Human Mobility in Epidemic Modeling

Xin Lu [a, +, *], Jiawei Feng [a, b, c, +], Shengjie Lai [d], Petter Holme [e, f], Shuo Liu [a], Zhanwei Du [g, h], Xiaoqian Yuan [a], Siqing Wang [b], Yunxuan Li [a], Xiaoyu Zhang [a], Yuan Bai [g, h], Xiaojun Duan [i], Wenjun Mei [b], Hongjie Yu [j], Suoyi Tan [a], Fredrik Liljeros [k]

[a] College of Systems Engineering, National University of Defense Technology, Changsha, China

[b] College of Engineering, Peking University, Beijing, China

[c] Innovation Centre of Sustainability, Energy, and Environment, City University of Hongkong, Shenzhen, China

[d] WorldPop, School of Geography and Environmental Science, University of Southampton, Southampton, UK

[e] Department of Computer Science, Aalto University, Espoo, Finland

[f] Center for Computational Social Science, Kobe University, Kobe, Japan

[g] World Health Organization Collaborating Center for Infectious Disease Epidemiology and Control, School of Public Health, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Hong Kong, China

[h] Laboratory of Data Discovery for Health Limited, Hong Kong Science and Technology Park, Hong Kong, China

[i] College of Science, National University of Defense Technology, Changsha, China

[j] Department of Epidemiology, School of Public Health, Key Laboratory of Public Health Safety, Ministry of Education, Fudan University, Shanghai, China

[k] Department of Sociology, Stockholm University, Stockholm, Sweden

+ These authors contributed equally to this work.

* Corresponding author: xin.lu.lab@outlook.com

Abstract

Human mobility forms the backbone of contact patterns through which infectious diseases propagate, fundamentally shaping the spatio-temporal dynamics of epidemics and pandemics. While traditional models are often based on the assumption that all individuals have the same probability of infecting every other individual in the population — a so-called random homogeneous mixing — they struggle to capture the complex and heterogeneous nature of real-world human interactions. Recent advancements in data-driven methodologies and computational capabilities have unlocked the potential of integrating high-resolution human mobility data into epidemic modeling, significantly improving the accuracy, timeliness, and applicability of epidemic risk assessment, contact tracing, and intervention strategies. This review provides a comprehensive synthesis of the current landscape in human mobility-informed epidemic modeling. We explore diverse sources and representations of human mobility data, and then examine the behavioral and structural roles of mobility and contact in shaping disease transmission dynamics. Furthermore, the review spans a wide range of epidemic modeling approaches, ranging from classical compartmental models to network-based, agent-based, and machine learning models. And we also discuss how mobility integration enhances risk management and response strategies during epidemics. By synthesizing these insights, the review can serve as a foundational resource for researchers and practitioners, bridging the gap between

epidemiological theory and the dynamic complexities of human interaction while charting clear directions for future research.

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1. Introduction

A disease outbreak, as defined by the World Health Organization (WHO) [1], is a sudden increase in disease incidence beyond what is usually anticipated within a specific population, community, geography, or season. These outbreaks are often driven by the spread of infectious agents through various pathways, including direct person-to-person contact, animal reservoirs, environmental exposure, or vector-borne mechanisms involving insects and animals [2–6]. At the core of these transmission routes lies human behavior, particularly the movement and interactions of individuals, which fundamentally shapes the dynamic contact structures that significantly influences where, when, and how pathogens spread [2,7–13]. Among behavioral drivers, human mobility plays a particularly critical role in the disease transmission dynamics. The sudden and large-scale movement of people, whether due to travel, migration, or social congregation, can amplify localized outbreaks into regional epidemics or even global pandemics [14]. When infected individuals move from areas of high to low disease prevalence, they probably introduce novel risk into previously unaffected populations or disease-eliminated regions. These dynamics underscore the importance of understanding and modeling mobility accurately in epidemiological frameworks for infectious diseases, to support timely epidemic control and mitigation.

Epidemic modeling has undergone significant advancements since its inception. The foundations of quantitative epidemiology were established through the statistical analysis of mortality data and further advanced by applying mathematical methods to evaluate the impact of smallpox vaccination [15]. Thereafter, a significant milestone was the development of the SIR (Susceptible-Infected-Recovered) model, which simplified the complex dynamics of diseases spread by categorizing populations into specific compartments [16]. These models, including SIR and its variations like SIS (Susceptible-Infected-Susceptible) and SEIR (Susceptible-Exposed-Infected-Recovered), not only simulate disease progression but also facilitate the derivation of key analytical indicators that characterize epidemic potential [17–22]. Foremost among these is the basic reproduction number [23], R_0, which quantifies the excepted number of secondary infections caused by a single infectious individual in a fully susceptible population.

However, traditional compartmental models rest on the assumption of homogeneous mixing, where each individual is equally likely to contact any other. Although some are analytically tractable (e.g., SI), they remain a significant simplification of real-world contact structures [4,24–27]. Real populations are spatially distributed, socially stratified, and temporally heterogeneous [28]. As such, contact rates vary over time and space, modulated by factors such as daily commuting, international travel, social distancing policies, and cultural practices [29]. To account for these complexities, epidemic models have been extended into metapopulation structures [28], network-based models[30], and agent-based simulations [31], where heterogeneous contact patterns are explicitly encoded, and mobility between subpopulations can be modeled stochastically. These methods also help estimate the effective reproduction number [32], $R_e(t)$, which reflects the average number of new infections per case at time t, under prevailing immunity levels, health behavior, and intervention measures.

When $R_e < 1$, the epidemic is expected to wane; otherwise, it stands ($R_e = 1$) or grows ($R_e > 1$).

Beyond average-case dynamics, individual-level heterogeneity in transmission may play a pivotal role in amplifying local outbreaks. Certain individuals due to higher connectivity, elevated viral load, or extensive mobility infect many others disproportionately [33,34]. This overdispersion in secondary infections violates the assumptions of deterministic models and necessitates stochastic modeling approaches, particularly in low-prevalence settings where chance events dominate [35]. The degree of overdispersion is often characterized using negative binomial distributions and has critical implications for outbreak predictability and control strategies [36].
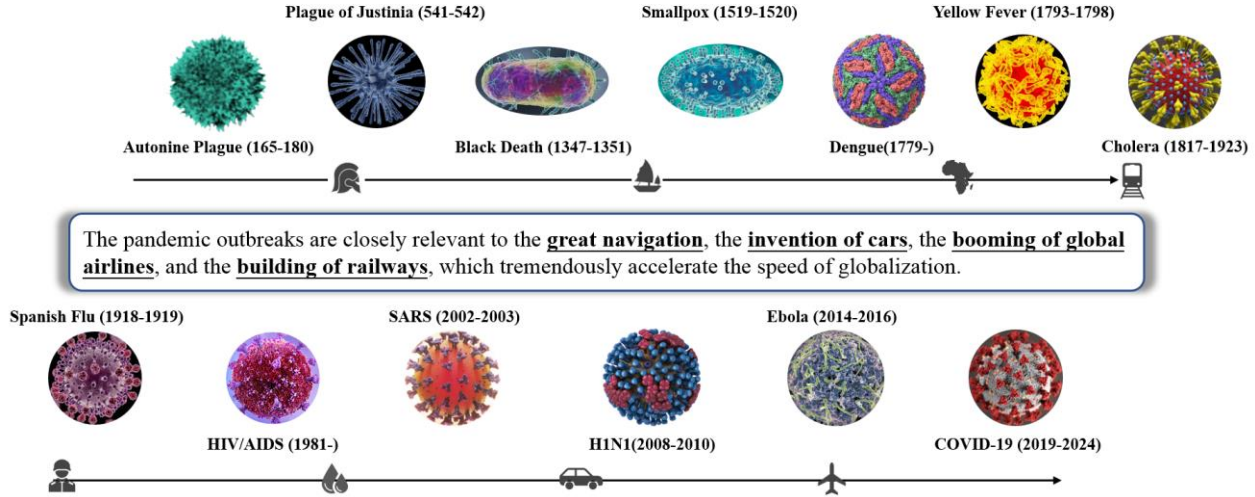
Figure 1 Chronological overview of major pandemics and epidemic events in human history.

Historically, major widespread epidemics have often coincided with advances in transportation and increase in global connectivity such as maritime expansion, industrialization, modern air travel, world wars and mass migrations, which have facilitated the movement of people and, by extension, pathogens [37,38]. **Figure 1** demonstrates a timeline of major pandemics and infectious disease outbreaks throughout history, showing the types of pathogens responsible involved and the temporal context. Although traditional epidemic models have provided valuable insights into disease dynamics, there is growing emphasis on explicitly incorporating mobility and social contact patterns, to more accurately represent complex, large-scale, and heterogeneous transmission dynamics across space and time [39,40]. For example, estimating time-dependent transmission metrics, such as the instantaneous reproduction number, R_t, has become essential for real-time epidemic assessment.

These estimates are typically inferred through Bayesian filtering or likelihood-based methods, incorporating diverse observational data streams including case counts, hospitalization records, mortality data, and sometimes mobility surveys or wastewater surveillance [31,41–43].

The addition of mobility data, especially from such as anonymized mobile phone signals, transportation usage logs, and geo-referenced digital footprints, further enables the ability of models to dynamically simulate contact networks, geographic importation risk, and location-specific onward transmission and intervention impacts [44–47]. Advances in modern transportation and technology have markedly enhanced the precise and real-time tracking of human movement, leading to substantial improvements in data collection and application [48]. Previous studies have shown that

mobility data is a more effective predictor for epidemic transmission than other indicators such as web search trends, population size, or city GDP [49]. Moreover, evidences suggest that using the distance from the outbreak source provides no advantage over mobility data in predicting the spread of infectious diseases [50,51]. These studies clearly demonstrate that the transmission of infectious agents occurs through individual movements, rendering other metrics less relevant.

During the early stages of the COVID-19 pandemic, researchers identified a strong correlation between population movement and outbreak trajectories across communities, cities, countries and continents [52]. Similar insights have emerged from earlier epidemics or pandemics, like H1N1 influenza [22], cholera [53], dengue [54], Mpox [24], and Ebola [55], each of which have demonstrated how mobility patterns uniquely shape transmission dynamics based on diverse mobility modes, from daily commuting and seasonal migration to international travel. Case studies have demonstrated that data on individual travel paths and contact patterns is critical for accurate epidemic modeling [20,49,54]. For instance, during the H1N1 outbreak, global air travel patterns were critical in predicting large-scale disease spread within a short period, while for cholera and dengue, localized community movement and interactions played a larger role [56]. This fusion of physics-inspired network modeling, high-resolution spatiotemporal mobility patterns, and data-driven statistical inference marks a shift toward quantitative, adaptive epidemiology, where control policies are informed not just by pathogen biology but by the evolving structure of human interactions [57,58]. Epidemic sources are frequently linked to highly mobile individuals who act as vectors by traveling from infected regions to susceptible areas. The spread of diseases such as COVID-19 and influenza has been shown to correlate strongly with international and domestic mobility patterns, as these movements help introduce infections to new, previously unaffected regions [59]. By tracking human movement patterns, public health officials can predict and manage the spatial spread of an epidemic, especially when mobility data is combined with real-time health surveillance [60]. This combination of mobility data and health metrics allows authorities to forecast where future outbreaks are most likely to occur and direct resources to these high-risk areas [59,61,62].

This review aims to summarize the sources and representations of human mobility data and discuss how to incorporate this data into epidemic modeling, risk assessment, and response strategies. In **section 2**, we provide an overview of main data sources of human mobility relevant to past infectious disease outbreaks and future epidemic control. In **section 3**, we introduce four types of representations of human mobility. These data representations provide convenient ways to capture human mobility patterns, enabling researchers to select the most suitable format for constructing epidemic models. In **section 4**, we explore the relationship between human mobility and epidemiology, focusing on determining whether and to what extent population flows, and contact behaviors contribute to the spread of infectious diseases. In **section 5**, we discuss widely adopted epidemic modeling approaches integrated with human mobility, including compartmental models, network-based models, agent-based models, and machine learning approaches. In **section 6**, we examine the role of human mobility in epidemic risk management, suggesting human mobility data can help identify high-risk areas, track infection pressure, and enhance monitoring effectiveness, thereby enabling timely risk management. In **section 7**, we provide an overview of policy responses implemented during pandemics, covering epidemic source identification and containment, as well as both pharmaceutical interventions (such as vaccines and treatments) and non-pharmaceutical

interventions (including social distancing and lockdowns). In **section 8**, we conclude with an outlook on the role of human mobility in epidemic modeling, highlighting methodological limitations, unresolved challenges, research gaps, and directions for future research.

2. Data Sources

2.1 Social surveys

Social surveys have long been a foundational method of data collection in epidemiology, providing invaluable insights into public behaviors, attitudes, and demographic characteristics [51,63], with ongoing advancements in data collection methods continually enhancing their value and applicability [64]. Through structured questionnaires or interviews, social surveys enable the collection of both qualitative and quantitative data, supporting nuanced analysis and cross-sectional comparisons. They allow researchers to obtain detailed, individual-level demographic and socioeconomic information from a wide range of populations [65,66]. In the context of public health and epidemic modeling, social surveys through questionnaires and follow-up studies are essential for capturing human behavior, mobility patterns, and social interactions that are critical to understand disease transmission dynamics [67,68].

Travel surveys, for instance, can reveal key details such as individuals' mobility trajectory, trip purposes, and the environmental contexts of visited locations (e.g., indoor or outdoor settings), while also including groups often underrepresented in digital datasets, such as young children without mobile phones or residents in low-connectivity, impoverished regions [69]. In addition, the emergence of digital survey tools has expanded both the scope and accessibility of traditional survey data collection, motivating real-time responses and improving coverage of previously hard-to-reach groups (e.g., individuals living with AIDS) [65,70].

Despite their strengths, social surveys face several challenges. Issues such as sampling bias [71], high non-response rates [72], and limitations in questionnaire design [73] can significantly affect the accuracy and representativeness of the collected data. Moreover, ensuring the confidentiality and ethical handling of sensitive personal information remains a critical concern in the survey process.

2.2 Public transportation records

As a classic source of human mobility data, public transportation records have long been used to acquire human movement patterns [74,75], including: (1) passenger transit card swipe records; (2) data autonomously collected at vehicle toll stations and video gates; and (3) ticket sales and passenger transport records from vehicles, ships, airplanes, and other modes of transportation. Passenger transit card swipe records provide detailed insights into individual travel patterns within public transit systems [76], while data collected at toll stations and video gates offer information on vehicular movement and traffic flows. Moreover, ticket sales and passenger transport records from various transportation modes provide aggregated data on traveler numbers and routes taken [77,78].

Public transportation data offers valuable multi-scale insights into human mobility patterns, ranging from local commutes to international travel. These data are essential for applications in urban planning, regional development, and public health, especially in tracking and managing the spread of infectious diseases. Intra-city traffic, primarily facilitated by buses and metros, supports daily commutes and short-distance travel within urban areas. These systems are heavily utilized, with daily

passenger volumes reaching millions in large cities, service frequencies ranging from a few minutes during peak hours to 30 minutes during off-peak times, and geographical coverage spanning 50 to 1,000 square kilometers. Inter-city traffic [79], served by trains and long-distance buses, is vital for connecting different cities and often crosses regional boundaries. This data is crucial for understanding regional connectivity and the flow of people between cities, with passenger volumes varying from thousands to hundreds of thousands per day. Service frequencies vary from multiple departures per hour on popular routes to just a few per day on less-traveled ones, with geographical coverage spanning several hundred to over a thousand kilometers. International traffic [80], primarily facilitated by air travel and ferries, plays a crucial role in understanding global connectivity and the spread of epidemics. This sector spans international routes that link countries across thousands of kilometers. Major transportation hubs handle daily passenger volumes ranging from thousands to over a million, with service frequencies varying from multiple departures per day at busy airports to weekly services on less-traveled routes.

2.3 Cellular signaling

Cellular signaling data (CSD), including both active and passive signaling data, is generated when a mobile phone connects to a Base Transceiver Station (BTS) during communication activities, such as powering on, making calls, and accessing the Internet. It includes a variety of information, such as call records, text messages, internet usage, and, most importantly for epidemic modeling, location data derived from the interaction between mobile devices and BTS [81,82]. Large-scale mobile phone data, at the national level, provides a finer-grained and high-quality characterization of human activities at unprecedented resolution and scale. As such, it is an increasingly valuable data source for enhancing epidemic preparedness and response efforts. With advancements in telecommunication technology and the expanding coverage of BTS, the reach and quality of cellular networks have increased significantly. The Call Detail Record (CDR) is one type of CSD, which contains information about the time of a call and the cell tower to which the mobile phone was connected when the call occurred [83,84]. In detail, CDR includes the precise time and date of each transaction, an anonymized yet distinctive identifier for both the calling and receiving parties, the call duration, and details of the cellular towers involved in the call (see **Table 1**).

Table 1 An example of mobile phone signaling data fields.

The table shows the anonymous user ID, interaction time, location, and base station code. According to the information, researchers can easily trace the users' spatiotemporal trajectories.

Fields	Examples
Time	20240210000040 (02/10/2024 0:0:40 PM)
User ID	99168999959434191
Phone number	1506179 (Top seven numbers)
User behavior	RAU-NORMAL
Location code	20512
Base station code	12321

In the context of pandemics, billions of mobile users generate a vast amount of CSD that can be

used to track human movement activities during epidemics. These CSD are typically aggregated (e.g., counties and states) for public release or further processed into index-based data to represent human mobility at the population level [47]. Population mobility data from BTS is often incomplete due to multiple operators within a country. For instance, China has China Mobile, China Unicom, and China Telecom, while the U.S. has AT&T, Verizon, and T-Mobile. Therefore, these data often need to be processed using machine learning algorithms to infer and model population mobility trends.

During COVID-19, CSD (Crowdsourced Data) demonstrated significant potential in enhancing outbreak response strategies [85,86]. However, several limitations also became apparent. Notably, datasets from major urban centers tend to be more reliable than those from rural areas, leading to an urban bias that limits representativeness. As a result, mobility patterns in less populated regions— often where healthcare resources are scarcest—may be overlooked [71]. Furthermore, concerns about privacy and restrictions on data accessibility hinder the widespread sharing and integration of CSD [87]. Addressing these challenges is critical to improving the accuracy and equity of epidemic modeling and ensuring the effectiveness of interventions across diverse populations.

2.4 Satellite positioning

Satellite positioning refers to the use of satellite systems to determine precise geographic locations on the Earth's surface. The most widely recognized satellite positioning system is the Global Positioning System (GPS), developed by the United States. However, several other systems exist, each serving similar functions: BeiDou (BDS) from China, Galileo from the European Union, and GLONASS from Russia. These systems collectively provide comprehensive global coverage, enabling fine-grained location tracking. Satellite positioning technologies have emerged as essential tools for tracking human movement. Numerous companies collaborate with mobile app operators to gather user data through app agreements, with user consent. The availability of such datasets significantly aided policy-making during the early stages of pandemics [12].

