should be suppressed by means of isolating the sick people as much as possible, improving medical treatment and reducing exposure rate.

In June 2009, Pu[5] first divided the population into six chambers and considered factors such as the density of the susceptible population and the mortality rate and cure rate of the patients to establish a new dynamic model to describe the SARS epidemic. In addition, according to the statistical data obtained during the PU modeling, the cured patients have immunity and the disease has an incubation

period. Then PU solved and analyzed the model and proved that the disease elimination equilibrium point of the model was globally stable under certain conditions, while the endemic disease equilibrium point was not asymptotically stable. At the same time, it was obtained that the model was permanently sustainable under appropriate conditions. Finally Pu summarized the model was very simple and limited, for example in assuming that the contact rate and mortality as a constant, in fact these parameters and the distribution characteristics of infected people is concerned, population distribution, contact rate is not the same, Pu facilitated the discussion of mathematics to simplify the related factors.

In August 2013, Green[6], Piper, and Keep discussed the application of microsimulation models of joint attacks, using plague and smallpox as examples. Green, Piper, and Keep also investigated possible interactions between people infected with the two diseases, and their impact on the spread of the disease and the number of deaths. The simulation involved 1,250 people and was based on NSW household and work statistics. Green, Piper and Keep then ran a series of simulations and concluded that the two substances were released simultaneously. Compared with smallpox, plague was introduced 0 d later and 35 d later, respectively. Green, Piper, and Keep also investigated the strength of the interaction between smallpox and plague deaths. The results are complicated because the death toll depends on the delay in the release of the plague and varies according to the number of people who infect them through the active release point. Green, Piper, and Keep argue that using microsimulations has advantages because there are many human factors that affect control delays, so the size of any epidemic can be easily incorporated into the simulation without affecting the rest of the simulation.

Dengue fever is a contagious viral disease in humans that is endemic in parts of Central and South America, Africa, India and Southeast Asia. Recent estimates indicate that there are several hundred million new infections worldwide each year. In January 2015, Lucas[7], Daniel and Stefanella developed a rather interesting SIR simplified model for studying the impact of population mobility on disease epidemics. In particular, when the model is used as a simplified version of dengue dynamics, local infection parameters express environmental attributes. Lucas, Daniel, and Stefanella also did not consider the incubation period of dengue fever in humans or mosquitoes in their model. Lucas, Daniel, and Stefanella then performed a stability analysis of the model and calculated the basic number of rebirths and deduced that introducing an infected individual into a non-patient population resulted in, on average, more than one secondary infection. Lucas, Daniel and Stefanella then used MATLAB to run numerical simulations based on dengue data from the city of Rio de Janeiro during the 2008 epidemic. In addition, Lucas, Daniel and Stefanella introduced a Gauss-like time-varying infection parameter to simulate the climate change of the city in one year (especially the impact of seasonal climate change), and got a better fit.

At the beginning of the 21st century, the outbreak and spread of SARS has brought a great impact on China's economy and people's life. Li[8] have gained a lot of experience and lessons from it. Li realized the importance of quantitatively studying the law of the spread of infectious diseases and creating conditions for the prevention and control of the spread of infectious diseases. In terms of epidemic control and disease prevention and treatment measures, there is still no more effective prevention and treatment method in medical treatment at present. Therefore, the most effective method is "early occurrence, early separation, early treatment", namely to prevent and control mainly. Li concluded from the constructed model that the number of cases would increase exponentially without considering the limit of the period of infection, and the change after the period of infection would deviate from the exponential growth and the growth rate would slow down. That is to say, this model has good applicability for the early stage of disease and has certain reference value, as the disease spreads. Finally, Li validated the model and commented on it. Taking the outbreak in Beijing as an example, taking April 30 as a base point, the duration of K value will be smaller if the quarantine

measures are taken in advance. In addition, Li stressed that our prevention and control measures need to be further developed to make them better and more reliable.

On April 25, 2018, Zhang[9] introduced the research background and significance of infectious disease models and the status quo of infectious disease prevention and control in China. Then Zhang introduced two models, one is a deterministic SIR model in the form of ordinary differential equations, the other is a stochastic SIR model driven by the birth and death process, and gave two methods to calculate the basic regenerative number. Compared with the determined SIR model, the stochastic SIR model takes into account the randomness and contingency in the transmission process of infectious diseases, and the state transfer is 'one' as the human unit, which is more reasonable in deconstructing the transmission process of infectious diseases. Stochastic SIR model can flexibly estimate parameters by using a variety of methods like maximum likelihood and least squares. Subsequently, Zhang proved that the mean value of the stochastic SIR model is equivalent to the deterministic SIR model after ignoring the covariance term, and briefly explained the rationality and superiority of the stochastic SIR model. Finally, Zhang used the real data after the outbreak of influenza to estimate the parameters using the least square method, and briefly explained the advantages of the stochastic SIR model in the calculation of the basic regeneration number and epidemic prevention and control.

