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Compartmental models in epidemiology: bridging the gap with operations research for enhanced epidemic control

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Abstract

Compartmental models have gained significant attention not only in public health studies but also in fields such as Operations Research (OR), social sciences, and logistics, particularly following the COVID-19 pandemic. Their broad applicability in epidemiology and their utility in understanding, predicting, and controlling the global spread of infectious diseases have made them indispensable across various disciplines. The appeal of these models lies in their simplicity yet effectiveness in capturing the essential dynamics of disease transmission. This paper provides a comprehensive review of compartmental models, focusing on the Susceptible-Infectious-Recovered (SIR) models and the key aspects of their structure. The primary objective of this review is to enhance the ability of researchers and practitioners to understand and manage infectious disease outbreaks through a twofold approach: (1) an evaluation of the assumptions, equations, and methodologies used for estimating critical parameters in SIR models, and (2) an exploration of the relationship between SIR models and optimization models. Additionally, a systematic micro-level review has identified the most significant research gaps in the literature on compartmental models, leading to recommendations for future research. A key finding emphasizes the need to revisit various assumptions to clarify the connection between SIR models and optimization approaches, which is expected to offer valuable insights for epidemic disease modeling.

Keywords Literature review · Compartmental epidemiological model · Pandemic · Operations research · Optimization

1 Introduction

For many years, infectious diseases have represented a significant global threat to public health. The emergence of diseases such as SARS in 2003 (He et al., 2004; Seto et al., 2003), the A/H1N1 influenza epidemic in 2009 (Jones & Salathe, 2009; Khan et al., 2009; Tang et al., 2010), Ebola virus disease in 2014 (Aylward et al., 2014; Baize et al., 2014), and the recent COVID-19 outbreak in 2019 have had profound impacts on human health, the global economy, and societal behaviors (Chintalapudi et al., 2020; Costantino et al., 2024; Huang

et al., 2020; Tang et al., 2020a, 2020b). Furthermore, the onset of infectious pandemics has caused significant disruptions in global supply chains (Ivanov & Dolgui, 2020, 2021; Queiroz et al., 2020). Unlike other disruptions, epidemics tend to begin gradually but can rapidly escalate, affecting diverse regions (Ivanov, 2020).

While the acute phase of the COVID-19 pandemic has largely been controlled through widespread vaccination and effective treatment strategies (WHO, 2023), the ongoing threat of emerging infectious diseases remains a pressing concern. This risk is amplified by factors such as globalization, urbanization, climate change, and the continuous evolution of pathogens (Carlson et al., 2023; Morens et al., 2022). As a result, there is an urgent need for robust, adaptable decision-support frameworks that integrate epidemiological modeling with operational realities to enable timely and effective responses to future outbreaks.

The implementation of both Medical Interventions (MIs) and Non-Medical Interventions (NMIs) is crucial for minimizing infection risks and mitigating disruptions during pandemics. Strategies like social distancing can reduce contact rates, while vaccination helps build immunity within the population. A key approach for limiting the spread of infectious diseases is reducing contact with infected individuals, as many diseases are transmitted through direct contact. For airborne infections, interventions like staying at home and wearing masks can significantly reduce transmission (Deng et al., 2021). Therefore, the timely implementation of MIs, such as vaccination, and NMIs, such as mask-wearing and quarantine, plays a critical role in controlling outbreaks and minimizing associated risks (Cui et al., 2008; Huang & Li, 2019; Tchuente et al., 2011; Wang & Xiao, 2013; Zhou & Fan, 2012).

A reliable tool is needed to monitor disease progression and assess the effectiveness of interventions in controlling outbreaks. In the absence of decision-support tools, especially during the early stages of an epidemic, mathematical models often serve as the primary guide for decision-making (McBryde et al., 2020). Various models, including Susceptible-Infected-Recovered (SIR)-type Ordinary Differential Equation (ODE) models (Anderson & May, 1979; Kermack & McKendrick, 1927), integral-differential models (Keimer & Pflug, 2020; Kermack & McKendrick, 1927), Bayesian Monte Carlo approaches (Stojanovic et al., 2019), and agent-based models (Kim et al., 2018; Bicher et al., 2020; Ng, 2020), are utilized to evaluate and simulate infectious disease dynamics. These models are essential for emergency planning, policymaking, risk assessment, improving health-economic outcomes, and defining control programs (Al-Sheikh, 2013).

