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# 数学建模国际赛

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# 第十届“认证杯”数学中国

## 数学建模国际赛

## 编 号 专 用 页

参赛队伍的参赛队号：（请各个参赛队提前填写好）：1528

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# Research on the Risk Model of Disease Transmission Based on Cellular Automata


## Abstract:

Nowadays, the spread of diseases has gradually aroused people's attention. The wanton destruction of SARS in 2003 and the COVID-19 have allowed people to gradually increase their awareness of the prevention and control of the spread of the disease. For the spread of disease, it can be spread through the air or through droplets. Based on the cellular automata's simulation of disease transmission, this paper realizes the exploration of the confined space disease transmission model.

**Firstly**, this paper establishes a **Wells-Riley Model** disease transmission model to explore the simple air mixing situation and the spatial division of the disease transmission situation successively. The Disease Transmission Model was established for the size of the confined space, the ventilation status, and the time of co-location. The computer simulation experiment showed that in a space with a **space size of** $\mathbf{58m^3}$, **the ventilation status** is $\mathbf{3.93\pm0.05m^3/s}$ and **the co-location time** is $\mathbf{2.14\pm0.01s}$, the possibility of disease transmission is higher

**Secondly**, this paper establishes a confined space disease transmission model based on the classic disease transmission equation, and uses the **Wells-Riley Model disease transmission model** and **the Wells disease transmission model based on multi-stage discrete dynamics**. The condition of the differential equation is constrained and a confined space with a volume of $58\pm3m^3$ is selected as the research object to establish the disease transmission model. According to **the $3\sigma$ principles** and **under 95% confidence**, the space size,the ventilation condition, co-location time and so on which their value are using a vector to desicribed as $\mathbf{\{58\pm3m^3, 3.94\pm0.05m^3/s, 2.14\pm0.01s, 2.2\pm0.1ind, 128.154\pm0.564Pa\cdot m/s\}}$, which in this condiction that probability of transmission is greater.

**Finally**, this article simulates the spread of the disease through computer simulation experiments, and chooses to use the **cellular automata model** to analyze the sensitivity of the model. The individuals in the confined space are set as the cell collection of the cellular automata, and the **infection rate** and **cure rate** of the disease are used as the **growth and reproduction parameters** of the cellular automata. Carry out a simulation of the disease broadcast process. Under the condition of $58\ m^3$ confined space, the **distribution of people** is $\mathbf{2.0\pm0.1\ ind}$ and the **airflow condition** is $\mathbf{125.267\pm0.564\ Pa\cdot m/s}$, the probability of disease transmission is the lowest, **with a value of 27% and degree is 94.3%.**



**Key words: Confined space disease assessment model; Dynamic diffusion equation; Cellular automata; Multi-stage Wells-Riley disease model**

# Contents

# I. Introduction

## 1.1 Restatement of the Problem

Nowadays, the spread of diseases has gradually aroused people's attention. The wanton destruction of SARS in 2003 and the new crown epidemic in 2019 have allowed people to gradually increase their awareness of the prevention and control of the spread of the disease. For the spread of disease, it can be spread through the air or through droplets. Airborne diseases can be spread by coughing, sneezing, spraying liquid or dust. In this paper, the disease transmission model in confined spaces is studied under the current situation where the spread of disease has attracted people's attention, and in order to study the law of disease transmission at a deeper level, the corresponding programming is implemented.


**Figure 1:Background introduction**

## 1.2 Assumptions

**a**. Assuming that the air is completely mixed, not to consider the random effects of small groups, nor to consider the susceptible population and the proximity of the source of infection.

**b.** Suppose that only a new disease infection may occur within a sufficiently small period of time.

**c**. During the period of disease transmission, the birth rate and mortality rate are approximately equal, and the total population can be considered to remain unchanged.

**d.**After treatment, the patient has obtained immunity, and no longer carry the disease virus, is considered to be not infected.

**e.** Both confirmed and suspected cases will be effectively isolated, and patients who die from the disease will no longer be infected with others.

## 1.3 Notations

The key mathematical notations uesd in this paper are listed in Table 1.

**Table 1:Notations used in this paper**

| Symbol | Description |
|---|---|
| $P_L(trans)$ | The spread of the disease |
| $E(size)$ | The size of the confined space |
| R(t) | Individual time situation in a confined space |
| $I(Con)$ | Air flow conditions in confined spaces |
| V(air) | Flow rate of airflow in a confined space |
| Exposed(t) | Have been in contact with an infected person |
| Susceptible(t) | Healthy people who have not been infected |
| Infectious(t) | Infected individuals who have been diagnosed |
| Recoverd(t) | Individuals with immunity after recovery |
| $p_s(loc)$ | The spatial position the individual in the confined space |

# II. The Description of the Problem

## 2.1 Problem analysis of the disease transmission risk model

According to the description of the problem, airborne diseases can be transmitted by coughing, sneezing, spraying liquids, or dust in the air. Some common infectious diseases can only be transmitted by droplets. Therefore, combined with the above description of infectious diseases, this paper establishes a risk assessment model for disease transmission to the air transmission and droplet transmission of disease in confined space, for the spread of disease, this paper intends to use the number of infections than the total number of values to be correspondingly expressed. And according to the requirements of the topic, the factors it wishes to consider are the size of space, space ventilation and co-positioning time, and give an accurate description of the distribution of personnel and airflow conditions.

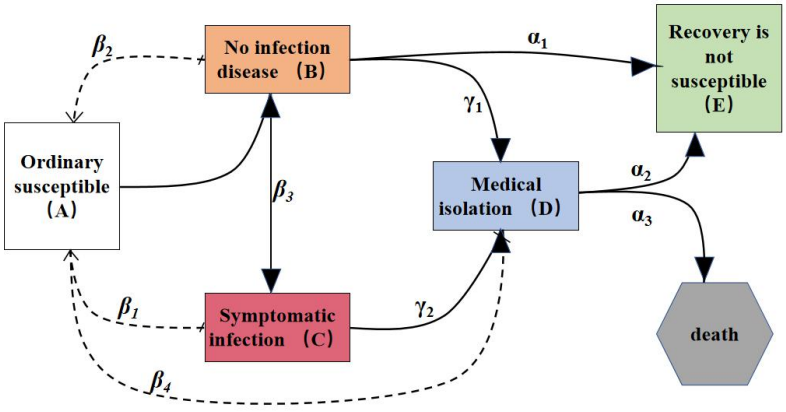


**Figure 2:Disease transmission risk model**

## 2.2 Problem analysis of computer simulation

Based on the establishment of the disease transmission risk model, the problem requires that the general results of disease transmission be given, and the model established is verified accordingly through specific living environments such as cabins and indoor stadiums, and the corresponding results are given. In this paper, the cell automaton model is intended to simulate the mobile population in the cabin, indoor stadium and other environments, and to simulate the probability and situation of disease transmission in the population through the interaction of space size, space ventilation, personnel distribution and airflow conditions. And by adjusting the above parameters, to simulate the spread of disease in different situations to verify the correctness of the model.

