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Mathematical Modeling of Novel Influenza Applying Contact Network Technique

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Abstract: The papers will analyze the complex Bio-mathematic model of novel influenza epidemic and determine its stability property by using the popular MathLab/Simulink software and relative software packages. In the recent year, the Bio-mathematics has become the main important trend of research direction which has applied to the epidemic models of disease mechanism, spreading regulation, and strategy of disease preventing in the field of medical and public health. In order to simulate the transmissions of vector-borne diseases and discuss the related health policies effects on vector-borne diseases, we combine the multi-agent-based system, social network, mirror identity concept, and compartmental model to develop an epidemic simulation model. In the identity level, we use the multi-agent-based system and the mirror identity concept to describe identities with social network features. In the vector level, we use compartment model concept to describe the vector populations and the transmission between populations. We will try to constructing epidemic dynamic system model and applying contact network technique to novel Influenza to find the quarantining parameters which are the most important factors to control epidemic situation. The results of experiment by numerical analysis may offer some prevention with reference to control epidemic situation of novel influenza.

Keywords: Bio-mathematic, Influenza, Social Network.

1 Introduction

Most of the human virus is not immune to the new force, because it can result in a short time a large amount of infection and death, making the entire healthcare system paralysis, the production line stopped, and caused public panic and not a very safe feeling. Twentieth century has occurred a total of three times current line infection pandemic, the most serious in years 1918 to 1919 the Spanish influenza infection caused by the impact of the line, not in just one year of time to cause about 40 million people, far more than the four years between World War I, the total number of deaths [2]. Influenza is considered the most potential pandemic infectious diseases [1]. As the influenza virus itself in the replication process is very easy to produce variance, with influenza virus type A virus with many variants and has to survive in different species, the body's ability, so it does not but cannot be completely eliminated, and can be taken between the hybrid viruses produced new strains of the virus, triggering a global pandemic. We called the new flu, refers to this may cause a pandemic of influenza viruses. To everyone close attention to the H5N1 avian influenza virus as an example: it was originally only in birds spread between the influenza virus, but in the 1997 Hong Kong's first degree has occurred of human infection with H5N1 avian influenza virus and the death of Case, 2003 and again degree spread Case of Human infection, So far the epidemic continued to spread (based on World Health Organization statistics, as of August 9, 2006 date, 236 have been produced In order to celebrities such type of avian influenza disease, of which 138 such patients have died). Current mode of transmission of H5N1 virus in birds is still limited contact between human beings and caused infection. But public health experts are worried that the H5N1 virus for re-variance and can be effectively transmitted between people, influenza pandemic of the plight of the possible occurrence of a further degree [3,4].

We will try to applying contactnetwork technique to novel Influenza and constructing epidemic dynamic system model to find the quarantining parameters which

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are the most important factors to control epidemic situation. The results of experiment by numerical analysis may offer some prevention with reference to control epidemic situation of novel influenza. Use mathematics in methods to understand the spread of the disease, can be traced to 1760 years using the mathematical methods used in infectious diseases on the pioneer David Bernoulli, he used mathematical applications on against smallpox this disease research , until 1927 one of the most famous now also applied quite widely used model is proposed that the Kermack-McKendrick's mathematics in SIR model [5], this basic model assumes a closed population, the total population number does not change case the population is divided into three types, not infected with S (Susceptible), infection I (Infected), restore the population R (Recovered), representatives of non-infected person infected by the disease but it cannot be infected, but infection is have been infected with the force of infection and ethnic groups, ethnicgroups that have been restored from a restore in case of infection, and disease immunity. Because according to the characteristics of different diseases, but also raised several other models. Some diseases have incubation period, although the infection was infected but did not have the ability, to join In order to latency groups E (Exposed), while SEIR model, two types of SIR and SEIR models of analog comparator, and the nonlinear effects caused by different can refer to [5]. And if the illness did not take long after the time of immunization, as this type of disease was restored after they did not become infected, the SIS model, etc.

