

Improved small-world network --model definition and generative function derivation in infectious disease scenarios

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Abstract: In recent years, there has been growing interest in predicting and simulating the spread and prevention of infectious diseases. The most commonly used model is the SEIR model, which characterizes the spread process by introducing parameters such as the infection rate, contact numbers, incubation period, and recovery rate. Despite its widespread application, this model has some limitations. Firstly, it is a quantity-based model that only reflects changes in quantity and cannot capture the spatial spread of the disease. Secondly, in the transmission of infectious diseases, there is a noticeable threshold phenomenon in terms of quantity, which the SEIR model cannot depict. The use of SEIR in specific scenarios can partially address the aforementioned issues. Common approaches include considering individuals as organized within a small-world network, where the proximity of individuals on this network influences the spread of infectious diseases. The model constructed in this paper attempts to introduce geographical space on this basis, defining a small-world network in geographical space and providing a generating function for the percolation phenomenon of disease transmission within it.

Keywords: Small-World Network; Percolation; Generating Function.

1. Introduction

In recent years, more attention has been paid to the prediction and simulation of infectious disease transmission and prevention. The most widely used model used for this purpose is the SEIR model. The SEIR model is a system of ordinary differential equations that characterizes the changes of four groups of people by combining the infection rate, the number of contacts, the incubation period and the recovery rate: susceptible, exposed, infected and recovered. Although this pattern is widely accepted, it also has limitations. First, it is a quantitative model that reflects only the numerical change and cannot represent the spatial spread of the disease, and second, it cannot explain the dynamic change in the behavior of the infection when the reproductive number reaches a certain threshold.

Many classical models in statistical physics, such as the Ising and spin-glass models, have been widely used in social science issues such as crowd and network public opinion. The above phenomena in disease transmission are similar to the phase transition phenomenon in statistical physics. Percolation model is a theoretical model used to describe the permeability characteristics of fluids in porous media, such as water diffusion in rocks or soil, and the transmission of electricity in the grid. There are many similarities between the epidemic transmission process and the override model, including: both can be regarded as stochastic processes: the override model models the penetration probability of each spatial location, while the epidemic transmission model models the probability of infection of each person. Both require consideration of the uncertainty of the influence of random factors on the outcome; both are nonlinear systems: percolation models usually exhibit a phase transition, while epidemic transmission usually has a similar "burst" effect. This means that the behavior of the system dynamics will change dramatically when certain parameters satisfy certain conditions. Both can be modeled through the network (such

as social networks) to predict their propagation effect. The override model can be used to study the transmission of electricity, epidemic diseases, etc., and the degree and frequency of contact between people play a decisive role in the transmission of the virus. Therefore, I hope to draw on the models and theories of statistical physics to establish an epidemic transmission model that includes the spatial transmission process of epidemic transmission, so as to better understand the law of epidemic transmission from the micro mechanism and optimize the epidemic prevention and control strategies accordingly.

My expected work includes: systematic learning of relevant statistical physics theories, models and methods; established the parameter model influenced by the seepage model; discussed the model, including its critical exponent and fractal structure; and evaluated and corrected the model through computer simulation experiment (Monte Carlo simulation) (the time reason is not yet realized).

2. SEIR Model and Research Thinking

The SEIR model is a mathematical model commonly used in the study of the transmission of infectious diseases. It divides the population into four main categories: susceptible, latent, infected, and recovered. The model, which describes the transfer process between categories and changes in the number of populations based on differential equations, can be used to predict disease transmission trends and explore strategies to control infectious diseases.

2.1. Model fundamentals:

The SEIR model describes the transmission process of the disease by considering the latency period (latent state), based on the mobility and contact behavior of the population. The basic principles are provided as follows:

Susceptible: Individuals in the population who have not yet been infected can be infected to spread the disease.

Exposed: Individuals who have been infected but have not

yet shown obvious symptoms are in the incubation period. During this period, lurkers can transmit disease to susceptible individuals.

Infectious: Individuals who have already been infected and can transmit the disease can directly infect susceptible individuals.