# III. Models

## 3.1Wells-Riley Model model for disease transmission

### 3.1.1 Background

In recent years, the air spread of infectious diseases has been a topic of great concern, more and more evidence that indoor air quality has an important impact on individual health, and plays an important role in the spread of infection. Although this problem has a wide impact on the world, there is less research on quantifying the risk of air propagation in closed space, and for past experience, many risk analysis and evaluation models are not perfect for solving this problem, and the study of space, population and other elements in the model is not well thought out. And previous model studies have not been able to explain the effects of proximity between infected and susceptible populations, so it can be said that previous studies have only quantified average risk rather than the expected range.

Therefore, based on the above description, it is urgent to study the risk of disease transmission in confined space, the preliminary idea of this paper is to combine with the mixed ventilation equation of simple areas by establishing a disease transmission model, so that the model can be initially in line with the variables required by the topic. And the risk test of disease transmission model can be carried out by air mixing on the risk of infection.

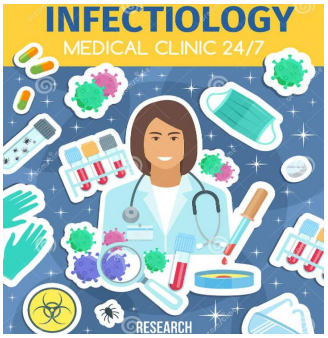


**Figure 3:Background introduction**

### 3.1.2 Simple mixed air disease transmission model

The Wells-Riley Model is used to predict the number of new cases of infection within a period of time t(S) within a constant rate of Q($m^3/s$) at the rate of indoor air flow, as follows:

$$N_C = S(1 - e^{-\frac{Iqpt}{Q}}) \quad (1)$$

Among them, S indicates the number of vulnerable people in space, I represents the number of infected people, p indicates the lung ventilation rate of susceptible people, q represents the unit of infection under the unit volume.

For formula (1), it is based on the small probability of Poisson's law, which assumes that only a new infection may occur for a sufficiently small period of time. This formula, which applies to most airborne infections, defines an equation for disease transmission within a near-standard time period, and although it is based on a probability approach, it is more commonly used for deterministic disease transmission.

Considering that S(t) is an infection constant under the time t of susceptible populations, further improvements can be made to formula (1), but before the improvement, a new variable, λ , is introduced in this article, which is expressed as:

$$\lambda = \frac{Iqp}{Q} \quad (2)$$

By considering the probability of an uninfected susceptible population at the t-moment, $P_S(t) = Pr(t)$,can be exported as equivalent random procedures. Within a very small interval dt, two outcomes may occur, with a probability of new infection of λdtS or no new infection probability of 1-λdtS, as follows:

$$P_S(t + dt) = P_S(t)(1 - \lambda dtS) + P_{S+1}(t)\lambda dt(S + 1) \quad (3)$$

When dt tends to 0, this article gets the differential equation:

$$\frac{dp_s}{dt} = -\lambda S p_S(t) + \lambda(S + 1)p_{S+1}(t) \quad (4)$$

Through the above formula (3) (4), this paper considers the disease transmission process to include a series of infection events, susceptible population reduced by one, by the feeling of one. When these different events occur, time does not run simulations based on fixed time steps, but is constructed using random variables to produce a more efficient numerical process and fewer simulation processes. For a susceptible population S, the time T to the next event is an exponentially distributed random variable:

$$Pr(T \geq t) = e^{-\lambda St} \quad (5)$$

At the same time, the above formula can be written as:

$$t = -\frac{\ln(Y)}{\lambda S} \quad (6)$$

Among them, λ can be learned from the formula (2). For the results of formula (6), this paper is easy to introduce the time corresponding to new cases of infection in susceptible populations in the ventilation indoor environment.

### 3.1.3 Model of disease transmission in the space domain

In view of the above simple hybrid air disease transmission model, this paper extends it to a space divided into multiple areas. The air in each area is considered evenly mixed. However, the mixing between these regions is limited, which leads to different concentration distributions throughout the space, so this paper divides the simple mixed air disease transmission model into two different stages, the first of which is the regional ventilation model, which is used to assess the distribution of infected bodies, and then extends the infection risk model to assess the prevalence of new infections in space.

#### 3.1.3.1 Area ventilation model

For the segmentation of the space domain, this paper first discusses the first stage of the disease transmission model, by using the infected quantum as a deterministic variable equal to the concentration of pollutants in the environment, the effects of air mixing are simulated, the specific formula is:

$$V_i \frac{dC_i}{dt} = q_i I_i - Q_{oi} C_i - \sum_k \beta_{ik} C_i + \sum_k \beta_{ki} C_k \tag{7}$$

Among them, the $q_i I_i$ indicates the rate of disease transmission in the space region, $Q_{oi}$indicates the ventilation rate of the i region, $\beta_{ik}$,$\beta_{ki}$represents the volume flow of air from the i, k region to each other.

By formula (7), this paper uses Gauss's elimination method to represent it in a matrix:

$$\begin{bmatrix} -(Q_1+\beta_{12}) & \beta_{21} & 0 \\ \beta_{12} & -(Q_1+\beta_{21}+\beta_{23}) & \beta_{32} \\ 0 & \beta_{23} & \dots \end{bmatrix} \begin{bmatrix} C_1 \\ C_2 \\ C_3 \end{bmatrix} = \begin{bmatrix} q_1 I_1 \\ q_2 I_2 \\ q_3 I_3 \end{bmatrix} \tag{8}$$

The above is the matrix expression of the regional ventilation model.

#### 3.1.3.2 Extended infection risk model

For the model established above, this paper improves it, replaces the infection rate described in formula (2) and has a replacement formula:

$$\lambda_i = C_i p \tag{9}$$

For the improved model, the Poisson hypothesis is still used, only one new infection occurs in a small time step dt, and the model is established for related simulation. However, now for new infections that may occur in any occupied area of the model, it is necessary to calculate the infection rate for each region to determine which region each infection occurs in. In each time step, the probability that the next infection event will appear in the i region is expressed as:

$$\frac{dp_s}{dt} = -\lambda \mathrm{Sp_S(t)\,R(k)} + \lambda(\mathrm{S}+1)\mathrm{p_{S+1}(t)} \tag{10}$$

And event t can be expressed as:

$$t = -\frac{ln(Y)}{R(k)} \tag{11}$$

The basic disease transmission model has been constructed for analysis by the most basic Wells-Riley Model disease transmission model, which assumes that the air in space is evenly mixed, and then improves the Wells-Model Riley model to accommodate the multi-segmentation of space and to describe the disease through the size of the space, the ventilation of the space, and the events of co-location. Next, this paper continues to model the effects of time stages on the spread of disease.

## 3.2 Disease model based multi-stage time dynamics

For the spread of disease In this paper, the modeling and analysis of the classical infectious disease dynamics model is carried out on the disease transmission model under the time domain, among which the classical infectious disease dynamics model SIR(susceptible,infectious,recovered)model,SIRS(susceptible,infectious,recovered,susceptible) model and SEIR (susceptible,exposed,infectious,recoverd) model. Its main idea is to divide the population into groups such as susceptibility, latent, infected and rehabilitated, and to establish differential equations through the communication mechanism of one group to another, thus revealing the law of disease transmission in the time domain.

