A metapopulation SEIR model with asymptomatic individuals based on human mobility patterns

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***Abstract*—In the post-pandemic era, new variants of COVID-19 continue to emerge and spread within communities across various regions, underscoring the importance of epidemic control and prevention. However, previous research has largely overlooked migration behaviors and individual awareness. In this paper, we propose a Susceptible-Exposed-Asymptomatic-Symptomatic-Recovered (SEI^aI^sR) model with a self-protection mechanism that simulates the impact of awareness in the metapopulation network. The proposed model incorporates analytical expressions for each state, derived from human mobility patterns using the microscopic Markov chain approach (MMCA). Simulation results highlight the significant influence of initial mobility rates and population size on disease transmission. We present an example of a real transportation network for metapopulations to illustrate its effectiveness in depicting epidemic dynamics.**

***Index Terms*—SEIR model, Metapopulation network, Mobility, Microscopic Markov chain**

I. Introduction

From the outbreak of SARS in 2003 to the emergence of the COVID-19 pandemic at the end of 2019, which rapidly swept through multiple countries and regions worldwide within a very short period, the pandemics have attracted significant public interest and drawn great attention from scientific researchers. The implementation of epidemic prevention measures by national governments and the improvement of individual awareness have made indispensable contributions to restraining the spread of viruses. Since the lifting of the comprehensive zero-COVID policy, outbreaks of diseases like H1N1 influenza [1] and more contagious variants of COVID-19, such as Delta (B.1.617.2) and Omicron (B.1.1.529), persist in localized urban or community setting [2]. Consequently, numerous researchers have employed various mathematical models to analyze these outbreaks, aiming to gain deeper insights into the transmission patterns of emerging diseases and provide evidence for assessing epidemic trends and prevention strategies.

The classical SIR and SIS compartmental models have been extensively used to describe the spread of infectious diseases, followed by a series of refined models based on these foundations [3]–[7]. Additionally, the epidemic models were applied and analyzed in various network structures, such as scale-free networks [8], temporal networks [9] and multiplex networks [10]. Among them, the SEIR model, which includes an incubation period, has been widely adopted for its ability to better explain the latent phase after infection and its advantage in considering interventions like movement restrictions or isolation measures imposed on infected individuals [11], [12]. Nevertheless, the structural characteristics of social networks (e.g., clustering effects or node degree distributions) are often overlooked in traditional SEIR models, which also categorize all infected individuals into a single class, despite the fact that different diseases or stages of the same disease can lead to varying degrees of severity among patients [13].

To better understand the micro-scale transmission processes of diseases within local communities and the long-distance spread of diseases caused by human mobility, Anderson and May first applied the concept of biological metapopulations to the SIR model in the field of epidemiological modeling, providing an effective modeling framework for the study of epidemic transmission from a spatial dissemination perspective [14]. Since then, an increasing number of scholars have been drawn to the research on disease modeling within metapopulation networks [15]–[17]. Once the metapopulation models are constructed, researchers utilize epidemiological parameters to track and forecast the spread of epidemics. Qi et al. studied epidemic transmission on different population network structures by considering comprehensive interventions and initial mobility rates [18], while Yang utilized discrete-time Markov chain methods to investigate infectious disease transmission with periodic population mobility within communities [19]. Studying the patterns of disease transmission during recurrent mobility contributes to a deeper understanding of epidemic propagation mechanisms, enabling the formulation of more effective immunization strategies. However, the uncertainty in human mobility patterns and awareness poses challenges to the study of epidemic dynamics.

Building on the discussions above, in this work we present an enhanced SEIR model in the metapopulation network, named the Susceptible-Exposed-Asymptomatic-Symptomatic-Recovered (SEI^aI^sR) model which divides the infected state into asymptomatic and symptomatic states based on the clinical symptoms exhibited by individuals. In order to take citizens' awareness of prevention into consideration, we introduce the self-protection mechanism as a changeable part related to

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the infected state mentioned above. In the proposed model, analytical expressions for each state are formalized with human mobility patterns by utilizing the microscopic Markov chain approach (MMCA). Finally, a real transportation network for metapopulations is presented to illustrate its effectiveness in depicting epidemic dynamics.