Recovered: After a certain period of time, the infected person may recover and have immunity, and can no longer be infected

. The transfer process in the SEIR model can be represented by the following formula:

$$\begin{aligned}dS/dt &= -\beta * S * I / N \\dE/dt &= \beta * S * I / N - \alpha * E \\dI/dt &= \alpha * E - \gamma * I - \theta * I \\dR/dt &= \gamma * I \\dD/dt &= \theta * I \\dN/dt &= -\theta * I\end{aligned}$$

Where, S is the number of susceptible persons, E is the number of latent persons, I is the number of infected persons, and R is the number of recovered persons. Where t is time, N is the total population, β is the infection rate, α is the reciprocal of the incubation period (the average incubation time is $1 / \alpha$), and γ is the reciprocal of the infection period (the average time of the infection period is $1 / \gamma$).

2.2. Model interpretation and application

Changes in the number of susceptible persons (dS / dt): The number of susceptible persons decreases with the contact between infected persons and susceptible persons, and the rate of reduction is related to the infection rate (β) and the proportion of susceptible persons and infected persons.

Change in the number of lurkers (dE / dt): The increase in the number of lurkers depends on the contact between the infected person and the susceptible person and the reciprocal of the incubation period (α), while the decrease depends on the conversion of the latency person to the infected person.

Change in the number of infected persons (dI / dt): The increase in the number of infected persons is related to the conversion of the latent person to the infected person, the increase rate depends on the reciprocal of the incubation period (α), and the reduction rate depends on the rate of recovery or death of the infected person (γ).

Change in the number of survivors (dR / dt): The increase in the number of survivors depends on the rate of recovery of the infected person (γ).

The SEIR model can help researchers to predict the transmission trend of infectious diseases in the population, and to understand the law of disease outbreak and the effect of prevention and control strategies. By adjusting the parameters of the infection rate, incubation period and infection period, simulating the transmission process of different diseases and evaluating the effects of different interventions can be performed.

To study the spread of infectious diseases in small-world networks, we can combine the small-world network model and the permeation model to construct a new model. This new model takes into account the local connection characteristics between nodes and the penetration and transmission process of infectious diseases to better describe the transmission rules of infectious diseases in the network.

Square Lattice Percolation Model Is one of the simplest and most classical models in overstepping theory. The model represents the medium as a grid of squares, and each grid point can be either an open or a closed state. By randomly

setting the open probability in the grid, we can study the occurrence probability of the connected path in the medium and its influence on the matter conduction behavior.

Here are the basic steps and key concepts of the grid overpenetration model:

Grid: The media in the model is represented by a grid where each node represents a tiny unit. The mesh can be either two-dimensional or higher-dimensional.

Open probability: each node has the probability of being set to an open state at some point. This probability is usually expressed as p, with values of p ranging between 0 and 1.

Connectivity: Connectivity is the key concept in the grid overpenetration model. If, starting from one position (starting node), along the open node can reach the other position (target node) on the grid, the two locations are said to be connected.

Clusters: Clusters are a collection of connected nodes. In the square lattice overstepping model, a cluster consists of connected open nodes that can be adjacent horizontally, vertically or diagonally.

Critical probability: Critical probability (Critical Probability) is an important concept, representing the probability threshold for forming infinite clusters in a medium. When the open probability exceeds the critical probability, infinite clusters appear in the medium.

Many interesting results and properties can be obtained by studying the lattice overpermeability model:

Critical probability: The critical probability in the square overstepping model is usually expressed as p_c . When the open probability p is less than p_c , no infinite clusters form; when p is equal to or greater than p_c , infinite clusters will form.

Connectivity probability: Connectivity probability is the probability of reaching from one position to another at a given open probability. By randomly setting the open probability in the square lattice override model, the connectivity probability between different positions can be calculated and studied with the open probability.

Critical exponential: Near the critical probability, the lattice overriding model shows the behavior of the critical exponential. The critical index describes different physical quantities (such as cluster size, average path length, etc.)

Model ideas:

Building small world networks: First, we build a network with local and random connectivity based on the small world network model. The Watts-Strogatz model can be used to generate small-world networks where parameters include the number of nodes, number of neighbors of each node and random reconnection probability.

Node state modeling: Each node is divided into three states: easily infected (Susceptible), infected (Infected), and recovered (Recovered). In the initial state, some nodes are marked as infected, while other nodes are easily infected.