For the model before the establishment, this paper set S(t) as the number of susceptible people in the t moment of the existing number, E (t) for the incubation period infected in the t moment of the existing number, R (t) indicates the cumulative number of healers at the t moment. For the cure there is a case of re-infection, in order to simplify the discussion of the problem, this case is ignored in this article.

### 3.2.1 Infection Healing Model

There is an incubation period of $t_1$ day before symptoms appear in an infected person, after diagnosis into a confirmed infection, after a $t_2$ day therapeutic observation period, it becomes a healer, that is, t-moment confirmed infected person in t-$t_1$ moment into incubation period infection, t-moment cure of the infected person in t-$t_1$-$t_2$ moment into incubation period infection, t-$t_2$ moment into a confirmed infection, the above description process can be shown in the following diagram:

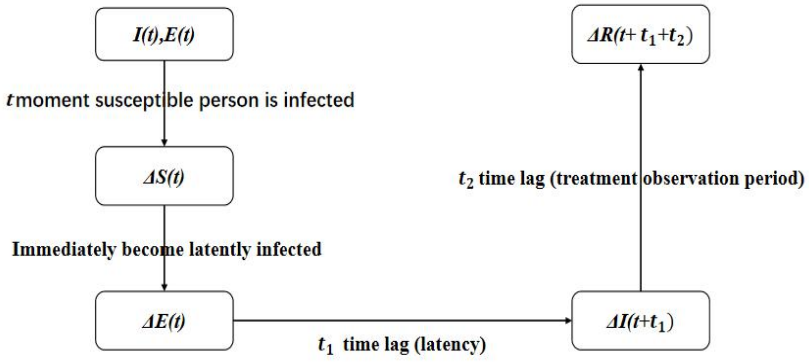


**Figure 4:Description process shown**

According to the disease transmission dynamics model, the infection healing model can be expressed as follows:

$$S(t+1) - S(t) = -\beta I(t) - E(t) \quad (12)$$

$$E(t+1) - E(t) = \beta I(t) + \gamma E(t) \quad (13)$$

$$I(t+1) - I(t) = \alpha I(t - t_1) + \beta E(t) \quad (14)$$

$$R(t+1) - R(t) = \theta I(t) + \gamma E(t) - \delta S(t) \quad (15)$$

## 3.2.2 Multi-stage time lag dynamic disease transmission model

For the spatial environment given by the topic, this paper assumes that the number of susceptible persons exposed to the confirmed infection in one day is $\theta_1(t)$, the number of susceptibility persons exposed to incubation period infection in a day is $\theta_2(t)$, and this paper assumes that both are decreasing functions of time t and have exponential form, the specific expression of which is as follows:

$$\theta_1(t)=\begin{cases} c_0, t \in [t_0, t_1] \\ (c_0 - c_1)e^{-r_1 t + b_1} + c_1, t \in [t_1, t_2] \\ (c_1 - c_2)e^{-r_2 t + b_2} + c_2, t \in [t_2, \infty] \end{cases} \quad (16)$$

$$\theta_2(t)=\begin{cases} c_3, t \in [t_0, t_1] \\ (c_3 - c_4)e^{-r_3 t + b_3} + c_3, t \in [t_1, t_2] \\ (c_4 - c_5)e^{-r_4 t + b_4} + c_4, t \in [t_2, \infty] \end{cases} \quad (17)$$

For this problem, this paper selected an indoor confined space as the research site, and the process of disease transmission was divided into two stages for discussion.

### 3.2.2.1 The first stage

Early for indoor confined Spaces, the spread of disease, the person inside the space does not have effective protective measures, and to the spread of the disease has not made the corresponding prevention and quarantine, so this article integrated the above conditions for the first phase of modeling, assume that the transmission coefficient for $\beta_{11}$ infected diagnosis effective contact number for $\theta_{11}$, latent infection of the transmission coefficient for $\beta_{21}$, The effective contact number is $\theta_{21}$. Based on this, the time-delay discrete dynamics model of the first stage is established as follows: The change of susceptible infection from time t to time t+1 is the difference between the number of infected persons in the incubation period at time t and the number of infected persons confirmed to be infected. The specific formula is as follows:

$$S(t+1)-S(t) = -\beta_{11}\theta_{11}I(t)-\beta_{21}\theta_{21}E(t) \quad (18)$$

From time t to time t+1, the change of the infected persons during the incubation period is the sum of the infected persons during the incubation period and confirmed infected persons at time t minus the sum of the infected persons during the incubation period and confirmed infected persons after the incubation period at time t-$t_1$. The specific calculation formula is as follows:

$$E(t+1)-E(t) = \beta_{11}\theta_{11}I(t)+\beta_{21}\theta_{21}E(t)-\beta_{11}\theta_{11}I(t-t_1)-\beta_{21}\theta_{21}E(t-t_1) \quad (19)$$

The change of confirmed infected persons at time t is the sum of the number of persons who become infected during the incubation period and become confirmed infected after the incubation period at time t-$t_1$, minus the sum of the number of persons who become infected during the incubation period at time t-$t_1$-$t_2$ and become cured after the incubation period and treatment period. The specific calculation formula is as follows:

$$I(t+1)-I(t) = \beta_{11}\theta_{11}I(t-t_1)+\beta_{21}\theta_{21}E(t-t_1)-\beta_{11}\theta_{11}I(t-t_1-t_2)-\beta_{21}\theta_{21}E(t-t_1-t_2) \quad (20)$$

$$R(t+1)-R(t) = \beta_{11}\theta_{11}I(t-t_1-t_2)-\beta_{21}\theta_{21}E(t-t_1-t_2) \quad (21)$$

As mentioned above in the discrete dynamic transmission model of disease in a confined space in the first stage, then individuals in a confined space began to take effective protective measures and actively cooperate with the effective measures of reducing disease transmission such as wearing masks in the medical system.

### 3.2.2.2 The second stage

The dynamic transmission model of the first stage has been given in the previous part. Then, for the second stage, individuals in a confined space will take effective medical protection measures, so the effective contact number of infected persons is set as $\theta_{12}$ and $\theta_{22}$. According to the discrete dynamic transmission model of the first stage, the formula is as follows:

$$S(t+1)-S(t) = -\beta_{11}\theta_{12}I(t)-\beta_{21}\theta_{22}E(t) \quad (22)$$

$$E(t+1)-E(t) = \beta_{11}\theta_{12}I(t)+\beta_{21}\theta_{22}E(t)-\beta_{11}\theta_{11}I(t-t_1)-\beta_{21}\theta_{21}E(t-t_1) \quad (23)$$

The above changes were made to the disease transmission model in the time domain of the second stage. The adjustment of the disease transmission model was realized by adjusting the effective number of contacts of infected persons, and then the third stage was entered.