The prevalence of telecommunication devices, particularly smartphones, enables the reveal of an individual's daily mobility behaviors through GPS traces, such as where and how long they remain in a particular location [88,89]. In the context of epidemics, GPS data can support the identification of contact events, assess mobility reduction during interventions, and help model the spatial spread of infections. However, its high resolution also raises privacy concerns, requiring strict anonymization and user consent measures [47]. For instance, some applications request access to the smartphone's GPS function in order to upload location data to cloud services and provide relevant functionalities. These data will be stored and analyzed in an anonymized form. **Figure 2** demonstrates the broad overview of anonymized GPS data applications, which includes data collection, cleaning and filtering, detection, inference, metrics construction, and visualization [89].

Data collection	Data cleaning and filtering	Detection of stops and trips	Inference of users home and visits	User metrics	User weights and population averages
• De-identified opted-in GPS data • Irregularly sampled signals	• Fraudulent signals and technical glitches • Minimum data thresholds	• Pings revealing stationary behavior • Parameter choices and robustness checks	• Recurrent locations • Stops to POI assignment	• Radius of gyration • Sheltering in place • Locations visited • Contact indices	• Post-stratification and non-response weights • Aggregation to administrative areas

Figure 2 Broad overview of anonymized GPS data applications.

2.5 IP and Wi-Fi location tracking

Internet protocol (IP) addresses can reveal the approximate geographic location of devices based on their network connections, aiding in the tracking of movements across different regions [90]. Wi-Fi data, particularly when combined from multiple access points, can provide even more precise information about an individual's location according to signal strengths, especially within buildings or urban areas. When devices connect to public networks, they interact with access points that log the device's presence, allowing inferences about the location and movement of users within the range of these access points. Wi-Fi data is instrumental in indoor environments where GPS signals may be weak or unavailable. Each device connected to the internet is assigned an IP address that can be used to approximate its geographic location. Although IP addresses are less precise than GPS or Wi-Fi data, they offer accessible information on mobility at the regional and city levels. This data is commonly leveraged by internet service providers, online retailers, and content delivery networks to enhance user experiences by providing localized content and services [91].

During the pandemic, Wi-Fi and IP address data proved useful for monitoring crowd density and movement patterns, as well as assessing the effectiveness of lockdown measures by tracking reductions in foot traffic within public spaces [92]. These data sources play a vital role in the broader human mobility data landscape, complementing other sources by providing additional detail and helping to fill gaps where GPS or other tracking methods may be less effective. Their integration supports a range of applications, including behavioral analysis and infectious disease modeling.

2.6 IoT location tracking

The Internet of Things (IoT), a vast network of interconnected devices exchanging data [93,94], offers a rich source of human mobility data. These mobility patterns can be inferred not just from common wearables like smartwatches, but from a diverse ecosystem that includes fitness trackers providing granular GPS traces, smartphones logging Wi-Fi and Bluetooth beacon interactions, and connected vehicles reporting their movement [95]. The core technical opportunity lies in the fusion of this heterogeneous data, which, when aggregated, can create a high-fidelity view of individual and collective movement over time [96].

This detailed, real-time data is invaluable for public health applications. For instance, it has been proven effective in monitoring compliance with public health measures like social distancing, tracking quarantine adherence during the pandemic, and identifying potential outbreak hotspots [97].

However, the use of such personal data necessitates robust privacy protections. Standard practices include anonymization, aggregation, and clear user consent managed through device settings and user agreements. To further enhance privacy, advanced techniques like federated learning can be employed, allowing analytical models to be trained on decentralized data without exposing raw location information. By leveraging these ethically managed IoT insights, public health authorities and researchers can complement other data sources, more effectively track disease spread, and implement timely interventions.

It is worth noting that a number of challenges may compromise the accuracy and ethical application of epidemic models. First, data biases, such as uneven geographic coverage, underrepresentation of rural or marginalized populations, and demographic skews, can lead to inequitable or misleading modeling outcomes [98]. Privacy concerns are also paramount, particularly with fine-grained data from GPS, cellular signaling, and IoT sources, where even anonymized data may still allow for re-identification. Moreover, the boundaries between data types are often blurred [93]; location-based service (LBS) data from platforms like Facebook or WeChat may fall simultaneously under GPS, IP, and cellular categories, making categorization and source attribution difficult [89]. In terms of interoperability, varying data formats, update frequencies, and spatial-temporal resolutions across sources complicate direct comparisons and integration efforts. **Figure 3** illustrates the measurement ranges and update intervals for various sources of human mobility data. The radius of each circle represents the level of data granularity, with larger circles indicating more aggregated mobility data points. Public transportation data may be collected via Bluetooth or CRFID, while IoT and GPS data typically transmit over Wi-Fi or cellular networks, further fragmenting the data ecosystem [94]. Overcoming these challenges requires the development of standardized protocols, robust ethical frameworks, and advanced data fusion methods to ensure responsible and effective use of mobility data in epidemic response.
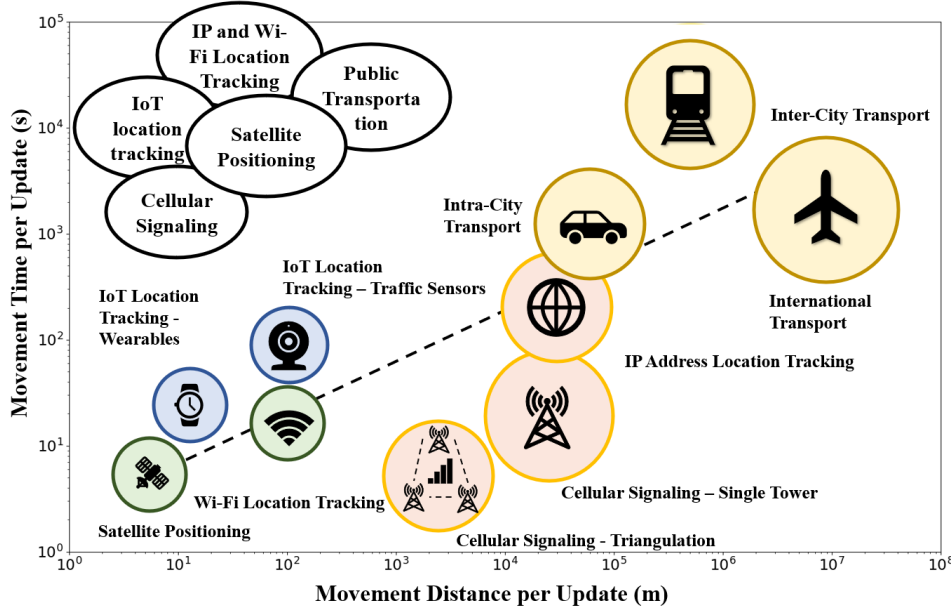
Figure 3 Estimated Spatiotemporal Resolution of Human Mobility Data Sources.

The radii of the circles represent data granularity, while the X-axis and Y-axis indicate the spatial distance of human movement and the temporal interval between record updates, respectively. It is important to note that the boundaries

between different human mobility data sources are often ambiguous. For instance, location-based service (LBS) data from platforms such as Foursquare, Twitter, Facebook, WeChat, and Weibo can fall under multiple categories, including IP-based, Wi-Fi-based, and cellular signaling. These platforms typically determine user locations using IP addresses and Wi-Fi networks, while also leveraging cellular signals to enhance positioning accuracy—particularly in scenarios where Wi-Fi is unavailable or unreliable.

3. Representation of Human Mobility

3.1 Trajectory

A trajectory refers to the movement path of an individual over time, typically represented as a sequence of geographic locations. Trajectory data is the primary data form of human mobility, which can (technically speaking) be captured from various sources such as social media platforms (Facebook, Twitter), GPS devices, and navigation applications (Google Maps, Baidu Map, and Amap). It is widely used in studies about urban mobility, travel behavior, and emergency response [99,100].

Generally, a trajectory can be seen as an alternation of stay and displacement, i.e., two states in which the individual spends time at a definite location and in which the individual moves between locations. It can be represented as a connotative chronological sequence $L_a \to L_b \to ... \to L_m$, where

L_i denotes the ith location, and the x-axis and y-axis represent longitude and latitude, respectively, as shown in **Figure 4**. Trajectory data can be used to build detailed co-occurrence or contact networks, identifying times and locations where individuals are likely to interact, which are essential factors in infectious disease modeling [97,101,101].
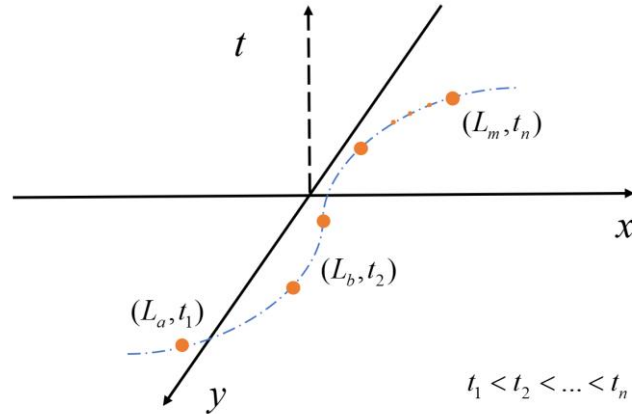
Figure 4 Human trajectory data example.

Trajectory data forms the basis for digital contact tracing during outbreaks by enabling the identification of close contacts and potential exposure events. This data allows health authorities to trace the movements of infected individuals and determine where and when they may have interacted with others, identifying potential transmission chains. However, the excessive granularity of trajectory data raises significant privacy concerns, as it can reveal sensitive information about individuals' daily routines, locations visited, and personal habits [102]. Consequently, after the COVID-19 pandemic, most trajectory datasets like Apple Mobility Trends Reports are no longer

collected and publicly available for researchers.

3.2 Mobility network

In principle, human mobility is the combined information of where people are as a function of time, but depending on data availability, questions asked about the data, and the particular disease spreading model used, one would try to assemble a more coarse-grained representation (e.g., mobility network) rather than the raw trajectories.

A mobility network refers to a graph-based representation of how individuals or populations move between different geographic locations, where nodes correspond to locations and edges represent the movements between these locations, as shown in **Figure 5**.
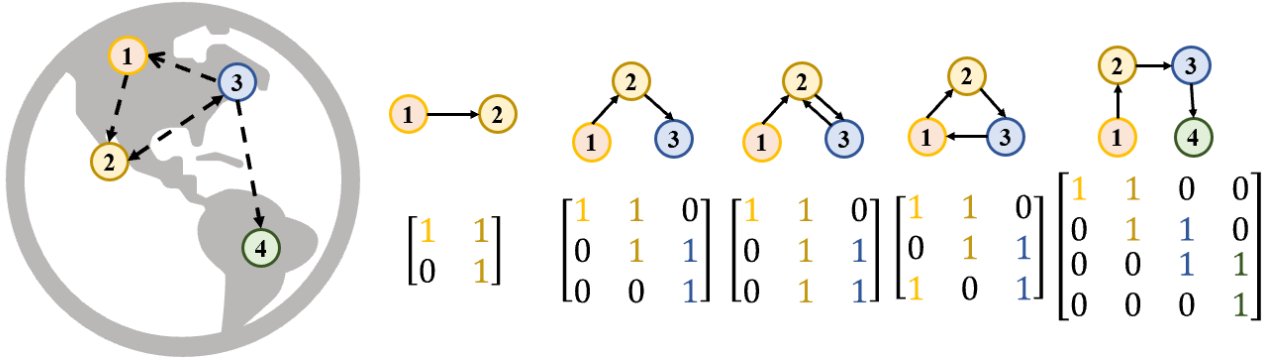
Figure 5 Example of the individual mobility network.

Each node is labeled with a number indicating the order of visits, and each edge is directed, indicating the origin-destination of trips made between the connected locations.

One of the most common forms of mobility networks is the Origin-Destination (OD) matrix, which captures the number of movements between different locations, defined as origins and destinations, over specific time intervals. In an OD matrix $\mathbf{A_{OD}}$, where a_{ij} and a_{ji} are the outflow and inflow from location i to j, respectively. The temporal OD matrix comprises multiple individual OD metrics in order of time. The temporal aspect of OD matrices allows for examining changes in movement patterns over time, providing insights into human mobility during epidemics, into daily, weekly, or seasonal variations. The backflow model is another representation of a mobility network, for each period k, the unidirectional netflow matrix can be denoted by E^k where $e_{ij} = a_{ij} - a_{ji}$ and

$e_{ji} = a_{ji} - a_{ij}$, which can be used to describe the net inflow and outflow mobility pattern in pandemics [79]. The OD matrix and its variants are standard analytical tools for examining population flow, capturing the movement behaviors and patterns of large groups across different regions [53,79]. In the context of a pandemic, these tools help describe and quantify population movement and settlement patterns, which is crucial for controlling virus transmission, optimizing public health strategies, and designing more effective preventive measures [103].

3.3 Contact network

A contact is, in general, a pair of people and a time interval when they are in sufficient proximity

for a disease to spread [104]. What a contact is depends strongly on the pathogen; for some diseases, people would not even have to be within visual range for a contact to happen [105]. In temporal network epidemiology, time is usually discretized for measurement technical reasons, and a contact is thus a triple (i, j, t) stating that individuals i and j have been in contact at time (interval) t. Although structures in time are known to have a potential impact on epidemic models [106,107], many epidemic models ignore time due to the need to simplify model assumptions.

Mathematically, a contact network is also a graph representation of individuals (nodes) and their interactions or contacts (edges) that can lead to the spread of epidemics [108–110]. It can be represented as a contact matrix C, which is a matrix with the number of individuals in the network. The elements of the matrix c_{ij}, represent the contact between individuals i and j. Specifically:

$$\mathbf{C} = \begin{pmatrix} c_{11} & c_{12} & \cdots & c_{1n} \\ c_{21} & c_{22} & \cdots & c_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ c_{n1} & c_{n2} & \cdots & c_{nn} \end{pmatrix}. \tag{1}$$

If c_{ij} is greater than 0, it indicates that there is a contact between individuals i and j, with the value represents the frequency or strength of the contact. If c_{ij} is 0, it suggests no contact between individuals i and j. By illustrating who interacts with whom and how frequently these interactions occur, contact networks enable epidemiologists to simulate the dynamics of disease transmission accurately, predict potential outbreak patterns, and identify critical intervention points. However, many real-life interactions occur within larger social contexts, such as households, schools, workplaces, or community gatherings, where multiple individuals simultaneously interact in groups rather than in simple pairwise encounters. These group interactions create clusters within the network, significantly affecting the overall connectivity and the speed at which infections propagate [111,112].

Contact networks map the interactions between individuals, capturing who comes into contact with whom. Unlike mobility networks, which emphasize aggregated flows between locations, contact networks focus on connections at the individual level. This allows for more granular representation of human movement and interaction, making them particularly relevant for studying contact-based infectious diseases [23,101]. In 2008, A study introduced the first large-scale, quantitative survey on contact patterns pertinent to the transmission of infections. This study focused on eight European countries (Belgium, Germany, Finland, Great Britain, Italy, Luxembourg, Netherlands, and Poland) and collected data between May 2005 and September 2006 to provide insights into how social contacts and mixing patterns impact the spread of infectious diseases across different populations [113].

3.4 Mobility trend and index

Relying solely on a data type makes it difficult to derive comprehensive and realistic human mobility patterns during epidemics. For instance, individual mobility trajectories and network data alone cannot capture actual contact events between susceptible individuals. Conversely, relying

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solely on contact network data fails to provide a comprehensive view of movement trajectories and cross-regional population flows. Furthermore, interdisciplinary studies often integrate various non-mobility datasets (e.g., demographic, transportation, social media, human behaviors, and geographic data) into human mobility datasets to enhance the analysis and understanding of epidemics [114]. However, from the perspective of data providers, who frequently possess additional information that could aid in understanding human mobility patterns, it is typically not feasible to share such data publicly due to concerns over business competition, legal and regulatory constraints, and privacy issues. As a result, many studies that incorporate population mobility into infectious disease modeling rely on publicly available mobility trends and indices, which are typically composites of diverse data types and sources.

Mobility trend and index datasets involve the aggregation and transformation of multi-source heterogeneous anonymous spatiotemporal mobility data, which presents processed data to the public to ensure privacy protection while providing valuable insights. Prominent examples of such practices include Google Community Mobility [85,115], Apple Mobility Trends [116], Spectus Mobility Data [117], Baidu Migration Index [118], Descartes Lab Mobility Index [119], and Facebook Data for Good [120]. **Table 2** summarizes the profiles of selected human mobility datasets. These datasets provide valuable insights while preserving individual privacy through anonymization and aggregation. They enable more accurate predictions and better-informed decision-making by leveraging the strengths of each data type while mitigating their respective limitations.

Table 2 Profile of selected human mobility datasets.

