Research on SI , SIS , SIR epidemic models and deeper investigation on diverse conditions

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Abstract

The modeling of infectious diseases is a tool which has been used to study the mechanisms by which diseases spread, to predict the future course of an outbreak and to evaluate strategies to control an epidemic. SI, SIS, SIR models[1] are three basic dynamics models of infectious disease. In this paper, we generate the models by simulating the process of disease propagation in a more realistic way and describe in detail the impacts of diverse conditions on the process. Before we come to a conclusion, we investigate more complex conditions such as different probabilities of contacting between each other. Finally, we give some suggestions[2] on preventing infectious disease based on what we get from the simulations.

Key Words: infectious disease dynamics; SI, SIS, SIR models; realistic simulation; complex conditions; preventive measures.

1.Introduction

Every year or several years, various viruses attacked us human beings or animals, which seriously endanger our assets and lives. For quite some time, Investigation of the mathematical model of infectious diseases to describe the spread of infectious diseases and the way to prevent or stop the propagation remain the focus of attention of experts and doctors. Early in the year of 1662, a scientist called John Graunt firstly systematically quantified causes of death by listing the numbers and causes of deaths publiced weekly, the analysis of which is considered the beginning of the “theory of competing risks”[3].The main idea of the method is well used among modern epidemiologists according to Daley and Gani. Later in the year of 1766, Daniel Bernoulli created a mathematical model to defend the practice of inoculating against smallpox, which preceded the development of germ theory. After Ronald Ross’s

research on the spread malaria, the modern theoretical epidemiology began, among which SI , SIR, SIS models are three basic dynamics models of infectious disease. Dynamics of infectious diseases, is one of the most important theoretical quantitative studies method. Based on the characteristics of population growth, the occurrence and spread of disease in the population, as well as related social and other factors, a mathematical model was established to reflect the dynamic characteristics of infectious diseases, analyze the development of the disease, reveal the epidemic law, and predict the trend of disease. It also plays a significant role in finding the optimal strategy for prevention and control and providing theoretical basis.

The models[4] mentioned above are types of deterministic compartmental models, in which individuals in the population are assigned to different subgroups or compartments, each representing a specific stage of the epidemic but with a probability to get contacted reciprocally. Based on these models, experts related can have a breakthrough in researching the growth of viruses, the spread of infectious diseases and the actions of drugs.

In this paper, firstly we will analyze the SI , SIR , SIS models and simulate the process of disease propagation respectively to make a comparison of the models, and change the parameters to see the impacts of one model. Secondly, we will regard the probability to get contacted as a variable, for as we all know, we tend to approach the acquaintance and stay away from strangers. Finally, suggestion will be given based on the results of above work.

2. Models and Methods

2.1 SI model

SI is an abbreviation of susceptible and infected.

2.1.1 Model:

a) The total population size remains invariant, set as N;

b) The probability to get into contact each other is deterministic, set as λ **;**

c) Once meeting the infected, one is to be infectious;

d) Once some individual is infected, it will never recover and stays infected as well as infectious to another susceptible.

2.1.2 Method:

Let S_0 be the number of susceptibles at time t=0;

Let S(t) be the number of susceptibles at time t;

Let I(t) be the number of infected at time t;

We have:

S(t)+ I(t)=N;

S(0)= S_0;

d I(t)/dt= λ ∗S(t)*I(t)/N.

Absolutely, we can get the solution:

$I(t)=1/(1+(1/(N- S_0)-1)*\exp(-\lambda t))$

However, in this paper, we will go to see the process of spread of the

infectious disease.

Firstly, we generate a two dimensional grid L*L, each individual takes up one grid.

Secondly, we choose one to be infected randomly;

Thirdly, we use the random number generators to judge whether the susceptible is infected or not. At the same time, we can count the number of susceptibles and infected, which must satisfy the equations above if N is large enough.

Finally, we will get the simulating process.

2.2 SIR model

SIR stands for susceptible, infected and recover with immunity.

2.2.1 Model:

a) The total population size remains invariant, set as N;
b) The probability to get into contact each other is deterministic, set as λ;
c) Every infected individual can recover with a deterministic probability, set as μ;
d) Once some individual recovers, it will never get infected again.

2.2.2 Method:

Let S0 be the number of susceptibles at time t=0;

Let S(t) be the number of susceptibles at time t;

Let I(t) be the number of infected at time t;

Let R(t) be the number of removals at time t， R(0)=0.