Definition of infection probability: defines the probability of infection between nodes, indicating the probability of transmission from an infected person to an easily infected person. The probability of infection can be determined based on factors such as the characteristics of infectious diseases and the distance between nodes.

Percolation model building: based on the idea of percolation model, to simulate the transmission process of infectious diseases in the network. Specifically, the infectious state of each node is updated according to the state of its surrounding nodes and the infectious probability. Infected patients can infect their neighbor nodes, the vulnerable to infected people may be infected, and the recovered people

will not be infected again.

Iteration: to simulate the transmission process of infectious diseases in the network by iteratively updating the infectious state in the node. Each round of iteration can be represented as a time step where the infectious state evolves over time.

formula derivation:

In this model, we introduce the following symbols:

N: The total number of nodes in the network

The t: time step (number of iterations)

S (t): the number of easily infected persons changes over time

I (t): the change in the number of infected persons over time

R (t): The number of survivors changes over time

β : Probability of infection

K: Number of neighbors of the node

And p: Random reconnection probability

Based on the model idea and the basic principle of the percolation model, we can derive the following formula:

Formula for changing the number of easily infected persons:

$$S(t+1) = S(t) - \beta * S(t) * I(t) + p * R(t)$$

It means that the number of easily infected people changes with time, and easily infected people may become infected through infected persons, or recover through random reconnection processes.

Formula for the change in the number of infected persons:

$$I(t+1) = I(t) + \beta * S(t) * I(t) - \gamma * I(t)$$

It means that the number of infected persons changes over time, and the infected persons may transmit to other nodes through contact with the easily infected persons. At the same time, some infected persons may recover due to recovery.

Formula for the number of recovered:

$$R(t+1) = R(t) + \gamma * I(t) - p * R(t)$$

It means that the number of survivors changes over time, and that the survivors may increase through the recovery of infected persons or decrease through the random reconnection process.

Among them, γ represents the recovery rate, namely the probability of recovery of an infected person.

Model interpretation:

Through the above model, we can simulate and study the transmission process of infectious diseases in small-world networks. The small-world network in the model considers the local connection and random connection properties between the nodes, and is closer to the real-world network structure. At the same time, the percolation model describes the penetration and transmission process of infectious diseases, and simulates the transmission path and transmission speed of infectious diseases through the contact and information transmission between nodes.

By adjusting parameters such as infection probability, number of node neighbors and stochastic reconnection probability, we can study the influence of different factors on the transmission process of infectious diseases. For example, increasing the probability of infection may accelerate the rate of infection, while increasing the probability of random reconnection may expand the range of transmission. Furthermore, we can also evaluate its inhibitory effect on the transmission of infectious diseases by introducing interventions, such as isolation and vaccination.

3. The process of point infiltration on the circular small world network

The following introduces the basic concepts and methods

of infiltration in the small world network. The concept of overstepping was first proposed by Broadbent and Hammersley in 1957 to describe fluid phenomena in disordered media. The concept was originally used to refer to that when the pore density in a disordered pore system reaches a certain degree, the system has a long-range correlation, which leads to a phase transition behavior in which a large number of pores are interconnected. In the complex process of the real world, there is often the feature of "critical point", that is, when a certain characteristic index of the system reaches a certain threshold, the original stable dynamic process of the system is mutated to another stable or non-stable state. Due to the above reasons, the superosmosis model is very effective in studying the scientific process of transmission and diffusion as the basic phenomenon, and has been successfully applied in materials, biology, social sciences and other fields. In 1967, psychologist Stanley Milgram conducted an experiment called "communication" to study social network structure. He devised a simple experiment, beginning in Kansas and Nebraska, by trying to pass it on to Boston targets through a series of traceable letters. People pass letters through their friends or acquaintances, record the transfer of each middleman, and finally count the number of deliveries. The results were surprisingly consistent, showing that an average of six passes from start to final delivery to the target person. This is called the "small-world" phenomenon, and raises the assumption of "six degrees of separation" that connections between any two people can be established by an average of six people. Despite some flaws in Milgram's experiments, his concept of a "small world" has been widely accepted. The "small-world" phenomenon was originally applied to sociological network analysis concepts, but it was not until 1998 that Watts and Strogatz proposed the first small-world network model. They constructed this model by tuning a parameter that moves the regular network over to a random network. The model was constructed by starting from a one-dimensional circular regular network with n nodes, each node connected to its nearest k nodes, and satisfied $n \gg k \gg \ln(n) \gg 1$, among $k \gg \ln(n)$ were ensure to form a random network. For each edge, changing its target connection point with probability p, reconnecting the edge, ensuring that no repeated edges appear, thus generating $pnk / 2$ long-range edges connecting a node to a distant node. By changing the value of p, you can transition from a regular network ($p=0$) to a random network ($p=1$).