In March 2019, Song[10] studied the reaction spread model of SIS infectious diseases with Neumann boundary conditions to characterize the basic reproductive number. If the basic regenerative number is less than 1, then the disease-free equilibrium is globally asymptotically stable; if the basic regenerative number is greater than 1, then the disease-free equilibrium is unstable. Then Song mainly studied the existence of the endemic equilibrium, using the implicit function existence theorem, eigenvalue principle, comparison principle, maximum principle and other methods to study the existence of the endemic equilibrium. Then Song studies the non-negative equilibrium solution of the system, characterizes the basic regenerative number of the system, and defines the variation expression of the basic regenerative number and its properties. Finally, the existence and uniqueness of the disease-free equilibrium were discussed, and the relationship between the basic reproduction number and the stability of the disease-free equilibrium was discussed. In addition, Song considers the influence of different risk domains on the stability of equilibrium solution under the condition that the diffusion coefficients of susceptible and infected persons are equal.

In March 2019, Qiu[11], An and Qi, in order to further explore the transmission laws of various epidemics and their relationship with prevention and control measures, established the dynamic difference equation of the transmission of infectious diseases through mathematical modeling and the transmission dynamics method to simulate the transmission laws of diseases. In the differential equation, Qiu, An and Qi divide the population into five categories: confirmed patients, suspected patients, cured patients, dead people and normal people, and give the relationship of mutual transformation among different patients. Subsequently, Qiu, An and Qi took A flu as an example and used MATLAB to conduct computer numerical simulation under different isolation intensities to obtain the development trend of disease transmission. The conclusion is that the number of confirmed cases and deaths is highly sensitive to the isolation intensity p , and the stronger the isolation intensity, the less confirmed number of cases and deaths. When the isolation intensity is less than the critical value $P \leq 52\%$, the epidemic will be out of control. Qiu, An and Qi also stressed improving China's infectious disease case reporting system, constantly detecting the epidemic and sharing data to provide reliable data for researchers.

In April 2019, Yuan[12] studied three groups in total. First, she introduced the research background and significance of the infectious disease model and the research status of transmission dynamics on complex networks. Secondly, Yuan built an improved SIRS infection model based on complex networks by considering such factors as population characteristics and the direct

transformation of infected individuals into susceptible individuals. The global dynamics of the equilibrium point is studied by Jacobian matrix method and Lyapunov function method. At the same time, the effects of the three immunization strategies are also discussed. Finally, the theoretical results are verified by numerical simulation. In addition, Yuan also studied a class of SIRS infectious diseases based on the weight network, obtained the basic reproduction number, provided the unique condition for the existence of the endemic disease equilibrium and proved the global asymptotic stability of the disease-free equilibrium. The persistence of the system is also studied and our results are verified by numerical simulation.

On May 24, 2019, Xu[13] first introduced the literature review of infectious disease research, and then described the research framework of this paper and the basic introduction of relevant knowledge. Then Xu introduced the SIR model of infectious diseases, including the SIR deterministic model and the SIR stochastic model, and introduced the basic properties of the model, the basic reproduction number and the threshold theorem in detail, and proved the relationship between the deterministic model and the stochastic model. Then Xu introduced the basic method of parameter estimation used in the empirical part - the least square estimation method. In the part of empirical analysis, Xu made empirical analysis and fitting of the SARS epidemic in Hong Kong on February 21, 2003, June 11, 2003, and used different models for fitting analysis. The whole SARS epidemic was divided into two stages. In stage II, the SIR determination model and the SIR stochastic model were used for parameter estimation and fitting respectively, and the results of parameter estimation and fitting were compared. In Stage I, the Logistic model was used to describe and analyze the whole process of SARS. Finally, some model applications were given.

On June 10, 2019, Yang[14] briefly introduced the background of tumor immune system and IVegs-mediated tumor immune escape, the current research status of tumor growth models and tumor immune system interaction models, and the basic concepts and theories of ordinary differential equations. Then Yang gave and studied A mathematical model of the tumor immune escape mechanism mediated by Tregs, a regulatory T cells. Yang constructed a four-dimensional model to study the dynamics of the interaction between immune cells and tumor cells by dividing the immune cell population into three categories: helper T cells, effector cells and Tregs. In terms of scientific behavior, the existence and stability of the model's tumor-free balance point and the tumor-free balance point were discussed. Yang did a branch analysis of some important parameters through numerical simulation. Then Yang constructed a tumor immunotherapy model. Yang considered three immunotherapies: adoptive T cell immunotherapy, monoclonal antibody immunotherapy and combined immunotherapy, and discussed the impact of these three immunotherapies on tumor growth and their efficacy. Finally, Yang concluded that the results of the study can help people better understand the role of Tregs in tumor immune escape, and provide scientific basis and theoretical support for immunotherapy.