We have:

$S(t)+ I(t)+R(t)=N;$

$S(0)= S_0;$

$R(0)=0;$

$dI(t)/dt= \lambda *S(t)*I(t)/N- \mu *R(t);$

$dS(t)/dt=- \lambda *S(t)*I(t)$

Absolutely, we cannot get the analytic solutions directly, but we can have a discussion on the set of equations, before which we can have a simulation similar to SI model.

The main difference is in the third step, while the is infectious to others, itself can recover as a removal with the probability of μ.Note that once having recovered, one will never get infected again.

2.3 SIS model

SIS represents for susceptible, infected and susceptible.

2.3.1 Model:

a) The total population size remains invariant, set as N;
b) The probability to get into contact each other is deterministic, set as λ_1;
c) Once meeting the infected, one is to be infectious;
d) Every infected individual can recover with a deterministic probability;
e) After recovering, one has a probability to get infected again, which in this paper is different from the probability for the susceptible who get infected for the first time, set as $\lambda 2$.

2.3.2 Method:

Let S_0 be the number of susceptibles at time t=0;

Let S(t) be the number of susceptibles at time t;

Let I(t) be the number of the infected at time t;

Let R(t) be the number of removals at time t,R(0)=0.

We have:

S(t)+ I(t)+R(t)=N;

S(0)= S_0;

R(0)=0;

dI(t)/dt=I(t) *(λ_1*S(t) + λ_2* R(t))/ N- μ *I(t);

dS(t)/dt=- λ *S(t)*I(t)/N;

Absolutely, we cannot get the analytic solutions directly, but we can have a simulation to see the spread of the infectious diseases.

Obviously the main difference with SI, SIR models is in the third step as well, where the susceptibles and the removals both has the probability of getting infected, and the infected may also recover. More complex, much closer to the fact, of course.

2.4 SHM model

SHM is an acronym of Sun Hui min, for the model is based on my comprehension of the models mentioned above and consideration of the different contact rate among individuals.

Based on the SIS model, we establish the SHM model. Generally, we tend to approach the acquaintance and stay away from strangers, hence we put the individuals into a two dimensional grid L*L, the summation of the row and column coordinate is regarded as a parameter related to the contact rate, set as RC, the difference of which is inversely proportional to the contact rate (here called infection rate) between two individuals. Substitute λ_1/RC and λ_2/RC for λ_1 and λ_2 respectively, we will get new simulation.

3. Algorithm

As analyzed above, there some common points among four models, such as how to get the first one infected and how to output the data.

3.1 Type of the individual

```
class SSR{
    public:
    int sup;//susceptibles
    int inf;//infectives
    int rev;//removed
};
```

3.2 Initiate of the individual

Note: the number of the initial infected persons is just one for SI and SHM model, and L(one in each row for the dyadic array) for SIR and SIS model, we should change it manually..

```
void InitiateSSR(SSR ssr[][L])
{ //initial condition:only one infected
    int k=rand()%L;

    for(int i=0;i<L;i++)
    {
        for(int j=0;j<L;j++)
        {
            if(i==k&&j==k)
            {
                ssr[i][j].inf=1;
                ssr[i][j].sup=0;
            }
            else
            {
                ssr[i][j].inf=0;
                ssr[i][j].sup=1;
            }
            ssr[i][j].rev=0;
        }
    }
}
```

3.3 Output of the data

File data.dat is used to store whether he individual is infected or not after some time.

File count_inf.dat is used to store the number of the infected individuals after some time;

File count_rev.dat is used to store the number of removals after some time.

```
void SaveSSR(SSR ssr[][L])
{
    int count_inf=0;//count for the infectives
    int count_rev=0;//count for the removed
    ofstream out1("SSS model data.dat",ios::app);
    ofstream out2("SSS model count_inf.dat",ios::app);
    ofstream out3("SSS model count_rev.dat",ios::app);

    for(int i=0;i<L;i++)
    {
        for(int j=0;j<L;j++)
        {
            out1<<ssr[i][j].inf<<'\t';
            if(ssr[i][j].inf==1)
            {
                count_inf++;
            }
            if(ssr[i][j].rev==1)
            {
                count_rev++;
            }
        }
        out1<<endl;
    }
    out1<<"**********************"<<endl;
    out2<<count_inf<<endl;
    out3<<count_rev<<endl;
    cout<<count_inf<<'\t'<<count_rev<<endl;
    out1.close();
    out2.close();
    out3.close();
}
```

