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## Review Article

# Modeling epidemic spread in transportation networks: A review

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## HIGHLIGHTS

- Reviewed epidemic spread models and their applications in transportation networks.
- Analyzed the advantages and limitations of epidemic spread model applications in transportation systems.
- Summarized the emerging modeling requirements brought by the COVID-19 pandemic.
- Proposed research trends and prospects for epidemic spread modeling in transportation networks.

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## ABSTRACT

The emergence of novel infectious diseases has become a serious global problem. Convenient transportation networks lead to rapid mobilization in the context of globalization, which is an important factor underlying the rapid spread of infectious diseases. Transportation systems can cause the transmission of viruses during the epidemic period, but they also support the reopening of economies after the epidemic. Understanding the mechanism of the impact of mobility on the spread of infectious diseases is thus important, as is establishing the risk model of the spread of infectious diseases in transportation networks. In this study, the basic structure and application of various epidemic spread models are reviewed, including mathematical models, statistical models, network-based models, and simulation models. The advantages and limitations of model applications within transportation systems are analyzed, including dynamic characteristics of epidemic transmission and decision supports for management and control. Lastly, research trends and prospects are discussed. It is suggested that there is a need for more in-depth research to examine the mutual feedback mechanism of epidemics and individual behavior, as well as the proposal and evaluation of intervention measures. The findings in this study can help evaluate disease intervention strategies, provide decision supports for transport policy during the epidemic period, and ameliorate the deficiencies of the existing system.

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## 1. Introduction

Over the past decade, the emergence of novel infectious diseases worldwide has become a serious problem requiring attention. The prediction and control of epidemics are major challenges for the global public health system. Following SARS, H1N1 influenza, Ebola virus, and Zika virus, the new coronavirus disease (COVID-19) pandemic has spread worldwide. Until October 14, 2020, the pandemic has spread to 216 countries and regions in the world, with a total of 38.36 million diagnosed cases and 1,090,811 deaths (Worldometer, 2020). Consequently, the major threat posed by infectious diseases has once again captured public attention. Monitoring, analyzing, and predicting the impact of epidemics on society is important for developing effective methods for the prevention, control, and management of the spread of epidemics. The use of models has become increasingly important in analyzing the spread of epidemics, designing interventions to control and prevent further outbreaks, and limiting their impacts on the population to control the spread of infectious diseases (Day et al., 2006; McKenzie, 2004).

An epidemic is a disease caused by various pathogens, which can be characterized by human-to-human, human-to-animal, or animal-to-animal transmission. Most of the pathogens are microorganisms, and a few are parasites. Usually, the disease can be transmitted via air, water, food, contact, and soil; humoral, fecal, and oral transmission are also possible by direct contact with infected individuals, body fluids, and the excreta of infected persons.

Modern epidemiological analysis and modeling theory began in the late 19th century and the early 20th century. Snow (1855) plotted the specific locations of cholera cases on a map, and assumed that contaminated water sources were the main reason for the spread of cholera in London in 1849. Arthur Ransome, who first described the cyclic behavior of measles, developed a discrete-time epidemic model for cholera transmission in 1906 (Roberts and Heesterbeek, 2003). Early studies combining spatial data and epidemiology, along with advances in biological research, have contributed important discoveries on the spread of epidemics. In addition to developing vaccines and drugs to combat epidemics, research on epidemics can provide decision support for the measures needed to manage and control the spread of epidemics; for example, elucidating the dynamic spatiotemporal characteristics of a disease can help mitigate the harm that it causes to society.

Initially, most disease models were mathematically modeled at the population level and assumed that populations are homogeneous. Classical mathematical models divided the host population into different units, and each individual interacted with his/her neighbors. The simplest of these models is the susceptible-infected-removed (SIR) model, originally proposed by Kermack and Mckendrick (1927) to describe a closed population. However, the spatiotemporal characteristics of spread and the effect of a disease outbreak in different communities often play more important roles in public health interventions (Auchincloss et al., 2012).

Traditional mathematical models assume population homogeneity and simulate the spread of epidemics on the premise of non-space. Although these models are useful in estimating the population size affected by the epidemic, they do not consider the factors affecting the spread of the epidemic.

Different modeling methods have been proposed to capture the behaviors of a large number of individuals with the development of computer technology and the increase in disease-related spatiotemporal data (Moore and Carpenter, 1999). The emergence of statistical models, network-based models, and individual-based statistical and simulation models has led to the increased consideration of various causal factors in models, such as individual behavior, interactions between individuals, and modes of interaction. Individual-based models are flexible for modeling the heterogeneity observed in disease transmission. At the same time, these models can take into account the impact of more spatial factors on the spread of epidemics, such as the effect of transportation systems.

Different types of epidemic spread models have been developed and used for modeling epidemic transmission characteristics (Duan et al., 2015; Grassly and Fraser, 2008). The shortcomings of the original model system are illustrated by the COVID-19 outbreak as well as the role of transportation in response and recovery periods. Peeri et al. (2020) showed that COVID-19 has spread more rapidly because of increased globalization. Wu et al. (2020) argued that the timing of the outbreak, which was near Chinese New Year, and the increased rail accessibility enabled the virus to spread rapidly. The emergence of modern transportation systems has intensified human contact, as the close proximity between travelers provides an opportunity for the virus to spread. To control the spread of COVID-19, governments worldwide decided to suspend transportation networks. However, the mechanism underlying the spread of the virus during the COVID-19 response and recovery period remains unclear.

This study conducted a comprehensive review of epidemic spread models and their applications in transportation networks. The emerging modeling requirements by the prevention and control of the COVID-19 pandemic are considered. The goal is to analyze and solve three problems: 1) how does the epidemic affect urban mobility? 2) how does urban mobility behavior affect the spread of the epidemic? and 3) how should the interventions of travel restriction strategies be evaluated? In this study, the basic structure and application of various epidemic spread models are reviewed; the emerging modeling requirements of the COVID-19 pandemic are summarized, and the advantages and limitations of model applications within transportation systems are analyzed, including the dynamic characteristics of epidemic transmission and decision supports for management and control. Finally, research trends are discussed and suggestion for future directions is given.