Data	Mobility Source	Mobility Type	Provider	Region	Available time	Publicly Available	Descriptions	Accessibility
Google Community Mobility	GPS/Wi-Fi/IoT/IP	Mobility trend and index	Google	Global	2020/2/15 - 2022/10/15	Yes	• The dataset shows the changes in visits and length of stay at different locations. • Data comes from users who have opted in to Location History for their Google Account.	https://www.google.com/covid19/mobility
Apple Mobility Trends	GPS/Wi-Fi/IOT/IP	Mobility trend and index	Apple	Global	2020/1/13 - 2022/4/12	Yes	• The dataset includes daily changes in requests for directions on the Maps app by driving, transit, and walking for several spatial levels. • Data is collected via Apple Maps using anonymized location services.	https://www.kaggle.com/datasets/caseycushing/apple-mobility
Baidu Migration Index	GPS/Wi-Fi/IP	Mobility network	Baidu	China Mainland	Up to now	No	• The dataset shows the number of people migrating from one city to another. • Data comes from (1) the users of Baidu Map, (2) Third-party Apps, and (3) government data.	https://qianxi.baidu.com
DL-COVID-19 Mobility Statistics	GPS	Mobility trend and index	Descartes Labs	America	2020/3/1 - 2021/4/20	Yes	• The Mobility statistics (representing the distance a typical member of a given population moves in a day) at the U.S. state and county level. • The datasets come from commercially available mobile device location datasets using cloud computing resources.	https://github.com/descarteslabs/DL-COVID-19
Spectus Mobility Data	GPS/Wi-Fi/IP	Trajectory/ Mobility network	Cuebiq	America	Up to now	No	• Spectus provides anonymous mobility data via a platform-as-a-service (PaaS). • Spectus mobility data is collected from its partner smartphone applications, whose location is at the core of the app's functionality.	https://spectus.ai
Data for Good	GPS/Wi-Fi/IP	Mobility trend and index	Facebook (Meta)	Global (except specific regions)	Up to now	Yes	• The data comes from Facebook users who opt into location history and background location collection. • The amount of movement is quantified by counting the number of 600m x 600m areas a person is observed in within a day.	https://dataforgood.facebook.com/

4. Interplay Between Human Mobility, Contact and Epidemiology

In this section, we introduce basic studies that reveal the correlation between mobility, contact behavior, and disease spread, and further explore how different forms of human movement contribute to transmission dynamics across spatiotemporal and social scales.
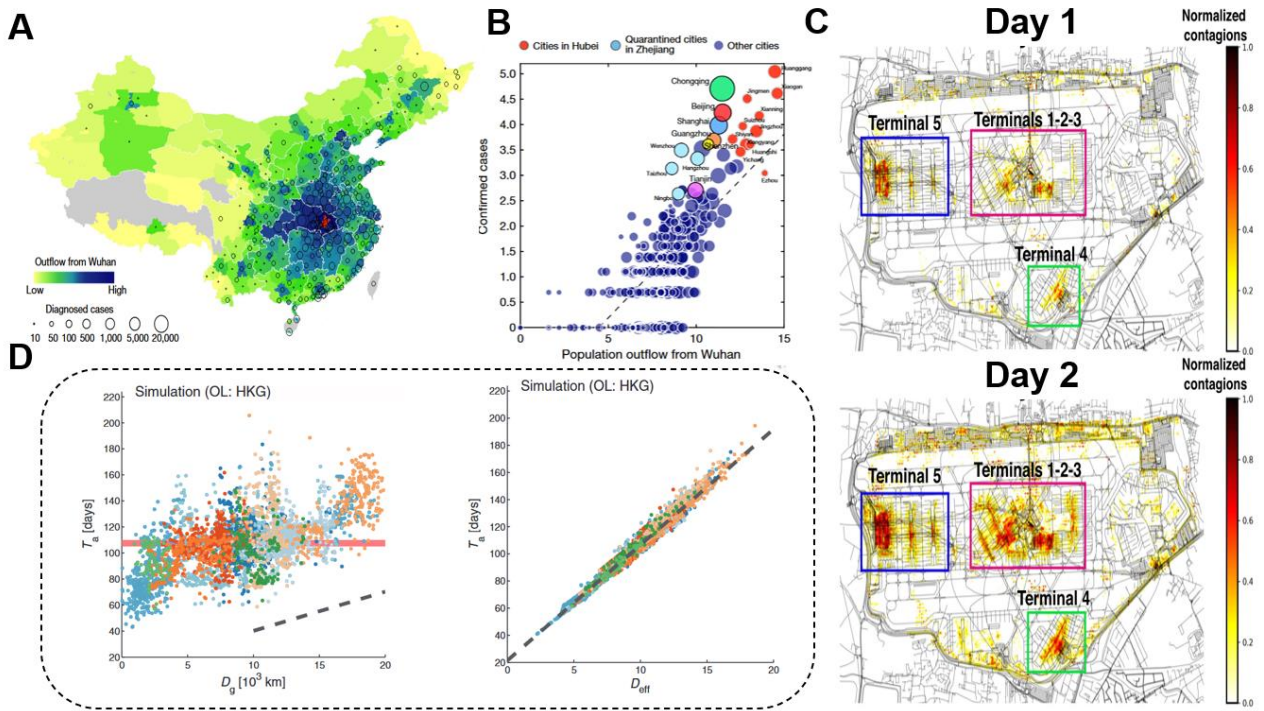
4.1 Transmission by population flow

Transmission by population flow in epidemics refers to the spread of infectious diseases facilitated by the movement of people across geographic regions [118,121]. This mechanism encompasses several critical dimensions: (1) the role of long-distance travel by infected individuals in disseminating pathogens across regions; (2) the significance of transportation hubs, such as airports, in early-stage transmission; (3) the correlation between mobility intensity and both local and international disease spread; (4) the impact of seasonal and demographic mobility fluctuations on transmission dynamics; and (5) the need for targeted interventions in high-traffic areas and among mobile, vulnerable groups.

Human mobility exhibits scale-free characteristics, whether long-distance travel or local commuting [122,123], which means that a small number of individuals with unusually high mobility can disproportionately contribute to pathogen spread [124]. For example, infected individuals with frequent and long-distance travel can quickly expand a localized outbreak into a regional or global health emergency. The examination of the correlation facilitates a more comprehensive understanding of and the ability to anticipate transmission patterns and implement timely control strategies [125]. One clear example of this correlation is the early-stage predicting role of transportation hubs in global disease outbreaks. International flight networks, for instance, link otherwise distant regions, enabling pathogens to travel thousands of miles in mere hours. Similarly, densely interconnected public transit systems, especially those involving enclosed and crowded spaces, often facilitate the rapid local spread of airborne and contact-transmissible diseases, like influenza or SARS-CoV-2 [44,79,126]. Meanwhile, domestic transmission within a country can show a strong correlation between the population outflow and the number of cases reported, as depicted in **Figure 6 (A, B)**. During the initial phase of the COVID-19 outbreak, for example, Chinese cities receiving large numbers of travelers from Wuhan exhibited significantly higher case counts. This association underscores the importance of focusing control measures on critical points of connectivity, such as railway stations, airports, and customs ports, where a large number of individuals interact and disperse.

The role of local contact environments is equally important. **Figure 6 (C)** illustrates that, as individuals traverse the airport, the infection can initially disseminate from an index case to nearby individual and subsequently propagate through the spatial layout of the facility [127]. Such hubs function as microcosms of epidemic processes, where short-duration, high-density contacts accumulate into macro-level transmission beyond transportation environments [79]. Beyond these physical spaces, the concept of effective distance, a metric derived from network topology rather than geographic distance, reliably predicts disease arrival times. As shown in **Figure 6 (D),** even if underlying epidemiological parameters remain unknown, mobility-based effective distance explains disease spread more accurately than linear geographic proximity, enabling early detection of transmission routes for outbreaks such as the worldwide 2009 H1N1 influenza pandemic and 2003

SARS epidemic [38].

Figure 6 Correlation between population flow and epidemic transmission.

(A) Heat map of outflow from Wuhan during the early stage of COVID-19, highlighting major destinations across mainland China [49]. (B) The correlation between population outflow and confirmed cases [49]. (C) Heatmap of the SIR model simulation within an airport environment, showing the cells in the airport area where infections occur. At the top after one simulation day and at the bottom after two days. The color scale is normalized for each period considered [127]. (D) Epidemic arrival time plotted against geographic distance from the source, and against effective distance derived from the mobility network, based on data from a simulated study [38].

Across various spatial scales, studies have shown that population flow is a more accurate predictor of infection spread than relatively static variables such as population size, economic status, or geographic distance from the epidemic origin [49,128]. This is primarily because most infectious diseases require physical contact or proximity, both of which are facilitated by human movement. This relationship has been particularly evident in past pandemics, where the speed, extent, and intensity of transmission have closely mirrored mobility patterns [129,130]. Research further suggests that specific types of movement—such as frequent commuting between densely populated urban centers—are especially conducive to accelerated transmission [131]. Additionally, variations in contact rates and mobility behaviors across different populations and regions introduce further heterogeneity into disease dynamics and detection efforts [132].

Transmission risk likely increase substantially during periods of seasonal or demographic mobility surges [133,134]. Holidays, school breaks, and labor migration events are marked by elevated social contact and crowding, creating ideal conditions for disease amplification during times of high population flux [135]. Vulnerable demographic groups, such as migrant workers, face heightened exposure due to their frequent movement and often substandard living and working conditions in areas where these populations converge, such as urban slums and temporary housing camps with limited access to healthcare [136–139]. For example, the resurgence of Ebola virus in

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Guinea in 2021 has been linked to population movement from affected areas [140]. The genomes form a well-supported phylogenetic cluster with those from the previous outbreak, suggesting that the new outbreak did not result from a novel spillover event from an animal reservoir, but rather from human-to-human transmission.

In addition, some migrant groups may originate from countries or regions with limited or disrupted healthcare and vaccination systems, leading to misalignment with the vaccination schedules of their host areas. This immunization gaps increase these populations' susceptibility to infection and may amplify outbreak risks in host populations [141]. Such findings highlight the need for targeted health interventions and policies to address mobility and immunization gaps in migrant populations [142]. It is significant to quantify the impact of population movement from one location to another and assess its influence on infectious disease transmission. Numerous studies suggest that human population movements are not random but exhibit high regularity and predictability across various spatial and temporal scales. These become a crucial factor in evaluating the effect of epidemic spread [143]. **Table 3** highlights six typical human mobility models used to quantify this impact. Each model defines the flow $T_{i,j}$ between regions i and j,

and provides unique insights into how human mobility contributes to disease spread. The models differ in how they account for population, distance, and opportunities, which play a specific role in simulating epidemic dynamics.

Table 3 Overview of population flow models in epidemics.

| Model	Formula	Explanation	Role in Epidemic Modeling
Gravity Model	$T_{ij} = \dfrac{G \cdot P_i^{\alpha} \cdot P_j^{\beta}}{d_{ij}^{\gamma}}$	P_i^{α} and P_j^{β} are the populations; α and β control the influence of population sizes, normally are 1; d_{ij} is the distance between areas; γ controls the deterrence effect of distance; G is a constant.	Predict how infectious diseases are transmitted between regions based on population size and distance.
Impedance Model	$T_{ij} = \dfrac{P_i \cdot P_j}{d_{ij}^{\gamma} + \varepsilon}$	P_i and P_j are the populations; d_{ij} is the distance or resistance factor; γ is the impedance factor that controls the effect of distance; ε is the resistance term.	Accounts for barriers or resistance (e.g., travel cost, time, distance) that may slow down disease spread. It helps model how travel restrictions or lockdowns can reduce transmission rates.
Intervention Opportunity Model	$T_{ij} = \dfrac{O_i \cdot D_j}{\sum\limits_{k \leq j} O_k}$	O_i is the opportunity at origin i; D_j is the attraction of destination j; the sum represents opportunities at intermediate locations.	It captures the spread of disease by considering the final destination and the intermediate stops where individuals might be exposed to the disease. Understanding how travel hubs like airports contribute to disease transmission is essential.
Radiation Model	$T_{ij} = \dfrac{P_i \cdot P_j}{(P_i + s_{ij})(P_i + P_j + s_{ij})}$	P_i and P_j are the populations; s_{ij} is the number of opportunities between the two areas.	Modeling disease spread based on opportunity distribution, not distance. It helps to simulate the regional spread of diseases without relying on arbitrary parameters like distance, particularly for diseases that do not rely heavily on distance for transmission.
Population Weighted Opportunities Model	$T_{ij} = P_i \cdot \dfrac{O_j}{\sum\limits_{k} O_k \cdot W_k}$	O_j is the opportunity at origin j; W_k is the population weight in other areas.	Incorporates population density into disease modeling to predict how densely populated areas are more likely to experience faster and broader spread of infections.
Opportunity Priority Selection Model	$T_{ij} = \dfrac{O_j^{\alpha}}{(d_{ij} + 1)^{\beta}}$	O_j is the opportunity at origin j; d_{ij} is the distance between areas; α, β are adjustable parameters for opportunity and distance.	Emphasizes the importance of specific destinations based on their priority (e.g., work or education opportunities), which helps identify high-risk regions for disease outbreaks.

4.2 Spread through contact behavior

Contact behavior refers to the patterns by which people interact with each other, including how often, how long, and in what situations those interaction occur [129,144]. These patterns shape the structural foundation for transmission and are critical for understanding the dynamics of infectious disease spread, informing both epidemic modeling and the design of intervention strategies [108,145]. The interplay between disease progression and human behavior is bidirectional: as infections spread, they often alter social behavior (e.g., via risk avoidance), which in turn reshapes future transmission potential. Comprehending this feedback loop is vital for building realistic models and developing interventions that not only mitigate disease spread but also consider the societal costs and behavioral responses. By examining how contact frequency, duration, and social contexts vary across different groups, researchers can enhance the granularity and accuracy of predictive epidemic models for tailoring targeted interventions [69]. Research on disease spread through contact behaviors focuses on three main aspects: (1) frequency and duration of contact, (2) social context and environmental influence, and (3) demographic and behavioral heterogeneity.

The frequency and duration of inter-host contacts are fundamental determinants of transmission probability [146]. High-frequency or prolonged contacts are more likely to lead to infections, particularly for pathogens transmitted via droplets, aerosols, or physical contact. Understanding the structure and dynamics of contact networks informs parameter estimation, interpretation, and the formulation of control measures such as social distancing, mask mandates, or quarantine guidelines [147,148]. **Figure 7 (A)** illustrates an example of disease propagation across a contact network, showing how an infectious individual transmits the pathogen to connected contacts over time [149]. Adaptive changes in behavior (e.g., by avoiding crowded places, wearing masks, or adhering to quarantine guidelines) can impact the infection rates and reduce infectious disease spread, reshaping the contact network. These behavioral shifts imply that traditional static models of disease transmission, which assume fixed contact rates, may not capture the full complexity of real-world epidemics. Understanding the relationship between human mobility, contact patterns, and disease transmission involves constructing contact networks and applying network analytics within predictive models. Epidemic models that integrate dynamic contact behavior more accurately reflect real-world epidemic trajectories and can inform better public health interventions [30,41,150,151].

The social context and environmental context in which interactions occur greatly influences transmission risk. Contact intensity and structure differ across settings, such as households, schools, workplaces and transportation hubs, as well as between groups with different social roles. Individuals with disparate social identities exhibit disparate contact patterns at a more localized level, giving rise to divergent transmission dynamics [152–154]. For instance, at London Heathrow Airport, airport staff had denser contact networks than transient passengers, making an infected worker far more likely to propagate disease than a single infected passenger [127]. While contacts in household setting dominate in many respiratory disease outbreaks, interventions like school closures can potentially reduce peak incidence by up to 40-60% and delay the epidemic peaks. However, such interventions are often insufficient alone and must be deployed with broader strategies. Incorporating these social and environmental layers into epidemic models allows us to capture the nuanced, real-world transmission dynamics shaped, enabling better precision in identifying high-risk interactions and

optimizing targeted interventions [155].
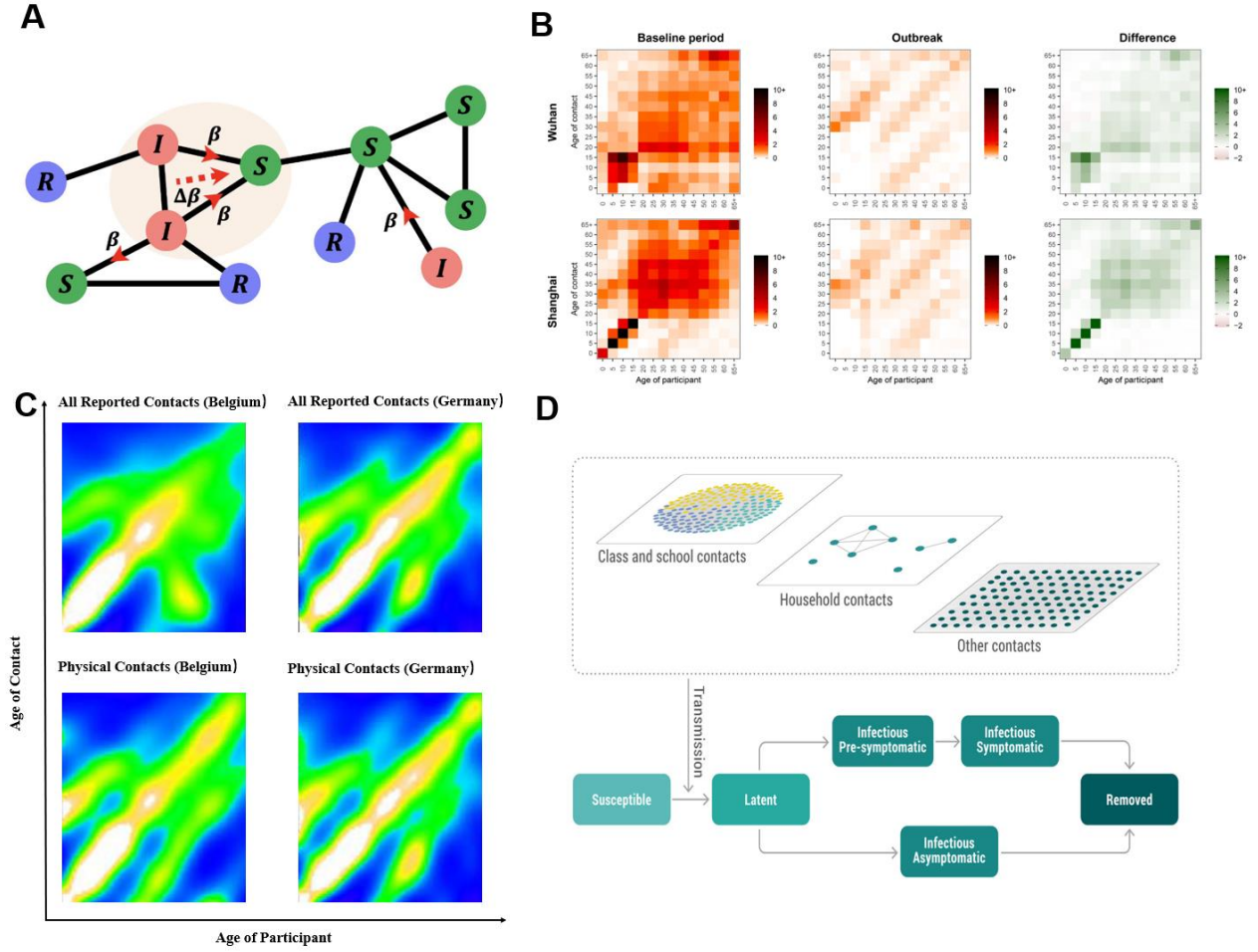
Figure 7 Epidemics spreading through contact patterns.

(A) Transmission of an infectious agent across a contact network, illustrating how person-to-person links facilitate the spread of disease [149]. (B) Age-stratified contact matrices from empirical studies, showing higher interaction rates within similar age groups [129]. (C) Smoothed contact matrices for Belgium and Germany. White indicates high contact frequency, green denotes intermediate, and blue represents low contact intensity [108]. (D) Schematic representation of the transmission model and contact networks in schools, households, and other places. Each environment features distinct connectivity patterns that shape transmission dynamics [156].