3.4Count the number of the infected

When calculating the contact rate for one individual, we should be aware of the number of the infected ,which is set as count_inf, then the contact rate is to be $\lambda *$ count_inf.

```
int CountInf(const SSR ssr[][L])
{
    int count_inf=0;
    for(int i=0;i<L;i++)
    {
        for(int j=0;j<L;j++)
        {
            if(ssr[i][j].inf==1)count_inf++;
        }
    }
    return count_inf;
}
```

3.5 The interrelationship function for SI model

```
void InterrelationShipSI(SSR si[][L])
{
    double k=0.0;
    double touchrate=TouchRate1*CountInf(si)/N;
    for(int i=0;i<L;i++)
    {
        for(int j=0;j<L;j++)
        {
            k=1.0*rand()/RAND_MAX;
            if(k<=TouchRate1)
            {
                si[i][j].inf=1;
            }
        }
    }
}
```

Main point: If the number generated randomly is less than the corresponding contact rate, the susceptible get infected, otherwise not.

3.6 The interrelationship function for SIR model

```
void InterrelationShipSIR(SSR sir[][L])
{
    double k=0.0;
    double touchrate2=TouchRate2*CountInf(sir)/N;
    for(int i=0;i<L;i++)
    {
        for(int j=0;j<L;j++)
        {
//susceptibles are infected with probability of TouchRate2
            if(sir[i][j].sup==1)
            {
                k=1.0*rand()/RAND_MAX;

                if(k<=touchrate2)
                {
                    sir[i][j].inf=1;
                    sir[i][j].sup=0;
                }
            }
//the infectives recover with probability of CureRate
            if(sir[i][j].inf==1)
            {
                k=1.0*rand()/RAND_MAX;

                if(k<=CureRate)
                {
                    sir[i][j].rev=1;
                    sir[i][j].inf=0;
                }
            }
        }
    }
}
```

Main point: For susceptibles, if the number generated randomly is less than the corresponding contact rate, the susceptible get infected, otherwise not; For infected, if the number generated randomly is less than the cure rate, the infected recovers and will never get infected again, otherwise not.

3.7 The interrelationship function for SIS model

```
void InterrelationShipSIS(SSR sis[][L])
{
    double k=0.0;
    double touchrate1=TouchRate1*CountInf(sis)/N;
    double touchrate2=TouchRate2*CountInf(sis)/N;
    for(int i=0;i<L;i++)
    {
        for(int j=0;j<L;j++)
        {
//the removed is again infected with probability of touchrate1
            if(sis[i][j].rev==1)
            {
                k=1.0*rand()/RAND_MAX;

                if(k<=touchrate1)
                {
                    sis[i][j].inf=1;
                    sis[i][j].rev=0;
                }
            }
//susceptibles are infected with probability of touchrate2
            if(sis[i][j].sup==1)
            {
                k=1.0*rand()/RAND_MAX;

                if(k<=touchrate2)
                {
                    sis[i][j].inf=1;
                    sis[i][j].sup=0;
                }
            }


//the infectives recover with probability of curerate
            if(sis[i][j].inf==1)
            {
                k=1.0*rand()/RAND_MAX;

                if(k<=CureRate)
                {
                    sis[i][j].rev=1;
                    sis[i][j].inf=0;
                }
            }
        }
    }
}
```

Main point: For susceptibles and removals, if the number generated randomly is less than the corresponding contact rate, the susceptible get infected, otherwise not; For the infected, if the number generated randomly is less than the cure rate, the infected recovers, otherwise

not.

3.8 The interrelationship function for SHM model

3.8.1 Touch Function

```
void TouchSSR(SSR* shm,int p,int q,int i,int j,int sup)
{
//TouchRate is different for the removed and the susceptibles
    double TouchRate;

    if(sup==0)
    {
        TouchRate=TouchRate1;//remove
    }
    else
    {
        TouchRate=TouchRate2;   //sup
    }

    double k=1.0*rand()/RAND_MAX;
//infected//the probility of two persons to meet one day is diff
    if(k<(0.2*TouchRate/(p+q-i-j)))
    {
        shm->inf=1;
        shm->rev=0;
        shm->sup=0;
    }
}
```

Main point: as we can see, the contact rate is different for susceptibles and the removals, if written in this way, the interrelationship function will be more concise and clear.