The rest of this paper is organized as follows: section 2 reviews epidemic spread models, including mathematical

models, statistical models, network-based models, and simulation models; section 3 summarizes the integration of epidemic models within transportation systems; section 4 summarizes the new modeling challenges posed by COVID-19; and section 5 discusses research trends, prospects, and conclusions.

## 2. Epidemic spread models

### 2.1. Mathematical models

Mathematical models have been used to understand the dynamics of epidemic transmission and quantitatively represent and predict spread risk for over 100 years. Because of the increased sufficiency of epidemic-related spatiotemporal data and the increase in the demand for analysis, mathematical models have evolved from extremely simple models, such as the SIR model, to complex partition models.

#### 2.1.1. Classic mathematical models

The classic population segmentation models use a population-based classification method to represent the spread of infectious diseases. The simplest form of the population-based mathematical models is the SIR model, originally proposed by [Kermack and Mckendrick \(1927\)](#) to explain the rapid change of the number of patients infected in epidemics, such as plague and cholera.

This model is based on an intuitive understanding of how infectious diseases affect the host in the real world. The SIR model includes three types of individuals: individuals who are susceptible (because of a lack of immunity) to infection after contacting infected persons (S), individuals who are infectious and can transmit the virus to susceptible individuals (I), and individuals who no longer participate in the infection process because of healing (with immunity) or death (R). Differential equations are used to describe the dynamic changes in the number of each subpopulation in the spread of epidemics. Within an analysis period, some people from susceptible individuals are infected, and some infected individuals recover, assuming that these changes are continuous. These processes can be described by Eqs. (1)–(3).

$$dS / dt = \alpha SI / N \quad (1)$$

$$dI / dt = \alpha SI / N - gI \quad (2)$$

$$dR / dt = gI \quad (3)$$

where S, I, and R represent the numbers of the susceptible individuals, infectious individuals, and recovered individuals, respectively, N is the total population (S + I + R),  $\alpha$  is the infection coefficient, g is the recovery rate of the infected person to health, and  $dS/dt$  represents the rate of change of S at time t.

The SIR model is the most basic model for indicating the spread of infectious diseases. When considering an exposed (or latent) compartment (explicitly containing those infected but not yet infectious), the model is called a susceptible-exposed-infected-removed (SEIR) model. [Kucharski et al. \(2020\)](#) used an SEIR model to analyze the early dynamics of

the transmission and control of COVID-19. [Prem et al. \(2020\)](#) used an SEIR model to analyze the effect of control strategies to reduce social mixing on outcomes of the COVID-19 epidemic in Wuhan. In the cases where susceptibility returns after recovery, the model is called a susceptible-infected-susceptible (SIS) model ([Lajmanovich and Yorke, 1976](#)). Other related models include susceptible-infected (SI), susceptible-exposed-infected (SEI), susceptible-exposed-infected-susceptible (SEIS), susceptible-infected-removed-susceptible (SIRS), susceptible-exposed-infected-removed (SEIR), and susceptible-exposed-infected-removed-susceptible (SEIRS) (structure is shown in [Fig. 1](#)). By considering additional variables, such as birth, death, and migration, or monitoring the spread of multiple epidemics simultaneously, these initial models have led to the development of more complex mathematical models ([Brauer, 2008](#)).

The mathematical models can establish and solve the differential equations of the current epidemic based on data relating to the past spread of the epidemic, which helps intuitively establish the basic laws of epidemic spread. These models are especially important when the details of the current epidemic transmission are not fully understood. Although the mathematical modeling approach has many advantages, some limitations are receiving increased attention. An important assumption of the mathematical models is that the group consists of a continuous entity that is not affected by the behavior of individuals; furthermore, the contact pattern is further simplified and assumed to be a transient event ([Koopman and Lynch, 1999](#)). In addition, the assumption of population homogeneity limits the models to assessing and characterizing how the disease spreads and whether the reduction of the disease is the result of intervention control measures or infection heterogeneity ([Dye and Gay, 2003](#)).

Similar models have revealed some important shortcomings because they do not consider spatial factors, such as population density. In addition, these models neglect the local characteristics of the spreading process, such as excluding the variable of individual susceptibility and cannot describe complex infection patterns well (which are mainly caused by the human interaction associated with modern transportation systems). In recent years, many studies have tried to improve the ability of mathematical models to solve these problems ([Jana et al., 2016](#); [Jiao et al., 2016](#); [Muroya et al., 2013](#)), as modern transportation systems have profound impacts on the spread of disease, and traditional modeling approaches cannot analyze the impacts of mobility on infection transmission. The lack of consideration of these effects in traditional models primarily stems from the complexity of the transmission of infections and individual travel characteristics.

#### 2.1.2. Spatiotemporal mathematical disease models

The spatial mathematical models assume that the spread of epidemics is a spatial process ([Ferguson et al., 2001](#); [Rhodes and Anderson, 1997](#); [Riley, 2007](#)) and permit the distribution of hosts or media and their motion characteristics to be represented in space. The models consider the boundary of the unit where the population is located. The simplest

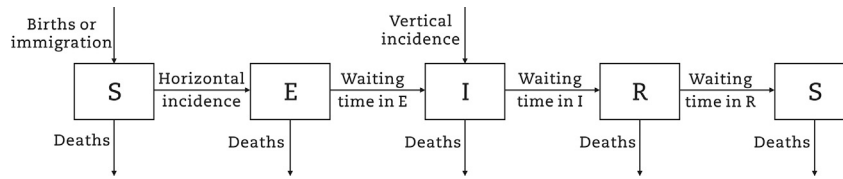


Fig. 1 – SEIRS model.

model based on Eq. (4) can define the speed at which the susceptible people in area  $j$  are infected by the patients in area  $j$ .

$$dS_j / dt = \alpha S_j I_j / N_j \quad (4)$$

where  $S_j$ ,  $I_j$  and  $N_j$  represent susceptible individuals, infectious individuals and the total population in area  $j$ , respectively.