Demographic traits (e.g., age, gender, or occupation) also shape contact patterns and, consequently, disease dynamics. Some diseases, such as HIV requiring prolonged or intimate contact for transmission, necessitate a more profound comprehension of the behavioral and social factors that contribute to their transmission dynamics [157]. In such case, the focus of prevention efforts must shift to understanding and addressing the exposure patterns within high-risk groups [158]. These include the frequency and nature of interactions within specific contact networks, such as those involving sexual partners or intravenous drug users. Identifying super-spreaders or hotspots of exposure within these networks can be crucial for implementing targeted interventions [159]. Besides, age-specific contact patterns offer another layer of insight. Empirical studies demonstrate that people are most likely to interact, and thus infect others within their own age group, especially in environments like schools and households [108,129]. This age-assortative mixing is visualized in

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Figure 7 (B, C), where contact matrices show stronger interactions within specific age bands. **Figure 7 (D)** further demonstrates the schematic representations of these contact and transmission networks across different circumstances, such as schools, households, and other social settings [156].

Analyzing contact patterns across these three dimensions, temporal dynamics, contextual settings, and demographic profiles, enables targeted and effective public health responses [160,161]. In particular, contact tracing conducted by field epidemiological investigations has proven instrumental in identifying and isolating cases within tightly connected social clusters [4,162]. In contexts where close-contact transmission dominates, tracing the structure of social interactions becomes critical to breaking chains of infection. New technologies have enhanced this capability [41]. For example, the utilization of digital contact tracing via mobile phone signaling, sensors and Bluetooth-based proximity data can now track interactions in real-time, allowing for rapid outbreak detection and early warning systems [41,150,163]. This advancement allows for the quicker identification of transmission chains, enhancing our ability to respond to outbreaks with greater speed and precision [129,164,165].

5. Epidemics Models Incorporated Human Mobility

5.1 Compartmental models

Compartmental models represent a class of population-based epidemiological modeling frameworks that simulate disease transmission dynamics by dividing the population into discrete compartments corresponding to different stages of infection, such as Susceptible, Exposed, Infectious, and Recovered [12,39,166–171]. These models typically rely on the assumption of homogeneous mixing, meaning that each individual in the population has an equal probability of coming into contact with others. Representative examples include the SI, SIS, SIR, SEIR, and SEIRS models, which have been widely employed to describe the spread of various infectious diseases. To date, compartmental models remain among the most commonly used mathematical frameworks in the field of epidemiological modeling [172,173]. However, the assumption of homogeneous mixing is often unrealistic in real-world contexts. Empirical studies have shown that human mobility follows a power-law distribution, wherein the majority of individuals engage in short-range movements while only a small proportion travel long distances [143]. This highly heterogeneous mobility pattern translates into non-uniform contact structures, meaning that the probability of interaction between individuals is far from evenly distributed. What's more, the studies of scale-free networks [174], and small world networks [175] in real human society can also demonstrate the heterogeneity in the actual epidemic spreading. Then, the result of traditional compartmental models may lack authenticity in a real pandemic.

A SEIR model integrated with human mobility was proposed in 2020 [176]. The model integrates human mobility by incorporating the probability of individuals traveling between communities and making contact, thereby simulating how movement across regions influences disease spread. The model divides the population into nine distinct compartments: susceptible (S), exposed (E), presymptomatic (P), infected (I), asymptomatic (A), hospitalized (H), quarantine (Q), recovered (R), and deceased (D). The model assumes frequency-dependent contact rates, whereby exposure occurs at a rate described by the force of infection. The force of infection for the community i is given by

$$\lambda_i = \sum_{j=1}^{n} C_{ij}^s \frac{\displaystyle\sum_{Y\in\{P,I,A\}} \sum_{k=1}^{n} \beta_Y C_{kj}^Y Y_k}{\displaystyle\sum_{X\in\{S,E,P,I,A,R\}} \sum_{k=1}^{n} C_{kj}^X X_k}, \tag{2}$$

where C_{ij}^X (with $X \in \{S, E, P, I, A, R\}$) is the probability ($\sum_{j=1}^{n} C_{ij}^X = 1$ for all i and X) that individuals in an epidemiological state X who are from the community i enter into contact with individuals who are present in the community j as either residents or because they are traveling there from the community k.

5.2 Metapopulation models

Classical compartmental models typically do not account for population heterogeneity, potentially limiting their ability to accurately represent the spatial dynamics of infectious disease spread [177]. To address this limitation, metapopulation models are developed as spatially explicit extensions of compartmental frameworks. These models divide the total population into multiple subpopulations (e.g., cities or communities) and explicitly incorporate migration rates to simulate individual movement across them, thereby capturing the heterogeneity in contact opportunities and mobility-driven transmission pathways [176,178].

A representative example is a study of the 2010 cholera outbreak in Haiti, which led to over 170,000 infections and more than 3,600 deaths by the end of that year. In this study, the researchers implemented a metapopulation-based SIR model that explicitly accounted for uneven population mobility between Haitian regions and hydrological mechanisms—such as rainfall-driven runoff—that facilitated the environmental spread of Vibrio cholerae through water systems [179]. Communities were modeled as interconnected nodes, linked by both human migration flows and waterway networks, thereby enabling both direct and indirect transmission across distant regions. This framework highlighted how spatial heterogeneity, particularly power-law mobility patterns, significantly influenced the outbreak's rapid geographic expansion and provided critical insights for designing more effective public health interventions.

Mathematically, the model extended the classic SIR equations by introducing inter-patch mobility terms. For a metapopulation consisting of N subpopulations, the dynamics for subpopulation i can be expressed as:

$$\frac{dS_i}{dt} = \mu(H_i - S_i) - \mathcal{F}_i(t)S_i + \rho R_i, \tag{3}$$

$$\frac{dl_i}{dt} = \mathcal{F}_i(t)S_i - (\gamma + \mu + \alpha)I_i, \tag{4}$$

$$\frac{dR_i}{dt} = \gamma I_i - (\rho + \mu)R_i, \tag{5}$$

$$\frac{dB_i}{dt} = -\mu_B B_i - I\left(B_i - \sum_{j=1}^{n} P_{ji}\frac{H_j}{H_i}B_j\right) + \frac{\rho}{H_i}\left[1 + \Phi J_i(t)\right]\left[(1-m)I_i + m\sum_{j=1}^{n} Q_{ji}I_j\right], \tag{6}$$

where S_i, I_i, and R_i are the abundance of susceptible, infected, and recovered in node i, and B_i is the concentration of node i, the total contact rate

$$\mathcal{F}_i(t) = \beta\left((1-m)B_i/(K+B_i) + m\sum_{j=1}^{n} Q_{ij}B_j/(K+B_j) \right)$$ incorporating both local disease transmission

within a given node and transmission associated with mobility between nodes. The human mobility patterns are modeled using an origin-destination (OD) matrix, wherein individuals depart from their origin node i with probability m, arrive at a destination node j with probability Q_{ij}, and subsequently return to their home node i. To characterize the connectivity between spatial units, a gravity-like model is employed, in which the connection strength Q_{ij} decays exponentially with the distance between nodes:

$$Q_{ij} = \frac{H_i e^{-\frac{d_{ij}}{D}}}{\sum_{k \neq i}^{N} H_k e^{-\frac{d_{ik}}{D}}}, \qquad (7)$$

Here, d_{ij} represents the shortest path distance between nodes i and j, while D denotes the deterrence cutoff distance that controls the rate of decay in interaction strength.

Although compartmental models provide a solid foundation for basic epidemic simulations, they struggle to accurately incorporate human mobility. This is largely because they presume uniform mixing within population groups and fail to represent the intricate web of interactions occurring among individuals in diverse locations. Consequently, these models often miss the complex dynamics of disease transmission driven by differing travel patterns, social networks, and highly connected hubs like transportation centers or crowded city centers. Complex network models present a more sophisticated framework to handle these intricacies, depicting populations as networks of interconnected nodes and edges. This approach effectively captures heterogeneous contact patterns and the flows of human movement.

5.3 Network-based models

Building upon the metapopulation framework introduced earlier, network-informed models offer a more granular and realistic representation of transmission dynamics by explicitly incorporating the heterogeneous structure of human interactions and mobility. Two primary types of networks are typically employed in the context of epidemics. The first is the mobility network, where nodes correspond to subpopulations or geographic regions, and edges reflect the probabilities or intensities of movement between them. The second is the contact network, which represents individuals as nodes and edges as potential disease-spreading interactions, such as social contact, co-residence, or workplace proximity. These network structures allow for more accurate characterization of transmission pathways, especially in systems where homogeneous mixing assumptions fail to reflect real-world complexity [180,181].

5.3.1 Mobility network models

Mobility networks capture the movement of individuals across different locations, enabling modeling of how infections propagate through spatially distributed populations. These networks are not static; rather, they evolve over time under the influence of various factors such as social behavior, economic activity, transportation infrastructure, and even public health interventions (e.g., lockdowns, quarantine orders, and travel restrictions). In these networks, nodes represent geographic units (e.g., cities, regions, countries), and directed edges encode the flow of individuals between these units. This approach generalizes the traditional compartmental models (e.g., SIR, SEIR), wherein individuals are assumed to mix homogeneously within each compartment or location but may migrate between compartments based on empirical or modeled mobility patterns. For example, an epidemic spread across countries via air travel routes can be effectively modeled using this framework, allowing researchers to simulate long-range transmission and assess intervention strategies across borders [182]. Traditional topological mobility network models are limited in representing the complex human mobility systems that include different types of relationships and nodal attributes [183]. They may overlook critical attributes like individual differences in behavior, social interactions, mobility frequency, and disease susceptibility, making it challenging to understand and predict disease dynamics in real-world scenarios fully.

The increasing availability of high-resolution human mobility datasets has significantly enhanced our ability to model real-world disease transmission across heterogeneous spatial scales. These data have made it possible to move beyond theoretical constructs and simulate disease dynamics with empirically grounded interregional mobility patterns. In this subsubsection, we introduce two representative mobility network models that capture distinct temporal and spatial patterns of human movement: the host movement network model [184,185], which reflects habitual and short-term displacements, the weekly mobility network model [186], which aggregates broader mobility trends over a weekly timescale.

In the host movement networks model [184,185,187], researchers evaluated the performance of two metapopulation models in capturing the dynamics of malaria transmission across a network of geographically isolated subpopulations. Their findings revealed that the choice of movement modeling framework plays a critical role in shaping epidemiological outcomes. Specifically, the models assume that each subpopulation remains demographically stable over time and that disease transmission occurs entirely through local interactions within each subpopulation. Under this assumption, individual movement between locations is described as a diffusive process, modeled as follows [184]:

$$\frac{dN_i}{dt} = -\sum_{j=1}^{K} f_{i,j} N_i + \sum_{j=1}^{K} f_{j,i} N_j, \tag{8}$$

where N_i represents the number of individuals currently located at site i, and $f_{i,j}$ is the rate at which

individuals travel from site i to site j, where $f_{i,i} = 0$ for all i. If visitors are allowed to interact with

residents at the destination site and then return to their home location at a fixed rate, the model incorporates a visitor-resident dynamic and can be reformulated as [184,185]:

$$\frac{dN_{i,i}}{dt} = -\sum_{j=1}^{K} \phi_{i,j} N_{i,i} + \sum_{j=1}^{K} \tau_{i,j} N_{i,j}, \tag{9}$$

$$\frac{dN_{i,j}}{dt} = -\tau_{i,j} N_{i,j} + \phi_{i,j} N_{i,i}, \tag{10}$$

where an individual from i who is currently located at j will be counted as belonging to the $N_{i,j}$ population, and the number of individuals whose home is i remains constant over time, even if members visit other locations. The constant $\phi_{i,j}$ represents the rate at which individuals whose home is i travel to j, while the constant $\tau_{i,j}$ is the rate at which individuals visiting j from i return home to i.

In contrast, the weekly mobility networks [186] utilizes empirical trip data to construct time-resolved mobility networks G_T for each calendar week T, capturing dynamic changes in population flows. The edge weights $w_{ji}(T)$ are then calculated as the average daily number of trips between counties during this week.

$$w_{ji}(T) = |D_T|^{-1} \sum_{t' \in \mathcal{D}_T} F_{ji}(t'), \tag{11}$$

where D_T denotes the set of days in calendar week T.

To investigate how the global reduction of mobility affects our observations in comparison to structural changes, we construct rescaled networks $G_{10}^*(T)$ by scaling the weights of the pre-lockdown network of calendar week ten by the flow lost during the week T, i.e.,

$$w_{ji}^{\star}(T) = w_{ji}(T) \times \frac{\sum_{i,j=1}^{m} w_{ji}(T)}{\sum_{i,j=1}^{m} w_{ji}(T=10)}. \tag{12}$$

According to formulas (10) and (11), researchers can incorporate human mobility into complex network models and analyze various lockdown-induced changes in mobility in Germany during the initial phase of the pandemic, finding a considerable reduction of mobility during the pandemic, similar to what was previously reported for other countries that passed and implemented comparable policies [184–186].

5.3.2 Contact network models

A growing body of research has focused on characterizing contact patterns by developing data-informed models that explicitly integrate human mobility with epidemic transmission dynamics. These models emphasize the heterogeneity of infection risk arising from both individual-level

interactions and mobility-induced exposure, thereby enhancing the accuracy and predictive power of epidemic forecasts. In this study, we present two representative modeling approach based on contact networks: temporal-evolving contact network model, which describes the dynamics of individual contact [188], scenario contact network model, which characterizes different kind contact in separated layer [23].

As showed in [188], temporal-evolving contact network model bases on a method for modeling time variant contact networks in epidemiology, explicitly linking individual-level interactions to disease transmission through mathematical frameworks. Contact networks are formally represented as graphs $G(t) = (V, E(t))$, where nodes $v \in V$ denote individual hosts, and time-varying edges $e_{ij}(t) \in E(t)$ represent contacts capable of pathogen transmission. Crucially, edges encode temporal features: duration τ_{ij}, concurrency $c_i(t)$ (number of simultaneous contacts per individual), and turnover rate ρ. Empirical data sources, such as cattle movement timestamps or human contact diaries recording pairwise touches/conversations. Disease transmission integrates contact dynamics via the SIR model. For an individual i, the infection hazard depends on contacts with infected neighbors $\mathcal{N}_i(t)$:

$$\frac{dI_i}{dt} = \beta \sum_{j \in \mathcal{N}_i(t)} 1_j^{inf} - \gamma I_i, \tag{13}$$

where β is transmission rate per contact, γ is recovery rate, and $\mathcal{N}_i(t)$ evolves dynamically.

Crucially, temporal contact features were shown to dictate epidemic outcomes: high concurrency accelerated outbreaks; frequent repeated contacts reduced transmission; and avoidance behavior (rewiring edges away from infected nodes) created modular networks, enabling sub-threshold persistence. Network topology metrics (degree distributions, clustering) further quantified how dynamic processes altered epidemic thresholds and intervention efficacy, proving that static models misestimate risks when contact fluidity is high.

The scenario contact network model was developed to assess the measurability and relevance of classical epidemic indicators, such as the basic reproduction number (R_0) and generation time (T_g) [23]. This model is structured as a multi-layer contact network, with each layer representing a distinct type of social interaction. Additionally, demographic stratification—including attributes such as sex, age, and occupation—can be incorporated as layered subpopulations. This stratification introduces both visible and invisible barriers to transmission, thereby enabling the modeling of targeted intervention strategies for specific demographic groups. The core methodology in [23] involves the construction of multiplex contact networks, which represent interactions within households, schools, workplaces, and the broader community. Each layer captures a specific interaction context, allowing for a more realistic representation of contact patterns. The node degree distribution aligns with empirical data, and the weighted number of contacts for each individual can be computed as follows:

$$\sum_{l \in \{h,s,w,c\}} w_l c_l(i), \tag{14}$$

where $c_l(i)$ is the number of edges node i has to other nodes in layer l and the influenza pandemics

with reproduction number $R^{index} = 1.3$ corresponding to an estimation results [189].

The infection dynamics follow a discrete-time SIR process with time step $t = 1$ day, which can be calculated by:

$$\begin{cases} S_i(t+1) = S_i(t)\left[1 - \displaystyle\prod_{l \in \{h,s,w,c\}} \prod_{j \in \mathcal{N}_l(t)} \left(1 - pw_l\rho(a_i)I_j(t)\right)\right] \\[2em] I_i(t+1) = I_i(t)(1-\gamma) + S_i(t)\left[\displaystyle\prod_{l \in \{h,s,w,c\}} \prod_{j \in \mathcal{N}_l(t)} \left(1 - pw_l\rho(a_i)I_j(t)\right)\right], \\[2em] R_i(t+1) = R_i(t) + \gamma I_i(t) \end{cases} \tag{15}$$

where $\mathcal{N}_l(t)$ is the neighbor set of i in layer l at time t, p is the transmission probability per contact, $\rho(a_i)$ is the age-specific susceptibility rates, and γ is the recovery rate. This layer-specific formulation allows for different transmission intensities across contexts.

Mobility-based and contact network models are increasingly utilized in epidemiological research to elucidate the complex, nonlinear dynamics of disease transmission. By explicitly representing the structure and temporal evolution of interactions among individuals, these models offer high-resolution depictions of epidemic spread [190]. Their advantages are substantial: they capture heterogeneous contact patterns, allow for more accurate forecasts of outbreak trajectories, and provide actionable insights into the roles played by individuals and subgroups in facilitating or impeding transmission. Such insights support the design of targeted interventions, including prioritized vaccination strategies and localized quarantine measures.

However, these network-based approaches also face several notable challenges. Their accuracy depends critically on the availability and quality of data describing contact and mobility behaviors—data that are often scarce, noisy, or difficult to collect at scale. In addition, simulating large-scale, multilayered networks can be computationally demanding, requiring significant computing resources and optimization techniques. Finally, model validation remains a persistent difficulty due to the dynamic and context-dependent nature of real-world contact structures, which may evolve over time or differ across populations and settings.

5.4 Agent-based models

5.4.1 Rule-based agent models

Epidemic models such as compartmental models and complex network-based frameworks, often simplify human behavior by assuming homogeneous mixing within groups or by downplaying the heterogeneity of individual actions. These approaches tend to emphasize macro-level state transitions, such as shifts between susceptible and infectious populations, while neglecting the nuanced

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interactions that occur at the individual level. However, human mobility behavior is inherently stochastic, diverse, and often guided by personal preferences or aversions. Failing to account for individual autonomy in movement and decision-making may severely limit a model's ability to simulate disease transmission dynamics accurately [71]. Integrating human mobility with agent-based models (ABMs) can help address the limitations of traditional approaches in capturing individual behavioral dynamics [191,192]. ABMs simulate the behaviors and interactions of individual agents, each representing a unique member of the population with independently evolving states over time. These highly flexible models are capable of incorporating detailed mobility patterns, enabling fine-grained, micro-level simulations of disease transmission processes.