### 3.2.2.3 The third stage

After the first and second stages, the confined space has developed strong space resistance and prevention measures against disease transmission. Therefore, in this stage, this paper believes that the confined space has reached a stable state for disease transmission. Therefore, for the first-stage dynamic propagation model, the following improvements are made in this paper:

$$I(t+1)-I(t) = \beta_{12}\theta_{13}I(t-t_1)+\beta_{22}\theta_{23}E(t-t_1)-\beta_{12}\theta_{13}I(t-t_1-t_2)-\beta_{22}\theta_{23}E(t-t_1-t_2) \quad (24)$$

$$R(t+1)-R(t) = \beta_{12}\theta_{13}I(t-t_1-t_2)+\beta_{22}\theta_{23}E(t-t_1-t_2) \quad (25)$$

For the models of the above three stages, the main difference lies in that the coefficient of the model is assigned according to different disease transmission conditions, and the different coefficient represents the infection coefficient and effective contact number of infected persons in different policies and actual situations.

## 3.3 Evaluation model disease transmission in confined space

In view of the disease transmission dynamics model established above, this paper further improves it by considering the space size, space ventilation, joint positioning time, personnel distribution and airflow conditions. In addition, according to the classical disease transmission equation (SI, SIR, SIRS, SEIR) mentioned in Part II, people in confined space are firstly divided into four categories, as shown in the following table:

**Table 2 Group classification in confined space**

| classification | Specific description |
|---|---|
| Susceptible | Is not infect healthy, easy to be infected |
| Exposed | Contact with an infected person, but no ability to transmit |
| Infectious | An infected individual has been identified |
| Recoverd | An individual who is immune after recovery |

For the problem of disease transmission in confined space mentioned in this question, this paper combined the wells-Riley Model and Wells Model of disease transmission based on multi-stage time-delay dynamics to improve it. Firstly, this paper selected the basic Model. It is intended to use SEIR model to simulate the transmission process of disease in a confined space. This basic model does not consider space size, space ventilation and other factors, but directly considers the infection rate of individuals in the space and other factors related to the transmission of disease. The following equation is given:

$$\begin{cases} \dfrac{dS}{dt} = -\dfrac{r\beta IS}{N} \\ \dfrac{dE}{dt} = \dfrac{r\beta IS}{N} - \alpha E \\ \dfrac{dI}{dt} = \alpha E - \gamma I \\ \dfrac{dR}{dt} = \gamma I \\ N = S + E + I + R \end{cases} \tag{26}$$

For the basic formula above, its pseudocode is:

**Basic formula code:**

```
def JBCB(seir,para,steps) :
    S,E,I,R = seir
    r,beta,alpha,gamma,N = para
    dS = -(r*beta*I*S)/N
    dE = (r*beta*I*s)/N-alpha*E
    dI = alpha*E-gamma*I
    dR = gamma*
    return [S+dS*steps, E+dE*steps, I+dI*steps, R+dR*steps]
```

Considering the influence of space size and space ventilation on confined space, it can be seen from literature that the size of space has a positive correlation with the

spread of disease to a certain extent. For space ventilation, its influence on disease is as follows: the better the space ventilation, the lower the probability of disease transmission. Accordingly, the ventilation equation of space size is:

$$P_L(trans) = P_S(size)(1-\lambda S) + P_{S+1}(val)\lambda(S+1) \quad (27)$$

As for the time of co-location, it mainly focuses on the changes of people's positions in confined space with time, and carries out inverse calculation of the spread of disease according to the time of location. Therefore, the equation is as follows:

$$\frac{dp_s(loc)}{dt} = -\lambda \mathrm{Sp_S(t)\ R(t)} \quad (28)$$

For personnel distribution and air flow conditions, the personnel distribution can be uniform distribution or aggregation distribution. This paper intends to use parameter q to represent the distribution of personnel in a confined space. As for air flow conditions, this paper comprehensively considers the types of air in the confined space, ventilation conditions and air flow rate in the space, and the formula is as follows:

$$\mathrm{V}\frac{dC}{dt} = qI - QC - \sum_k B_k + \sum_k C_k \quad (29)$$

According to the above considerations of space size, space ventilation, time of joint positioning, personnel distribution and airflow conditions, together with the Wells-Riley Model and the Wells Model of disease transmission based on multi-stage time-delay dynamics, the disease transmission Model of confined space is obtained:

$$\begin{cases} \dfrac{dp_s(loc)}{dt} = -\lambda \mathrm{Sp_S(t)\ R(t)} \\ \dfrac{dE}{dt} = \dfrac{r\beta IS}{N} - \alpha E(size) \\ \dfrac{dI}{dt} = \alpha E(Dist) - \gamma I(Con) \\ \mathrm{V(air)}\dfrac{dC}{dt} = qI\,(air) - QC(loc) \\ P_L(trans) = P_S(1-\lambda S) + P_{S+1}\lambda(S+1) \end{cases} \quad (30)$$

Among them:

$p_s(loc)$: The spatial position of an individual in a confined space

$\mathrm{R(t)}$: The time profile of individuals in a confined space

$E(size)$: The size of the confined space

$I(Con)$: Air flow conditions in confined Spaces

$\mathrm{V(air)}$: The flow rate of air in a confined space

$P_L(trans)$: The spread of disease

$\lambda$: Wells-Riley Constants, its specific expression is shown in Formula (2)

## 3.4 Cellular automata simulation of disease transmission model

Cellular automata (CA), also known as lattice automata or cellular automata, is a discrete model consisting of infinite regular and rigid squares, each of which is in a finite state. The entire grid can be any finite-dimensional and discrete at the same time.

The state of each cell of cellular automata at t is determined by the state of a set of finite cells at t-1. The adjacent cells of each cell have been fixed. When cellular automata evolves each time, each cell evolves together in accordance with the same rule. For visualization of disease transmission model in confined space, cellular automata is selected in this paper for demonstration. Cellular automata has the characteristics of parallel computation, locality and consistency, which provides help for demonstration of disease transmission model.

### 3.4.1 Composition of cellular automata

For a standard cellular automata (A), it is mainly composed of cellular domain, cellular state, ingot dimension, state update rule, etc., which can be expressed by mathematical expression as:

$$A = (L,d,S,N,f) \tag{31}$$

Where, L is cellular space, d is the dimension of cellular space within cellular automata, S is the set of finite and discrete states of cellular, N is the set of all cellular in a certain field, and f is the reproduction rule of cellular.

The cellular space refers to the collection of the cellular space distribution by branch, ideally, cellular space is infinite extension in various dimensions, and a cellular automata is usually in a moment only taken from a finite set of a state, in here, this article take {0, 1}, where 0 means uninfected individuals, 1 infected individuals. Cellular status can represent individual infection to facilitate the exploration of disease transmission models.

### 3.4.2 Cellular automata reproduction rules

In this paper, cellular automata was used to simulate the disease transmission model in a closed space, and parameters were adjusted, such as space size, space ventilation, time of joint positioning, personnel distribution and airflow conditions. For the reproduction rule of cellular automata, this paper first defines its state at time t, and then calculates it through the spatial disease transmission model to update its state at time t+1. At time t, its state is expressed as follows:

$$S_t = (E_t, R_t, I_t, \lambda_t, \gamma_t) \tag{32}$$

Where, $E_t$ is the state of individuals in the incubation period in the confined space at time t, $R_t$ is the state of susceptible persons in the confined space at time t, and $I_t$ is the state of confirmed infected persons at time t.