Under the influence of all infected patients, the infection rate of the susceptible population in area  $j$  can be calculated as follow.

$$S_j \frac{\alpha}{\sum_{i=1}^K M_{ji} N_i} \sum_{i=1}^K M_{ji} I_i \quad (5)$$

where  $M_{ji}$  is the mixing rate of area  $j$  and its neighboring area  $i$  (note  $M_{jj} = 1$ ), which can be constructed through the common boundary between areas,  $I_i$  is the number of infected persons in area  $i$ ,  $K$  is the total number of areas,  $N_i$  is the total population in area  $i$ , and  $\alpha$  is the transmission coefficient.

Another spatial approach is to treat the spread of disease as an infection wave spreading across the map. In this model, the spread of epidemics in space is related to traveling waves. Epidemics invade from infected areas to uninfected areas through the travel of infected persons and their contact with susceptible people (Wang et al., 2012; Zhang, 2009). These models are mainly used to predict the spread of epidemics between human settlements such as from cities to cities and from cities to rural areas and the expansion of epidemic areas. Population-based modeling methods treat people in a community as homogeneous entities, while traveling wave models treat a relatively smaller number of people as homogeneous units, such as neighbors. Although this model allows a certain degree of spatial heterogeneity in performance, it is still similar to the traditional mathematical models as it is not applicable to individual-based models and cannot explain the impact of transportation systems.

## 2.2. Statistical models

A statistical model is usually specified as a mathematical relationship between one or more random variables and other non-random variables. Different from theoretical-based models, the mathematical relationships in statistical models are used to directly express the relationship between variables of interest and reproduce the dynamic real-world relationship through the trend and dependence of empirical data without directly expressing causality in epidemiological analysis.

Statistical models often use exploratory data analysis (EDA) to obtain the main characteristics of disease data, or

confirmatory data analysis (CDA) to test statistical hypotheses. Ecological analysis in statistical models is used to analyze the relationship between the spatial distribution of disease incidence and the influential factors that may affect the epidemic spread at a spatial level. Spatial regression analysis often uses the spatial weighting matrix to calculate the autocorrelation between variables and residuals. Eq. (6) shows the classical spatial regression model.

$$Y = X\beta + \epsilon \quad (6)$$

where  $Y$  is the epidemic incidence vector observed in multiple regions,  $X$  is a matrix of explanatory factors,  $\beta$  is the parameter that needs to be estimated, and  $\epsilon$  is a random error vector with a Gaussian distribution. In classical least squares regression,  $\epsilon$  should be independent. However, when there is spatial autocorrelation in epidemiological data,  $\epsilon$  is not independent. To calculate the spatial autocorrelation, the spatial error model uses a spatial adjacency matrix to incorporate the structural relationship of the spatial region into the regression model, as shown in Eqs. (7) and (8).

$$Y = X\beta + \mu \quad (7)$$

$$\mu = pW + \epsilon \quad (8)$$

where  $W$  is the adjacency matrix,  $\mu$  is the error process, and the parameter matrix  $p$  represents the degree to which the change in  $Y$  can be explained by its adjacent values.

Another spatial regression model, called the spatial autoregressive model (SAR), uses a spatial weight matrix as shown in Eq. (9).

$$Y = pWY + X\beta + \epsilon \quad (9)$$

More complex models can build a hybrid SAR model (Beale et al., 2010; Lesage, 1997) by synthesizing Eqs. (7)–(9). For example, the generalized linear mixed model and the spatial hierarchy model can combine the spatial effects at the individual and regional levels (Breslow and Clayton, 1993). Individual-level statistical models have also been developed to simulate the spread of epidemics and the transition between disease states at the individual level (Deardon et al., 2010).

Over the past few decades, tremendous progress has been made in the use of machine learning models and Bayesian statistical methods to analyze the features of epidemics (Bernardinelli et al., 1995; Dunson, 2001; Xia et al., 2004). These models analyze the observed input and output data and use statistical algorithms to learn structured relationships in the data. Since machine learning models can use adaptive mathematical structures to represent any complex

relationships, effective support can be obtained for decisions that control the spread of epidemics.

The statistical models are highly flexible in the structures and parameters of the input data, which makes the statistical models suitable for exploring the spatiotemporal impact on epidemics having few data. The structure of the models indicates that the statistical models are suitable for analyzing the structural relationship between variables, but the statistical models are still not adequate for analyzing the impact of transportation systems and individual mobility on the spread of epidemics.

### 2.3. Network-based models

Network-based epidemiological models originate from the concept of meta populations. These models rely on several basic assumptions. For example, the spread of epidemics follows some specific contacts or transmission paths, such as social contact networks (Kretzschmar and Morris, 1996). Another assumption is that the local populations of subpopulations are isolated from each other in space but are connected through travel. Network models are used to generalize complex contact networks to estimate the probability and the path of epidemic transmission. The network model structure shown in Fig. 2 is a set of nodes and links that is typically denoted as the network  $G = (V, E)$ .  $V$  is a set of nodes that represents individuals, and  $E$  is a link that represents the relationships between individuals. The attributes of nodes, links and the topology of the graph can be assigned multiple parameters to describe the spatiotemporal characteristics of the epidemic.