2 Epidemiological SIR Models.

The most widely used method is called by Kermack and McKendrick in 1927, The development of the SIR model (Figure 1.), is a typical differential equation system, all individuals of the whole society is divided into three sub-groups, and a set of differential. The equation is the future of individual mobility between ethnic groups to follow the child dynamic process: S (susceptible) on behalf of groupsvulnerable to infection, denotes the population of individuals susceptible to infection, but not sick; I (infected) on behalf of infectious population, denotes population of individuals infected with diseases not only in itself, but will spread to other trading infected persons; R (recovery) denotes the population, that is, groups of individuals have recovered or are no longer infectious ability (or dead).

(1)

Eq.(1) γ is the infection rate, δ is the removal rate, and N is population size.

The traditional concept of a simple SIR model, but also simplifying many problems for the spread of disease to explore the threshold value, and the simulation calculation

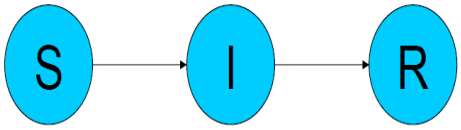


Fig. 1: SIR epidemiological model

of the required resources and time spent little. However, this model has two disadvantages:

1. The concept of the lack of social contacts, in the SIR model, the contact between any two individuals with the same probability, however, in reality, only individual regular contact with the crowd in a small part of society, while the vast majority of people rarely or Absolutely have no contact.

2. SIR Model for the transmission of the disease can only be regenerated to a disease rate (R_0), can not understand the dynamics of disease transmission, but also can not be discussed in depth by SIR model to compare the infection or the denial of the effectiveness of policies.

Mathematical problems concerning infectious diseases is one of the most useful threshold parameters and sometimes referred to as a rate or ratio. It is widely used in mathematical epidemiology models. The basic reproduction number denoted as , is the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual [1,2]. It was obtained that the basic reproduction number determining whether the disease becomes endemic. is simply the product of the infection rate and the mean duration of the infection. If $R_0 < 1$, then on average an infected individual produces less than one new infected individual over the course of its infectious period, and the infection cannot grow. Conversely, if $R_0 > 1$, then each infected individual produces, on average, more than one new infection, and the disease can spread in the population. For the case of a single infected compartment.

3 Simulate the Spread of Disease and Contact Network.

Simulate aspects of disease transmission, the first to be made ahead, is the most widely used, convenient storage compartment model is the so-called (Compartmental Model). In this model, all individuals according to their disease state is divided into certain sub-groups, and the number with the letter to denote the number of sub-groups of individuals. Then using of differential equations to describe the function of the number of changes and the relationship between the number of letters Contact relationships between individuals, in essence, be seen as a network, so we use the Contact Network ,The term representative of the future spread of the virus in the community when they rely on

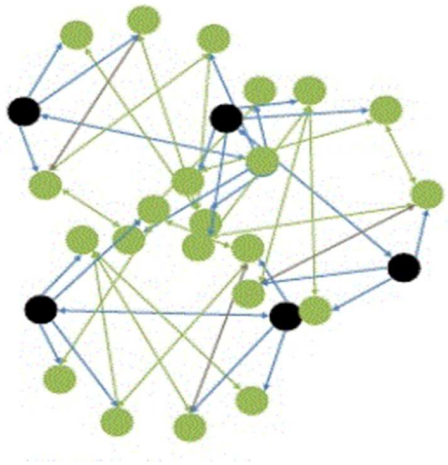


Fig. 2: Social network model

interpersonal contact with ties. And how to construct a catenary line with real-world network, In order to facilitate the researcher into an important issue.