The rest of the paper is presented as follows: We first introduce the proposed SEI^{a}I^{s}R compartmental model and the detailed formulation of each state in the metapopulation framework in Section II. Section III shows the numerical results and conclusions of three experiments, and in Section IV we conclude the findings and discuss the prevention measures and isolation interventions when facing future epidemics.

II. Model Description

A. Compartmental dynamics with SEI^{a}I^{s}R model

The traditional SEIR model divides people during a disease infection process into four parts: Susceptible (S), Exposed (E), Infected (I), and Recovered (R). Specifically, infected individuals effectively contact the susceptibles at a transmission rate λ, turning them into exposed individuals. Exposed individuals then progress to the infected state after an average latent period, with a transmission rate of β. Infected individuals recover at a recovery rate μ and become immune to the virus. However, for the same type of infectious disease or different strains of the same infectious disease, individuals may experience milder symptoms due to continuously increasing resistance. For example, symptoms tend to be milder and recovery time shorter when individuals are reinfected with variants of the COVID-19 virus. Therefore, we divide the infected state into Asymptomatic Infectious state (I^{a}), where individuals become asymptomatic or show mild symptoms, and Symptomatic Infectious state (I^{s}), where individuals exhibit typical clinical symptoms. Once the incubation period ends, two paths emerge, as shown in Figure 1.

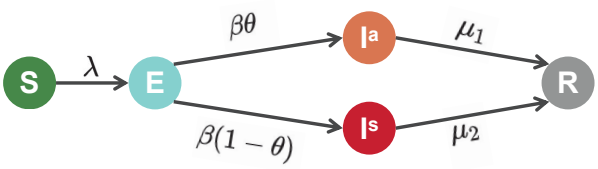

Fig. 1. **State transition process of the disease compartment model.** The S-state individuals transform into the E-state individuals with probability λ, and θ represents the conversion rate from exposed state to asymptomatic infectious state, while μ_1 and μ_2 denote the recovery rates of asymptomatic and symptomatic infectious individuals, respectively.

B. Theoretical analysis with mobility patterns

The metapopulation network comprises N nodes, with each node i containing n_i individuals. In this scenario, each node in the metapopulation network represents a subpopulation or patch with varying population sizes. Infection occurs within each patch under the well-mixing approximation, and individuals can move between patches. The patches refer to small local sites usually(e.g., classrooms, dormitories, or workplaces, depending on the living environment) where individuals are able to contact each other with the same probability. The weights between edges of different nodes represent the probability of an agent moving to a specific patch, called mobility probability [20]. Our metapopulation model is constructed by utilizing the microscopic Markov chain approach proposed for the first time in disease transmission dynamics modeling [21], which provides a better description of epidemic spreading at the node level. Unlike traditional MMCA, we use $\rho_i^m(t)$ to represent the proportion of individuals in state m at time t, with location at patch i. The other explanation says that it is the probability of individuals staying at a specific patch with the given state.

We assume contacts among individuals within each community are uniform, meaning pathogens infect healthy individuals in the community at the same probability. The next part of the structured metapopulation network concerns the mobility patterns among individuals. Considering the impact of self-protection awareness on mobility, individuals tend to move towards communities with either a lower prevalence of disease or where the symptoms experienced after infection are mild. Therefore, we define a variable $\varphi_i(t)$ to represent the proportion of individuals with symptomatic infectious states among the total infected population in patch i at time t, expressed as

$$\varphi_i(t) = \frac{\rho_i^{I^s}(t)}{\rho_i^I(t)} \tag{1}$$

where $\rho_i^I(t)$ donates the sum of the density of individuals in Asymptomatic Infectious state(I^{a}) and Symptomatic Infectious state(I^{s}).

Additionally, we define a function f that represents the tendency of individuals moving to a specific patch with a range from 0 to 1. The greater the willingness of individuals to enter a certain area, the higher the corresponding function value will be. Thus, the self-protection mechanism f reads

$$f = e^{-\varphi_i(t)} \tag{2}$$

Each agent can move to neighbor patches, thereby influencing the spread of the disease. The movement of agents is depicted within a metapopulation network, and the reaction-diffusion process based on individual mobility patterns is illustrated in Figure 2. At each time step, the migration patterns between distinct patches are dictated by the mobility matrix C, where C_{ij} denotes the probability an individual leaves the current location i with probability p and occupies any other patch connected. We have

$$C_{ij} = \frac{W_{ij}}{\sum_{l=1}^{N} W_{il}} \cdot e^{-\varphi_j(t)} \tag{3}$$

where the probability of selecting patch j is proportional to the corresponding entry of the adjacency matrix W_{ij}, in conjunction with the function f, which represents the likelihood of individuals moving to patch j.