The network-based models can be population-based or individual-based, depending on the data analyzed. In a study simulating the H1N1 influenza outbreak in 2009, an airline network from Mexico to other cities was used, and a global connectivity network was established. The population-based mathematical models were used to simulate the potential

epidemic risk of different cities based on flight travel volumes on the connected network (Khan et al., 2009). Meloni et al. (2009) and Yang et al. (2015) analyzed the impact of the structural characteristics of the network model on the spread of the epidemic in this situation. Individual-based social connection networks are used to simulate epidemic transmission within the city (Bian and Liebner, 2007; Carley et al., 2006; Eubank et al., 2004). In the model of Bian and Liebner (2007), individual health status and the length of the latent and infectious periods are used to describe the properties of individuals (node), and the attribute of the link is the probability of infection through this link. Three parameters are used to describe network links (topological relationships): 1) the number of links between individuals, 2) the degree of interconnection between family members and colleagues, and 3) the proportion of work connections and family connections. This constitutes a network model framework to simulate the epidemic spread. Finally, the parameters are determined and the vulnerability of the communities responding to the diseases is assessed based on multiple data sources.

A major challenge for network-based models is data collection. Eubank et al. (2004) and Eubank (2005) used census data, land-use data, travel data, and transportation network data for modeling. Bian and Liebner (2007) introduced a more complex dataset containing personal survey information to describe multiple parameters, such as individual attributes and link attributes.

With a certain understanding of the behavioral characteristics, interaction methods, and epidemic transmission characteristics of each type of population, network-based models can more realistically simulate epidemic transmission. However, the inability to describe micro-individuals in the network-based models is a major limitation in the analysis of infectious diseases with alienated individual structures.

### 2.4. Simulation models

#### 2.4.1. Cellular automaton simulation

Cellular automaton (CA) was proposed by von Neumann and Ulam in the 1950s, and their purpose was to better understand the biological systems composed of many relatively simple objects. CA is a discrete spatial model for simulating the spatiotemporal dynamics of events (Sirakoulis et al., 2000). CA models are composed of regular discrete grids, grid boundary conditions, finite state sets, interacting neighbor cell sets, and transition rules for cell states. Each cell is assigned a state from the finite state set at each time  $t$ . According to some fixed rules (usually a mathematical function), the state of the cell is updated at each time step based on the current state of the cell and the state of the neighboring cell. The common topologies of CA are chains and regular lattices, but CA in two-dimensional space has some shortcomings. For example, the connection topology among the cells is restricted to the predetermined homogeneous lattice.

The premise of the CA models is that the spread of disease is a spatial process, which is contrary to the mathematical models, as basic mathematical models do not consider spatial factors. In the CA models, grid-shaped cells represent agents, and the disease is transmitted from infected individuals to

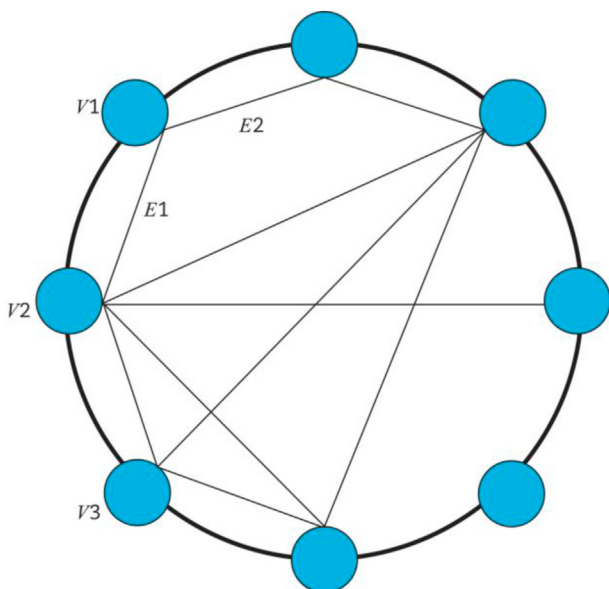


Fig. 2 – Structure of network-based model.

susceptible individuals based on the rules of infection (usually the extended SIR models) (Beauchemin et al., 2005). Individuals can be in different stages of infection, such as incubation period, infection period, and immunization period. The CA models integrate the disease state transition rules, which determine the individual state at the next time point based on the disease state of the individual and its neighbors, and the disease transmission characteristics. The state of each individual in the network is calculated by discrete time steps, and the same rules are applied to all individuals.

The advantage of the CA models is that it can integrate environmental factors, such as land use and terrain, and population distribution, such as population density and age structure, into the model (Fuentes and Kuperman, 1999). In addition, simulating and visualizing the dynamic characteristics of the epidemic spread in the population is straightforward. Computer-aided analysis that simulates the epidemic spread has been used to understand the spreading characteristics of diseases as well as making emergency management and control measures for diseases (Beauchemin et al., 2005; Doran and Laffan, 2005; Pfeifer, 2008; Xiao et al., 2006).

In recent years, this method has been used extensively to study the mechanism of infectious disease transmission and evolution. With the in-depth study of epidemiology, the CA models have a major advantage over non-spatial models. The models are intuitive, interactive, dynamic, and the simulation results of the models can be obtained by determining relatively simple local evolution rules, multi-step iteration, and parallel evolution, which demonstrate the complex spatiotemporal evolution process.

However, the CA models still focus on the population level. Cells can only communicate locally and cannot engage in rapid global communication. Daily activities of individuals cannot be modeled using the CA models (Pfeifer, 2008), which limits their applicability. Based on the CA model, Chen and Tong (2018) divided the regions into static and dynamic and established a cross-regional transmission model of infectious diseases with population migration functions that considered the infectious disease transmission and interregional population transfer. In addition, the effect of the dynamic regional position and the area on the spread of infectious diseases across regions was analyzed. Although the movement of the cells can be simulated and the epidemiological transmission law can be analyzed in the case of population migration, the CA model is still not adequate for simulating transportation systems and providing decision support for travel restrictions and other management and control measures.