Among these models, SIR models have been used for decades to analyze and understand the spatial and temporal patterns of infectious disease spread. Their importance has grown significantly following the COVID-19 outbreak, as they are effective in simulating disease transmission and assessing various interventions, such as vaccination (Blasioli et al., 2023; McBryde et al., 2020). During the COVID-19 pandemic, SIR models were instrumental in understanding the transmission dynamics of the virus, surpassing their applications in previous health crises (Eubank et al., 2020; Holmdahl & Buckee, 2020; Rhodes et al., 2020). A key feature of SIR models is compartmentalization, which categorizes individuals into different states, enabling a more accurate simulation of pandemic dynamics.

Compartmental models can be extended to achieve a more comprehensive understanding of disease dynamics. These extensions may include a focus on socioeconomic and demographic parameters (Manna et al., 2024), the addition of compartments for vaccination or different disease stages, time-dependent parameters to capture seasonal effects (Bents et al., 2023), multi-group structures based on age and health status, and human demographic

parameters that align with disease dynamics, such as immigration rates, birth and death rates, and disease-related mortality.

In various studies, compartmental models have evolved to include additional states, such as "exposed," "pre-symptomatic infectious," or "vaccinated" individuals, leading to the development of SEIR or SVIR models (Enayati & Özaltın, 2020; Ghostine et al., 2021). These models can be adapted to consider vaccination status, varying based on the type of disease, vaccine, and number of doses, resulting in either single- or multi-dose SVIR models (Aguilar-Canto et al., 2021). On the other hand, OR can address several challenges in epidemic management, including: (1) determining the optimal allocation of resources to control an outbreak or prevent disease spread, (2) identifying the necessary resources for disease control, and (3) selecting the appropriate resources for disease control interventions (Brandeau, 2008). These capabilities are essential for practical decision-making in dynamic and resource-limited environments. Although epidemics are inherently dynamic, operations research models by themselves often fail to capture this complexity. Therefore, integrating epidemic models with operations research enhances the relevance and accuracy of the results. Moreover, combining optimization techniques with epidemiological modeling enables the identification of optimal solutions.

However, the integration of epidemiological models with OR optimization approaches remain an underexplored area, particularly with regard to its direct impact on public health policy and pandemic preparedness. This paper seeks to address this gap by examining the question: *How can compartmental epidemic models, when integrated with OR optimization techniques, enhance epidemic control measures and reinforce supply chain resilience under uncertainty?* By addressing this question, we aim to advance knowledge at the intersection of public health and operations research, providing actionable insights for policymakers and specialists facing complex epidemic management challenges.

The motivation behind this research arises from the evident need for adaptable, data-driven frameworks that can respond to rapidly evolving epidemic situations. The COVID-19 pandemic highlighted the crucial importance of integrating epidemiological insights with operational decision support to formulate timely, effective responses, especially in the face of new variants, changing public behaviors, and supply chain disruptions (Blasioli et al., 2023). Yet, these fields have largely developed in parallel with limited cross-disciplinary translation, which limits their collective effectiveness. This review endeavors to bridge that divide by synthesizing research advancements in both compartmental epidemiological modeling and OR methodologies, emphasizing their complementary strengths and integration potential.

Given the limited comprehensive reviews focused on SIR and related compartmental models from an OR perspective, this work provides an in-depth treatment of model classifications, methodological assumptions, parameter estimation techniques, and the application of optimization tools for epidemic control. We also highlight key research gaps and challenges to equip researchers—particularly those new to epidemic modeling—with a coherent framework for developing effective models and intervention strategies.

The remainder of the paper is structured as follows: Sect. 2 details the search strategy for gathering relevant literature. Section 3 reviews the components of epidemiological models and related equations. Section 4 categorizes assumptions into population, intervention, and epidemiological factors. Section 5 examines parameter estimation for these models. Section 6 discusses the relationship between these models and optimization, emphasizing the

importance of optimizing interventions and epidemic control strategies. From a practical perspective, Sect. 7 addresses the role of epidemiological models in supply chains during pandemic disruptions. Finally, Sect. 8 summarizes the findings, and Sect. 9 identifies research gaps and offers recommendations for future studies in epidemiological modeling.