The proposal of small-world network models provides an important basis for our understanding and studying the structure and properties of complex networks. It reveals the features present in many real networks, such as social networks, Internet and neural networks, where the connections between nodes are characterized by short path length and high clustering. Small-world network models provide us with a new perspective to understand the phenomena of information transmission, disease transmission, and social impact.

When using small-world networks to study infectious disease problems, the nodes in the network are first arranged in a nearest neighbor ring network, but the network does not destroy the original connection, but only adds new connections to the nearest neighbor ring network with a small probability. Therefore, the SIR model on the network in the traditional method can be equivalent to the overstepping process.

Infiltration theory is the best theoretical approach for

treating systems with strong disorder and random geometric structures. It has two basic types: seat overpenetration and key overpenetration. These methods start from the periodic lattice array of rules, and specify the non-geometric properties reflecting the statistical characteristics of the problem, so as to transform the regular geometry into a random geometry. The transition from regular geometry to random geometry has a critical value, namely the overpermeability threshold p_c , which is only possible when this threshold is reached.

As p represents the proportion of easily infected people in the whole population, ϕ represents the ratio of the number of newly added edges and the original number of the edges, and k represents the number of nodes connected to a node in a clockwise or counterclockwise direction in the nearest-neighbor ring network. The critical value of the network can be expressed in implicit representation.

$$\phi = \frac{(1 - q_c)^k}{2kq_c[2 - (1 - q_c)^k]}$$

Point overinfiltration model

In epidemiology, there are two simple parameters of interest, respectively, susceptibility and transmissibility. Susceptibility is the probability of an individual exposed to the disease being infected, while transmissibility is the probability of an infected person after contact with a healthy but susceptible individual. In this paper, we assume that a disease starts with an infected person. Individuals are represented by sites of the small-world model, while disease spreads along edges representing interindividual contacts. We denote sites as occupied depending on whether the individual is susceptible to the disease, and edges as occupied depending on whether contact spreads the disease to the susceptible individual. If the distribution of occupied site or edge is random, then determine when the outbreak of epidemic problem is equivalent in the small world map: how many proportion for p_c site or edge is occupied, a composed of connected site "huge cluster" formation, its size and the proportion of the total station L increased significantly.

We will start with the case of site penetration, where each healthy but susceptible individual whose contact with an infected individual causes transmission, but not all individuals are susceptible. The proportion of occupied sites, p , is exactly equal to the susceptibility as defined above. Consider a one-dimensional small-world graph, as shown in Figure 1. L sites are arranged on a one-dimensional lattice according to the periodic boundary conditions, and connect the edges between all sites separated by no more than k distances. (For simplicity, we chose $k=1$ in Fig.) Now, add shortcuts between randomly selected pairs of sites. The parameter ϕ is usually defined as the average number of shortcuts at each edge on the underlying lattice. For a large L , the probability of a shortcut between two randomly chosen sites is:

$$\psi = 1 - \left[1 - \frac{2}{L^2}\right]^{k\phi L} \approx \frac{2k\phi}{L}$$

On a small-world graph, a connected cluster consists of multiple local clusters composed of occupied sites joined together by nearly adjacent edges on the underlying one-dimensional lattice, while these local clusters are interconnected by shortcuts. For $k = 1$, the average number of local clusters with length i is:

$$M_i = (1 - q)^2 q^i L$$

For the general k there is $M_i = (1 - q)^{2k} q^i (1 - (1 - q)^k)^{i-1} L = (1 - q)^2 q q^{i-1} L$,