#### 2.4.2. Agent-based models

Agent-based models are based on the heterogeneity of individuals. This assumption is fundamental to epidemiological research (Koopman and Lynch, 1999). These models based on the contact between discrete individuals were developed mainly to study the spread of epidemics (Ghani et al., 1997). The agent-based models account for personal social networks and contact activities better than other models, such as mathematical models. Because these factors significantly affect the spread of epidemics (Bian,

2004; Koopman and Lynch, 1999; Roche et al., 2008), and agent-based models represent a fundamental shift in epidemiological thinking.

Assumptions are made within the agent-based simulation framework to account for heterogeneity and the interaction between individuals as well as the spatiotemporal heterogeneity of the epidemic transmission process. To simulate the spread of epidemics within the scale of a city, agent-based models often assume that 1) individuals are different from each other in terms of age, race, occupation, and infection status; 2) individuals contact a certain number of other individuals within a certain period; 3) the number of individual activities varies from person to person; and 4) individuals are spatially separated and movable. These assumptions are suitable for modeling epidemic transmission in urban environments (Bian and Liebner, 2007).

Based on the above assumptions, the conceptual framework of agent-based models consists of the disease section, the agent society, transportation systems, and the environment (Hunter et al., 2017). The disease section describes how the disease spreads between individuals and how individuals transfer at different stages of the disease, such as transferring from susceptible to infected. Agent society characterizes the individual's characteristics and behavior as well as the individual's social network and interactions. Transportation systems, which are important places of interaction, characterize the movement of individuals in the simulation system. The environment, which is a place where individuals interact and obtain information, contains information such as land use.

Agent-based models can be used to study how diseases are transmitted (Duan et al., 2013; Epstein et al., 2008) and understand the dynamic transmission characteristics of epidemics, which can help research on the efficacy of control measures. Agent-based models can also determine which measures can effectively suppress the spread of epidemics and how they can be combined to obtain the most social benefits, such as isolation (Barrett et al., 2008), school suspension (Lee et al., 2010), vaccine development (Olsen and Jepsen, 2010), and travel restrictions (Duan et al., 2013). Agent-based models can also be established based on historical experience. For example, Frías-Martínez et al. (2011) tried to model epidemic outbreaks in the past and analyzed whether enough time and appropriate control measures had been taken to stop an epidemic or other outbreak. Chinazzi et al. (2020) used agent-based models to analyze the effect of travel restrictions on the spread of the COVID-19 outbreak.

Individual modeling methods are significantly different from population-based approaches. Most agent-based models are not used for prediction, instead they are tools for evaluation, decision support, and visualization. Multi-agent models are the most suitable models for observing and analyzing the relationship between individual behavior and epidemic transmission characteristics, as well as the developmental trend of epidemics. They also support quantitative simulation experiments for analyzing measures for controlling epidemics. Each agent can be assigned different attributes and make different decisions in a multi-agent-based model, which allows the model to capture every detail of behavior and

interaction. Therefore, the models have greater flexibility and greater freedom in simulation design.

The multi-agent-based model simulation framework has the ability to integrate large-scale data heterogeneity, but due to the complexity of individual behavior and the consequent lack of data, parameter adjustment for individual heterogeneity is a great challenge (Chao et al., 2010).

### 3. Modeling epidemic spread in transportation networks

Transportation systems play extremely important roles in the context of epidemic transmission. Taking measures to stop the spread of epidemics in the transportation system is necessary because the transportation system is a place that is highly conducive to the spread of infections. At the same time, transportation systems permit public travel and allow individuals to return to their activities after the epidemic. Realizing both of these roles of transportation is a major challenge.

To provide a theoretical basis for the prevention and control of epidemics in transportation systems, the models, methods, and goals of epidemiological studies considering transportation networks in recent years are analyzed to identify where future research efforts are needed. The search terms “epidemic”, “transport”, and “transportation” were input in Google Scholar to identify relevant studies over the past decade. After screening the retrieved documents, 62 articles from 39 different journals and conferences were obtained. Because the study of transportation management and control for epidemics is an interdisciplinary issue, the relevant journals included those relating to the fields of mathematics, biology, and transportation. The models, methods, and research objectives used in these studies are summarized in Table 1. The research purposes include model method research to expand the analytical capabilities of the model, the dynamics of disease transmission in specific scenarios, and the effects of interventions in specific scenarios.

Over the past decade, statistical models have rarely been used to study epidemics in transportation systems. The reason is that statistical models often use EDA to obtain the main characteristics of disease data or CDA to test statistical hypotheses. Statistical models require a large amount of data related to human mobility, and the model performance is limited. Few studies have used CA models, as it is difficult for CA to simulate transportation systems, let alone make decision supports for management measures, such as travel restrictions. Below, the applications of mathematical models,

network-based models, and agent-based models for transportation systems are summarized.

#### 3.1. Mathematical models

The most significant advantage of mathematical models is that little data are needed and parameters can easily simulate the epidemic spread characteristics over a large area. Therefore, many studies have tried to expand mathematical models to adapt them to scenarios of human mobility. To understand the spatial distribution of epidemics, the direction of expansion of the mathematical models is primarily based on the transmission dynamics in the event that the total population changes. In this case, the epidemic transmission in multiple regions is analyzed. In this framework, the spatial structure is represented by a finite number of distinct patches. In each analysis period, the population dynamics in each patch are partly transferred to other patches to account for the mobility between regions. The parameters of epidemic dynamic transmission in different regions are different because of the proportion of infected people and the stage of epidemic spread. Wang and Zhao (2004) proposed an  $n$ -patch SIS model and applied it to the scenario of 2-patches, where the infected and susceptible people in each region migrate to another region in a certain proportion. Based on this model, a threshold that determines the persistence and extinction of the epidemic was obtained. Wan and Cui (2007) proposed an SEIS model to analyze the impact of transport-related infection on disease transmission and control measures, which showed that only restricting the travel of infected people cannot inhibit the spread of the epidemic, as latent patients can also lead to the spread of the epidemic. Many studies (Cui et al., 2006; Takeuchi et al., 2007) have reached the same conclusion and have extended the scenario to SIR (Hyman and Tara, 2003; Li and Zou, 2010), SIRS (Liu and Zhou, 2009), and other models. However, these expansions assume that individuals leaving a certain region and reaching their destination region immediately. However, travel can be time-consuming, and passengers are in a relatively closed environment during travel, often with a high-density configuration of seats. The transportation used for travel is also one of the places where diseases spread, especially for diseases that spread rapidly, such as SARS and influenza. The models can explain how human behaviors affect the spread of the epidemic through these methods. In addition, models can represent some simple behaviors by adjusting the parameters.