2 Review methodology

2.1 Search methodology

To identify relevant studies, the search began with a combination of terms: (“Medical intervention” OR “Non-Medical intervention” OR “Vaccine”) AND (“Epidemiological Model” OR “SIR Model” OR “SEIR Model”) in the titles, abstracts, and keywords of studies published between 2019 and September 2024. This time frame was selected because research in this area has intensified since the COVID-19 outbreak. Figure 1 illustrates the primary steps of the paper selection process using a PRISMA diagram.

The search was conducted using Google Scholar, SCOPUS, and major publishers such as ScienceDirect and PubMed. Initially, the search yielded 965 publications based on the specified keywords within the selected time frame. After removing duplicates, the remaining papers underwent a comprehensive full-text screening to eliminate irrelevant studies, including those addressing the epidemic's effects on psychological issues, animal infectious diseases, childhood diseases, and sexually transmitted infections. The aim of this paper is to review literature specifically related to epidemic diseases, such as COVID-19, that impact humans across all age groups. To ensure a focused examination of compartmental SIR models, papers that analyzed SIR models in fractional, spatial, or network contexts were also excluded. This process guarantees that the reviewed papers are cohesive and well-integrated. During the full-text screening, the references of the selected papers were also reviewed to confirm their relevance. Ultimately, a total of 236 papers were included.

Figure 2 illustrates the number of papers published each year surveyed in this research. Following the outbreak of COVID-19 (SARS-CoV-2 virus) in late 2019, only a limited number of papers were published that year. However, it is evident that the pandemic sparked a surge in research interest in 2021 and 2022, resulting in a peak in the number of published papers during that period.

The VOS software is used for bibliographic analysis, specifically to extract repeated keywords from the selected papers. Figure 3 visualizes the frequency of keywords and their interrelationships. The size and shape of each keyword represent its repetition rate, while the thickness of the connecting lines indicates the strength of their associations. The keywords identified in the studies are organized into four themed clusters, each represented by a distinct color. From Fig. 3, it is evident that the keyword “COVID-19” appears most frequently in the papers and is closely associated with the SIR model, vaccination, and epidemiological models. Several other keywords, such as non-pharmacological interventions, vaccines, and optimization, are also featured in the figure and are discussed in the paper.