As the real world of catenary road in the construction of the time required a large amount of human investigation, and sampling process is also often have a bias, so to establish a sperm does a catenary road is almost a not possible, Therefore, researchers start with some simple convenience network to explore the network structure and some properties of the network dynamics of the spread of disease. Computer simulation will be MatLab / Simulink simulation and other related ancillary software, so software is a very powerful numerical simulation software, not only very strong in numerical analysis, the use of its epidemic, the establishment of a variety of reaction dynamics mathematical model of novel influenza, Find the best of its prevention and control strategies for the prevention and treatment decision-making theory and quantitative basis [10]. The paper will be updated in addition to the micro perspective to take into account the interaction between the individual and the individual, not only the real situation more closely, but also enables more subtle research, and to network-based Model, it is to focus on the individual and the individual links between the major research methods and impact, a simple social network model of the basic concepts as to each individual on the network as each point, between the individual and the individual If the existence of a relationship, for example: this time is the same place, we link the next link two points (individuals), the joint statement of the relationship may be expressed as a signaling communication links, disease transmission and so on.

Social network theory views social relationships in terms of ties and nodes. Ties are the all-important relationships or connections between them, and Nodes are the entities within a network. Entities may be individuals, businesses or organisations. That any two people on the planet are linked to each other by only six ties, on average., we can give more properties representation, such as: disease status, immune competence ... and so on, so more light can be achieved easily in the setting of individual differences, this is also the network model and the traditional SIR model is the biggest difference. Model of the joint between the midpoint and end point that has a relationship between individuals, if the AIDS analog speaking, this link may be representative of the relationship between or shared needles, if the existence of links between individuals, the disease may be passed to another individual, if the SARS simulation speaking, this link represents the two individuals in close geographic or location away from a contact. In each unit time or the status of each individual property are likely to change, and change the rules according to their original status of the nearby state of the individual or the link between a state and so on.

In epidemiologics R_0 is a very important parameter, the parameter definitions and establish ment are made without a structural model. In other words, this parameter did not include the geometric concept, due to the parameters are built up in a mathematical form, which is defined as the fact that the infected, was a first time infection, caused by the second infection, the average population quantity. And this definition may understand disease in infected people stays, and the relationship of the size of the rate of infection how long leads to the number of infections produced by him. This concept is essentially the next word in the life of a parasite that can produce the average number of successful offspring. In this regard, the introduction and information can refer to [9]. When $R_0 > 1$, this disease will have spread of disease and the outbreak of the phenomenon. In SIR model type R0 is expressed in mathematical formula (2).

$$R_0 = \beta/\alpha \qquad (2)$$

The premises of β is the infection rate, α is a restored rate, essentially the basic reproductive number is the infection rate divided by the restored rate.

Small world network is a Watts and Strogatz proposed network structure, it has two important properties, high clustering and low degree of segregation level, these two properties are important to modern society characteristics. High level of expression of clusters is the reality of society, close relationships, this close of Rapoport's triangle is closed (Triadic Closure) the concept of, for example: when A and B are Know C, then A and B are also likely knowledge of each other. The knowledge of each other order for people to form a closer relationship between the groups (such as one family, or a group of very good friends), and in this relationship more closely within the population, the relationship between people is a strong link. Low separation level of expression is a "small world" concept, which is the Milgram proposed six degrees separated; society any two individuals in interpersonal distance of only about 6; than we thought

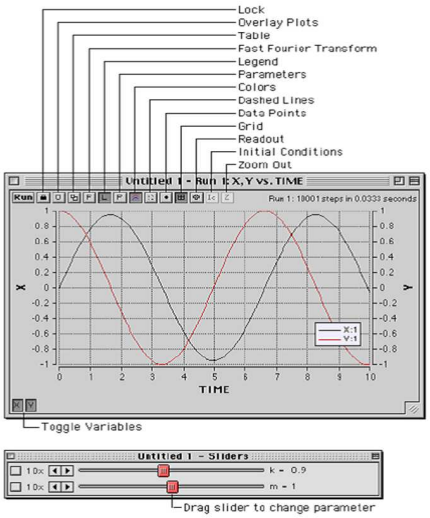


Fig. 3: Adjust the size parameters, graphical changes in the results.

but also the future too short. Watts and Strogatz's model to explain through them this phenomenon. They found that as long as a regular network by adding a small portion of the long-distance links, enables to greatly reduce the separation of the whole network level. Of these long-distance links, corresponding to the real life that is so-called weak links, such as more regular contact is not friends or distant relatives.