Mathematical models can represent simple reactions of people to the epidemic, such as reducing the number of trips.

**Table 1 – Summary of current studies.**

Model	Count	Purpose		
		Method	Dynamics	Intervention
Agent-based	20	13	14	7
Network	20	10	13	7
Mathematical model	16	12	5	5
Cellular automaton	1	1	0	0
Custom model	5	0	2	5



Based on the directed graph to describe the traffic network structure in the context of population migration, the regions are the nodes of the graph, and nodes are connected by the directed link if there is transportation of individuals from region to region. Generally, the traffic network is strongly connected (one can go from any region to any other region), but when an epidemic occurs, the structure of the traffic network may change from strongly connected to weakly connected because of control measures or personal instinct. All of these factors need to be considered in epidemic models. Nakata and Gergely (2015) established an epidemic model for the spread of an infectious disease along with population dispersal by a system of delay differential equations. By increasing the possibility of infection in the process of travel and assigning different parameters related to travel to susceptible and infected people, the sub-epidemic transmission model through the transportation systems was improved. The concept of a directed graph was used to describe the spatial structure, the connectivity of different regions, and the population migration characteristics when the network was not strongly connected because of the epidemic.

Mathematical models are based on the population. Therefore, mathematical models can be effective at macro-scales for considering the impact of inter-regional travels through transportation systems on the spread of epidemics. They are also suitable for providing the basis for formulating control measures during the early stage of epidemic spread. However, mathematical models cannot describe and analyze individual travel within the region, and they cannot provide decision supports for refined management and control measures.

### 3.2. Network-based models

The spatial structure of populations is a key element for understanding the large-scale spread of epidemics. The network approach focuses on the network structure formed by the connections among regions (populations), and the link between nodes can represent the travel path. Therefore, network-based models can provide additional important insights for understanding the role of mobility patterns in the transmission of infectious diseases.

Airlines are one of the major infection channels for the global spread of epidemics. Poletto et al. (2012) analyzed the impact of the stay time of different travelers at the destination after long-distance travel. In analyzing the spread of epidemics within the city, Balcan and Vespignani (2011) and Xu et al. (2013) analyzed the commuting network and the public transportation network, respectively. Colizza and Alessandro (2008) presented a thorough analysis of the characteristic of infectious disease in metapopulation models characterized by heterogeneous connectivity and mobility patterns and derived the basic reaction-diffusion equation describing the metapopulation system at the mechanistic level.

The network-based model can also be used to analyze the interplay between human and epidemic dynamics and evaluate different interventions. Meloni et al. (2011) analyzed the impact of individual travel decisions, such as avoiding epidemic areas, on the spread of epidemics. Bóta et al. (2017)

attempted to model passenger behaviors during the outbreak process. Yang and Wang (2016) analyzed the effect of different interventions on the spread of epidemics. The use of network models combined with transportation systems has inherent advantages as the connection between nodes can be used as a travel path. However, the complexity of network structure often makes it effectively become a population-based model; thus, characterizing the impact of microscopic traffic behavior on the spread of epidemics is difficult.

### 3.3. Agent-based models

In agent-based models, each agent can be assigned different attributes and make different decisions, which allows the model to capture every detail of interaction and behavior. Because of the modernization of urban transportation, human travel is becoming increasingly dependent on public transportation systems relative to travel on foot and via cars. This shift in the use of transportation has caused major changes in the spatiotemporal characteristics of human activities and has complicated the individual contact network. Therefore, transportation system modeling is extremely important in agent-based epidemic spread models.

Because of the flexibility of simulation design, agent-based models can simulate transportation systems of any complexity. Some researchers have used simple forms of simulation, such as an agent moving between a starting point and an end point along a line at a constant speed (Duan et al., 2013). A more practical transportation system model may include the choice of the shortest path or the next shortest path. Some specific models also include using mobile phone data to simulate the activity trajectory of the agent (Frias-Martínez et al., 2011). The most complex transportation system models include public transportation systems (Rakowski et al., 2010) because public transportation is a high-risk place for the spread of epidemics. These models can explain how human behaviors affect the spread of epidemics, but these models often analyze routine behaviors. Because the simulation design is flexible, there is a need for more research to focus on specific behaviors in the context of epidemic spread, such as the distribution of medical materials and living materials.

As agent-based models consider the heterogeneity of individuals, individual travel decisions can also be modeled and analyzed. Most simulations are based on the social structure and agent behavior rules to make travel and activities decisions. Usually, travel activities assigned to the agent are simply from the residential place to the workplace. Some more complex models include shopping, entertainment, religion, and other travel purposes (Crooks and Hailegiorgis, 2014; Mao, 2014). Research conducted by Crooks and Hailegiorgis (2014) permitted agents to make their own travel decisions based on their own attributes, health status, and other factors. These decisions included home isolation because of illness (Duan et al., 2013) and traveling with strangers (Simoes, 2006).

Because agent-based models can simulate complex transportation systems, the models can consider the simplified versions of problems in other models, such as the

transmission mechanism of epidemics in different transportation facilities, making individual travel plans based on individual attributes and epidemic information. These problems have yet to be resolved.