3.8.2 Cure Function

```
void CureSSR(SSR* shm)
{
    double k=1.0*rand()/RAND_MAX;

    if(k<CureRate)    //cured
    {
        shm->inf=0;
        shm->rev=1;
    }
}
```

Main point:it is just for convenience.

3.8.3 The interrelationship function for SHM model

The function is a little long, you can read it in the appendix.

Main point:

In a two dimensional grid, considering each individual as a point, for the origin point, the point whose both the row and column coordinate are larger than or equal to the origin point's is called the field point, we should consider the interrelationship between the two point.

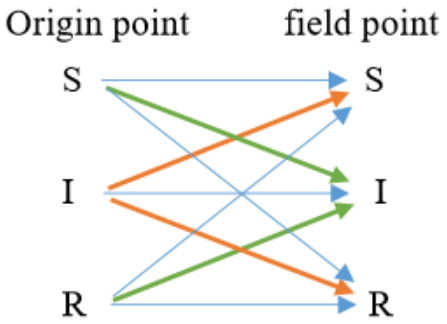

Figure 1: the interrelationship between the origin and field point.

As we can see in the figure 1,the interrelationships between the two points are not 9 but 4.The red lines represents the impacts which the origin point plays on the field point, causing it infected with probability. Once the field point is infected by one origin point, it is infected in the observation of next time in spite of the impacts of other origin points, but remains uninfected this time. The green lines represents the impacts which the field point plays on the point point, causing it infected with probability. As for the calculation of the interrelationship, it is similar to other models, the main difference is that the contact rate is a variable, as shown in the

Touch Function in 3.8.1.

4. Results and Analysis

4.1 SI model

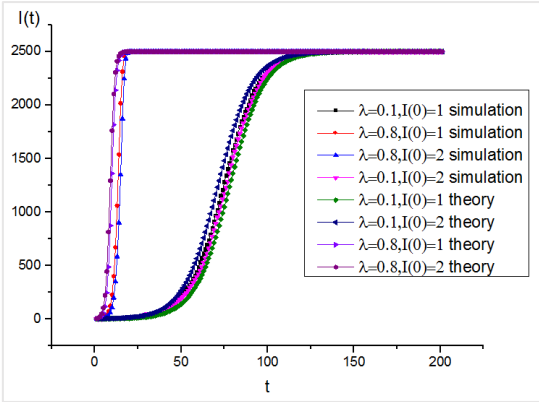

Figure 2: The simulating image and theoretical image of the relationship between the number of the infected and time under different environment in SI model.

From Figure 2, we can conclude as followed:

1) As mentioned in 2.1.2, in SI model, we can get an analytic solutions directly, and from Figure 2, we can see that under different environment, the simulating lines almost coincide with the corresponding theoretic line, which implies the way we simulate the model is right.
2) With the contact rate increasing, the number of the infected gets to the maximum faster.
3) The initial number of the infected is 1 or 2 has little impact on the results.

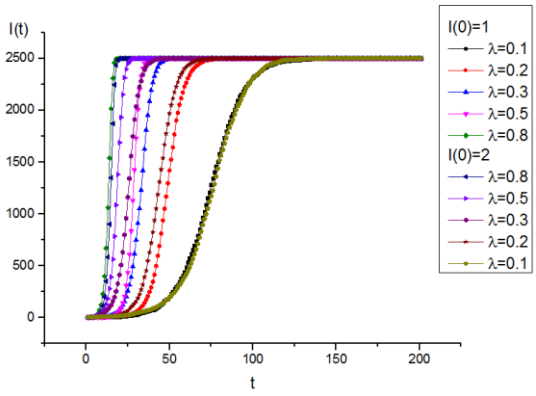

Figure 3: The relationship between the number of the infected and time under different environment and initial conditions in SI model.

Based on Figure 2, and from Figure 3, we can see that the initial number of the infected is 1 or 2 does have little impact on the results.