4 Mathematic Models Based on Matlab to Simulation Platform

A simulation platform of mathematic dynamics model is developed by using Matlab. The simulation platform can be used in dynamics simulation of epidemic dynamics modeland the simulation could be used in results analysis. The software is a very powerful numerical simulation software, not only very strong in numerical analysis, the use of its tuberculosis epidemic, the establishment of a variety of reaction dynamics mathematical model of novel influenza.The software is the fastest, most convenient tool for solving differential equations, the relative price inexpensive, and can run on Windows systems, widely used in academic and commercial institutions as a mathematical model to establish research and teaching tool. The first equation with dynamic behavior of advanced parameter setting [10]:

After setting, press Run, the system immediately computed results of the differential equations, and draw diagram types in the Fig 3. Size by adjusting the parameters, but also observe the changes in graphics [10].

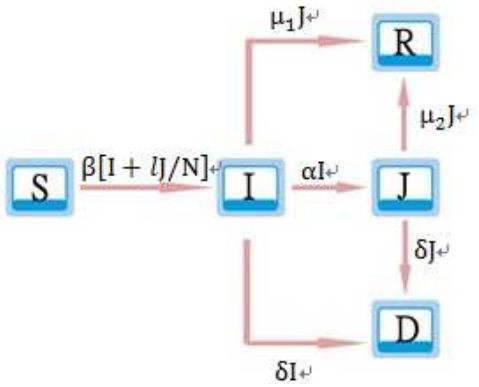


Fig. 4: SIJR model

5 Construct New Theoretical Model and Simulation of an SIMR

Mathematical model of the disease stage of development is still ongoing, and some mechanisms of infectious diseases present the possibility of overturning later scholars, up to now hence there is still. As time for a new derivation the models of this study are built on top of these two models, one is Chowell, PhD, published SIJR model (Fig 4).These two models are given in the year that the SARS outbreak arose [12].

$$\begin{cases} \frac{dS}{dt} = -\beta\left(I(t) + lJ(t)\right) \\ \frac{dI}{dt} = [\beta - (\alpha + \mu_1 + \delta)]I(t) + l\beta J(t) \\ \frac{dJ}{dt} = \alpha I(t) - (\mu_2 + \delta)J(t) \\ \frac{dR}{dt} = \mu_1 I(t) + \mu_2 J(t) \\ S(0) \approx N(0), I(0) \approx 0, J(0) = R(0) = 0 \end{cases} \quad (3)$$

This model is obtained, from the SEIR model by Aron et al (SEIR model is derived from the SIR model), in this model N = S + I + J + R, E is infected yet still latency diseases. The number of asymptomatic, called latent; J indicates the number of confirmed cases, namely, the number of being diagnosed; S1 and S2, are not vulnerable to infection and vulnerable to infection are not infected two people respectively, S2 is less susceptible to infected people, whose value is p; q is no symptoms yet having the potential proportion of contagious; k is the proportion of patients becoming latent, l for the isolation rate; α is the proportion for patients to be diagnosed and being diagnosed; the μ is divided into two parts $\mu 1$ and $\mu 2$; $\mu 1$ expressed by the patient recovered as immunization, the proportion, and $\mu 2$ is the proportion of immune persons recovered by the diagnosis; other parameters are the same as the previous model introduced, will not be detailed [15].