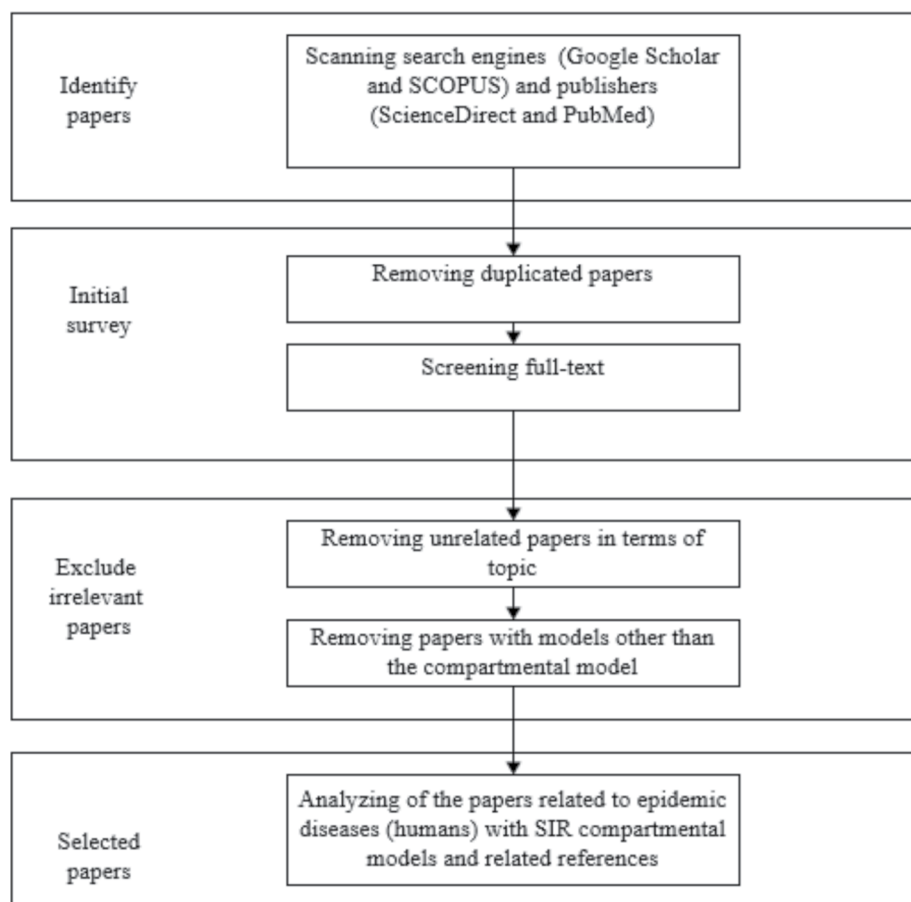


Fig. 1 The PRISMA process for paper selection

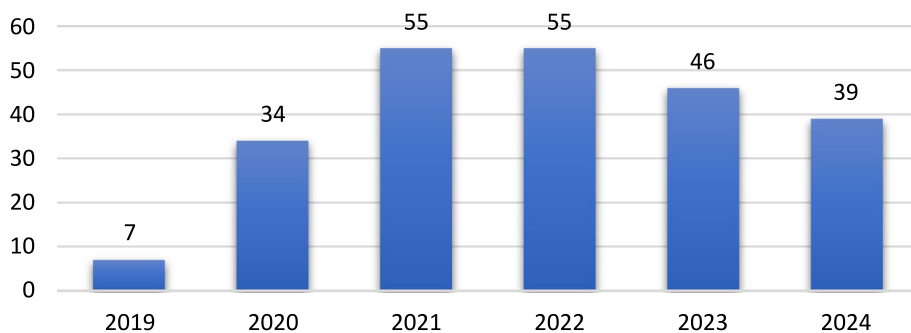


Fig. 2 Number of reviewed papers in this paper

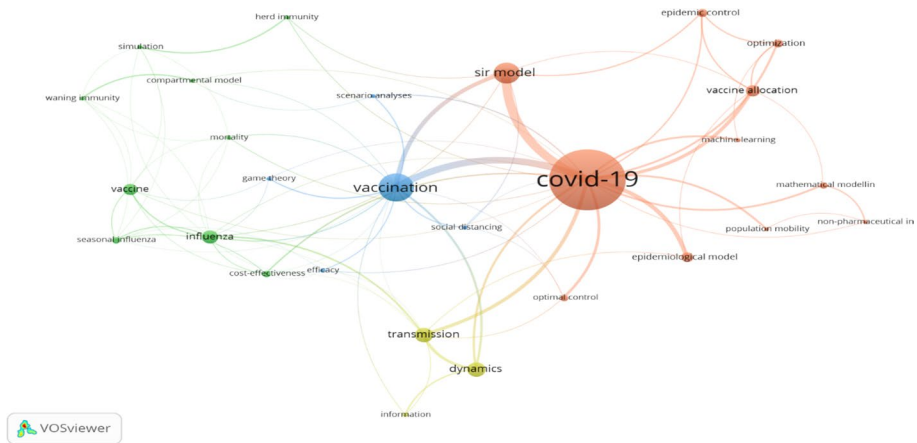


Fig. 3 Important keywords in the selected references

2.2 Contributions of this paper

Several review papers have been published in the field of epidemic control. Table 1 compares these papers with the current research. The modeling perspective emphasizes the specifics of modeling, including assumptions and equations. Mutalik (2017) identified various mathematical models used to predict H1N1 outbreaks and highlighted the usefulness of these models in estimating the magnitude of such outbreaks. Arefi and Poursadeqiyani (2020) reviewed global studies to prevent the spread of Coronavirus. Given that no effective vaccine was available at the time of their writing, the authors discussed the impact of non-medical interventions in controlling the disease. Tang et al., (2020a, 2020b) outlined the fundamentals of multi-compartment infectious disease models from deterministic and stochastic viewpoints. Rezapour et al. (2021) also provided a comprehensive summary of economic evaluations of preventive strategies, programs, and treatments for COVID-19, classifying studies into cost-effectiveness, cost-utility, and cost–benefit analyses.

Additionally, Callegari and Feder (2022) reviewed the pandemic's effects on long-term economic development, encompassing various economic and historical debates. Zhang et al., (2022a, 2022b, 2022c) conducted a retrospective evaluation of the predictive performance of compartmental models. They subsequently discussed potential enhancements to these models in detail and provided examples of how they can support policymaking. Kong et al. (2022) aimed to clarify the compartmental structures used in COVID-19 dynamic models as a reference for future dynamic modeling of COVID-19 and other infectious diseases. Blasioli et al. (2023) explored mathematical models in operations research focused on efficiently organizing vaccine distribution and allocation. Finally, Dey et al. (2024) provided a comprehensive overview of optimization models developed by researchers during the COVID-19 era, specifically aimed at improving vaccine distribution.