The individual-based network models and agent-based models can use actual census data, family structure information, population mobility data, and relational network data to make the heterogeneous performance of epidemic transmission more realistic. Therefore, using these two types of models to study the dynamics of epidemic transmission in the context of regional human mobility and travel restriction measures is more appropriate. A population-based network model is more appropriate for addressing research questions at larger scales, such as in global epidemiological research. The global connectivity network is built through the airline network to connect various geographic regions, and the individual flows through transportation and travel represent the connection between groups in each region.

#### 4. Modeling challenges brought by COVID-19

On December 31, 2019, the Wuhan Municipal Health and the Health Committee of Hubei Province, China issued the “Notice of Pneumonia in Wuhan” after 27 cases of pneumonia had been reported. On January 7, 2020, the virus was preliminarily identified as a novel coronavirus. On February 11, 2020, the World Health Organization announced that the novel coronavirus disease was to be named “Coronavirus disease-2019” (COVID-19). As of October 14, 2020, COVID-19 has become a pandemic with more than 38 million confirmed cases worldwide.

Some studies argued that high rail accessibility and increased globalization have enabled the virus to spread rapidly (Peeri et al., 2020; Tan and Ma, 2020; Wu et al., 2020). Many countries have responded with non-pharmaceutical interventions to diminish viral transmission, including intercity travel restrictions, the early identification and isolation of cases and contact restrictions in many countries (Flaxman et al., 2020; Lai et al., 2020). These measures have undoubtedly hindered the spread of the epidemic, but which aspects of the emergency response were most effective remain unclear (Tian et al., 2020). The fact that COVID-19 is still spreading rapidly indicates that there are many deficiencies in the existing model systems.

COVID-19 imposed new modeling requirements to existing model systems. To better support the prevention of the epidemic, three questions need to be addressed: 1) how does the epidemic affect urban mobility behavior? 2) how does urban mobility behavior affect the spread of the epidemic? and 3) how should the interventions of travel restriction strategies be evaluated?

##### 4.1. How does epidemic affect urban mobility behavior?

Human beings engage in self-protection behavior based on epidemic information to reduce the risk of epidemic infection. For instance, many people choose to maintain social distance to avoid being infected. However, most previous epidemic models only consider the impact of human mobility on

epidemic spread, but the impacts of the pandemic on the urban mobility behavior have received little attention, especially changes in travel behavior (e.g., reduced travel in public transport). Previous studies on urban mobility behavior during epidemic spread have generally adopted one of the three following perspectives.

##### 4.1.1. Economic epidemiology

Economic epidemiology is a field at the intersection of epidemiology and economics. Its premise is to incorporate incentives for behavior and their attendant behavioral responses into an epidemiological context to better understand how diseases are transmitted. The utility function, such as the Behrman equation (Zhang et al., 2011), provides the basis of individual behavior decision-making in the outbreak of an epidemic (Fenichel et al., 2011). The Bellman equation considers changes in individual health states because of their behaviors and defines the utility of escaping from infection and the utility of being infected. Researchers have also used game theory to study changes in individual behavior (Reluga, 2010; Shim et al., 2010).

##### 4.1.2. Psychological epidemiology

Researchers have also studied changes in human behavior in epidemic outbreaks from the perspective of psychology. Specifically, they have proposed the health belief model (HBM) (Rosenstock, 1974), the theory of rational action, and other models to study changes in individual behavior during the outbreaks associated with an epidemic. The HBM has been widely used to describe individual psychological dynamics and behavioral decision-making during the outbreaks of an epidemic. It uses logical regression to quantify individual beliefs and perceptions (Tang and Wong, 2004).

##### 4.1.3. Epidemiological information

Epidemiological information is the information through which individuals know about the dynamics of epidemic spread; this information can be either centralized or local (Tommasi and Weinschelbaum, 2007). Centralized epidemic information consists of news released by the media (Dredze, 2012) and the government, which is the center of disease control and prevention. Local epidemic information refers to information transmitted through individual social networks. Researchers have also studied a dual diffusion process of epidemic information and epidemics as well as urban mobility change and epidemics (Mao and Bian, 2011).

#### 4.2. How does urban mobility behavior affect the spread of the epidemic?

Urban mobility behavior can drive the spread of epidemics. The feedback loop between human dynamics and epidemic dynamics is responsible for their interaction (Ferguson, 2007). Most previous epidemic models have considered the impact of human dynamics on epidemic spread (Funk et al., 2010; Segbroek et al., 2010). However, the concept of human behaviors should be extended because of COVID-19. Typical behaviors, such as wearing a facemask, avoiding crowds, improving personal hygiene, and taking antiviral drugs, have

been analyzed (Bagnoli et al., 2007), yet COVID-19 spread in unexpected ways.

In addition, more attention needs to be given to examine epidemic spread via cold chain logistics. On June 11th, Beijing reported a 52-year-old confirmed case in Xicheng after no new confirmed cases had been reported in Beijing for 56 days. Within 10 days, over 200 cases were diagnosed in Beijing. Almost all of these cases were found to be associated with activities in the wholesale market of agricultural products in Xinfadi. When novel coronavirus was detected on a salmon-chopping board in Xinfadi Market, salmon, as well as the cold chain logistics behind it, received increased attention. For example, freezing technology and refrigeration technology are frequently used in the logistics process of fresh products to ensure that perishable and vulnerable products are maintained in low-temperature environments during every stage, including production, storage, transportation, sales, and consumption, to ensure quality and reduce losses (i.e., cold chain logistics). However, cold environments allow the virus to survive; consequently, the survival of the virus in cold chain logistics can infect people in the freight chain. This possibility is a reminder that human behaviors associated with the freight transportation system can be reservoirs mediating virus spread. The distribution of medical and living materials in the context of epidemic spread should also receive increased attention to clarify how transportation affects the epidemic.