For the reproduction rule of cellular automata, this paper defines a reproduction function, which is expressed as:

$$S_{t+1} = \varphi(E_t, R_t, I_t, \lambda_t, \gamma_t) \quad (33)$$

Here φ(·) is a five-dimensional discrete function, which defines its own automata rules and constraints the rules of each dimension cellular automata. Meanwhile, for the disease transmission model, this paper limits its state, which is a binary variable of 01. Therefore, the description of the above state will produce two to the fifth power of situations in total, and it is stipulated in this paper that for each position in the confined space, the occurrence of the state is equally probable.

## 3.5 Data sources and measurement methods

For the parameters used in the above model building, the source or measurement method will be given in this section.

### 3.5.1 Measurement method of space size

For the measurement of the size of the space, this article intends to use the method of photogrammetry, by measuring the known small-scale objects, and using the fisheye camera to measure the size of the confined space. The selected confined space is as follows:

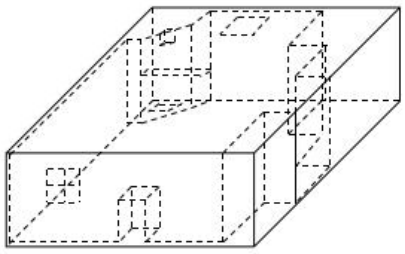

**Figure 5:Schematic diagram of confined space**

### 3.5.2 Measurement method of space ventilation

Use CFD technology to measure the ventilation of the confined space, install the device for measuring the ventilation of the space in the space, and use SolidWorks software to monitor the ventilation of the space in real time, and finally obtain the gas diffusion law in the confined space and the ventilation of the confined space Condition.

### 3.5.3 Measurement method of co-location time

For the measurement of positioning, this article carries out GPS tracking for people in confined spaces, which mainly uses applications on mobile phones to implement corresponding functions.

### 3.5.4 Measurement method of personnel distribution

For the measurement of personnel distribution, this article intends to use the co-location time measurement method to count the total number of individuals per unit area in a confined space, and perform real-time updates, and finally obtain the personnel distribution.

$$D_t = \frac{Num_{total}}{S_{space}} \tag{34}$$

### 3.5.5 Measurement method of airflow conditions

For the measurement of airflow conditions, electromagnetic sensors such as thermal resistance are used for measurement. When the fluid in the confined space passes through the sensor, the conditions of the fluid are recorded by the sensor, and then passed through the sensor verification system, sensor calibrator, etc. The device captures the airflow conditions and finally returns the data to the terminal.

# IV. Conclusions

## 4.1 The confined space disease transmission evaluation model

For the analysis of a specific scene in the title, this article selects a confined space, and for this confined space, its top view is as follows:

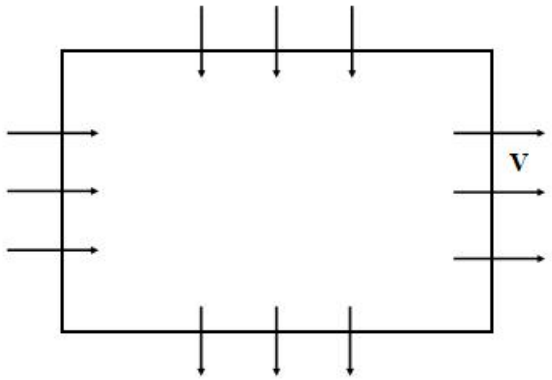


**Figure 6:Top view of confined space**

For the establishment of a simple mixed-air disease transmission model, for different ventilation conditions, its impact on the disease is shown in the following figure:

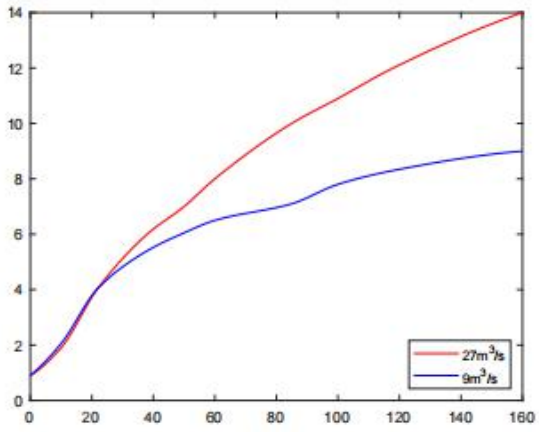


**Figure 7:The effect of mixed air on the spread of disease**

For the multi-stage time-lag dynamic disease transmission model, the transmission of diseases in a confined space is roughly divided into three stages through segmentation in the time domain, and this paper simulates different conditions (that is, different space ventilation conditions, personnel distribution) And the influence of the confined space environment of airflow conditions on the spread of diseases, the following results are obtained:

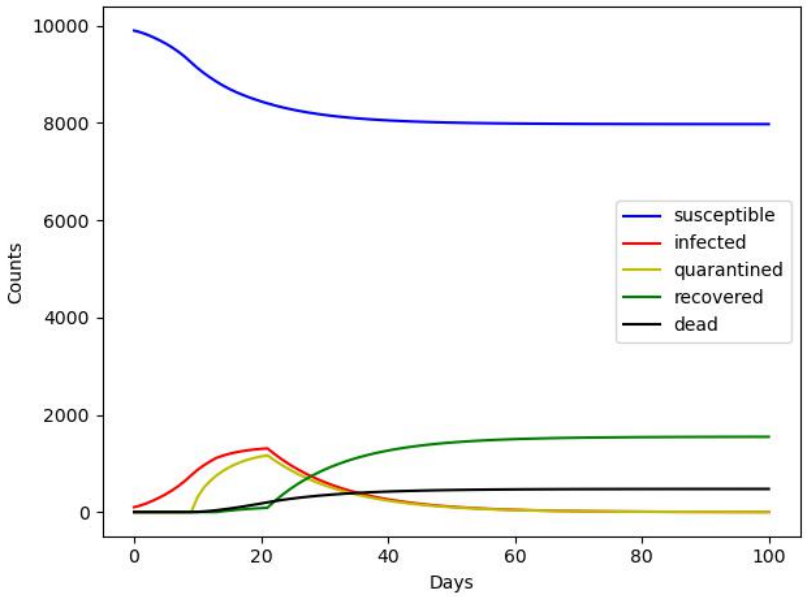


**Figure 8:Multi-stage dynamic disease transmission model**

For the results given above, this paper matches the decision vector (space size, space ventilation, co-location time, personnel distribution, airflow conditions) with the possibility of fluid-borne diseases, and makes decisions based on the 3 principles, and obtains the following results :