Despite this breadth, existing literature often treats epidemiological modeling or optimization in isolation or adopts either macro-scale analyses or focused case studies. This research advances the state of the art by providing a comprehensive and interdisciplinary examination of epidemic models from an operations research perspective, with a strong

Table 1 Comparison of review papers with this research

Reference	Modeling view	Scale	Period		NMIC	OM	Type of models					
			From	To			SIR	SEIR	SIRD	SVIR	SIHR	Other models
Mutalik (2017)	+	Ma	2004	2015	+	–	+	+	–	–	–	±
Arefi and Poursadeqiyan (2020)	–	Ma	2019	2020	+	–	–	–	–	–	–	–
Tang et al., (2020a, 2020b)	±	Mi	1927	2020	+	+	+	–	–	–	–	–
Rezapour et al. (2021)	–	Ma	2019	2020	+	–	+	+	–	–	–	±
Callegari and Feder (2022)	–	Ma	1970	2021	–	–	–	–	–	–	–	–
Zhang et al., (2022a, 2022b, 2022c)	±	Ma	2019	2022	±	–	+	+	–	±	±	±
Kong et al. (2022)	±	Ma	2021	2021	+	–	+	+	±	±	±	±
Blasioli et al. (2023)	±	Ma	2020	2021	+	+	–	±	–	–	–	±
Dey et al. (2024)	+	Mi	2020	2023	–	+	+	+	±	–	–	±
Current research	+	Mi	2019	2023	+	+	+	+	+	+	+	+

± = Satisfied, – = Not satisfied, ± = Partially satisfied, Ma = Macro, Mi = Micro, NMIC = Non-Medical Intervention Classification, OM = Optimization Methods

+ = Satisfied, – = Not satisfied, ± = Partially satisfied, Ma = Macro, Mi = Micro, NMIC = Non-Medical Intervention Classification, OM: Optimization Methods

emphasis on integrating epidemiological dynamics, intervention strategies, and supply chain resilience. The key contributions are summarized as follows:

- *Comprehensive and updated review of epidemic models:* In light of the significant increase in epidemiological modeling literature following the COVID-19 outbreak in 2019, this study systematically reviews and categorizes recent research, offering a time-relevant, structured overview that captures contemporary advances. By focusing predominantly on publications from 2019 onward, the research fills an important gap by reflecting the evolving landscape of epidemic modeling and optimization applications during a critical global health crisis.
- *In-depth analysis of compartmental models and their extensions:* The study rigorously examines classical compartmental frameworks such as SIR, SEIR, SIRD, SVIR, and SIHR models, emphasizing their mathematical foundations, assumptions, and parameter estimations. Unlike prior reviews that often omit detailed model dynamics or focus primarily on operational research applications, this work delivers a balanced and thorough exploration of these epidemiological models and highlights extensions that incorporate vaccination and demographic heterogeneity, enhancing realism and predictive power.
- *Evaluation of model extensions incorporating demography and operational complexity:* By reviewing multi-group and multi-compartment extensions that account for age, health status, and migration, as well as time-varying parameters such as seasonality, the study highlights the importance of demographic and operational diversity in epidemic dynamics. These nuanced models support the design of tailored interventions and enrich optimization contexts.
- *Advancing epidemic control through operations research methodologies:* The paper explicitly couples epidemiological modeling with optimization techniques—including resource allocation, dynamic intervention planning, and multi-objective optimization—to enhance decision-making frameworks. This integration enables more accurate and adaptable epidemic control strategies, improving efficiency and equity in public health responses amid uncertainties characteristic of infectious disease outbreaks.
- *Application-oriented insights for vaccine supply chains and healthcare logistics:* The research surveys state-of-the-art models that integrate epidemiological processes with supply chain logistics to optimize vaccine campaign planning, inventory management, and distribution routing. It highlights frameworks that apply Mixed Integer Programming (MIP), Fuzzy Inference Systems (FIS), and optimal control techniques to respond agilely to evolving outbreak scenarios, thereby supporting healthcare system preparedness and improving public health outcomes.
- *Bridging epidemiological modeling and non-pharmaceutical supply chain resilience:* A novel and critical contribution of this research lies in the exploration of how epidemiological models, particularly compartmental frameworks like SIR and SEIR, are increasingly employed to analyze and forecast supply chain risks triggered by global pandemics. By integrating disease transmission dynamics with supply chain management challenges—including labor shortages, demand surges, logistical disruptions, and production capacity constraints—this study demonstrates how OR methods can optimize supply chain reconfiguration, vaccine distribution, and resource allocation to improve resilience. This interdisciplinary link advances the understanding of both short-term

crisis management and long-term supply chain adaptability.