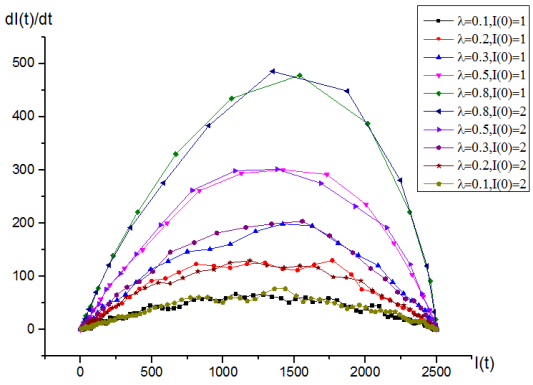

Figure 4: The relationship between the derivative of the number of the infected and itself in SI model.

As we can see from Figure 4, with the increase of the number of the infected, the derivative of it shows a trend of increasing first and then decreasing. We can make a Gaussian fitting, as shown in Figure 5.

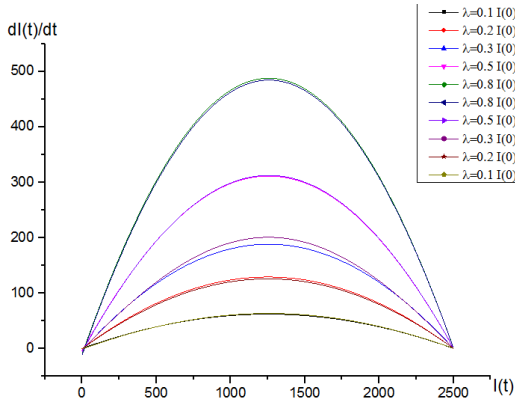

Figure 5: The Gaussian fitting of curves in Figure 4.

After fitting, we can intuitively see that under different conditions, the value of dI(t)/dt gets to its maximum almost at the same value of I(t), when the number of the increasing patients grows fastest. According to the data, relevant departments can predict the climax of infectious diseases and make sufficient preparations.

4.2 SIR model

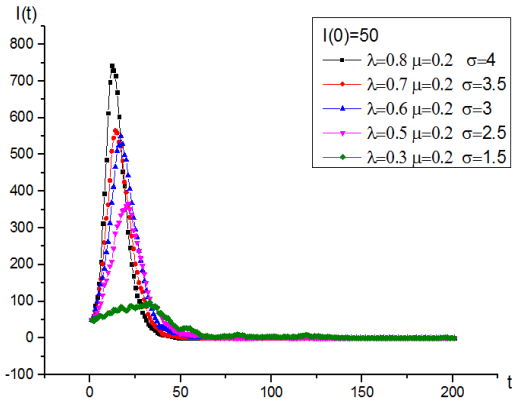

Figure 6: The relationship between the number of the infected and time under different conditions when σ is more than 1 in SIR model.

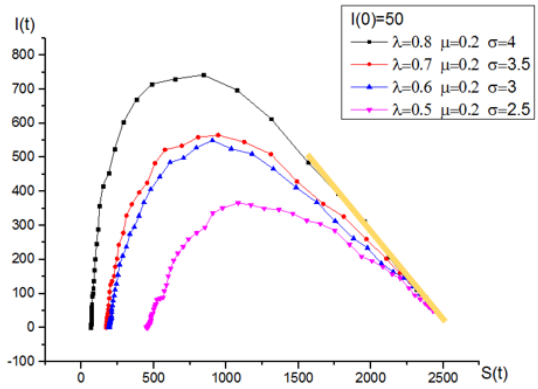

Figure 7: The relationship between the number of the infected and the susceptible under different conditions when σ is more than 1 in SIR model.

From Figure 6 and 7,we can conclude as followed:

1) With time passing by,the number of the infected shows a trend of increasing to the maximum first and then decreasing to zero when σ is more than 1.
2) With the decrease of the contact rate, the value of the maximum of I(t) is getting smaller, which means that isolating the patients does good to controlling the spread of the disease.
3) With the increase of the number of the susceptibles, the number of the infected shows a trend of increasing first and then decreasing when σ is more than 1. What matters most is that the four lines have a common tangent when the number of the infected converges to zero, which is shown in yellow line in the figure.

In other words, this kind of infectious disease won't spread in the crowd and will be cured finally.

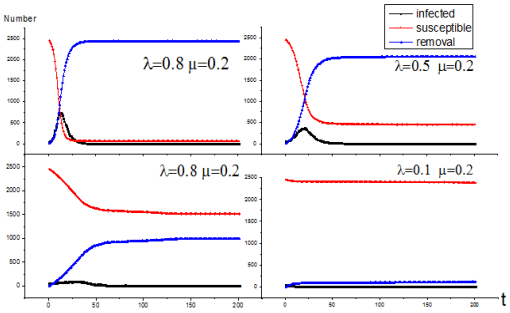

Figure 8: The image of the number of the infected, the susceptibles and the removals with time changing under different conditions in SIR model.