**Table 3:Evaluation of the possibility of disease transmission**

| Size of space ($m^3$) | Ventilation ($m^3$/s) | Co-location time(s) | Staff distribution(ind) | Airflow conditions(Pa • m/s) | Probability of spread(%) |
|---|---|---|---|---|---|
| 58.32 | 3.59 | 2.32 | 3.7 | 121.375K | 78 |
| 58.34 | 3.96 | 2.15 | 2.1 | 127.264K | 86 |
| 58.62 | 3.12 | 2.35 | 2.9 | 120.342K | 82 |
| 58.19 | 3.87 | 2.13 | 2.4 | 129.325K | 89 |
| ... | ... | ... | ... | ... | ... |

According to the above table, this paper takes a combination with a propagation probability of more than 85%, and it can be concluded that the propagation probability of the two sets of decision vectors (58.34,2.96,2.35,3.1,117.264) and (58.19,2.87,2.13,3.0,119.325) is greater than 85%. Therefore, based on these two sets of decision vectors, this article judges the factors studied accordingly, that is, when the size of the space is around $58m^3$, the ventilation is $3.93\pm0.05m^3$/s, the co-location time is $2.14\pm0.01$s, and the personnel distribution is $2.2\pm0.1$(ind) , When the airflow condition is $128.527\pm0.564$(Pa • m/s), the transmission probability is higher. At this time, the possibility of disease transmission by fluid in the confined space is higher. At this time, attention should be paid to the spread of disease.

## 4.2 Cellular automata simulation of disease transmission conclusion

The infection rate and other results of the confined space disease transmission model have been given in the first part, and then this article carries out the sensitivity test of the model, and wants to use the cellular automata to simulate the disease transmission process.

In this model, this paper assigns corresponding values to the element composition of cellular automata (A), which is mainly composed of cell domain, cell state, yuanbao dimension, state update rules, etc. It is expressed by mathematical expression as :

$$A = (L,d,S,N,f) \tag{31}$$

Among them, L is the location space composed of individuals in the confined space, d is the dimensionality of individuals in the confined space, S is the state of the individuals in the confined space, which is a binary variable representing infection or uninfected respectively, and N is A collection of all individuals in a confined space, f is the transmission rule of diseases in a confined space.

For the spread of the disease, this article simulates it from the spatial domain. In order to simplify the study of the problem, this article simply represents the confined space as a two-dimensional square space, where each individual is a pixel block, The color of the pixel block represents the state of different individuals. This article makes an individual in a confined space become infected with a disease, and divides it into two situations to study the possibility of disease transmission in a confined environment under different conditions. The simulation process is as follows:

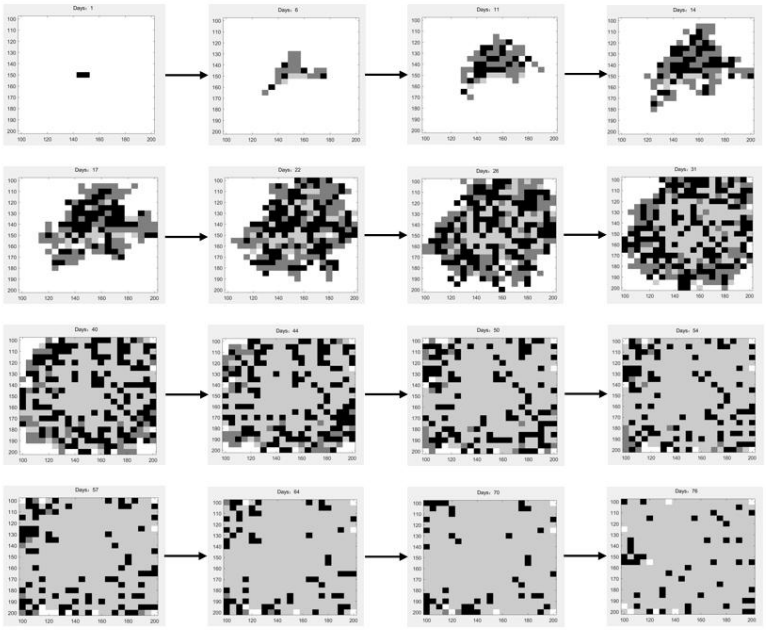

**Figure 9:Cellular Automata Simulation Process under Low Defense**

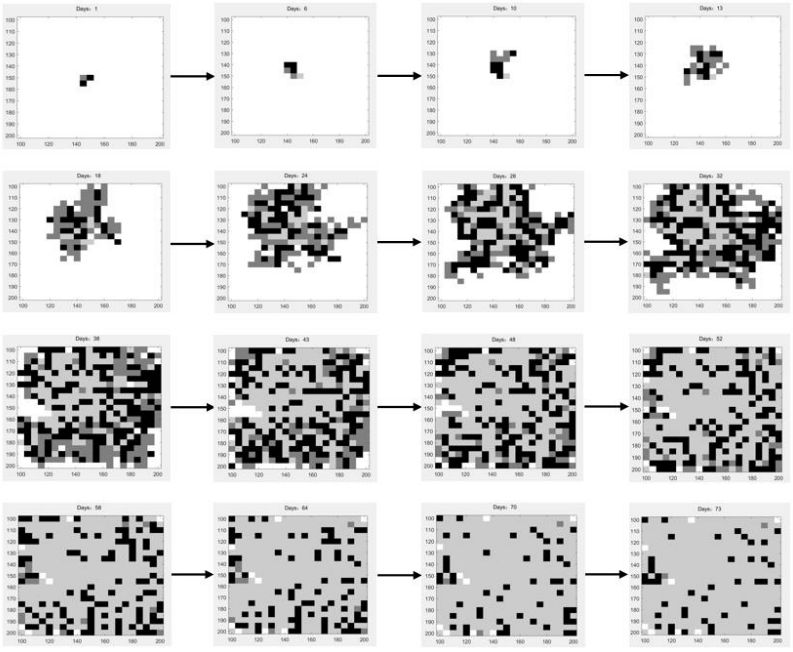

**Figure 10:Cellular Automata Simulation Process under High Defense**

In this paper, the simulation process of disease transmission is adjusted by adjusting the space ventilation, co-location time, personnel distribution and airflow conditions and other parameters, and a program suitable for simulating the disease transmission process is obtained through programming. The interactive interface is as follows:

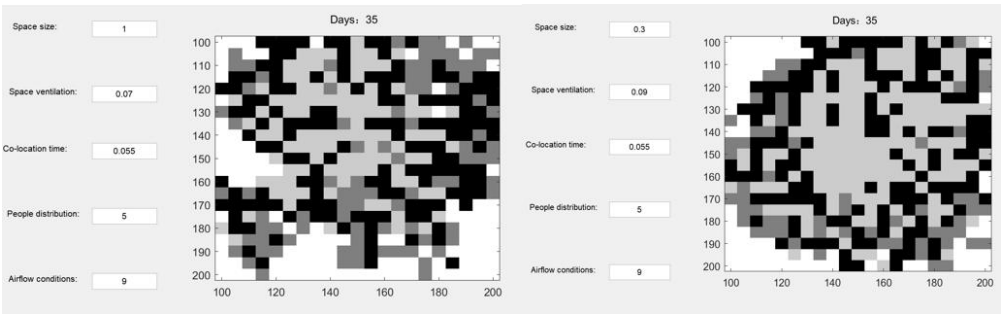


**Figure 11:Disease spreading simulation interface**

The above is the disease transmission model and the test of the model. Through the test of the cellular automata, the model established in this paper is verified to prove the rationality and correctness of the model establishment, and the simulation process of the disease transmission is given at the same time.