Now we construct a connected cluster from these local clusters in the following way. We start with a specific local cluster, by first adding to it all other local clusters that can be reached by a single shortcut. We then add all local clusters that can be reached along a single shortcut from these new local clusters, and so on until the connected clusters are complete. Let us define a vector v at each step of this process, with a cluster v_i equal to the probability of a local cluster of size i just being added to the overall connected cluster. We wish to calculate the value v' of this vector according to the value v of the previous step. At or below the penetration threshold, v_i is small, so that the v'_i will be linearly related to v_i according to the transition matrix M , i. e.: $v'_i = \sum_j M_{ij} v_j$,

$$M_{ij} = M_i (1 - (1 - \psi)^{ij}). (*)$$

Here N_i is the number of local clusters with size i as described previously, $(1 - \psi)^{ij}$ is the probability of a shortcut from local clusters of size i to local clusters of size j , since there are ij pairs of possible sites that can be connected by them. Note that M is not a random matrix, i. e., it is not normalized such that the sum of its rows is equal to units.

Now consider the maximum eigenvalue of M , λ . If $\lambda < 1$, the iterative equation (*) will shift v to zero, so that the rate of new local cluster addition will decay exponentially and the connected clusters are finite, with an exponential size distribution. Conversely, if $\lambda > 1$, v grows until the cluster size is limited by the overall system size. The penetration threshold occurs at $\lambda = 1$.

For a finite L , it is difficult to find the maximum eigenvalue of M . However, if ϕ remains constant, when L , it approaches zero ψ , so for large L , we can approximate M as: $M_{ij} = ij\psi M_i$

This matrix M is the fork product of two vectors, once the above equation * can be expressed as

$$\lambda v_i = i\psi M_i \sum_j j v_j,$$

Among $v'_i = \lambda v_i$. M 's eigenvalue form of $v_i = C\lambda^{-1} i\psi M_i$, where the constant $C = \sum_j j v_j$. So there is

$$\lambda = \psi \sum_j j^2 M_j$$

For $k = 1$,

$$\lambda = \psi L q \frac{1 + q}{1 - q} = 2\phi q \frac{1 + q}{1 - q}.$$

Suppose q_c set to 1 yields the ϕ value at the permeation threshold p_c :

$$\phi = \frac{1 - q_c}{2q_c(1 + q_c)},$$

The reverse solution is obtained:

$$q_c = \frac{\sqrt{4\phi^2 + 12\phi + 1} - 2\phi - 1}{4\phi}.$$

To the general k

$$\lambda = \psi L q \frac{1 + q}{1 - q} = 2k\phi q \frac{2 - (1 - q)^k}{(1 - q)^k},$$

$$\phi = \frac{(1 - q_c)^k}{2kq_c(2 - (1 - q_c)^k)}.$$

The threshold density p_c is the root of a polynomial of order $k + 1$.

4. Over Infiltration model of infectious diseases on two-dimensional lattice

This chapter tries to model the two-dimensional lattice points in geographical space to describe the infiltration process of infectious diseases spreading in geographical space. The traditional SEIR model is a pure quantitative model, which can only describe the change of four types of population of a city with time, and does not explore the transmission mechanism of infectious diseases from the micro process of transmission. However, "more is different", the transmission of infectious diseases is a complex process, and the variables of the infectious process in the macroscopic (total population) often do not have a single or simple law, and the characteristics of the change themselves also change with the change of the transmission stage of infectious diseases, the infection proportion, the population density and other factors. When this change is large, the original parameter model becomes invalid. For example, the SEIR model is continuous and stable due to the form of the one-order differential equation, which cannot explain the critical phenomenon similar to the "phase transition" in the spread of infectious diseases. Therefore, in the previous article, we use the infiltration process on the small world network in a one-dimensional ring to describe the temporary phenomenon by discussing the permeability threshold.