Collectively, this work fosters a robust interdisciplinary framework at the intersection of epidemiological modeling, optimization, and supply chain management, delivering both theoretical advancements and practical decision-support tools. The synergies highlighted herein offer significant value to operations researchers, epidemiologists, and policymakers striving to enhance pandemic preparedness, response strategies, and supply chain resilience in an increasingly interconnected and uncertain global environment.

3 Compartmental analysis

This section examines content related to model construction and equations for each model. The SIR model, a vital tool in infectious disease modeling (Erkayman et al., 2023), comprises three primary compartments: *Susceptible* (S), *Infectious* (I), and *Recovered* (R). The characteristics of each compartment are described below. The SIR system, excluding vital dynamics such as birth and death (demography), can be represented by a set of ordinary differential Eqs. (1)–(3) and Fig. 2a.

Susceptible: Susceptible individuals are those who have not been infected with the disease and are susceptible to infection (Erkayman et al., 2023). They can become infected through contact with infectious individuals. Each susceptible individual is defined by Eq. (1).

$$\frac{dS}{dt} = -\frac{\beta SI}{N} \quad (1)$$

where t is the time and β represents the transmission rate.

Infectious: Infectious individuals can transmit the disease to susceptible individuals. Also, each infected individual is transferred to the recovered compartment at a rate of γ as described by Eq. (2).

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I \quad (2)$$

Recovered: In the simplest scenario, once individuals transition from infectious to recovered, they are assumed to be immune to re-infection (Libotte et al., 2020). This concept is captured by Eq. (3).

$$\frac{dR}{dt} = \gamma I \quad (3)$$

Researchers utilize the SIR model for various purposes, such as predicting infection cases and hospitalizations (Storlie et al., 2021b), analyzing the impact of vaccination on virus spread (Ai et al., 2022; Chang et al., 2020; Storlie et al., 2021a), assessing community intervention measures (Mehmood et al., 2021), and understanding the effects of vaccination and social distancing on epidemics (Batistela et al., 2021). Additionally, the model is employed to manage hospitalization rates (Dias et al., 2022), study factors influencing virus spread

(Erkayman et al., 2023), explore gender dynamics in influenza transmission, investigate the effects of mass vaccination (Safan, 2019), assess the economic and clinical impacts of vaccination campaigns (Fust et al., 2024), and evaluate the impacts of booster programs and different vaccination strategies on COVID-19-related morbidity and mortality (Mendes et al., 2024).

In some studies, researchers have expanded upon the SIR models to forecast the progression of epidemics. They have introduced additional compartments into the model to allow for a more detailed examination of the issue and to achieve results that closely align with real-world data. Each subsequent subsection evaluates the extended models based on their incorporation of one or more compartments into the SIR model.

3.1 Single extension models

In addition to susceptible, infectious, and recovered, there are crucial components such as exposure, asymptomatic cases, mortality, pharmaceutical interventions (including vaccination and medication), medical interventions (such as hospitalization), and non-pharmaceutical interventions (such as quarantine). Figure 4 shows the SIR model and examples of single-extension models. Table 2 outlines these components and their corresponding equations, further discussed in the following. The impact of adding compartments to epidemiological models is assessed from both updated and new equations perspectives. In updated equations, the effect of the factors on the equations is shown in comparison with Eq. (1)–(3).

The models employed in Table 2 focus on the most basic states for simplicity. Consequently, these equations do not explore the impact of various states and assumptions on the equations. For instance, in the SIQR model, it is assumed that the recovery rate of individuals in quarantine is the same as that of other infectious individuals. In contrast, some studies suggest that these rates may differ. To examine the equations in this section more thoroughly, various assumptions are explored in Sect. 4.