Agent-based models (ABMs) have been widely used to assess how mobility restrictions and behavioral changes influence infection rates. Traditional ABMs operate based on predefined rules, simulating movement behaviors and interactions at a high level of detail [31,193–195]. In particular, reference [196] proposed a rule-based ABM designed to evaluate the disease transmission risks in facilities, aiming to capture the spatiotemporal dynamics of epidemic spread. In this model, agents are categorized into two distinct types that make decisions according to specific rule sets—Type A and Type B, corresponding to Rule I and Rule II, respectively. Each agent is assigned a unique mobility pattern, enabling precise simulation of daily activities and interpersonal interactions. These interactions are characterized by various health states, such as susceptible, exposed, infectious, and recovered, which evolve based on predefined rules and interactions with other agents. The rules are aligned with the spatial movement patterns and infection conditions of the agents to represent the transmission process accurately. Furthermore, each agent is assigned a personal profile that includes key social attributes and health status, which govern behavioral responses during interactions. These individual-level features play a critical role in shaping agents' interaction behaviors, as illustrated in **Table 4** [196–198].

Table 4 Pseudo-code for the epidemic transmission risk model based on rules.

ABM algorithm	
Input: A, B, l_{in}, l_{cm}, u_{cm}, $[L_x, U_x, L_y, U_y]$, α, $maxiter$, R, S, $k=1$	
$Pri_i \leftarrow$ **InitializeProbInf**(A, l_{in}, u_{in}); $Prcm^B_i$, $Prcm^B_j \leftarrow$ **InitializeProbMob**(A, B, l_{cm}, u_{cm}); $A(k)$, $B(k) \leftarrow$ **InitializePos**(A, B, [Lx, Ux, Ly, Uy]);	Initialization
while $k <= maxiter$ **do**	

for each $a_i(k) \in A(k)$
  $F \leftarrow$ **FindAnInfectedAgentInNeighbor**($B(k)$, R);
  If ($F == 1$) **then**
    If ($rand \leqslant Pri_i$) **then**
      $A(k) \leftarrow$ **DeleteFromA**(a_i);
      $B(k) \leftarrow$ **IncludeInB**(a_i);
    end If
  end If
  end for
	Rule Ⅰ

for each $a_j(k) \in A(k)$
  If ($rand \leqslant Prcm^A_i$) **then**
    If ($rand \leqslant \alpha$)
    $a_i(k+1) \leftarrow$ **LocalMovement**($a_i(k)$, S);
	Rule Ⅱ for A

else
        $a_i(k + 1) \leftarrow$ **LongMovement**($[L_x, U_x, L_y, U_y]$);
        end If
     else
     $a_i(k + 1) = a_i(k)$
     end If
   end for	

for each $b_j(k) \in B(k)$
     If ($rand \leqslant Prcm^B_j$) **then**
       If ($rand \leqslant \alpha$)
       $b_j(k + 1) \leftarrow$ **LocalMovement**($b_j(k), S$);
       else
       $b_j(k + 1) \leftarrow$ **LongMovement**($[L_x, U_x, L_y, U_y]$);
       end If
     else
     $b_j(k + 1) = b_j(k)$
     end If
   end for
	Rule ‖ for B

$k = k + 1$ **end while**	

A recent example of applying agent-based modeling (ABM) to epidemic simulation involves representing individuals as agents who move within urban areas, travel between cities, and interact in various public settings [199]. This model tracks how mobility restrictions and behavioral adaptations (e.g., social distancing) impact infection rates over time. Agents' mobility patterns determine the likelihood of contact between individuals, thereby directly influencing the dynamics of disease transmission. Another study investigating how objective mobility affects epidemic spread found that increased mobility significantly raises the final number of infections. For mobile individuals, infection rates at nodes were found to be proportional to their betweenness centrality, while for non-mobile individuals, infection rates were approximately proportional to nodal degree [200]. These ABM frameworks focus on the core mechanisms of epidemic spread, particularly human behaviors such as movement, dwelling, and social interactions, enabling them to capture the complexity of human mobility and interaction more effectively than aggregate models. Each agent is assigned a mobility trajectory that dictates their daily routines, interactions, and transitions between locations. Decisions such as whether to visit a public venue or remain at home directly affect their exposure risk. Broader patterns of human movement influence the probability of agent contact, thus shaping the overall dynamics of transmission.

5.4.2 Stochastic agent models

In contrast to rule-based agent models, where agent behaviors follow explicitly defined interaction protocols, stochastic agent-based models introduce inherent randomness and unpredictability in agent interactions, better capturing the complexity and variability observed in real-world social dynamics [201,202].

In [203], it develops a stochastic agent-based microsimulation model is developed to evaluate the potential effects of non-pharmaceutical interventions (NPIs) on the trajectory of the COVID-19 epidemic in France. Each agent in the model represents an individual characterized by demographic

and health attributes drawn from national statistics, including age, sex, household composition, and comorbidities known to increase the risk of severe SARS-CoV-2 infection. The synthetic population was constructed to reflect the real-world distribution of risk factors in France, with approximately 36.4% of the population categorized as vulnerable due to age (over 65 years) or pre-existing medical conditions. The agents interact within a dynamic social contact network, which simulates daily activities such as work, school, family gatherings, public transport, and grocery shopping. Each interaction is parameterized by distance, duration, and frequency, thereby generating probabilistic exposure events. The disease model is overlaid on this network, allowing for infection to spread across contact edges according to a transmission probability function that decays with physical distance and is modulated by preventive behaviors such as mask-wearing and physical distancing. By integrating epidemiological parameters, the model simulates disease progression on an individual level, accounting for the heterogeneity of both exposure risk and clinical severity. Crucially, the stochastic nature of the model enables it to capture the probabilistic and emergent behavior of an epidemic in a heterogeneous population.

Recent advancements further enhance these models by integrating real-world modeling technologies, such as generative agents with Large Language Models (LLMs). **Figure 8** demonstrates a framework to model spreading behaviors using generative artificial intelligence [204]. By employing LLMs, researchers can more realistically simulate individual decision-making processes, social behaviors, and communication patterns, substantially improving the fidelity of epidemic simulations. Such integration allows stochastic agent models to more effectively reflect the unpredictability inherent in human behavior, thus offering more accurate and actionable insights into disease spread dynamics and potential interventions [200].
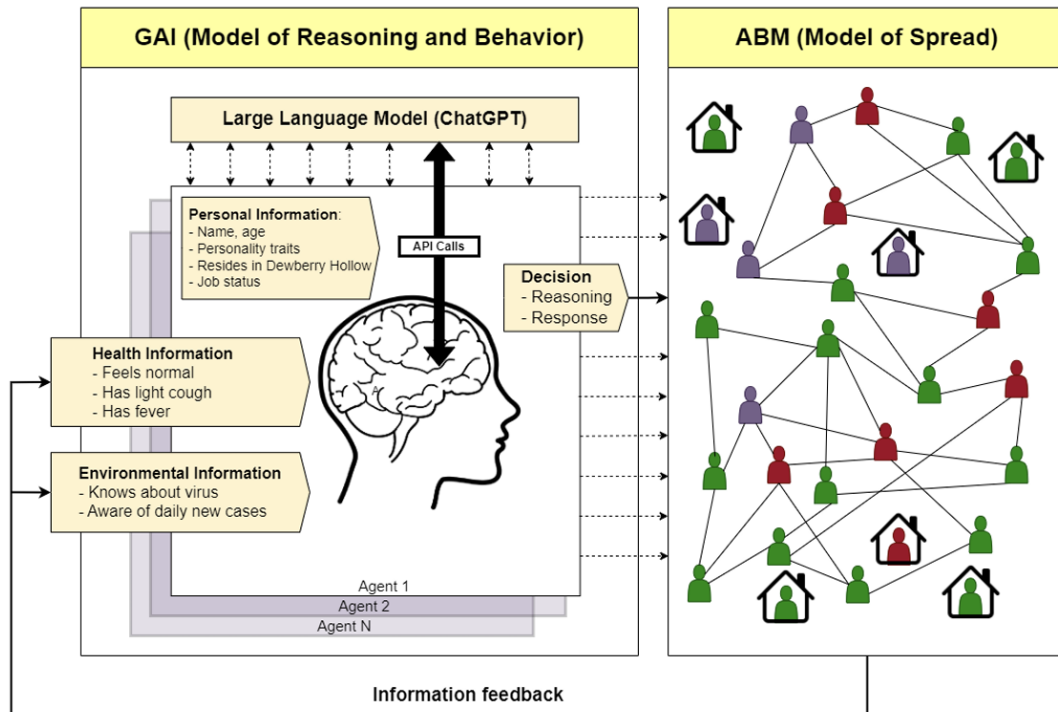
Figure 8 Generative agent-based modeling for spreading behaviors.

Generative agent-based modeling provides reasoning and decision-making ability for each agent through closed feedback between an AI-based large language model of reasoning (GAI) and a simulation model of spread (ABM) [204].

The strength of ABMs lies in their ability to simulate individual behaviors and interactions, providing detailed insights into disease transmission that are often unattainable through more aggregated modeling approaches. However, the inherent diversity and unpredictability of human behavior pose significant challenges to accurately simulating real-world scenarios. Detailed ABMs can be computationally intensive, but advances in computational technology have increasingly enabled large-scale and efficient simulations. By integrating human mobility with ABM techniques, researchers can develop powerful epidemic modeling tools that effectively capture the complexity of human behavior and movement.

5.5 Machine learning models

With advancements in computational and statistical technologies, machine learning (ML) models have been extensively explored and applied in infectious disease modeling [205–207]. ML techniques offer new avenues for predicting contagious disease spread and evaluating intervention strategies[208], as shown in **Figure 9**. These models can handle large, complex datasets and enhance the real-time response capabilities. Traditional ML models, such as Bayesian [209], Autoregressive Integrated Moving Average (ARIMA) [210], Support Vector Machine (SVM) [211], and Ensemble Learning (EL) [212], provide clear insights into how human mobility influences disease transmission, while balancing predictive performance with interpretability. In addition, deep learning models such as Deep Neural Networks (DNNs) [213], Graph Neural Networks (GNNs) [214], and Long Short-Term Memory (LSTM) [215], have also demonstrated strong performance in epidemic prediction tasks due to their ability to capture complex nonlinear patterns. However, their lack of interpretability and reliance on large-scale data can limit their applicability in some policy-sensitive contexts. Recently, large language models (LLMs) have emerged as powerful tools for extracting knowledge from unstructured data, such as scientific literature, policy documents, and social media. While not directly used for mechanistic modeling, LLMs can support epidemic analysis by synthesizing insights, generating hypotheses, and enhancing decision-making workflows [216].

5.5.1 Traditional machine learning models

To forecast outbreaks and assess interventions, interpretable machine learning models harness historical mobility data reflecting fundamental human movement behaviors, helping discern the factors influencing disease spread. Bayesian models are a prevalent forecasting tool, enhancing accuracy by combining mobility data with prior insights into mobility or epidemiology. Within this framework, the prior distribution represents initial parameter assumptions, updated by observed data into the posterior distribution for final parameter estimation. By treating mobility probabilistically, these models gauge the likelihood of cross-regional transmission, leading to more accurate identification of infection pathways and emerging hotspots. For instance, a conditional Batesian spatial modeling framework was offered to assess perceived infection risk, modeling the relationship between county-level demographic, socioeconomic, and business attributes across the U.S. [209]. This approach treats mobility patterns as probabilistic inputs to model transmission likelihood across regions. Conditional on the selected covariates, the percentage in mobility is assumed to follow a Beta distribution:

$$\mathbb{E}[y \mid \mathbf{x}] \sim B(\mu(\mathbf{x}), \phi), \tag{16}$$

where **X** is the set of fixed covariates, given by the selected principal component constructed in Principal Component Analysis and the epidemiological covariate; ϕ is the precision parameter of the Beta distribution and $\mu(\mathbf{x})$ its mean, linked to the linear predictor $\mu(\mathbf{x})$ by the default logit-link. Such integration enables the Bayesian model to trace how covariates modulate mobility behaviors and propagate transmission risk. Beyond improving hotspot and pathway detection accuracy, the probabilistic treatment explicitly quantifies model uncertainty, transforming it into a decision-support tool for public health planning.

As time-series techniques, ARIMA models identify trends, cycles, and seasonality in human mobility. When extended to ARIMAX with mobility as an exogenous regressor, they assess both the impact of population movement on disease spread and temporal dependencies in transmission. The models' interpretable parameters clarify mobility-infection linkages. This study further develops the framework by: (1) analyzing mobility-infection correlations, and (2) introducing a hybrid EEMD-ARIMAX forecasting method where mobility serves as the exogenous input [210]. The parameters of the ARIMAX(p, d, q, n) model are: p, the number of autoregressive terms; d, the number of nonseasonal differences needed for stationary; q, the number of lagged forecast errors in the prediction equation; n, the number of exogenous variables; η, a constant; and, ϕ_i, for $i = 1, \ldots, p$, θ_j, for $j = 1, \ldots, q$, and ζ_l, for $l = 1, \ldots, n$, the model parameters. Mathematically, this model can be formulated as

$$W_t = \eta + \sum_{i=1}^{p} \phi_i W_{t-i} - \sum_{j=1}^{q} \theta_j e_{t-j} + \sum_{l=1}^{n} \zeta_l Y_l, \tag{17}$$

where W_t and W_{t-i}, for $i = 1, \ldots, p$, are the predicted values of the time series; Y_l, for $l = 1, \ldots, n$, are the exogenous variables of human mobility; and e_{t-j}, for $j = 1, \ldots, q$, represent the error terms. This model incorporates external inputs into the ARIMA model to forecast the number of confirmed cases in epidemics. The external variables encompass meteorological data and human mobility data. By integrating these variables into the ARIMAX model, we can more accurately predict the epidemic development trend of different cities and enhance the prediction accuracy by combining the empirical mode decomposition (EMD) method.

In the human mobility and epidemic modeling context, Support Vector Machines (SVMs) are supervised learning algorithms used for classification and regression tasks. In infectious disease modeling, SVM can classify regions or periods based on the risk level of disease spread by utilizing features extracted from human mobility data, such as travel frequency, distance, and connectivity. On the other hand, Ensemble learning methods (e.g., Random Forests) combine multiple models to enhance predictive performance. They are especially adept at handling large datasets with numerous features, making them suitable for analyzing complex human mobility patterns. Random Forests can identify critical predictors of disease spread by evaluating the contribution of different mobility factors. These models provide feature importance scores, which are interpretable and help clarify which mobility factors most significantly influence transmission dynamics. Here is research where

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SVM and Random Forests are used to identify everyday activities between infected and uninfected individuals to help stop the spread of pandemic diseases [211]. Another research focuses on classifying whether an individual will exhibit flu-like symptoms based on their mobility pattern. The Random Forest classifier predicts symptom presence, focusing on short-term mobility behaviors by analyzing features such as the number of different places visited, the total displacement, and other movement-related data. The model achieves notable performance, with an Area Under the Curve (AUC) score of 0.57 and an F1-score of 0.77, demonstrating its ability to identify key mobility features that signal impending symptoms [212].

Both SVM and Random Forests can effectively incorporate human mobility data, such as travel frequency, distance, and connectivity, to classify regions or periods based on the risk of disease spread. These models can also identify critical predictors of transmission by evaluating various mobility factors, such as travel hubs, transportation modes, and population density. It helps assess and mitigate transmission risks. For example, datasets like Google Community Mobility Reports, SVM, and Random Forests can correlate movement patterns with infection rates, providing valuable insights for controlling disease outbreaks and identifying which aspects of mobility have the most significant impact on transmission dynamics.

5.5.2 Deep learning models

Deep learning models are growing prominent in mobility-aware epidemic forecasting. Their foundation lies in multilayered neuron assemblies: individual neurons apply trainable weight parameters to incoming signals before outputting transformed results via nonlinear activations. For instance, DNNs can predict infection rates by processing high-dimensional features derived from human mobility data, such as GPS traces. These networks mimic the human brain's neural connections, allowing them to model intricate, non-linear relationships in large datasets. They can identify hidden patterns that are difficult for traditional models to detect. Study [213] proposed an IPSO-DNN model to predict social distancing efficacy through mobility pattern analysis. This model consists of three key stages, namely, data preprocessing, IPSO-DNN hyperparameter optimization, and model evaluation. Human mobility data is scaled and split into training and testing sets, ensuring features are normalized to improve model learning. Then, the IPSO algorithm minimizes the mean squared error of the DNN's prediction on training data. At last, the optimized DNN model predicts the impact of social distancing based on the testing data. The model quantifies how social distancing reduces transmission rates and confirms its critical role in pandemic containment. Furthermore, intervention duration and compliance intensity significantly influence epidemic trajectories.

GNNs are particularly well-suited for epidemic modeling due to their ability to work with graph-structured data such as the OD matrix and contact network. The features of human mobility networks make GNNs ideal for modeling the interconnectedness of such systems. However, in real-world situations, strict privacy data protection regulations result in severe data sparsity problems (i.e., limited case and location information). To address these challenges of data sparsity, researchers propose a Deep Graph Diffusion Infomax (DGDI) from the micro perspective mobility modeling to compute the relevance score between a diffusion and a location [214]. From an alternative standpoint, researchers have put forth a network-based deep learning approach to address the changes in spatiotemporal travel mobility and community structure detection induced by the pandemic, which is

based on the premise of normalized preparedness. By jointly optimizing graph learning and network analysis in an end-to-end system, this approach models evolving transportation networks. The resulting complex network metrics reveal spatiotemporal mobility transformations and statistical dependencies between travel modes. The findings reveal a reduction in connectivity and travel diversity across various modes, with post-pandemic recovery characterized by polycentric structures and increased bike-sharing usage [217]. These GNN models spatial and structural interconnectivity within mobility networks, identifying complex contagion dynamics across population clusters through learned relational dependencies. Their ability to model changes in travel behavior and community structures during a pandemic makes them particularly useful for developing targeted intervention strategies and understanding the long-term impacts of mobility shifts on epidemic dynamics.
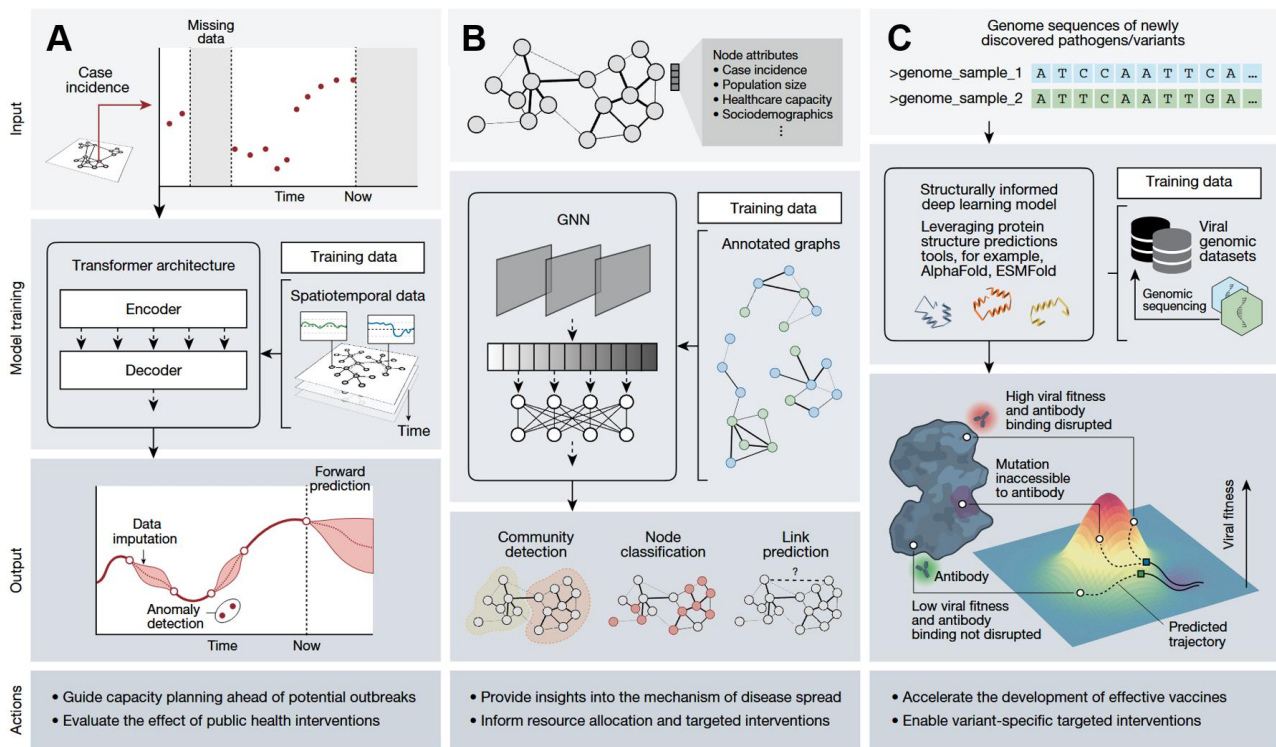
Figure 9 Machine learning approaches to tackling key epidemiological questions.