Obviously, when σ >1, isolating the patients does good to controlling the spread of the disease.

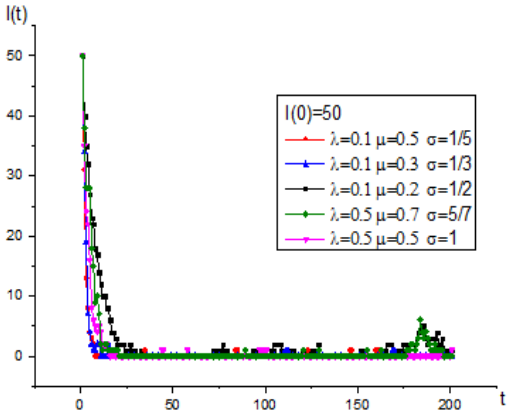

Figure 9: The relationship between the number of the infected and time under different conditions when σ is less than or equal to 1 in SIR model.

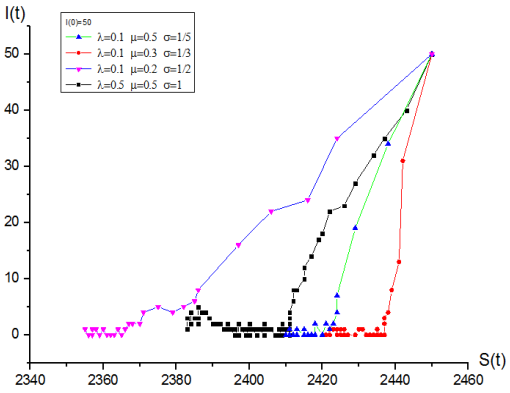

Figure 10: The relationship between the number of the infected and the susceptible under different conditions when σ is less than or equal to 1 in SIR model.

Compared to Figure 6 and 7,we can obviously get from Figure 8 and 9, the number of the infected converges to zero at fast speed when σ is less than or equal to 1, which means the infection rate of the disease is very small and isolation is of no necessity.

4.3 SIS model

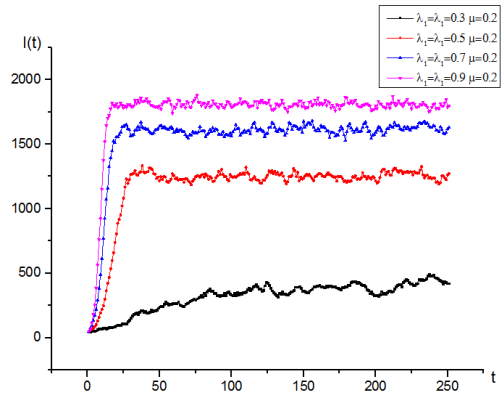

Figure 11: The relationship between the number of the infected and time under different conditions where the cure rate remains invariant and when σ is more than 1 in SIS model.

As we can see from Figure 11, the number of the infected increases rapidly with time and then keeps invariant, the value of which increases with the contact rate increasing.

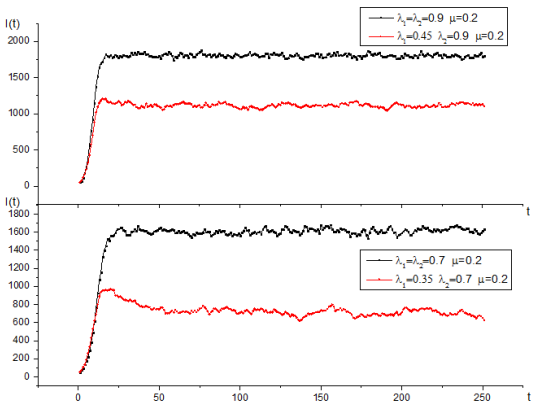

Figure 12: The compasion of the number of the infected when the contact rate is different for the removals and susceptibles under different conditions in SIS model.

Obviously from Figure 12, if the contact rate of the removals is half of that of the susceptibles, although the trend of the number of the infected is the same, but the value of the maximum is much less than that of the susceptibles.