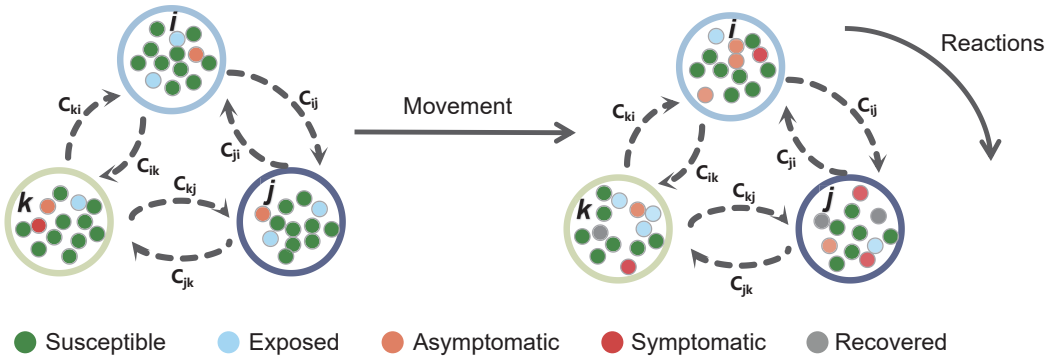

Fig. 2. **Diagrammatic representation of one single time step within the reaction-diffusion system in a metapopulation network.** The illustration is composed of $N = 3$ patches based on SEI^{a}I^{s}R model, in which each color of a node represents a single state. At each time step, the individuals either remain at their residence or decide to move to neighbor patches according to the mobility matrix $\mathbf{C}$. Then they contact with others under the well-mixing approximation and undergo reactions within the current patch. At last, individuals return to the residence or move to another patch and start another round of the infection.

Here, combined with the proposed epidemic model, the microscopic Markov chain equations for the evolution of each state over time are given by

$$\begin{cases} \rho_i^S(t+1) = (1-\Pi_i(t))\,\rho_i^S(t) \\ \rho_i^E(t+1) = \rho_i^S(t)\Pi_i(t) + (1-\beta)\rho_i^E(t) \\ \rho_i^{I^a}(t+1) = \beta\theta\rho_i^E(t) + (1-\mu_1)\rho_i^{I^a}(t) \\ \rho_i^{I^s}(t+1) = \beta(1-\theta)\rho_i^E(t) + (1-\mu_2)\rho_i^{I^s}(t) \\ \rho_i^R(t+1) = \rho_i^R(t) + \mu_1\rho_i^{I^a}(t) + \mu_2\rho_i^{I^s}(t) \end{cases} \tag{4}$$

The susceptible population in patch i is infected by contact with asymptomatic and symptomatic carriers, with a total infection rate of $\Pi_i(t)$, given by

$$\Pi_i(t) = (1-p)P_i(t) + p\sum_{j=1}^{N} C_{ij}P_j(t) \tag{5}$$

The first side of Eq. (5) represents the probability of individuals staying in patch i and getting infected, while the second term signifies contagions occurring in any surrounding area. $P_i(t)$ denotes the likelihood of catching the disease within patch i, thus expressed as

$$P_i(t) = 1 - \prod_{j=1}^{N}\left[1 - \lambda\rho_j^E(t) - \beta\rho_j^I(t)\right]^{n_{j\to i}} \tag{6}$$

where $n_{j\to i}$ donates the total number of individuals moving from patch j to patch i:

$$n_{j\to i} = \delta_{ij}(1-p)n_i + pC_{ij}n_j \tag{7}$$

where $\delta_{ij} = 1$ when $i = j$ and $\delta_{ij} = 0$ otherwise.