#### 4.3. How should the interventions of travel restriction strategies be evaluated?

Early intervention measures can effectively curb epidemic spread, including reducing the peak medical demand and the number of deaths (Hoertel et al., 2020). However, which part of the emergency response is most effective remains unclear (Tian et al., 2020). The positive consequences of mandatory travel restrictions are recognized, yet the epidemic can rebound when such measures are relaxed.

To mitigate these negative effects, robust disease control and prevention planning is becoming increasingly important as globalization and climate change are expected to make the occurrence of new diseases more common in the future (Baker et al., 2019). Previous models have primarily focused on moderate measures, but evaluations of more rigorous interventions, such as extensive travel restrictions and travel demand scheduling under strict control, are required because of COVID-19. New models should provide decision support for the policymakers.

## 5. Research trends and prospects

### 5.1. Research trends

Over the past few decades, the focus of epidemiological model research has shifted from group-based modeling to individual-based modeling. Individual-based models are more appropriate for relatively small spatial scales and numbers of populations, such as cities, communities, or other regions with mobility and heterogeneity. Population-based models

are best suited for simulating the spread of epidemics with a certain degree of homogeneity within a large area. Most mathematical models of epidemic spread use differential equations based on the assumption of uniformity among individuals. Individual-based models use actual census data, family structure data, human mobility data, and relational network data to make the heterogeneous performance of epidemic transmission more realistic.

Several challenges associated with individual-based statistical models or network models require consideration. First, the data used by individual-based epidemiological models often come from different data sources; thus, the quality of data often results in insufficient analysis. Papoz et al. (1996) pointed out that the quality of data obtained from different data sources is usually far below the standard of specific epidemiological prevalence surveys. Second, individual-level data is used to better estimate individual parameters, while many variables are estimated from overall data. Therefore, potential ecological fallacies need to be considered when the representativeness of parameters is evaluated. Different spatiotemporal scales can also lead to different results. Third, data loss and zero counts caused by frequently used count data lead to problems, such as excessive data dispersion.

Disease analysis and modeling techniques are essential for understanding and controlling the dynamics of infectious disease transmission. Recognizing the conditions of an epidemic occurrence, as well as the mode of transmission of specific diseases, is critical to designing and implementing effective public health measures. The modeling methods used depend on the research data available and the purpose. The advantages, disadvantages, and spatial scale appropriate for different models in studying epidemics in transportation systems are shown in Table 2.

### 5.2. Research prospects

The use of individual-based epidemiological models for decision support research has become mainstream, and the various measures include travel restrictions, bus shutdowns, and others. With the development of technology and the diversification of data, the demand for differentiated management and control has gradually increased; consequently, higher requirements have been placed on related models. COVID-19 exposed the shortcomings of the existing model system. To better plan control measures, evaluate disease intervention strategies, and determine the best use of public health resources, further research is needed in the following three aspects.

First is the impact of epidemics on urban mobility behavior. Human beings engage in self-protection behavior based on epidemic information to reduce the risk of epidemic infection; however, most previous epidemic models only consider the impact of human dynamics on epidemic spread. Some models consider simple behaviors triggered by epidemics. With the awareness of the severity of the epidemic increasing, individual responses become increasingly diverse and complex. The models need to better represent the impact of epidemics on individual behavior. By doing so, these models could provide new insights into the interplay between

**Table 2 – The advantages, disadvantages, and spatial scale appropriate for different models.**

Model	Advantage	Disadvantage	Appropriate spatial scale
Mathematical model	Simplicity and certainty	Unable to analyze spatial and interactive scenarios	Large
Statistical model	Shows the relationship between disease transmission and potential factors	Difficult to reflect individual's initiative and interactivity	Small and large
Network-based model	Merges multiple data sources and considers individual interaction	Difficult to reflect individual behavior	Small and large
Cellular automaton	Simple and intuitive rules	Unable to simulate travel activities	Small
Agent-based model	Combines personal behavior and mobility information	Complicated compilation and large number of calculations	Small

humans and epidemics, thus helping to prevent epidemics from occurring.

Second is the impact of urban mobility behavior on the spread of epidemics. Human behaviors can drive the spread of epidemics. Most previous epidemic models have considered the impact of human dynamics on epidemic spread, but COVID-19 shows that the concepts of human behavior need to be extended, including freight transportation system and travel demand scheduling under strict control. Characterizing the impact of microscopic traffic behavior on the spread of epidemics would clarify the mechanism by which the epidemic spreads and help develop transport-based interventions.

Third is the proposal and evaluation of intervention measures. The outbreak of COVID-19 was so rapid that the government only had time to implement non-pharmaceutical interventions. However, which aspects of the emergency response have been most effective remains unclear, and the epidemic is prone to rebounding when such measures are relaxed. Therefore, models need to propose and evaluate appropriate interventions for preventing outbreaks and for stopping the spread of epidemics in transportation systems, which mediate public travel and facilitate the reopening of the economy after the epidemic.

## 6. Conclusions

This study conducted a comprehensive review of epidemic models within transportation systems to provide insights into the interplay between transportation networks and epidemics. Three major types of models were introduced, including mathematical models, network-based models, and agent-based models, and the principles, applications, advantages, and limitations for applications of these models in transportation networks were discussed. Specifically, modeling challenges brought by the COVID-19 pandemic were summarized, including the interaction mechanism between urban mobility via transportation networks and epidemic spread, as well as the evaluation method for intervention strategies. Then, three future research directions in epidemic modeling within transportation networks were proposed, including the impact of epidemics on individual behavior, the impact of individual behavior on the spread of epidemics, and the proposal and evaluation of intervention measures.

Further work is needed in the proposed future research prospects, especially understanding the mechanism between travel behavior and virus spread during epidemic outbreaks. In addition, a generalized agent-based testbed model is needed to compare and verify the above mechanism. At last, a retrospective analysis of the effects of travel restriction policy in different countries during COVID-19 pandemic is needed to obtain evidence-based conclusions.

## Conflict of interest

The authors do not have any conflict of interest with other entities or researchers.

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