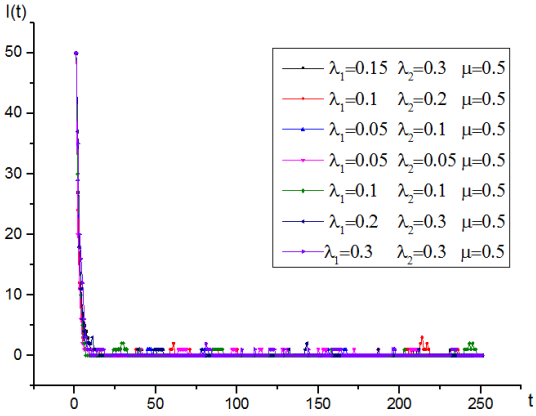

Figure 13: The relationship between the number of the infected and time under different conditions where the cure rate remains invariant and when σ is less than or equal to 1 in SIS model.

4.4 SHM model

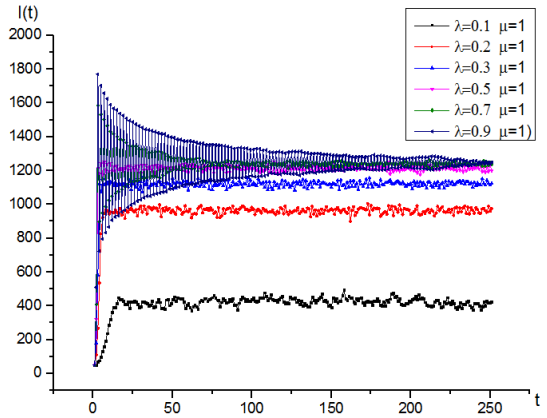

Figure 14: The relationship between the number of the infected and time under different conditions when the cure rate=1 in SHM model.

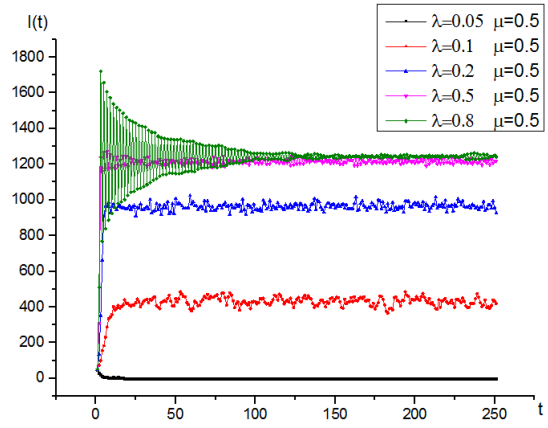

Figure 15: The relationship between the number of the infected and time under different conditions when the cure rate=0.5 in SHM model.

From Figure 14 and 15, we can conclude as followed:

1) When the cure rate=1, the infection rate is more than 0.1, the number of the infected is increasing rapidly at first and then come to the platform, the value of which increases with the infection rate increasing.
2) When the cure rate=0.5, the infection rate is more than 0.1, the number of the infected is increasing rapidly at first and then come to the platform, the value of which increases with the infection rate increasing as well. But when the infection rate is 0.05, the number of the infected converges to zero rapidly, which means isolation is of significant importance.

Let us have a look at the spread of SHM model under the condition:

λ =0. 1 μ =1

(yellow represents infected, green means uninfected)

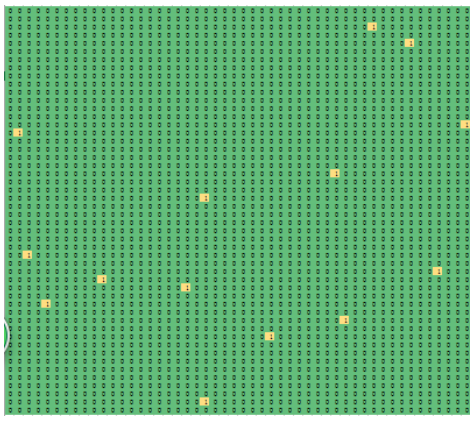

Figure 16: the simulation of day 2.