III. Simulation Results

In this section, we conduct numerical simulations in the metapopulation network with $N = 20$ patches. The population size of each patch follows a random distribution ranging from 100 to 500 individuals. Thus, we set up a directed complete graph as the metapopulation network, where the weights of edges are randomized. To simulate the initial stage of disease transmission, we assume that the proportion of susceptible individuals in the entire metapopulation network is $\rho^S(0) = 0.98$, while the exposed density is $\rho^E(0) = 0.01$ and the sum of infected density is $\rho^I(0) = 0.01$. To avoid errors caused by the randomness of experiments, we derive the mean values of each state over 100 times in the Monte Carlo simulations. The parameter values based on the real epidemic data are presented in Table I.

TABLE I
PARAMETER VALUES OF THE EPIDEMIC MODEL

Parameter	p	λ	β	θ	μ_1	μ_2
Value	0.6	0.001	0.2	0.7	0.4	0.2

A. Comparison of mentioned models

In order to clarify the influence of individual protective consciousness on epidemic dissemination within a metapopulation network, we compare the epidemic trends of susceptibility density ρ^S and recovery density ρ^R between our proposed model with the self-protection mechanism and the traditional model over time steps, as depicted in Figure 3. The solid line represents the trend in population density for our proposed model, while the dotted line represents that of the traditional SEIR model. By comparing these two models, we find that the density of susceptible individuals in our model decreases at a slower rate compared to the traditional model. Additionally, the increase in the density of recovered individuals is also more gradual, and the time to reach the epidemic equilibrium point is later. This phenomenon suggests that if people move freely without protective awareness, the epidemic could potentially lead to more intense outbreaks between communities, infecting a larger portion of the population within a shorter period and significantly impacting local public healthcare resources.

Figure 4 illustrates the variation in the infection probability Π changing with time in the same metapopulation network. It

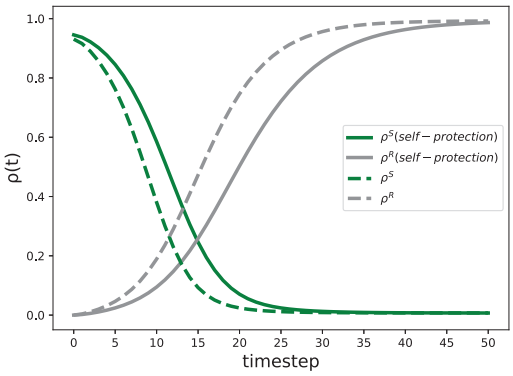

Fig. 3. **The epidemic state densities of susceptible proportion and recovered proportion change over time.** The green curve denotes the proportion of susceptible individuals, and the grey one denotes the proportion of recovered individuals with a self-protection mechanism in our model. By comparison, the dashed lines indicate the change in the proportion of the corresponding states in the traditional SEIR model in 50 time steps.

can be seen that the infection rate of the SEIR model ascends and reaches its peak more rapidly, indicating the fact that the population within the entire community becomes infected at a faster pace. Subsequently, the infection rate declines until it reaches zero. Through a series of comparisons, the results better underscore the crucial role of public awareness in controlling the spread of the epidemic.

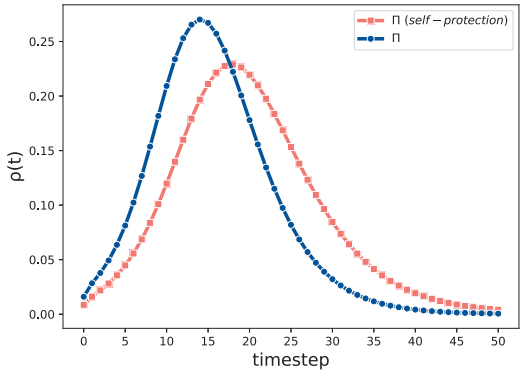

Fig. 4. **The epidemic state densities of the infection probability between different models in 50 time steps.** The parameter Π denotes the probability of individuals in a patch catching the disease, which reflects the speed of the epidemic transmission. The blue circle denotes the infection probability of the traditional SEIR model, while the red circle denotes the infection probability of our proposed model with the self-protection mechanism.

B. Analysis of peak proportion densities

The peak infection density within patches serves as an indicator of the severity of an epidemic to a certain extent. In addition, the final recovery density represents the proportion of the population that is ultimately affected by the disease, thereby reflecting the extent of its transmission to some degree.