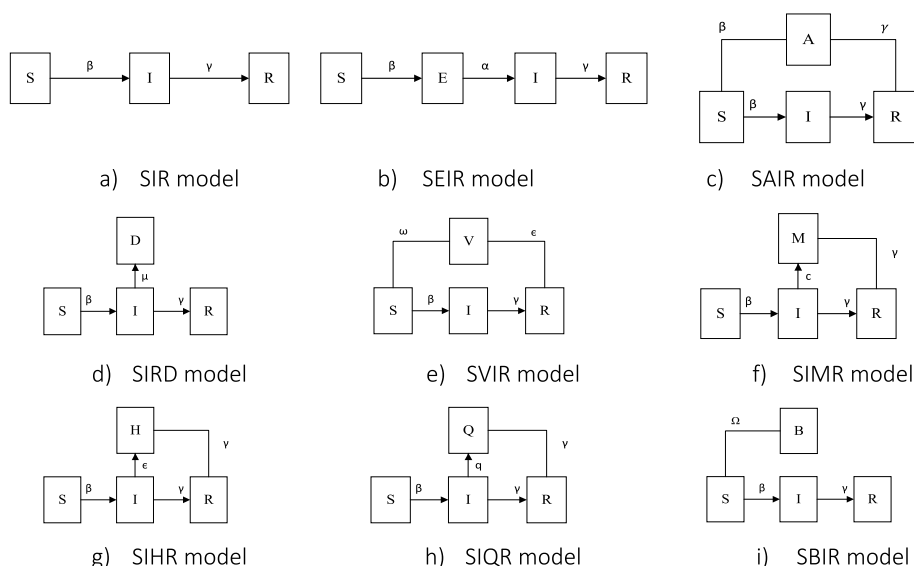


Fig. 4 SIR model and examples of standard single extension models

Table 2 Common and extended compartments of SIR models and associated equations

Compartment name	Compartment notation	Model	Equations	
			$\frac{dS}{dt}$	$\frac{dR}{dt}$
Susceptible	S	SIR	$-\frac{\beta SI}{N}$	γI
Infected (Infectious)	I			
Recovered (Removed)	R			
Exposed	E	SEIR	Updated $-\frac{\beta SI}{N}$ $\frac{\beta SI}{N} - \gamma I$	$\gamma I + \alpha E$ $\gamma I + \gamma A$
Asymptomatic	A	SIAR		
Deceased	D	SIRD	$\frac{\beta S}{N} - \gamma I$	New $\frac{dE}{dt} = \frac{\beta IS}{N} - \alpha E$ $\frac{dA}{dt} = \frac{\beta S}{N} A - \gamma A$
	V	SVIR	$\frac{\beta SI}{N} - \gamma I$	
	M	SIRM	$\frac{\beta SI}{N} - \gamma I - cM$	
Hospitalized	H	SIHR	$\frac{\beta SI}{N} - \gamma I - \xi I$	$\gamma I + \gamma H$
Quarantined	Q	SIQR	$\frac{\beta SI}{N} - \gamma I - qI$	$\gamma I + \gamma Q$
Insusceptible	B	SBIR	$\frac{\beta SI}{N} - \gamma I$	γI

α^{-1} : Average incubation period; μ : Death rate; ω : Vaccination rate; ζ^{-1} : Mean amount of time to achieve immunity; c : The effective rate of the medication; ξ : The hospitalization rate of infectious individuals; q : Quarantine rate; Ω : Effect of non-medical interventions

Exposed: This model is an extension of the SIR model, known as the SEIR model, which introduces a fourth “exposed” (E) compartment shown in Fig. 2b. Individuals in this compartment are infected but not yet capable of transmission. This feature is particularly relevant for many significant infections, as there is often a substantial incubation period during which individuals are infected but asymptomatic. An exponential distribution with parameter α is considered for the incubation period (where the average incubation period is α^{-1}).

Asymptomatic: Melis and Littera (2021) surveyed undetected infected individuals. These individuals subtly affect the spread of infection and can be classified into two categories: (1) pre-symptomatic individuals, who will later show symptoms, and (2) asymptomatic or paucisymptomatic individuals, who do not develop noticeable symptoms during infection. Individuals in the pre-symptomatic stage undergo a process similar to that of exposed individuals. In contrast, asymptomatic individuals remain undetected and eventually transition to the R compartment after a certain period, as shown in Fig. 2c. Some papers have also explored the possibility of asymptomatic individuals being transferred to the infected compartment (Kühn et al., 2021; Saha et al., 2022).