In October 2020, when COVID-19 broke out all over the world, Manuel[15] and Asier first described and explained an epidemic model. Although the Logistic Stee equation, Malthusian parameters and parameterized load-capacity parameters are all time-varying in general, then the model is applied to COVID-19 popular by using some recorded data. Among them, Malthusian parameter is related to the growth rate of infection solution, and the carrying capacity is related to its maximum reachable value. In the simplest epidemic model, the quotient between the absolute value of the Malthusian parameter and the carrying capacity determines the rate of transmission of the disease. Thus, Manuel and Asier argue that the logical version of the pandemic description is attractive because it provides a simple explanation of the evolution of the data, especially during the outbreak of a pandemic. The SIR model built by Manuel and Asier includes recruitment, demographic and mortality parameters. Manuel and Asier also discuss numerical simulation examples.

3. Methodology

Assume in time t , the number of susceptible population $S(t)$,

Assume in time t , the number of infective people $I(t)$,

Assume in time t , the number of removed people $R(t)$.

Based on the above three assumptions, the classical SIR model is expressed by the differential equations as follows:

$$\begin{cases} \frac{dS}{dt} = -\beta SI \\ \frac{dI}{dt} = \beta SI - rI \\ \frac{dR}{dt} = rI \end{cases}$$

β : vulnerable people become infected people at a rate of β .

r : infected people recover at a rate of r .

On the basis of the classical SIR model, we additionally consider the birth rate of the population, recorded as a . We assume that the new born population is healthy. Therefore, we can give an SIR model with born rate a .

$$\begin{cases} \frac{dS}{dt} = -\beta SI + aS + aI + aR \\ \frac{dI}{dt} = \beta SI - rI \\ \frac{dR}{dt} = rI \end{cases}$$

On the other hand, we give an SIR model of the transmission of the disease in mice.

Assume in time t , the number of healthy mice $E(t)$,

Assume in time t , the number of dying mice with infectivity $D(t)$,

Assume in time t , the number of dying mice without infectivity $F(t)$.

$$\begin{cases} \frac{dE}{dt} = bE - \alpha ED \\ \frac{dD}{dt} = \alpha ED - nD \\ \frac{dF}{dt} = nD \end{cases}$$

b : healthy mice were born at a rate of b .

α : healthy mice become dying mice at a rate of α .

n : remove the died mice without infectivity at a rate of n

Finally, we consider the cross-infection of the disease between mice and humans, and we give a double-SIR model, which describes the transmission of the disease.

$$\begin{cases} \frac{dS}{dt} = -\beta SI + aS + aI + aR - cSD \\ \frac{dI}{dt} = \beta SI - rI + cSD \\ \frac{dR}{dt} = rI \\ \frac{dE}{dt} = bE - \alpha ED - mEI \\ \frac{dD}{dt} = \alpha ED + mEI - nD \\ \frac{dF}{dt} = nD \end{cases}$$

c : susceptible people contact with dying mice at a rate of c .

m : infected people contact with healthy mice at a rate of m .

In order to describe the mathematical model of the dynamic behavior of this type of infectious disease, the total population needs to be divided into three categories: susceptible, infected and recovering. The recovering person will not become susceptible again, because the recovering person is no longer involved in the spread of the disease. Sometimes the remover is also called the expatriate. This is the SIR model of infectious disease dynamics. Based on this model, I added new parameters such as the birth rate of the population (and assuming that people born with immunity), normal people and disease. It belongs to the infection rate of contact, and the infection rate of normal mouse and patient contact, so I constructed my model.

4. Algorithm

```
Function dy=df1(z, y)
```

```
dy=zeros (6,1)
```

```
dy (1) = $\beta$ *y (1) *y (2) +a*y (1) +a*y (2) +a*y (3)-c*y (1) *y (5);
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```
dy (2) = $\beta$ *y (1) *y (2)-r*y (2) +c*y (1) *y (5);
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```
dy (3) =r*y (2);
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dy (4) =b*y (4)- $\alpha$ *y (4) *y (5)-m*y (4) *y (2);
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```
dy (5) =- $\alpha$ *y (4) *y (5)-m*y (4) *y (2)-n*y (5);
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dy (6) =n*y (5);
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5. Conclusions

This article first introduces the research problems of the Inner Mongolia pneumonic plague based on the SIR model in detail, and secondly introduces the source of the plague, the time of the plague outbreak in history, the source of the SIR model, and how people connect the SIR model and the plague together. There is an optimization process of the SIR model. Then, on the basis of the SIR model of infectious disease dynamics, I added the birth rate of humans, the rate of mutual infection between mice and humans, and finally I established a double SIR model of two-way infection. Then I used MATLAB to the differential equations are encoded and the corresponding images are obtained. There are still many shortcomings in this article. The first is the coefficient estimation. Since there has been no large-scale plague outbreak in recent years, I cannot find useful data for numerical simulation. For plague data, I will use the least squares method to estimate the coefficients in the model and run the code to generate the changing trend of the epidemic. Secondly, I want to use the Logistic model to characterize the analysis, simulate the changes of the infected person over time during the period, and the results are analyzed, and specific epidemic prevention and control measures are given. Finally, in the future universities, I hope to model and analyze covid-19, and realistically consider every influencing factor such as the incubation period of the epidemic, secondary infections, etc. Use logistic regression method for data analysis, then use MATLAB to plot the data of different countries, and finally emphasize the significance of the model again.

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