We investigate the impact of recurrent mobility patterns by varying the number of patches and population sizes. Figure 5 demonstrates the changes in peak infection density with increasing mobility rates from 0 to 1 under different population sizes. It has been demonstrated that a larger population size, coupled with an increased mobility rate, positively influences the spread of the epidemic.

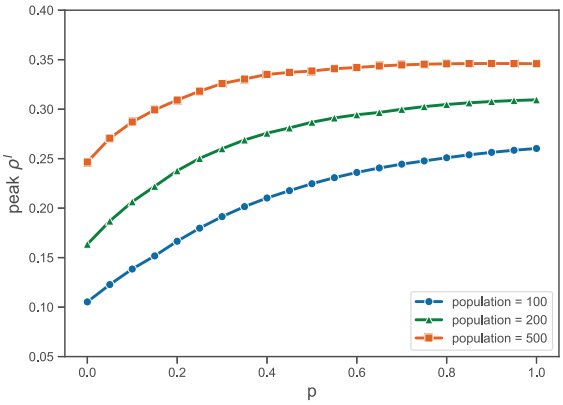

Fig. 5. **The comparison of the peak infection densities with varying mobility rates for different population sizes.** The simulations for each curve are performed using N=20 patches across an average of 100 experiments. As the mobility rate p increases, and the peak infection density is represented by different shapes for various population sizes, where the blue circle corresponds to a population size of 100, the green triangle to a population size of 200, and the red square to a population size of 500.

Figure 6 illustrates the relationship between peak infection density and mobility rates across various patch scales. It indicates that holding the number of patches and population size constant, the peak infection density of a single curve is significantly influenced by the mobility rate. In other words, as the mobility rate increases, the peak infection density on a single curve also rises. Furthermore, we have deduced that there is a positive correlation between the number of communities, population size, and the peak infection density as the mobility rate increases, which means that restricting unnecessary movement of people, implementing effective quarantine measures, and monitoring epidemic data in real-time can suppress the spread of the epidemic.

Subsequently, in Figure 7 we explore how mobility probabilities influence the final recovered density $\rho^R(\infty)$. Experiment results show that disease can hardly spread at the beginning of the epidemic. As time goes by, the proportion of recovered individuals increases gradually. We get that in small-scale towns, the higher the mobility rate, the faster the spread of diseases.

C. Epidemic trends in a real transportation network

Finally, we analyze a real urban transportation system, the city of Sioux Falls (America). We collect population distribution data for 5.9×10^4 residents, divided into 24 areas. The network is established by linking these 24 subpopulations through traffic arteries, where the traffic flow between roads determines the weights of each edge. We conduct numerical simulations

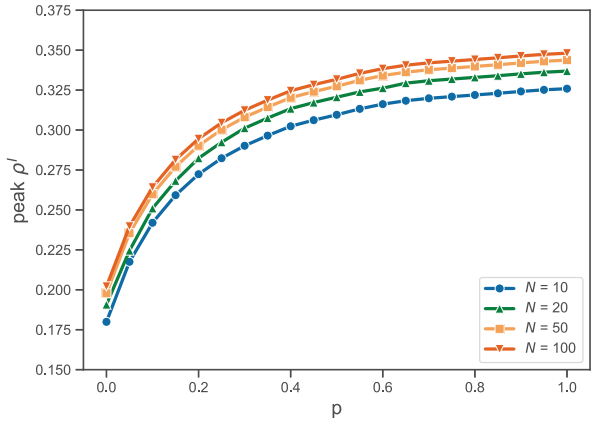

Fig. 6. **The comparison of the peak infection densities with varying mobility rates for different numbers of patches.** The population size for each curve follows a random distribution ranging from 100 to 500 individuals. As the mobility rate p increases, the peak infection density is represented by different shapes for the various number of patches, where the blue circle donates the peak infection density with $N = 10$, the green triangle with $N = 20$, the yellow triangle with $N = 20$, and the red inverted triangle with $N = 50$.