(A) By pre-training large-scale foundation models with transformer architecture using time-series epidemic data—whether empirical or simulated—it becomes possible to apply these models in a zero-shot manner for tasks such as forward prediction, data imputation, and anomaly detection. The outputs generated by these models can be utilized to assess the impact of public health interventions and inform capacity planning for future outbreaks. (B) Modeling the spread of infectious diseases with Graph Neural Networks (GNNs) involves representing pathogen transmission through annotated graphs. In these graphs, nodes represent locations or individuals, and edges symbolize potential transmission routes, such as human or vector interactions. Each node is linked to a set of features, like case incidence and population size, which serve as indicators or drivers of disease spread. GNNs can learn intricate patterns from this data, facilitating tasks such as node classification (predicting disease prevalence), community detection (identifying infection clusters), and link prediction (uncovering hidden transmission pathways). These insights offer a deeper understanding of the mechanisms behind disease spread and support efficient resource allocation and targeted interventions. (C) Leveraging biologically informed deep learning models to predict immune-escape mutations involves utilizing recent advancements

in protein structure prediction, like AlphaFold and ESMFold. These models can help identify pathogens or variants that are prone to developing mutations that disrupt antibody binding, potentially leading to resistance against current vaccines or therapeutics. Such predictive capabilities can assist in the development of next-generation vaccines and help prioritize containment strategies aimed at emerging variants[208].

LSTM networks are effective for time-series forecasting in epidemic modeling, as they can process sequences of mobility data and infection rates, capturing patterns and trends in human movement and infection spread. By learning these dynamics over time, LSTMs enable more accurate predictions of future outbreaks and support timely interventions. This feature of LSTM is helpful for rapidly probing and quantifying the effects of government interventions, such as lockdown and reopening strategies. This study presents a deep learning framework based on LSTM networks for epidemiology system identification from noisy and sparse observations with quantified uncertainty, which is trained on Google and Unicast mobility data [215]. The method integrates graph learning and optimization to model travel networks dynamically, uncover changes in user mobility patterns, and explore the relationships between different travel modes. The findings reveal significant trip volume and connectivity reductions during the pandemic, with post-pandemic recovery showing a shift towards more polycentric travel patterns and increased use of bike-sharing services. By capturing temporal patterns and trends in human movement, LSTMs model the non-linear relationships between past mobility behaviors and current infection levels, providing accurate predictions even when dealing with complex, time-dependent data. These networks are instrumental in assessing how changes in human mobility such as those caused by lockdowns or public health interventions affect the trajectory of an epidemic. However, while LSTMs offer predictive solid performance, their internal mechanisms, like gates controlling information flow, are complex and hinder interpretability. This trade-off between model transparency and predictive accuracy remains challenging, as LSTMs focus more on accurate forecasting than explanation.

5.5.3 Large language models

In recent years, Large language models (LLMs) have catalyzed a pivotal transformation in the field of natural language processing. LLMs can not only simulate individual behaviors to form ABMs, but also infer future disease dynamics based on population data and textual information. This study proposes the PandemicLLM framework, which applies multimodal large language models to the field of infectious disease forecasting, transforming traditional epidemic prediction problems into text-based reasoning tasks, integrating real-time, complex, non-numerical information, including public health policy texts, genomic surveillance data, and spatiotemporal and epidemiological time-series data [216]. The overview of this method is showed in **Figure 10**. It transforms traditionally heterogeneous data (e.g., epidemiological time-series, public health policy descriptions, genomic surveillance reports, and spatial-demographic indicators) into structured textual prompts. These prompts, typically around 300 words long, are carefully crafted through a cooperative design involving both human experts and AI systems. To handle the time-dependent nature of epidemiological data, the framework uses a recurrent neural network (GRU-based encoder) that converts sequential numerical data (like hospitalization rates) into dense embeddings. These embeddings are injected into the LLM's input space via a special token mechanism, allowing the model to incorporate both temporal and textual information. Forecasting is formulated as a categorical

classification problem, where the model predicts the future hospitalization trend of each U.S. state (for 1-week and 3-week horizons) into one of five categories: substantial decrease, moderate decrease, stable, moderate increase, or substantial increase. The LLM used (a fine-tuned version of Meta's LLaMA2) is trained to generate the most likely category token based on the prompt. The model is evaluated across several time periods using not only conventional metrics like accuracy and mean squared error, but also probabilistic ones such as Brier score and ranked probability score, which better capture forecast uncertainty. Notably, three versions of PandemicLLM are trained on progressively larger datasets, and tested over extended periods without retraining, demonstrating the model's robustness and adaptability.
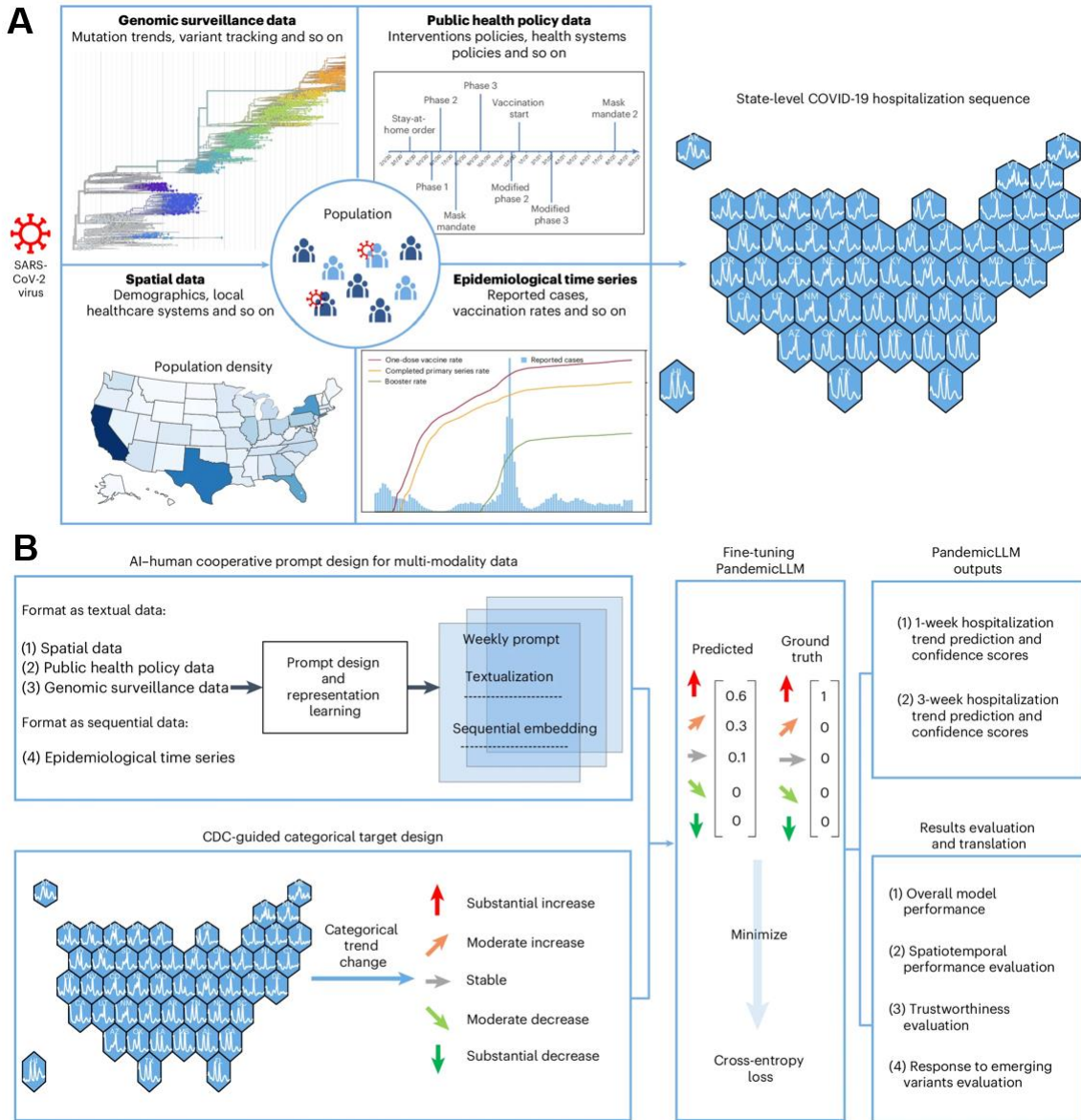
Figure 10 Overview of pandemic data streams and pipeline in PandemicLLM.

(A) The study utilizes a comprehensive dataset that brings together four key types of information related to the pandemic: spatial characteristics, epidemiological time series, public health interventions, and genomic surveillance. (B) In designing the PandemicLLM framework to forecast hospitalization trends during the pandemic, the problem is treated as an ordinal classification task. It adopts five outcome categories based on CDC guidelines: ranging from substantial

decrease to substantial increase. To enable model training, multi-modal data are first reformatted into textual inputs through a collaborative prompt design involving both AI and human input. PandemicLLM is then fine-tuned using these text-based prompts and the associated prediction targets, focusing on both 1-week and 3-week timeframes. Careful evaluation procedures are applied to ensure the predictions are both accurate and reliable [216].

6. Human Mobility and Epidemic Risk Management

This section aims to illustrate how human mobility data can be used to identify risk sources, measure infection pressure, and reveal transmission mechanisms, particularly in outbreaks driven by emerging pathogens. It also highlights studies related to early warning and outbreak detection.

6.1 Epidemic source identification

The rapid, large-scale, and diffuse movement of people can significantly amplify localized outbreaks into widespread epidemics through long-range travel, daily commuting, and socio-spatial congregation [218]. Empirically, epidemics often originate from a few key locations or events, such as high-density transportation hubs or mass gatherings where large numbers of individuals converge [152,153]. Epidemic sources are frequently linked to highly mobile individuals who act as vectors by traveling from infected regions to susceptible areas. The spread of diseases such as COVID-19 and influenza has been shown to correlate strongly with international and domestic mobility patterns, as these movements contribute introducing infections to new, previously unaffected regions [59]. **Figure 11 (A)** illustrates that nationwide outbreaks of infectious diseases often begin in a small number of early-affected regions that serve as risk sources. These initial outbreaks gradually trigger a chain of transmissions across the country, driven by human mobility and social interactions. While the overall epidemic may appear as a single nationwide curve, it can be decomposed into distinct regional timelines, each reflecting localized transmission dynamics. In this process, infections spread from the source regions to others via observable population movements and hidden social contact routes, highlighting the importance of early detection and intervention at the source to contain further spread. By tracking epidemic sources, public health officials can predict and manage the spatial spread of an epidemic, especially when mobility data is combined with real-time health surveillance [60]. This combination of mobility and individual health status of people from epidemic sources allows us to forecast where future outbreaks are most likely to occur and direct resources to these high-risk areas [59,61,62].

With the increasing availability of mobile phone data, travel records, and other real-time datasets, several approaches have been developed to track and pinpoint epidemic sources based on population mobility patterns. For instance, the use of smartphone apps such as COVID Safe in Australia, Trace Together in Singapore, and Exposure Notification in the United States has demonstrated the potential of mobile technology to assist in contact tracing efforts at a national scale. These apps use Bluetooth technology to detect proximity between individuals and inform them if they have been in contact with someone who tested positive for the virus. By using Bluetooth technology, these apps ensure that personal data remains minimal, as they only store anonymized identifiers rather than sensitive personal information. Studies have shown that digital contact tracing systems can significantly reduce the time lag between an individual becoming infected and being isolated, thus curbing the spread of infections by identifying high-risk individuals faster [219–221]. **Figure 11 (B)** demonstrates the

process of identifying risk source via human mobility. The inputs are a series of GPS trajectories of individuals that have visited the outbreak origin (blue circle) and trajectories of other, unaffected individuals (grey, dashed lines). Using these data, researchers can infer the location and timing of an outbreak by identifying instances where infected individuals were in close proximity. The most prominent cluster is then identified as the estimated outbreak location through inference methods [222,223].

Researchers develop a spatiotemporal risk source model that utilizes population flow data (which operationalizes the risk emanating from epidemic epicenters) not only to forecast the distribution of confirmed cases but also to identify regions with a high risk of transmission at an early stage [14]. The model yields a benchmark trend and an index for assessing the risk of community transmission of epidemics over time for different locations. This risk-source model operationalizes the risk emanating from the epidemic source. The effect of outflow on infection by using the following multiplicative exponential model:

$$y_i = c \prod_{j=1}^{m} e^{\beta_j x_{ji}} e^{\sum_{k=1}^{n} \lambda_k I_{ik}} \quad . \tag{18}$$

In which y_i is the number of cumulative (or daily) confirmed cases in the prefecture i (depending on the model); x_{1i} is the cumulative population outflow from Wuhan to prefecture i; x_{3i} is the population size of prefecture i; m is the number of variables included; c and β_j are parameters to estimate. λ_k is the fixed effect for province k; n is the number of prefectures considered in the analysis; I_{ik} is a dummy for prefecture i and $I_{ik} = 1$, if $i \in k$ (prefecture i belongs to province k), otherwise $I_{ik} = 0$. This model leverages observed population flow data to operationalize the risk emanating from the epidemic source. It makes no assumptions regarding travel patterns or practical distance effects, allows for nonlinear estimations, generates a non-arbitrary, source-linked risk score, and is easily adapted to other empirical contexts. **Figure 11 (C)** demonstrates the predictive model based on population outflow. The left subgraph represents the outflow population from Wuhan, China, along with time, and the right subgraph represents the risk scores over time, providing a dynamic picture of shifting transmission risks in different prefectures in China.

Identifying the sources of an epidemic as early as possible is essential for effective disease control and mitigation, as it allows public health authorities to implement timely interventions and limit the spread of infectious diseases [224]. However, privacy concerns and public reluctance to adopt source identifying technologies remain major barriers to effective implementation. For instance, studies have shown that voluntary participation in digital contact tracing applications is often significantly lower than expected, mainly due to fears of surveillance and data misuse [225]. These challenges undermine the timely identification of infection sources, which is essential for early intervention and targeted

response.

To overcome these limitations, future efforts should focus on improving the accuracy, reliability, and public acceptance of source identifying systems. By integrating multiple types of data, including mobile location traces, social media activity, environmental factors, and demographic information, researchers can build more comprehensive models for outbreak detection. In addition, advances in machine learning can enhance the predictive performance of these models, allowing for more adaptive and real-time epidemic management strategies [226,227].

6.2 Epidemic risk models incorporated infection pressure

The effectiveness of infectious disease response and containment can be significantly improved by concentrating healthcare efforts and control measures in areas at highest risk of new outbreaks. Calculating infection pressure provides a quantitative method for evaluating the level of risk in specific areas. Infection pressure refers to the force exerted by pathogens' presence and transmission potential within a population, which influences the likelihood and degree of disease spread [228]. It is determined by factors such as population density, mobility patterns, contact rates, and the virulence of the infectious agent. High infection pressure often arises in areas with large, mobile populations or frequent interactions, such as urban centers, transportation hubs, or regions with high rates of human mobility.

Previous studies have demonstrated that infection pressure, calculated by mobility flows or contact rates, can serve as a valuable proxy for identifying early outbreaks [14,229]. For instance, a study based on mobile phone data during the early COVID-19 outbreak in China proposed a spatio-temporal risk model to estimate infection pressure from Wuhan to 296 prefectures across mainland China, demonstrating that the intensity of outflows from Wuhan explained over 96% of the variance in case distributions during the early spread phase [14]. Another study analyzed the travel-related risks associated with the SARS-CoV-2 Omicron variant in China, demonstrating that mobility data from air and rail travel were essential for estimating the importation and exportation risks of emerging variants, particularly in highly connected urban regions [230]. Similarly, researchers leveraged air passenger itinerary data to estimate global infection pressure from high-risk Chinese cities, showing a strong correlation between air travel volumes and case importation risk, particularly before international travel restrictions were enacted [231,232]. These models above calculate risk by population inflow rather than local population size, highlighting the directional and dynamic nature of infection risk propagation [233]. They offer operational value for real-time risk assessment, early warning, and resource allocation, especially when combined with global travel data and local health system vulnerability indices such as the Infectious Disease Vulnerability Index (IDVI) [234].

Infection pressure serves as a foundational metric for quantifying the epidemic risk imposed by population movements from an infected source to susceptible regions [14,229]. Conceptually, it integrates both the intensity of human mobility and the prevalence of infection at the origin, formalized as the product of population flow and incidence rate [153,231]. This indicator reflects not only the probability of seeding infections in target areas but also the temporal synchronization between mobility peaks and epidemic surges [235]. At the early stage of the outbreak, by constructing infection pressure indicators through real-time analysis of big data on population mobility, it is possible to predict the potential infection risks in various regions, assist the

government in implementing regional graded control, and formulate refined prevention and control strategies to reduce the impact on the economy and society [236,237].