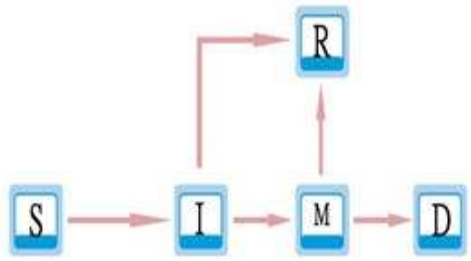


Fig. 5: SIMR model flow chart

A new theoretical model is constructed. It is derived from the SIJR model, tentatively called the SIMR. Because the treatment is not completely, wrong treatment, and other diseases (such as HIV/AIDS) co-infection, the patient in SIJR model is replaced Multiple drug resistant patient. M (Multiple drug resistant) is resistant strains represents the total number of infected patients, and in unit time t, the number of patients with resistant strains are denoted by M (t). γ denotes the ratio that a potential patient (infected by Mycobacterium tuberculosis but not contagious) disease complicated as those who (by Mycobacterium tuberculosis infection but infectious), but I means that these people are TB patients. TB is a still prevalent in the world, especially in the undeveloped and developing countries, chronic diseases, it is caused by the Mycobacterium tuberculosis infection in the initial infection, approximately 95% of people will heal themselves because of their immunity, and self- more, but there will be lifelong re-activation (Reactivation) potential danger, and only 5% of people infected with TB may at first by the spread of blood or lymph fluid caused by pulmonary or TB meningitis. Therefore, μ in the model as with the SIJR is divided into two parts M1 and $\mu 2$; $\mu 1$ is the rate expressed in units of time t, caused by the general TB patients recovered into immune. However, $\mu 2$ is the rate in unit time t, the TB complicated by drug-resistant patients, recovered as immunization, the death rate of TB patients is almost 0 as the above, the dead are almost all drug-resistant patients given anti-TB drugs or improper treatment of patients, so δ in unit time t, the rate of disease mortality is not necessary as μ and δ in the SIJR model which is divided into two parts for discussion. $l$is the isolation rate, one thus obtains the flow chart of the SIMR model (Fig 5) [13].

When M (t) is obtained, it will be able to obtain $D(t) = \int_0^t \delta M(\tau)\, d\tau - D(0)$When I (t), M (t) is obtained, it will be able to obtain $S(t) = \int_0^\tau -\beta[(\tau) + lM(\tau)]\, d(\tau) - S(0)andR(\tau) = \int_0^\tau [u_1 I(\tau) + u_2 M(t)]\, d\tau - R(0)$, thus, we only analyze model (4)

$$\frac{dM}{dt} = \gamma I(t) - (u_2 + \delta) M(t) \qquad (4)$$

If the parameters of linear systems (4) are greater than 0, and less than or equal to 1, the eigenvalues of the coefficient matrix A are $\lambda_1 \lambda_2$ different real numbers; in addition

a. If $D_1 + D_2 - \beta > 0$ and, $D_1 D_2 - \beta D_2 - l\gamma\beta > 0$
b. If $D_1 + D_2 - \beta > 0 D_1 - \beta > 0$
and $D_1 D_2 - \beta D_2 - l\gamma\beta > 0$then $\lambda_2 < 0 < \lambda_1$
A characteristic polynomial

$$p(\lambda) = d\,|et\,(\alpha - \lambda_2) = \begin{pmatrix} \beta - D_1 - \lambda \\ \gamma \end{pmatrix} \begin{pmatrix} l\beta \\ -D_2 - \lambda \end{pmatrix}$$

Have two characteristics value

$$\lambda_{1,2} = \frac{-\left(D_{1+D_2-\beta}\right) \pm \sqrt{(D_1 + D_2 - \beta)^2 - 4(D_1 D_2 - \beta D_2 - l\gamma\beta)}}{2}$$

of which the λ_2 table is the loser.

The compounded characteristic value $\lambda_2 \lambda_1$ is meaningful, therefore$\lambda_2 \neq \lambda_1$.