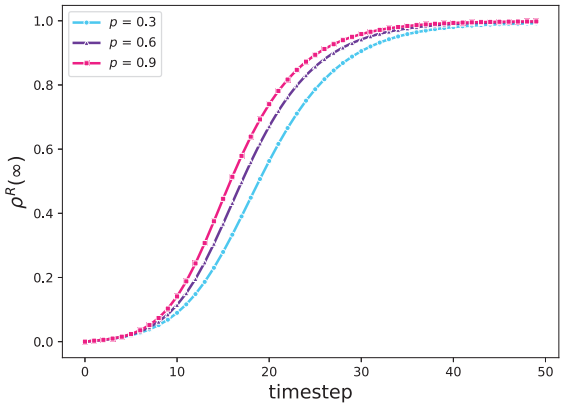

Fig. 7. **The final recovered density changes over time under different mobility rates.** The population size for each curve follows a random distribution ranging from 100 to 150 individuals with a total of 50 patches. As time evolves, recovered densities increase and then remain unchanged. The final recovered density is represented by different shapes for the various number of mobility rates, where the blue circle donates the final recovered density with $p = 0.3$, the purple triangle with $p = 0.6$, and the red square with $p = 0.9$.

of reaction-diffusion dynamics by computing Markov Eq. (4). Figure 7 displays the evolving trend of population density in different infection stages over 50-time steps. As illustrated in the Figure, the percentage of individuals in the susceptible (S) state drops sharply as the disease spreads. With the progression of time, the fraction of S-state individuals diminishes further until it approaches zero, while the proportion of those in the recovered (R) state grows until nearly all individuals have reached the R-state. Simulation results reveal the trend of disease transmission under a realistic community structure, with comprehensive and sufficient contact among people. It is worth noting that there is a point of intersection between the density curves of symptomatic and asymptomatic individuals at a specific time step. This occurs because we assume that individuals in the asymptomatic state experience a shorter recovery period compared to those in the symptomatic state, leading to the stabilization of the population density in the symptomatic state ultimately.

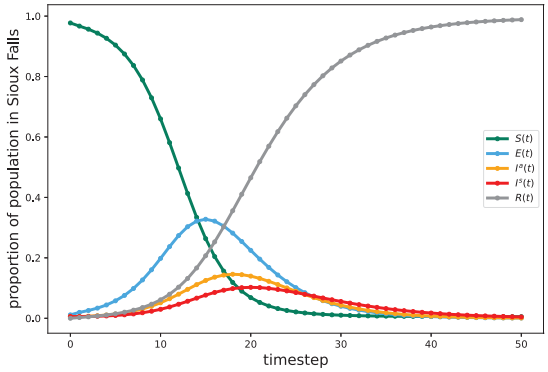

Fig. 8. **The evolution of the fractions of population in different infection stages in Sioux Falls.** The metapopulation network of the city of Sioux Falls (composed of 24 communities) where links denote transportation flows between pairs of subpopulations. Each curve of the figure obtained by Markovian equations respectively shows the trend of the proportion of individuals with the SEI^aI^sR model.

IV. Conclusion

In this paper, we propose and elaborate a new metapopulation SEI^aI^sR epidemic model to study the influence of human mobility patterns and individual protective awareness on disease transmission in small-scale communities. Based on the microscopic Markov chain approach, we get the theoretical formalism of each state under the proposed model. Furthermore, the simulations we set up show the initial mobility rate, awareness dissemination between individuals, the size of communities or, any other important factors that are closely associated with the epidemic spreading. At last, we emphasize the feasibility and effectiveness of the MMCA equations in forecasting the trend of infection in a real case study in the city of Sioux Falls. The proposed model can provide valuable insights into the epidemic dynamics and the role of individual protective awareness in controlling the spread of the epidemic. The results suggest that governments or regions aiming at overcoming localized outbreaks put better prevention strategies such as blocking personnel contact, implementing effective isolation measures, and strengthening public control education.

Despite the metapopulation framework we propose achieves definite advantages in epidemic modeling, it still possesses many limitations. For example, in order to make the model more simplified, we assume that the mobility rate of individuals remains the same for each experiment. However, in reality, the mobility rate varies across different regions and individuals and can be influenced by various factors such as age, gender,

and geographic location. Moreover, we expect to enhance our study further by considering the effect of individual behavioral factors such as social distancing, mask-wearing, and hygiene.

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