As previously mentioned, it is significant to assess the infection pressure of importation of the virus from a risk source and its potential impact on the local transmission of the disease in regions impacted by the ongoing pandemic [153,154,238]. Lee et al. focus on the country-specific importation risk based on the number of international travelers, confirmed cases in the originating countries, and the population of the originating countries [239], proposing the risk assessment model:

$$\text{Risk}_{c,t} = \frac{I_{c,t}}{pop_c} T_{c,t}, \tag{19}$$

where t is the month and c is a group of countries. $I_{c,t}$ stands for the monthly confirmed cases in a month t and an originating country c. The population-adjusted density of infectious travelers was obtained by $I_{c,t}$ dividing its population pop_c of country c. $T_{c,t}$ represents the number of passengers traveling from country c in a month t. **Figure 11 (D)** shows the normalized country-specific risk of case importation from the top 13 countries to South Korea from January to October 2020.

Wu et al. used data on flight bookings and human mobility in China to predict the infection pressure of the COVID-19 virus and accounted for the effect of the Wuhan quarantine [74]. They consider the infection pressure in the following SEIR model:

$$\begin{cases} \dfrac{dS(t)}{dt} = -\dfrac{S(t)}{N}\left(\dfrac{R_0}{D_I}I(t) + z(t)\right) + L_{I,W} + L_{C,W}(t) - \left(\dfrac{L_{WI}}{N} + \dfrac{L_{WC}(t)}{N}\right)S(t) \\[2mm] \dfrac{dE(t)}{dt} = \dfrac{S(t)}{N}\left(\dfrac{R_0}{D_I}I(t) + z(t)\right) - \dfrac{E(t)}{D_E} - \left(\dfrac{L_{WI}}{N} + \dfrac{L_{WC}(t)}{N}\right)E(t) \\[2mm] \dfrac{dI(t)}{dt} = \dfrac{E(t)}{D_F} - \dfrac{I(t)}{D_I} - \left(\dfrac{L_{WI}}{N} + \dfrac{L_{WC}(t)}{N}\right)I(t) \end{cases}, \tag{20}$$

where $S(t)$, $E(t)$, $I(t)$, and $R(t)$ is the number of susceptible, latent, infectious, and removed individuals at the time t; D_E and D_I are the mean latent and contagious period; R_0 is the primary reproductive number; $z(t)$ is the zoonotic force of infection equal to 86 cases per day in the baseline scenario before market closure on Jan 1, 2020, and equal to 0 after that. This model estimates the outbreak size of COVID-19 thus far in Wuhan and the probable extent of disease spread to other cities domestically. The results clearly indicate that if the pandemic had spread rapidly everywhere at the same rate as in Wuhan, outbreaks would have quickly emerged in many major Chinese cities.

Overall, tracking human mobility is essential for quantifying infection pressure, as it helps identify where a disease is likely to spread and assess the intensity of transmission dynamics across different regions. Moreover, understanding infection pressure is crucial for implementing targeted interventions, as it highlights areas where containment measures, such as social distancing, vaccination, or travel restrictions, should be prioritized to reduce the risk of outbreaks.

6.3 Epidemic risk assessment based on network transmission

The spread of epidemics depends on contact between people. Constructing a complex network of interpersonal contacts is not only the basis for understanding, analyzing and predicting the risk of infectious disease transmission, but also an important part of computational epidemiology.

Effective epidemic control requires targeted interventions in regions under high infection pressure. Combined with human mobility, researchers find that the risk of an area experiencing an outbreak within seven days showed a strong dose-response relationship with the mobile phone-based infectious pressure estimates [240]. They use the human mobility network M^{phone} with elements m_{ij}^{phone}, indicating the average daily proportion of mobile phones relocating from the study area i to j, comparing their last registered location on the day t with their previous registered location on the day $t-1$, and then they propose the infection pressure $P_j(t)$, in which $c_i(t)$ is the number of reported cases in study area i on day t.

$$P_j(t) = \sum_{i, i \neq j}^{n} \left[m_{ij}^{phone} \sum_{k=1}^{7} c_i(t-k) \right]. \tag{21}$$

Based on this infection pressure model, all areas they studied experienced outbreaks within several days over a specific pressure level. The findings indicate that the probability of an epidemic occurring in a specific region and the initial severity of local outbreaks could have been predicted during the initial stages of the epidemic by utilizing case reports and the mobility patterns of mobile phones.

To empirically characterize human contact heterogeneity, large-scale studies have quantified age-specific interaction patterns. A study based on characteristic data of 97,904 interpersonal contacts from 7,290 participants in multiple European countries, found that contact patterns showed clear age homogeneity, with contacts in families, schools or leisure places more likely to involve physical contact (and thus potentially more susceptible) than contacts in the workplace or during commuting. When the population is fully susceptible, the 5-19 age group has the highest risk of infection in the early epidemic stage of an emerging infectious disease [241].

From the perspective of transmission sources, the contact network effectively identified high-risk node types. In response to the COVID-19 pandemic, the contact transmission network constructed based on digital contact tracing (DCT) estimated that the basic reproduction number R0 in the early stage of the epidemic in China was 2.0. Among them, pre-symptomatic individuals contributed 46% of the transmission risk, symptomatic individuals accounted for 38%, asymptomatic infections accounted for 10%, and the remaining 6% came from environmentally mediated transmission [242].

In addition to node heterogeneity, the spatiotemporal characteristics of contacts further reveal the mathematical principles of super spreading. The RFID-based real contact network of the population found in multiple scenarios that the duration of interpersonal contact follows a power-law distribution, and individuals with high numbers of connections maintain longer contact time at the same time, thus revealing the mathematical principles of "super-spreading events" in epidemics [243].

The seminal framework of network disintegration proposed by Brockmann & Helbing employs effective distance metrics to conceptualize epidemics as percolation processes across spatial networks

[153]. Within this paradigm, nodes represent epidemic-relevant locations (e.g., cities, airports), while edges encode population mobility (e.g., air travel, commuting). During the COVID-19 pandemic, empirical validation demonstrated that targeted removal of <5% of high-traffic hub airports (modeled as removing connecting edges) reduced global transmission risk by 37% [237]. By isolating certain specific nodes (such as their caregivers), the disease can be effectively prevented from spreading to vulnerable groups such as infants and the elderly. The Targeted Iterative Avoidance (TIA) proposed by Zhang et al. has application advantages in resource-limited scenarios. In WS and BA networks, the TIA method calculates that the number of nodes required to be removed is 30%-50% less than that of T-Katz. In the C. elegans neural network and the COVID-19 mobile network with 10,914 nodes, TIA only needs to immunize 16% of the nodes to isolate 80% of the elderly population, while T-Katz requires 60% [244].
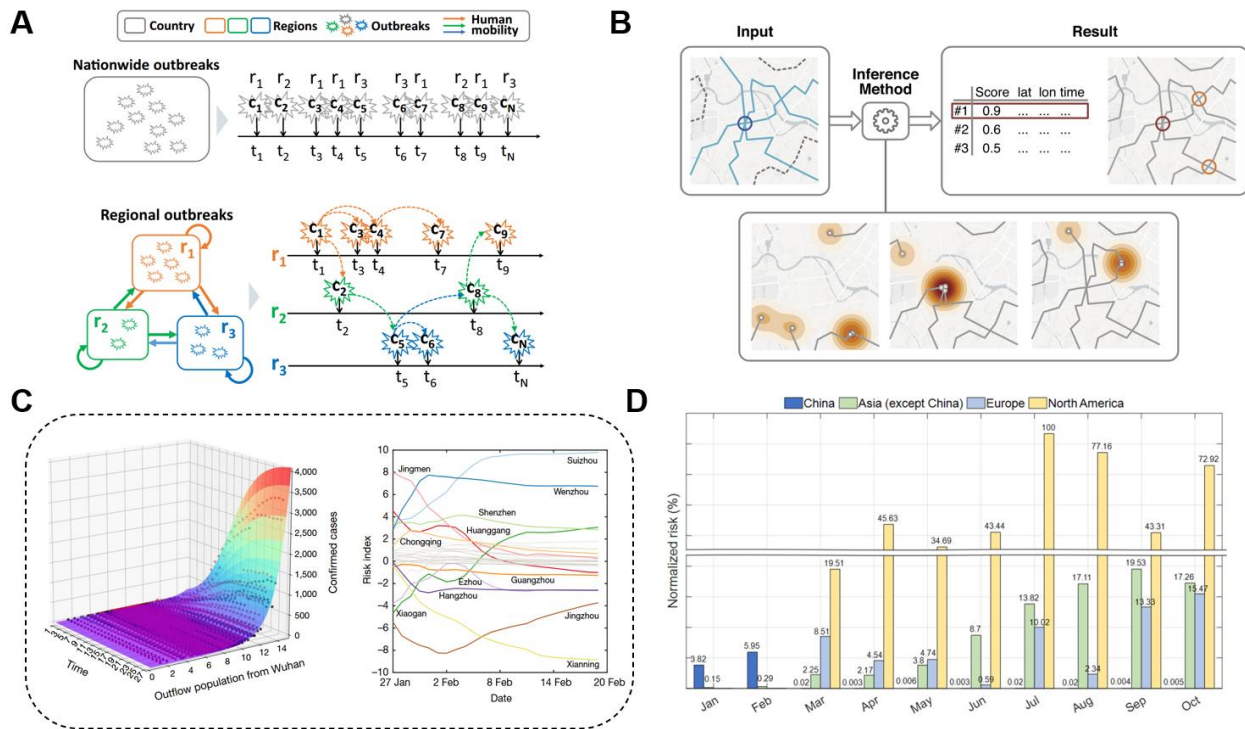
Figure 11 Human mobility and epidemic risk assessment.

(A) National outbreaks of epidemics often originate from a limited number of initial risk sources, with each outbreak event characterized by a contagion c_i occurring at time t_j in region r_k [245]. (B) The method to infer the outbreak occurrence via human mobility data [222]. (C) Risk index calculation based on the outflow population from epidemic sources [14]. (D) The country-specific risk of case importation from the top 13 countries to South Korea from January to October 2020 [239].

7. Human Mobility and Response Strategies Design

This section covers intervention strategies that incorporate mobility restrictions and travel bans. It introduces some quantitative indices, simulations, and experimental studies that explore how to block and mitigate outbreaks. In addition, it discusses evaluation methods and models used to assess the effectiveness of these interventions, including the relationship between policy stringency indices and health outcomes, as well as insights from natural experiments.

7.1 Disrupting transmission pathways of epidemics

In addition to early source identification, cutting transmission pathways is a critical step in reducing the spread of diseases, particularly when these pathways involve large-scale human mobility. Effective interventions targeting key nodes of transmission can prevent localized outbreaks from evolving into widespread epidemics, thereby minimizing the impact on public health and economies [10]. Advances in data analytics, mobility modeling, and public health strategies have enabled more precise identification and intervention in these transmission pathways. Still, challenges remain in balancing the need for control with socio-economic considerations when disrupting transmission pathways of epidemics [246,247].

7.1.1 Quantitative index for measuring intervention

At the beginning of the COVID-19 pandemic, Stringency Index (SI) was proposed the to quantify the intensity of government non-pharmaceutical interventions (NPIs) [248]. SI assigns nine scores to school closures, workplace closures, public event cancellations, gathering restrictions, public transportation closures, stay-at-home orders, domestic mobility restrictions, international travel restrictions, and public information campaigns. The SI is then calculated as the average of these scores. Let k represent the number of policy indicators included in the assessment, and I_j represent the stringency score of the j-th policy. Then:

$$SI = \frac{1}{k}\sum\nolimits_{j=1}^{k}I_j . \tag{22}$$

A study based on 113 countries showed a strong correlation between SI and the infection rate: for every 10-point increase in SI, the mortality rate decreased by 6% [249]. In addition, some study focused on the timeliness of cutting off the transmission pathways explored the quantitative relationship between reaching a high SI level earlier and reaching the peak of the epidemic earlier: from the initiation of response measures and the reporting of the first case, for every day earlier the high SI level is reached, the daily peak of new cases can be reached 0.44 days and 0.65 days earlier, respectively [248]. For example, a study based on barangay-level COVID-19 data in the Philippines found that the correlation between SI and the number of cases was affected by population density: when population density increased from 26,903 per km^2 to 44,290 per km^2, the correlation coefficient decreased by 20% (from 0.70 to 0.56) [250].

7.1.2 Network theory for interrupting the transmission path

Utilizing network-based interventions has proven effective in disrupting disease transmission routes [251–253]. From a network theory perspective, epidemic dynamics can be modeled as complex systems where individuals, regions, or transportation hubs constitute nodes and mobility-driven connections form edges. As demonstrated by Pastor-Satorras et al. in their foundational review, strategic disruption of transmission pathways relies on identifying critical nodes or edges that act as "superspreading conduits" for pathogens, enabling targeted interventions that maximize containment efficiency [254].

The network disintegration framework, pioneered by Brockmann & Helbing using flow distance

metrics, conceptualizes epidemics as percolation processes across spatial networks [153]. Within this paradigm, nodes represent epidemic-relevant locations (e.g., cities, airports), while edges encode population mobility (e.g., air travel, commuting). As empirically validated during COVID-19, targeted removal of <5% of high-traffic airport nodes (modeled as edge removal) reduced global transmission risk by 37% [237]. During the Wuhan outbreak, Kraemer et al. quantified node centrality that governs outbreak scalability through three key metrics[236], as shown in **Table 5**.

<p align="center">Table 5 Node centrality and epidemic scalability.</p>

Centrality Type	Epidemiological Role	Intervention Impact
Betweenness	Bridge between communities	Lockdown reduced inter-city spread by 53%
Degree	Hub connectivity	Airport closures cut international exportation by 64%
Closeness	Rapid accessibility	Roadblocking delayed peak incidence by 8.2 days

Percolation theory provides mathematical rigor for disintegration strategies. The critical percolation threshold fc defines the minimal fraction of nodes/edges whose removal fragments the network. Cohen et al. proved fc scales with network heterogeneity [255,256], explaining why targeting just 2% of global airports (high-degree nodes) collapsed the pandemic's connectivity backbone during COVID-19 [237,257]. Li et al. further revealed that dynamic traffic bottlenecks lower fc by 19% in real-world mobility networks [258], enabling precision targeting.

While the theoretical frameworks of network disintegration and percolation thresholds provide robust foundations for epidemic control, their real-world implementation reveals critical spatial heterogeneities and temporal dynamics. As evidenced by mobility interventions across diverse geopolitical contexts, the effectiveness of node or edge targeting strategies is profoundly shaped by local community structures and phased policy deployment.

7.1.3 Spatial correlation and timeliness of strategies

In actual epidemic prevention and control, strategies are not formulated in isolation, and the epidemic intensity in surrounding areas is a key factor affecting NPIs in the region. While a region has only a few independent positive test results and no direct link to known imported cases, the region can be considered to be in the early stages of the epidemic. And the closure of the border between two regions is effective only if one of the regions is at the early stage the epidemic and that if there is an imbalance between the regions in terms of the number of infected. If several independent cases are reported from several parts of the region, the region should be considered to have left the first stage and entered the main stage of the epidemic. When both regions have reached the main stage, the boundary should be opened, as the closure no longer adds anything to other types of social distancing. Moreover, travel restrictions have no effect if the infection is evenly spread in the population. If the proportion of infected varies locally, for example varies between cities and rural areas, decreased travel between cities and rural areas may have an effect. If the number of infected persons is higher in the district than surrounding districts, the import cases will not have any significant effect on the spread of the epidemic.

On the contrary, an uncoordinated blocking strategy will significantly affect the prevention and

control effect, and even cause a rebound in the epidemic. If all European countries jointly take 4, 8 or 12 weeks of intervention measures, and if one of them terminates non-drug intervention measures prematurely, the epidemic in continental Europe may rebound up to 5 weeks earlier, as shown in **Figure (A, B)** [259].
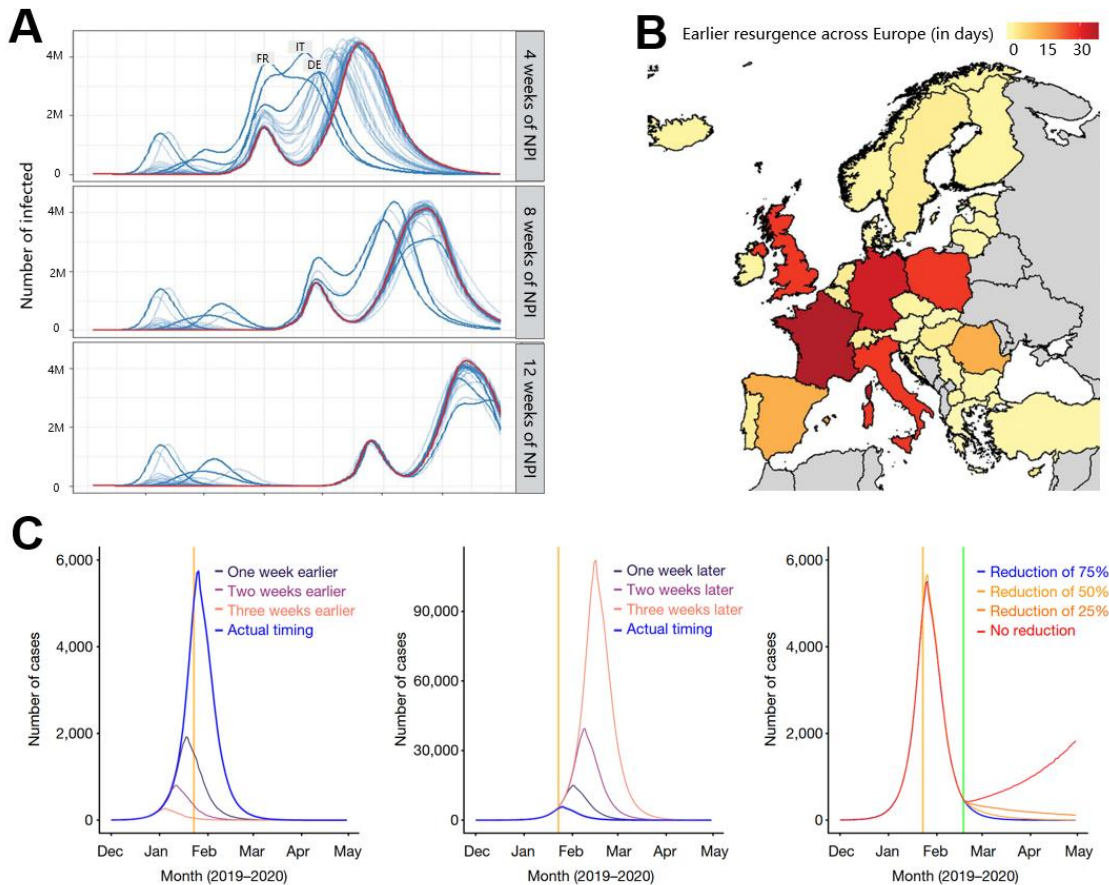
Figure 12 Epidemic spread if all countries but one maintain existing NPIs.