In addition to focusing on the prediction of its transmission by infectious disease models, we also focus on whether the calculation results of the model can guide us to take what measures to counter its transmission. In experience-oriented practice, we often isolate geographical units of different sizes, such as buildings and blocks as controlled Spaces. However, although the above one-dimensional ring in the small world on the network process this model, compared with the traditional quantity parameters model more clear on the microscopic mechanism, but because the model is essentially based on social network, did not fully put the geographical space in the model, makes the model is difficult to predict the spread of infectious diseases in the geographical space. The latter is often more important in developing practical epidemic responses, because we often have to solve the problem of how to prevent the spread of infectious diseases from A to B. At the same time, the real geographical space itself has heterogeneity, and the distribution of population in the city itself has an unbalanced structure, which results in different infection risks of different lattice points. Therefore, the use of a single p -value to depict the critical threshold of overinfiltration lacks the reflection of spatial heterogeneity. Therefore, we tried to model the two-dimensional lattice point in geographical space, and use some means to correct the seepage threshold, so as to restore the real situation of infectious diseases in geographical space.

4.1. Overtone phase transition at two-dimensional lattice points

In this section, we briefly describe the transition phase transition at two-dimensional lattice points. On a two-dimensional positive square lattice, each lattice site or connection has two occupied and non-occupied states. Several connected lattice points form a cluster (cluster). For the bond overpenetration model, the connection of each team in the grid has a probability of p . If the two keys can be connected by the connected keys, the two keys are said to belong to the same cluster. When p is small, many small

clusters are distributed in the lattice. As the value of p increases, the number of connected bonds in the whole system increases, resulting in the generation of new clusters compared with the growth of the preexisting small clusters. Small clusters have the opportunity to connect with other clusters to form larger clusters during growth. When p reaches the critical threshold q_c , the first cluster appears through the whole region in the finite lattice point in the system, or the infinite cluster in the infinite two-dimensional plane, which makes the system change in the connectivity angle.

The override probability $P(p)$ is defined as the probability that an arbitrarily connected bond belongs to a connected or infinite cluster. Usually in disordered systems, when p is close to the critical overpermeability threshold q_c , dP/dp tends to infinity. This indicates that the system acts similar to the phase transition at the overpermeability threshold q_c .

The significance of overinfiltration for the study of infectious diseases is that it can describe whether infectious diseases can spread indefinitely in people or geographical space through connectivity, and how to explain the above situation.

4.2. Model building

In this chapter, we directly model the geospace. Here are some basic assumptions of the model:

- 1). Because most of the human living space is flat, the space can be considered as a one-or two-dimensional continuous plane;
- 2). The space is divided into more homogeneous square units according to the spatial heterogeneity, so as to facilitate mathematical derivation and simulation calculation;
- 3). Infectious diseases are only transmitted directly between people and between people, regardless of the presence of pathogens carried by animals and express delivery as agents of infection;
- 4). Because of the continuity of geographical space, each unit only affects the spread of infectious diseases, so this model is an Ising model;
- 5). The increase of the number of infections in A geographic unit A is proportional to the number of people from A to B

In order to describe the geographical heterogeneity, the population flow matrix between geographical units is first defined, which is the units connecting different populations and different infection rates, and is given weight through the keys of different flows. Using urban daily commuting data as the source of different geographic units for $m \times n$, the element A_{ijpq} in the matrix of mn ($mn \times mn$) is the number of commuter population from the cell in row i , column p to the unit in row j and q . Because of the continuity in the geographical space, to reach the nonadjacent geographical units, one must pass through several intermediate units on the way. That is, the factors affecting each key do not include only the elements in the matrix characterizing the commuter population between the two geographic units connected by this bond. Therefore, compared with specific commuting destinations, we focus more on the tendency of population movement in different directions within each geographical unit to simplify the calculation of population mobility (because it is also difficult to directly obtain flow data between adjacent plots). So we use the vector field mode to characterize the population flow. We create vector fields by using each geographic unit as a starting point to calculate the unit vector pointing to other destination geographic units.