Through the calculation of the available matrix A eigenvalues $\lambda_2 \lambda_1$ only the $\lambda_2 < 0 < \lambda_1$, or $\lambda_2 < \lambda_1 < 0$ of both cases, are proved.

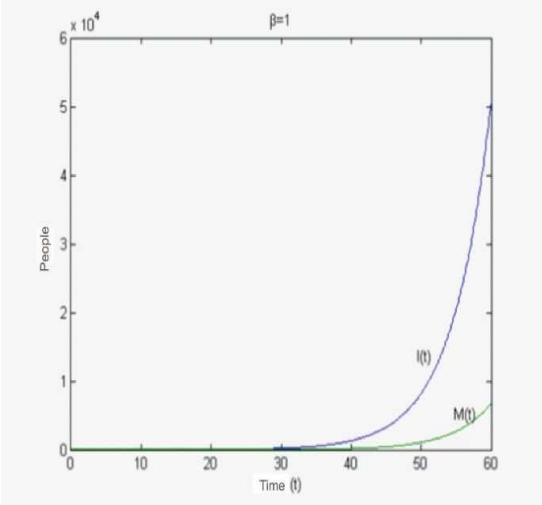
Eigenvalue $\lambda_2 \lambda_1$, there is a positive real number in the$0 < \lambda_1$, then the epidemic will spread.
If the characteristic value $\lambda_2 \lambda_1$ of two non-positive real numbers is $\lambda_2 < \lambda_1 < 0$, then the epidemic will be controlled

When the only change is in the value of β, we calculate the eigenvalues and its graphics for comparison:
When $\beta = 1$, $(\lambda_1 \lambda_2)$approximation: (0.1825, -1.0825)
When $\beta = 0.7$, $(\lambda_1 \lambda_2)$approximation: (-0.1230, -1.0770)
When $\beta = 0.4$, $(\lambda_1 \lambda_2)$approximation: (-0.4338, -1.0662)
Of $\beta \to 0$, $(\lambda_1 \lambda_2)$approximation: (-0.7677, -1.0323)

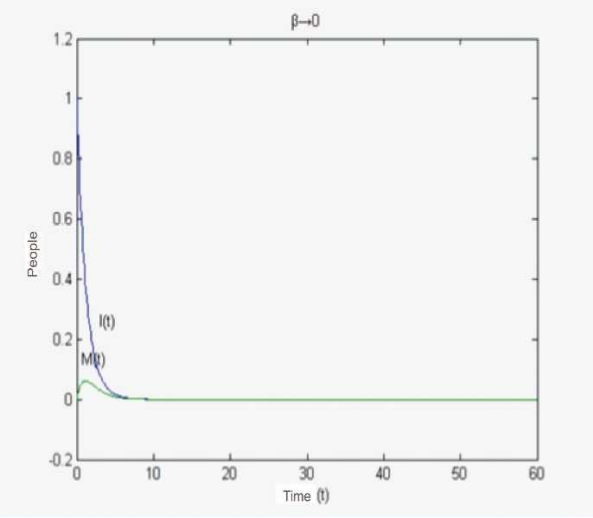
It can be seen that when $\beta$is less than 0.7, the I (t) and M (t) decrease with the increased t, can be seen by the infectious diseases there is no proliferation of opportunity; When$\beta = 1$, I (t) and M (t) with increasing t is increased, indicating that the epidemic will continue to spread, so the βcontrol can not be greater than 0.7.

When the only change is in the value of l, we calculate the eigenvalues and its graphics for comparison:
When $l = 1$, $(\lambda_1 \lambda_2)$approximation: (0.0199, -1.0799)
When $l = 0.7$, $(\lambda_1 \lambda_2)$approximation: (-0.0156, -1.0444)
When $l = 0.4$, $(\lambda_1 \lambda_2)$approximation: (-0.0538, -1.0062)
Of $l \to 0$, $(\lambda_1 \lambda_2)$approximation: (-0.1085, -0.9515)
Evident when $l$is less than 0.7, the I (t) and M (t) with the increase of t close to zero, can be seen by the infectious diseases there is no proliferation of opportunity; and $l = 1$, the I (t) and M (t) will rise with the increase of t, indicating that the epidemic will continue to spread.