# V. Future Work

## 5.1 Advantages

**a.**Cellular automata can simulate isotropic phenomena better, and the model is more suitable for the actual situation.

**b.**The classic disease transmission equation can better describe the situation of disease transmission, which is conducive to the research of the problem.

**c.**The multi-stage discrete dynamic disease transmission model divides the disease transmission into multiple stages, which is beneficial to the study of the disease transmission process.

## 5.2 Shortcomings

**a.**Cellular automata is more difficult to express and display, and it is difficult to program.

**b.**The differential equation of disease transmission is difficult to solve, and sometimes there will be no solution.

**c.**The multi-stage discrete dynamics disease propagation model will produce multiple solutions, thereby increasing the complexity of problem solving.

## 5.3 Outlook

Regarding the confined space disease infection model established in this article, although computer simulation experiments have been performed on it and the disease transmission process has been simulated, there are still many areas for perfecting and improving the disease transmission model. The classic disease infection equation is used to establish an equation for the situation encountered in this topic, but there are still imperfections in the consideration of special circumstances. In the process of improving the model in the future, by adding the description and resolution of special situations, the model can be more perfect.

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# VII. Appendix

## Covid_sim.m

```
clear;clc;
N = 1300000000;
E = 600;
I = 400;
S = N - I;
R = 2;

B_11 = 0.09;
B_21 = 0.055;
B_12 = 0.015;
B_22 = 0.022;
r_11 = 5.29
r_21 = 8.11

T_1 = 1:14;
for idx = 1:length(T_1)-1
    S(idx+1) = S(idx) - B_11*r_11*I(idx) - B_21*r_21*E(idx);
    E(idx+1) = E(idx) + B_11*r_11*I(idx) + B_21*r_21*E(idx) - B_11*r_11*I(max(idx-7,1))*(idx-7>0) - B_21*r_21*E(max(idx-7,1))*(idx-7>0);
    I(idx+1) = I(idx) + B_11*r_11*I(max(idx-7,1)) + B_21*r_21*E(max(idx-7,1)) - B_11*r_11*I(max(idx-21,1))*(idx-21>0) - B_21*r_21*E(max(idx-21,1))*(idx-21>0);
    R(idx+1) = R(idx) + B_11*r_11*I(max(idx-21,1))*(idx-21>0) + B_21*r_21*E(max(idx-21,1))*(idx-21>0);
end

%T_2 = 15:21;
for idx = 14:20
    r_12 = (5.29-1.91)*exp(-0.96*idx-15)+1.91;
    r_22 = (8.11-1.88)*exp(-1.61*idx-15)+1.88;
    S(idx+1) = S(idx) - B_11*r_12*I(idx) - B_21*r_22*E(idx);
    E(idx+1) = E(idx) + B_11*r_12*I(idx) + B_21*r_22*E(idx) - B_11*r_11*I(idx-7) - B_21*r_21*E(idx-7);
    I(idx+1) = I(idx) + B_11*r_11*I(max(idx-7,1)) + B_21*r_21*E(max(idx-7,1)) - B_11*r_11*I(max(idx-21,1))*(idx-21>0) - B_21*r_21*E(max(idx-21,1))*(idx-21>0);
```

```
30.       R(idx+1) = R(idx) + B_11*r_11*I(max(idx-21,1))*(idx-21>0) + B_21*r_21*E(
    max(idx-21,1))*(idx-21>0);
31.   end
32.
33.   for idx = 21:27
34.       r_12 = (5.29-1.91)*exp(-0.96*idx-15)+1.91;
35.       r_22 = (8.11-1.88)*exp(-1.61*idx-15)+1.88;
36.       r_13 = (1.91-0.47)*exp(-1.86*idx-22)+0.47;
37.       r_23 = (1.88-0.96)*exp(-1.89*idx-22)+0.96;
38.       S(idx+1) = S(idx) - B_12*r_13*I(idx) - B_22*r_23*E(idx);
39.       E(idx+1) = E(idx) + B_12*r_13*I(idx) + B_22*r_23*E(idx) - B_11*r_12*I(id
    x-7) - B_21*r_22*E(idx-7);
40.       I(idx+1) = I(idx) + B_11*r_12*I(max(idx-7,1)) + B_21*r_22*E(max(idx-7,1)
    ) - B_11*r_11*I(max(idx-21,1)) - B_21*r_21*E(max(idx-21,1));
41.       R(idx+1) = R(idx) + B_11*r_11*I(max(idx-21,1))*(idx-21>0) + B_21*r_21*E(
    max(idx-21,1))*(idx-21>0);
42.   end
43.
44.   for idx = 28:34
45.       r_12 = (5.29-1.91)*exp(-0.96*idx-15)+1.91;
46.       r_22 = (8.11-1.88)*exp(-1.61*idx-15)+1.88;
47.       r_13 = (1.91-0.47)*exp(-1.86*idx-22)+0.47;
48.       r_23 = (1.88-0.96)*exp(-1.89*idx-22)+0.96;
49.       S(idx+1) = S(idx) - B_12*r_13*I(idx) - B_22*r_23*E(idx);
50.       E(idx+1) = E(idx) + B_12*r_13*I(idx) + B_22*r_23*E(idx) - B_12*r_13*I(id
    x-7) - B_22*r_23*E(idx-7);
51.       I(idx+1) = I(idx) + B_12*r_13*I(idx-7) + B_22*r_23*E(idx-7) - B_11*r_11*
    I(idx-21) - B_21*r_21*E(idx-21);
52.       R(idx+1) = R(idx) + B_11*r_11*I(idx-21) + B_21*r_21*E(idx-21);
53.   end
54.
55.   for idx = 35:59
56.       r_12 = (5.29-1.91)*exp(-0.96*idx-15)+1.91;
57.       r_22 = (8.11-1.88)*exp(-1.61*idx-15)+1.88;
58.       r_13 = (1.91-0.47)*exp(-1.86*idx-22)+0.47;
59.       r_23 = (1.88-0.96)*exp(-1.89*idx-22)+0.96;
60.       S(idx+1) = S(idx) - B_12*r_13*I(idx) - B_22*r_23*E(idx);
61.       E(idx+1) = E(idx) + B_12*r_13*I(idx) + B_22*r_23*E(idx) - B_12*r_13*I(id
    x-7) - B_22*r_23*E(idx-7);
62.       I(idx+1) = I(idx) + B_12*r_13*I(idx-7) + B_22*r_23*E(idx-7) - B_12*r_12*
    I(idx-21) - B_22*r_22*E(idx-21);
63.       R(idx+1) = R(idx) + B_12*r_12*I(idx-21) + B_22*r_22*E(idx-21);
64.   end
65.
```

```
for idx = 60:79
    r_12 = (5.29-1.91)*exp(-0.96*idx-15)+1.91;
    r_22 = (8.11-1.88)*exp(-1.61*idx-15)+1.88;
    r_13 = (1.91-0.47)*exp(-1.86*idx-22)+0.47;
    r_23 = (1.88-0.96)*exp(-1.89*idx-22)+0.96;
    S(idx+1) = S(idx) - B_12*r_13*I(idx) - B_22*r_23*E(idx);
    E(idx+1) = E(idx) + B_12*r_13*I(idx) + B_22*r_23*E(idx) - B_12*r_13*I(idx-7) - B_22*r_23*E(idx-7);
    I(idx+1) = I(idx) + B_12*r_13*I(idx-7) + B_22*r_23*E(idx-7) - B_12*r_13*I(idx-21) - B_22*r_23*E(idx-21);
    R(idx+1) = R(idx) + B_12*r_13*I(idx-21) + B_22*r_23*E(idx-21);
end
speed = 0.3;
restart_flag = 0;