(A) Epidemic curves, with varying numbers of weeks that NPIs are implemented. Curves indicate numbers of active cases at any given time, rather than numbers of new cases per day. Red lines indicate epidemic curves where all countries maintain NPIs for the denoted number of weeks. Blue lines indicate epidemic curves if one country ends intervention policies early (each line represents one randomly chosen country that ends its policies early); France, Germany, and Italy are highlighted. (B) For the 4 weeks of NPI scenario, the number of days earlier that an uncontrolled second epidemic occurs continent-wide if each country ends NPIs early, measured as the time to 25% of the population of Europe having had COVID-19. Movement data were not available for countries in grey [259]. (C) The estimates of the COVID-19 outbreak under various scenarios of intervention timing and lifting of travel restrictions across China [260].

The timeliness of taking measures to block the transmission path is also a key factor affecting the effectiveness of prevention and control. In the early stages of the COVID-19 pandemic, China took proactive, strong and comprehensive non-drug intervention measures in a timely manner. Through simulation of China's epidemic spread and intervention scenarios based on daily transportation networks, it was found that early and comprehensive application of non-drug intervention measures can produce the strongest and fastest prevention and control effects. As shown in **Figure (C)**, if China's intervention measures were implemented one week, two weeks or three weeks earlier than the actual implementation time, the number of new coronary pneumonia cases may

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be reduced by 66% (50-82%), 86% (81-90%) or 95% (93-97%) respectively; however, if the implementation time of non-drug intervention measures is one week, two weeks or three weeks later than the actual situation, the number of cases may increase by 3 times (IQR 2-4), 7 times (5-10) or 18 times (11-26) respectively[260].

7.2 Protecting vulnerable groups

The equitable protection of vulnerable populations, such as older adults, immunocompromised individuals, and residents of socioeconomically deprived areas, remains a cornerstone of effective epidemic response [261]. Vulnerability in epidemics arises from two distinct but often intersecting factors: biological susceptibility (e.g., elderly, immunocompromised individuals) and occupational exposure intensity (e.g., essential workers in public-facing roles). Strategies to protect vulnerable populations can be divided into non-pharmaceutical interventions and pharmacological interventions.

7.2.1 Non-pharmaceutical interventions

The pandemic and the measures taken by authorities to control its spread have altered human behavior and mobility patterns in an unprecedented way. The timely implementation of interventions, such as quarantine and isolation, plays a key role in limiting transmission and minimizing socioeconomic disruptions [237,262]. **Figure (A)** illustrates that before the implementation of lockdown measures in eastern Shanghai, China, mobility reductions exhibited considerable heterogeneity across cells, with the most pronounced decreases observed in those severely impacted by the epidemic. **Figure (B)** demonstrates the community structures were observed during the pre-outbreak period, the targeted intervention phase, the citywide lockdown phase, the targeted lifting of the intervention phase, and the reopening phase, respectively. Each node was found to correspond to a community, and the node's centre was found to coincide with the centroid of the community. The size of each node was found to be proportional to the community's area (number of cells). The width of the directed arrow was found to be proportional to the flows between communities.

During the pandemic, policy responses varied significantly across countries. In the United Kingdom (UK), the evolution of mobility under lockdown shows that mobility first reverted towards fine-scale flow communities already found in the pre-lockdown data and then expanded back towards coarser flow communities as restrictions were lifted. Besides, there are temporal to lockdown differences, as shown in **Figure 13 (C)**. The most significant changes in fine-scale coverage have been observed in urban centers such as London, Birmingham, Liverpool, and Manchester, with recovery times being notably faster. In contrast, rural areas, which were already more constrained to local communities before the lockdown, have demonstrated more negligible but long-lasting effects on the coverage at the regional level. The effectiveness of the lockdown in preventing a severe secondary outbreak is evidenced by the implementation of a strict travel ban [263].

Public-facing workers, including healthcare personnel, transit operators, retail staff, and first responders, face elevated infection risks during epidemics due to frequent population contact and unavoidable exposure scenarios. Standard precautions mandated by WHO form the foundation of occupational protection. Universal precautions, treating all contacts as potentially infectious, reduce transmission through strict hand hygiene, barrier protection (gloves, gowns, masks), and environmental decontamination. During COVID-19, adherence to these protocols reduced healthcare

worker infections by 37% in settings with compliance monitoring. For non-clinical public workers (e.g., bus drivers), WHO recommends twice-daily disinfection of high-touch surfaces, ventilation upgrades, and shift staggering to minimize close contact [264].

Moreover, targeted health education has been shown to be a cost-effective non-pharmaceutical intervention. For instance, digital exclusion in certain demographic groups (e.g., the elderly or low-income populations) may further limit the reach of digital contact tracing tools, leaving these groups less protected. Digital exclusion can significantly affect the effectiveness of epidemic containment strategies, as individuals without access to smartphones or those unfamiliar with technology may not participate in digital tracing efforts [265]. Studies have shown that populations with lower digital literacy or limited access to technology are often at a higher risk of infection due to their exclusion from real-time contact tracing and exposure notifications [57,266].

7.2.2 Pharmaceutical interventions

Vaccination is the most typical pharmacological intervention to protect populations susceptible to epidemics. Since 2007, Beijing, China has provided free influenza vaccines to people aged 60 and above and primary and secondary school students, which has greatly reduced the health hazards of influenza to the public [267]. Moreover, infants and the elderly are the main susceptible populations of respiratory syncytial virus (RSV), based on the weekly positive rate data and vaccination results reported by 13 countries during the 2018-2019 respiratory syncytial virus (RSV) epidemic season, it was found that vaccination of older adults would prevent hospitalizations by a median of 35-64%, while vaccination of pregnant women could avert infant hospitalizations by 5-50%, and vaccine coverage is positively correlated with protection effect [268]. **Figure 13 (D)** shows the estimated reduction in RSV-related hospitalizations in the elderly and infants due to RSV vaccination. The error bars represent the median and 95% uncertainty range (UR) from 500 random simulations, where (a) is the simulation result for vaccination of the older adults and (b) is the simulation result for vaccination of pregnant women.

In a low-transmission scenario (Re=1.2), RSVpreF would avert a total population of 2.35 (95% CrI 1.24-3.77) million infections, 12.80 (95% CrI 8.60-17.06) thousand hospital admissions, and 0.93 (95% CrI 0.69-1.25) thousand deaths, with 1.82 (1.41-2.33) million infections, 12.44 (95% CrI 8.50-16.38) thousand hospital admissions, and 0.93 (95% CrI 0.67-1.23) thousand deaths averted for people aged 60 years and older. In a high transmission scenario (Re=2.0), RSVpreF would avert 2.01 (95% CrI 1.37-2.68) million infections, 14.67 (10.05-18.33) thousand hospital admissions, and 1.12 (95% CrI 0.80-1.35) thousand deaths. The majority averted would still be among older adults [269].

In addition, allowing susceptible people to take some proven effective preventive drugs in advance before the epidemic season is also a means of pharmaceutical intervention for susceptible people. For example, taking neuraminidase inhibitors such as oseltamivir before the flu season can reduce the risk of pneumonia by 15% (RR 0.85, 95%CI: 0.73, 0.98) by blocking the release and spread of the virus. Among them, the probability of illness in children aged 6-12 years (RR 0.43, 95% CI: 0.26, 0.71) and children aged 1-2 years (RR 0.48, 95% CI: 0.24, 0.99) was reduced even more, at 57% and 52% respectively [270]. A randomized controlled trial (RCT) of oseltamivir 75 mg (n = 493) or placebo (n = 462) once daily given to close contacts of household index cases within 48 hours of symptom onset in household quarantine following household exposure found that the overall

protective effect of oseltamivir against clinical influenza was 89% (95% CI: 67%-97%; P < .001) for individuals and 84% (95% CI: 49%-95%; P < .001) for households [271].

The equitable protection of vulnerable populations, such as older adults, immunocompromised individuals, and residents of socioeconomically deprived areas, remains a cornerstone of effective epidemic response [261]. Human mobility data provides critical insights for identifying at-risk groups and optimizing targeted interventions, bridging the gap between broad epidemiological trends and granular community needs [272].

Vulnerability in epidemics arises from two distinct but often intersecting factors: biological susceptibility (e.g., elderly, immunocompromised individuals) and occupational exposure intensity (e.g., essential workers in public-facing roles). Human mobility data provides granular insights into both dimensions. The limitation of digital contact tracing is that incomplete or inaccurate data can hinder its effectiveness. For instance, digital exclusion in certain demographic groups (e.g., the elderly or low-income populations) may further limit the reach of digital contact tracing tools, leaving these groups less protected. Digital exclusion can significantly affect the effectiveness of epidemic containment strategies, as individuals without access to smartphones or those unfamiliar with technology may not participate in digital tracing efforts [265]. Studies have shown that populations with lower digital literacy or limited access to technology are often at a higher risk of infection due to their exclusion from real-time contact tracing and exposure notifications [57,266].

Moreover, public-facing workers, including healthcare personnel, transit operators, retail staff, and first responders, face elevated infection risks during epidemics due to frequent population contact and unavoidable exposure scenarios. Standard precautions mandated by WHO form the foundation of occupational protection. Universal precautions—treating all contacts as potentially infectious—reduce transmission through strict hand hygiene, barrier protection (gloves, gowns, masks), and environmental decontamination. During COVID-19, adherence to these protocols reduced healthcare worker infections by 37% in settings with compliance monitoring. For non-clinical public workers (e.g., bus drivers), WHO recommends twice-daily disinfection of high-touch surfaces, ventilation upgrades, and shift staggering to minimize close contact.

Digital contact tracing platforms enable precision identification of high-exposure populations by algorithmically detecting proximity events through Bluetooth signal attenuation, anonymized GPS patterns, and venue check-in histories. These systems dynamically flag essential workers facing sustained exposure risks, such as healthcare staff in COVID-19 wards or transit operators interacting with 500+ daily passengers for prioritized interventions. Real-world implementations demonstrate significant efficiency gains: Singapore's Trace Together reduced vaccination targeting costs by 42% compared to census-based approaches while achieving 37% higher seroconversion rates among high-risk groups through mobile clinics deployed to geofenced exposure zones [273,274]. Integrated AI-driven technologies provide multilayered protection for essential workers facing elevated pathogen exposure, optimizing both predictive surveillance and real-time risk mitigation. Next-generation epidemiological platforms like BlueDot synthesize global mobility patterns, flight itineraries, and clinical surveillance data to forecast regional outbreaks in advance, enabling preemptive resource stockpiling [275].

The strategic protection of vulnerable populations during respiratory virus outbreaks requires leveraging human mobility data to optimize vaccine delivery and exposure reduction, as evidenced

by recent advances in RSV prevention modeling. In high-transmission scenarios (Re=2.0), RSVpreF vaccination would avert 2.01(1.37–2.68) million infections, 14.67(10.05–18.33) thousand hospitalizations, and 1.12(0.80–1.35) thousand deaths, mainly in older adults [276].
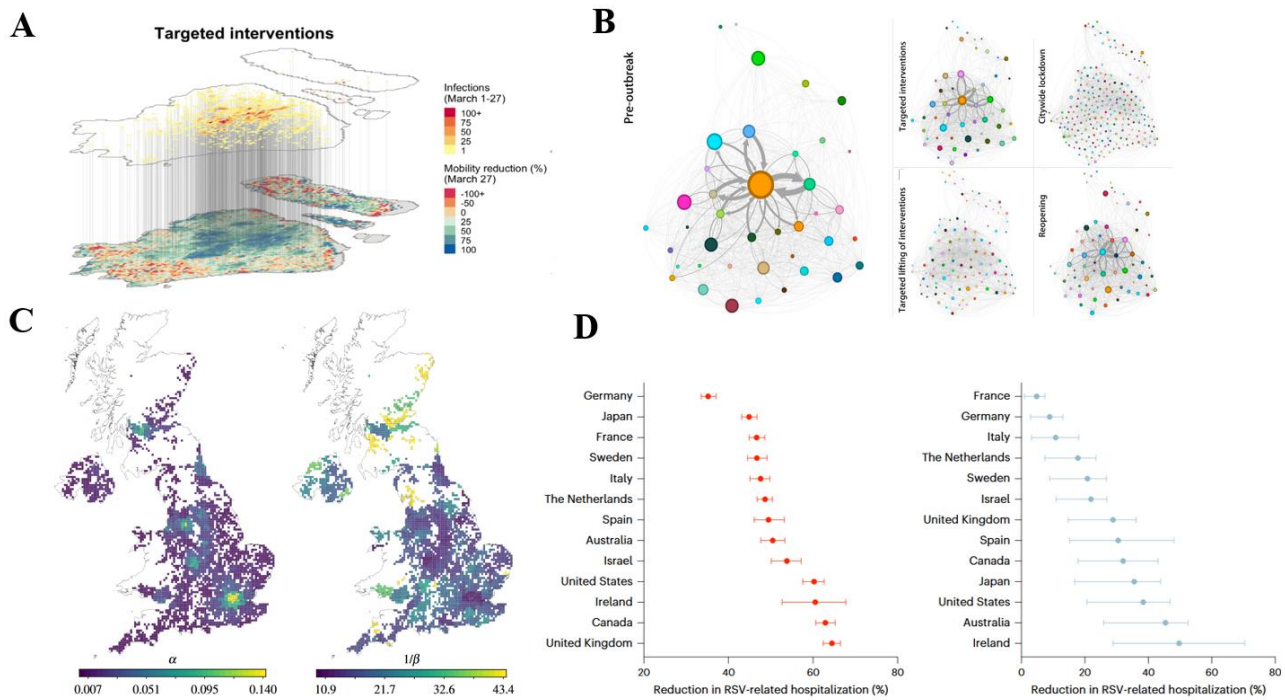
Figure 13 Policy response under pandemics.

(A) The geographic distribution of infections and mobility reduction during the targeted interventions phase [12]. The upper map shows the number of infections at the grid level as of March 27 (i.e., before the lockdown of eastern Shanghai). The lower map shows the reduction in mobility. (B) The network structure changed during each phase: before the outbreak, during the lockdown, after the lockdown, and after reopening [12]. (C) Regional differences in the temporal response to the lockdown [277]. (D) Estimated reduction in RSV-related hospitalizations among older adults (red) and infants (blue) attributable to RSV vaccination [268].

8. Conclusion and Outlook

Human mobility has become a cornerstone for better understanding, predicting, and mitigating the spread of infectious diseases [49,164]. With the advancement of technologies, a diverse array of mobility data sources is now available, including social surveys, public transportation, cellular signaling, satellite positioning, IP and WiFi addresses, and IoT information. These data can be represented in various forms, such as trajectories, mobility networks, contact networks, and aggregated indices, providing flexible and scalable frameworks to model complex human interactions and movement patterns [89,278]. Through these representations, researchers have uncovered valuable and quantifiable insights of correlations between population flow and epidemic transmission, offering new opportunities to develop more precise risk assessments and more responsive public health measures [59,61,62].

A pandemic with a high R0 value that has gained a foothold somewhere in the world cannot be stopped — no matter how good the data is — but that good data can help mitigate its impact [279]. However, the integration of mobility data into a range of epidemic modelling paradigms, such as

compartmental models, complex network models, agent-based simulations, and machine learning approaches, has significantly enhanced the resolution and realism for epidemiological forecasts and interventions [12,39,166–171]. For example, informed by near real-time mobility data, SIR and metapopulation models can simulate spatially resolved disease dynamics with higher fidelity, while agent-based simulations capture individual-level heterogeneity across different geographical regions [224]. Moreover, machine learning techniques are increasingly used to process large-scale mobility datasets and extract latent features that drive epidemic propagation, thereby strengthening early warning systems and supporting adaptive policy responses [216].

Despite these advancements, several methodological limitations and challenges need to be addressed to maximize the effectiveness of mobility-informed epidemic modeling. One critical area is the presence of demographic and socioeconomic biases in mobility datasets. Human mobility and contact patterns, derived from novel digital sources like mobile phones, GPS, and digital platforms, often tend to disproportionately represent urban, affluent, or tech-savvy populations, while under-representing others, particularly rural, low-income, or digitally excluded [71,89]. These biases might distort model outputs and lead to inequitable or ineffective public health interventions. Although techniques such as statistical re-weighting, data imputation, and demographic re-calibration have been proposed to correct for these disparities, the effectiveness and generalizability of these methods across different contexts and populations remain an active area for further investigation.

Additionally, data gaps can emerge during crises, where the influx of real-time data exceeds processing capacities or when critical data sources become unavailable due to infrastructure failures, leading to incomplete or delayed datasets. In such situations, data fusion approaches, which combine data from multiple sources (e.g., mobile data, transportation systems, social media, and healthcare records), offer a promising strategy to fill gaps and triangulate insights [214,216]. However, integrating datasets from heterogeneous sources introduces new challenges in terms of data consistency, quality, and interoperability, necessitating the development of robust methodological approaches to ensure reliability.

The ethical and privacy concerns are always paramount when working with granular human mobility data, especially from personal devices. Location tracking and contact tracing systems can potentially expose sensitive information, contributing to surveillance risks or societal misuse [280]. Although privacy-preserving techniques like differential privacy and data anonymization have been proposed to mitigate these concerns, their implementation in real-world epidemic modeling remains limited. Moving forward, it is imperative that epidemic modeling frameworks adopt transparent, ethical standards for data use.

Addressing these limitations requires a multi-pronged, interdisciplinary approach [26]. First, an integrated approach that combines emerging digital data streams with traditional methods (e.g., household surveys) can improve coverage and enable cross-validation and extrapolation of real-world human mobility patterns. Second, enhancing multi-institutional data-sharing protocols across sectors, fostering collaborative research frameworks, and establishing standardized data processing approaches can help correct data bias to improve the accuracy, privacy and inclusivity of mobility-informed epidemic models. Moreover, the development of advanced statistical methods and validation techniques for handling missing or uncertain data will also enhance the robustness and credibility of model predictions. As artificial intelligence and machine learning continue to evolve,

these technologies can be leveraged to identify hidden patterns and correlations in complex, large-scale mobility datasets, thereby improving model precision [216]. However, it is equally important that researchers and policymakers collaborate to establish clear ethical guidelines and privacy safeguards to ensure responsible use of human mobility data and sophisticated analyzing technology.

Integrating human behavioral data into epidemic models still represents one of the most promising frontiers in infectious disease research, with immense potential for enhancing our understanding and control of infectious diseases. As the global community prepares for future public health crises, it is critical to continue investment in data infrastructure, analytic capability, and privacy-preserving innovation. In particular, strengthening the foundations for real-time mobility monitoring, digital contact tracing, and precise epidemic simulations in more inclusive, ethical, and actionable ways, will enhance our collective ability to respond swiftly and equitably to emerging threats.

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CRediT author statement

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