Model analysis and conclusions:

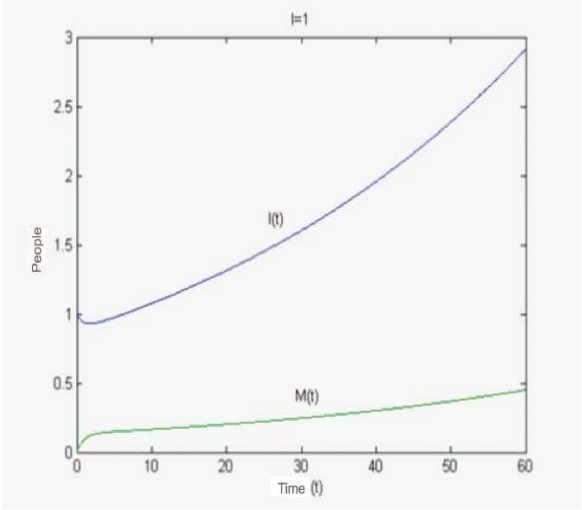


(a)

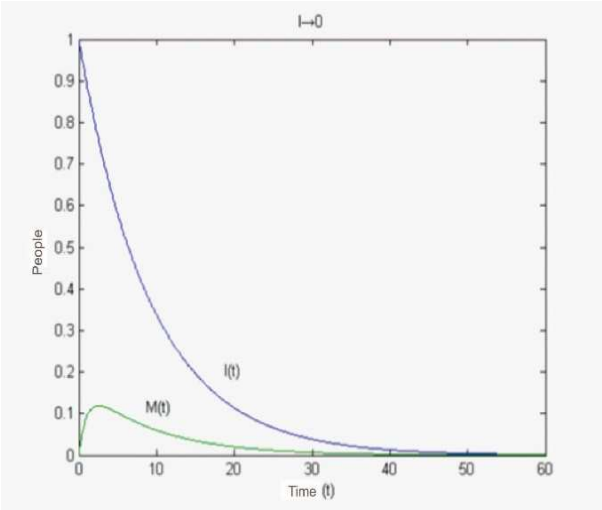


(b)

Fig. 6: (a)when β is 1, I (t) and M(t) will increase with rising t , suggesting the epidemic will continue to spread.(b)when β is 0, I(t) and M(t) will decrease with rising *t*.



(a)



(b)

Fig. 7: (a) when l is 1, I (t) and M(t) will increase with rising t. (b)when l is 0, I (t) and M (t) will increase of t close to zero.

1.A computer simulation, conducted through the calculation of eigenvalues $(\lambda_1\lambda_2)$ can distinguish the future of the variations of the epidemic.
2.A lower infection rate(β), means the epidemic can be controlled.
3.Improve the therapeutic ratio (u_1u_1) and enhance the isolation rate (*l*lower for treatment (u_1u_1) close to 0) in order to control the epidemic, and obtain better results, thus, there is a similar infectious disease, with an isolation rate(l) able to control the epidemic.

6 Conclusions

In this study, we have established more realistic models of Novel influenza with a variety of factors. via theoretical analysis, data processing, as well as computer modeling to predict the future trend of the new influenza. In order to find the best treatment and control measures, we need to provide a quantitative basis so that the dynamics of infectious diseases play a key role in disease prevention and control. Besides, the study of quantitative approach to the treatment will facilitate the practical application and control and the control of infectious disease epidemics cost-benefit assessment of trends, and help establish a disease prevention policies, evaluation and revision.

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