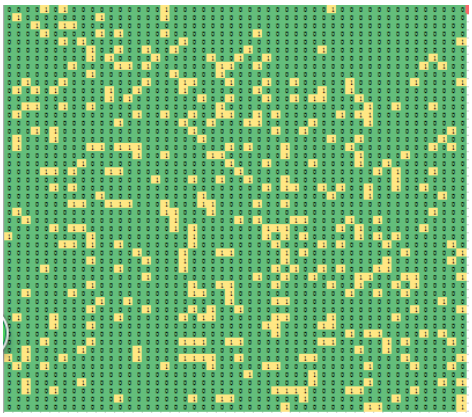

Figure 17: the simulation of day 10.

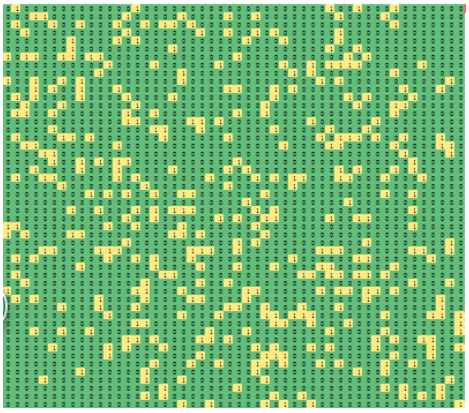

Figure 18: the simulation of day 20.

As we can see from three figures above, we can notice that once one person is infected by some factors and no preventive or quarantine measures are taken, it is very easy for individuals near the patient to get infected in SHM model, because everyone in this model is coupled so strongly that spread of the disease seems much easier.

5. Conclusion

We have used four models, which have both common and different points, to simulate the spread of the infectious diseases and analyze the results in details.

Here we make a brief conclusion based on the results above.

For the disease which cannot be cured completely or almost impossibly cured, once one person is checked to have infected, the one is ought to volunteer to isolate himself in case of infecting others, or everyone will get infected at last. Meanwhile, improving the health care facilities or reducing the contact rate, can delay the arrival of the peak of infectious diseases.

For the disease which can be cured with immunity, the number of the infected will converge to zero finally without any measures, so don't worry although getting far away from the infected is better to avoid getting infected. Improving the health level is a pretty way to control the spread of infectious diseases.

For the disease which can be cured without immunity, if the cure rate is bigger than the contact rate, the number of the infected will converge to zero rapidly. However, if the contact rate is bigger than the cure rate, the number of the infected will remain at certain value, while improving the level of medical and care, diminishing the contact rate is the best way to avoid diseases, namely getting far away from the patient.

Thanks to the flexibility of the models, they can be applied to predict the future trend of infectious diseases, simulate the interaction between the drug and body or some sociological problems such as the spread of rumors and so on.

Reference:

[1] The models of the infectious diseases.

[2] Problems of the spread of the infectious diseases.

[3] Wikipedia

[4] Argimiro Arratia & R. Ferrer-i-Cancho, Epidemic models over networks.(2016)

Appendix

The interrelationship function for SHM model in 3.8.3:

```
void InterrelationShipSHM(SSR shm[][L])
{
    SSR newshm[L][L];
    //copy ssr first
    for(int i=0;i<L;i++)
    {
        for(int j=0;j<L;j++)
        {
            newshm[i][j]=shm[i][j];
        }
    }
    //change later
    for(int i=0;i<L;i++)
    {
        for(int j=0;j<L;j++)
        {
            for(int p=i;p<L;p++)
            {
                for(int q=j;q<L;q++)
                {
    //regard shm[i][j] and shm[p][q] as the origin point and the field point in electromagenetic field respectively
                    if(p==i&&q==j);
                    else if(shm[i][j].inf==1)
```

```
//i.e:the origin point may change the field point
            {
                CureSSR(&newshm[i][j]);
//the origin point may be cured
                if(newshm[p][q].inf==0)
//the field point is not infected yet.
                {
                TouchSSR(&newshm[p][q],p,q,i,j,sh
            m[p][q].sup);
//the field point may change
                }
            }
            else if(shm[p][q].inf==1)
//i.e:the field point may change the origin point
            {
                TouchSSR(&newshm[i][j],p,q,i,j,shm
            [i][j].sup);
//the field point may changes
            }
            if(i==L&&j==L&&shm[i][j].inf==1)
            {
                CureSSR(&newshm[i][j]);
            }
//other occasions: neither the origin point nor the
field point is infected
                            }
                        }
                    }
                }
//final paste
            for(int i=0;i<L;i++)
            {
                for(int j=0;j<L;j++)
                {
                    shm[i][j]=newshm[i][j];
                }
            }
        }
```