fig3=figure( 'Name',',','Position',[0,0,700,500] ,'NumberTitle','off','toolbar','none','menubar','none','visible','off');
movegui(fig3,[800,200]);
set(fig3,'visible','on');
fig3_flag = gcf;
uicontrol('Style','pushbutton','Position',[50,50,100,30],'String','start','callback',@start);
uicontrol('Style','pushbutton','Position',[180,50,100,30],'String','restart','callback',@restart);
uicontrol('Style','pushbutton','Position',[370,50,100,30],'String','Pause','callback',@btnPause);
uicontrol('Style','pushbutton','Position',[500,50,100,30],'String','Go on','callback',@btnGoOn);
uicontrol('Style','text','Position',[20,450,80,20],'String',':');


function restart(x,y)
    restart_flag = 1;
end

function set_temp(x,y)
    speed = str2num(get(edit_speed,'string'));
    B = str2num(get(edit_B,'string'));
    B2 = str2num(get(edit_B2,'string'));
    r = str2num(get(edit_r,'string'));
    r2 = str2num(get(edit_r2,'string'));
    a = str2num(get(edit_a,'string'));
    y1 = str2num(get(edit_y1,'string'));
```

```
end

function start(x,y)
    restart_flag = 0;
    Day = 140;
    T = 1:Day;
    for idx = 1:length(T)-1
        S(idx+1) = S(idx) - r*B*S(idx)*I(idx)/N - r2*B2*S(idx)*E(idx)/N;
        E(idx+1) = E(idx) + r*B*S(idx)*I(idx)/N - a*E(idx) + r2*B2*S(idx)*E(idx)/N;
        I(idx+1) = I(idx) + a*E(idx) - y1*I(idx);
        R(idx+1) = R(idx) + y1*I(idx);
    end
    fig2=figure( 'Name','曲线图','Position',[0,0,600,400] ,'NumberTitle','off','toolbar','none','menubar','none','visible','off');
    movegui(fig2,[200,200]);
    set(fig2,'visible','on');
    plot(T,S,T,E,T,I,T,R);grid on;

    pro_E_I = 1-B;
    pro_E_E = 1-B2;
    pro_III = 1-r/8;
    pro_EEE = 1-r2/8;
    pro_I = 1-a;
    pro_R = 1-y1;

    for mbmb = 0 : Day
        if(restart_flag == 1)
            break
        end
        for len = 0:mbmb
            if(restart_flag == 1)
                break
            end
            for xxx = -len:len
                if(restart_flag == 1)
                    break
                end
                yyy = len - abs(xxx);
                if (M+abs(xxx)<=Unit-1 && M+abs(yyy)<=Unit-1)
                    if Temp(M+xxx,M+yyy) == 3
                        for x = -1:1
                            for y = -1:1
```

```
                                if Temp(M+xxx+x,M+yyy+y) == 0 && rand > pro_
    E_I && rand > pro_III
                                    Temp(M+xxx+x,M+yyy+y) = 2;
                                end
                            end
                        end
                    end
                    if Temp(M+xxx,M+yyy) == 2
                        for x = -1:1
                            for y = -1:1
                                if Temp(M+xxx+x,M+yyy+y) == 0 && rand > pro_
    E_E && rand > pro_EEE
                                    Temp(M+xxx+x,M+yyy+y) = 2;
                                end
                            end
                        end
                    end
                end
                if (M+abs(xxx)<=Unit-1 && M+abs(yyy)<=Unit-1)
                    if Temp(M+xxx,M-yyy) == 3
                        for x = -1:1
                            for y = -1:1
                                if Temp(M+xxx+x,M-yyy+y) == 0 && rand > pro_
    E_I && rand > pro_III
                                    Temp(M+xxx+x,M-yyy+y) = 2;
                                end
                            end
                        end
                    end
                    if Temp(M+xxx,M-yyy) == 2
                        for x = -1:1
                            for y = -1:1
                                if Temp(M+xxx+x,M-yyy+y) == 0 && rand > pro_
    E_E && rand > pro_EEE
                                    Temp(M+xxx+x,M-yyy+y) = 2;
                                end
                            end
                        end
                    end
                end
                        if Temp(temp_x,temp_y) == 2
                            for x = -1:1
                                for y = -1:1
                                    if Temp(temp_x+x,temp_y+y) == 0 && rand>
```

```
    pro_E_E && rand > pro_EEE
                                        Temp(temp_x+x,temp_y+y) = 2;
                                    end
                                end
                            end
                        end

function btnPause(x,y)
uiwait();
end

function btnGoOn(x,y)
uiresume();
end
end
```

**Cellular_automata_sim.m**

```
close;
clear;
clc;

Map = [1 1 1; 0 0 0];
colormap(Map);

gap = 0.5;
test = 2;

S = 21;
L = zeros(S);

M = (S+1)/2;
L(M,M) = 1;
Temp = L;
imagesc(L);

length_max = 2*M;

for length = 1 : length_max
    for x = -length : length
        y = length - abs(x);
        if M+abs(x)<=S && M+abs(y)<=S
            if(rand>gap)
                Temp(M+x,M+y) = 1;
            end
```

```
            if(rand>gap)
                Temp(M+x,M-y) = 1;
            end
        end
        for z = 1:test
            x_1 = fix(rand*length*2-length); y_1 = fix(rand*length*2-length)
;
            if(M+abs(x_1)<=S && M+abs(y_1)<=S && abs(x_1)+abs(y_1)<length)
                if(rand > gap && Temp(M+x_1,M+y_1) == 0 )
                    Temp(M+x_1,M+y_1) = 1;
                end
            end
        end
    end
    pause(0.5);
    imagesc(Temp);
end
while 1
    for z = 1:100
        x = fix(rand*S+1);y=fix(rand*S+1);
        if(x >0 && y>0 && Temp(x,y) == 0)
            if(rand > gap)
                Temp(x,y) = 1;
            end
        end
    end
    pause(0.1);
    imagesc(Temp);
end
```