These vectors are summed to form a synthetic vector representing the average outgoing flow direction for each geographic unit. This vector field is critical for understanding flow patterns and can help us determine the average out-of-flow direction for each geographic unit. By dividing the vector by its "quality" or population quantity, we can define the vector field more accurately to better understand and analyze the complex flow patterns within the city. The vector field allowed us to visualize and analyze the human flow behavior in the city and to speculate on the changes and trends of the flow under different conditions.

$$\vec{W}_i = \frac{\vec{T}_i}{m_i} = \sum_{j \neq i} \frac{T_{ij}}{m_i} \vec{u}_{ij}$$

In this study, the main object of the vector field is the vector defined at the mesoscopic unit scale $\vec{W}_i$, Which represents the average mobility of each resident. Our source of data is commuting data. For practical considerations, we defined the local mass m_i of the geographic unit i as the total number of commuters living in that geographic unit. It means that $M_i = \sum_j T_{ij}$, Where summing includes the term of $j=i$. This definition allows us to apply a consistent treatment to all databases, and it approximately represents the total workforce in each geographic unit. As shown in [46], the mass defined in this way yields better results for flow estimates of gravitational and radiation models, more accurate than the actual geographical unit population.

Empirical results suggest that we considered population migration from work back to home. In this case, the vector T_i is still defined in the residence cells in opposite directions, but the modulus remains constant. Therefore, the organization of the spatial field is invariant and does not affect the results presented below (except for the symbols). On the other hand, if we define the synthetic vector on the working unit: $\vec{T}'_j = \sum_i T_{ij} \vec{u}_{ji}$ and $\vec{W}'_j = \vec{T}'_j / m_j$, The value of the vector itself changes at each position, but the behavior of the mesoscopic field and the main properties of the studies below are robust

After defining the field, we can compute the flux on any closed perimeter directly from the empirical data, through the surface integration $\Phi_W^S = \oint d\vec{l} \vec{n} \vec{W}$, among $\vec{n}$ is the unit vector perpendicular to each point, $d\vec{l}$ is the minute element of length. It is then integrated with the volume of the divergence of the vector field $\vec{W}$, $\Phi_W^V = \int dV \nabla \cdot \vec{W}$ compare in the enclosed areas within the circumference (where dS is a minute element of the area). This allows us to assess whether the experimental vector field $\vec{W}$ satisfies the Gaussian divergence theorem. The Gaussian divergence theorem shows that $\Phi_W^S = \oint d\vec{l} \vec{n} \vec{W} = \int dV \nabla \cdot \vec{W} = \Phi_W^V$, This means that the field is generated by the source, and that the flux through the surface must obey the conservation law. After obtaining the weight of the key, the key seepage is used to calculate the seepage threshold. Is that all individuals are susceptible, but spread less than 100% more efficiently. This situation can be described as bond

overstepping on a small world graph, where epidemics occur when a sufficient proportion of the graph are occupied, forming a giant cluster proportional to the size of the graph. The proportion of occupied bonds p is the transmission ability of the disease. The generating function deduction of the key overstep is given below.

For $k=1$, the penetration threshold p_c is actually the same as that for point penetration. On the one hand, now a local cluster is composed of $i-1$ occupied bonds and two unoccupied bonds, so that the number of local clusters is $N_i = (1-p)^2 p^{i-1}$, This is a factor less than the case. On the other hand, the probability of a shortcut between two random points now has an additional p factor, namely ψp , and not just ψ . Two factors of p cancel each other, and we finally get the same characteristic value expression for M and the same threshold density as before. For a larger k , computing N_i becomes complicated. Instead of directly calculating N_i , a generation function $G(z)$ is introduced so that the derivative of i at $z=0$. For $k=2$, the lengthy derivation yields the following generating function:

$$G(z) = [z(1-q)^4(1-2qz+q^3(1-z)z+q^2z^2)] / [1-4qz+q^5(2-3z)z^2-q^6(1-z)z^2+q^4z^2(1+3z)+q^2z(4+3z)-q^3z(1+5z+z^2)],$$

So as to get

$$M_1/L = (1-q)^4, \quad M_2/L = 2q(1-q)^6, \\ M_3/L = q^2(1-q)^6(6-8q+3q^2).$$

$$\lambda = \psi q \sum_i i^2 M_i = 2k\phi q \left[\left(z \frac{d}{dz} \right)^2 G(z) \right]_{z=1},$$

$$\text{So the } k=2 \text{ excess limit is } \phi = \frac{(1-q_c)^3(1-q_c+q_c^2)}{4q_c(1+3q_c^2-3q_c^3-2q_c^4+5q_c^5-2q_c^6)}$$

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