Deceased: With the addition of the mortality factor, the Susceptible-Infectious-Recovered-Deceased (SIRD) model is created. The SIRD model distinguishes between individuals who have recovered (indicating those who survived the disease and are now immune) and those who have died (Bailey, 1975). The SIRD model is illustrated in Fig. 2d, where μ is the death rate due to the disease.

Undergoing pharmaceutical intervention: The vaccinated (V) compartment plays a crucial role in pharmaceutical interventions, as vaccination is recognized as the most effective method of controlling infections. The SVIR model assumes that vaccinated individuals have permanent immunity, as shown in Fig. 2e. Other vaccination-related assumptions are discussed in Sect. 4. Qundus (2023) illustrated the SIRM model, demonstrating an expanded equation system that includes ωM , representing vaccinated and immune individuals, and cM , representing those infected and treated with medication. Both vM and cM develop immunity through different mechanisms and form a new group, as shown in Fig. 2f. In some models, hospitalization is considered merely an assumption and not explicitly modeled, as seen in the models proposed by Mesa et al. (2022) and Caulkins et al. (2023). However, in some epidemiological models, the Hospitalized (H) compartment is included, as depicted in Fig. 2g.

Undergoing non-pharmaceutical intervention: Quarantine plays two critical roles in epidemic control: isolating infected individuals and implementing regional quarantines. Figure 2h illustrates quarantined infectious individuals as an additional compartment; however, regional quarantine can affect transmission dynamics without requiring a separate compartment. Other non-pharmacological interventions, such as social distancing, also significantly influence disease transmission rates. Rajaei et al. (2021) introduced a new compartment for insusceptible individuals who are protected through public health improvements, as shown in Fig. 2i. It is important to note that insusceptible individuals are also considered in Saha and Samanta (2021), but they are not allocated to separate compartments.

3.2 Multi-extension models

Some papers used a combination of different compartments. Filho et al. (2021) introduced the SEIAHRV model (Susceptible, Exposed, Infected, Asymptomatic, Hospitalized, Recov-

ered, and Vaccinated), building upon the model utilized by Moret et al. (2021). Albani et al. (2021a) proposed an epidemiological model that considers the distribution of the population into n age ranges. Within each age range, individuals are categorized into nine compartments: susceptible (S), vaccinated (V), exposed (E), asymptomatic and infective (IA), mildly infective (IM), severely infective or hospitalized in wards (IS), critically infective or admitted to the ICU (IC), recovered (R), and deceased (D). Symptomatic infective individuals not requiring hospitalization are classified as mildly infective, while those needing hospitalization are placed in regular hospital beds, and those in the ICU are considered critically infective. Moreover, Asplin et al. (2024) and Zhu et al. (2024) incorporated symptom severity into the SEIR model by adding additional compartments.

In the study by Saha et al. (2022), the entire population (N) is allocated into several sub-populations: the susceptible population (S), the population that is infected asymptotically or pre-symptomatically exposed to the coronavirus without displaying symptoms (I_1), the symptomatically infected and quarantined population (I_2), the hospitalized population (H), the recovered population (R), and the vaccinated population (V). In a susceptible environment, individuals contract the infection and shift to an asymptomatic state upon contact with the asymptotically infected class (I_1) and the symptomatically infected class (I_2). Differential equations for vaccinated and hospitalized populations are included in their model. Equation (4) indicates that individuals from the symptomatically infected class move to the hospital at a rate denoted by ϕ . Upon hospitalization, individuals transition to the recovered class after appropriate medical treatment at a rate denoted by ψ . Equation (5) denotes that a proportion ω_1 of the susceptible population and a proportion ω_2 of the asymptotically infected population move to the vaccinated compartment upon completing an entire two-dose vaccination procedure.

$$\frac{dH}{dt} = \phi I_2 - \psi H \quad (4)$$

$$\frac{dV}{dt} = \omega_1 S + \omega_2 I_1 \quad (5)$$

Gorji et al. (2023) utilized compartmental models to analyze epidemic dynamics, incorporating age-stratified social mixing and accounting for vaccination status and waning efficacy. The model's fundamental structure follows the SIR type, encompassing susceptible (S), infected (I), hospitalized in general wards (H), hospitalized in ICUs (IU), and removed (R) populations. Their study demonstrated the model's ability to capture key aspects of epidemic dynamics and the resulting healthcare requirements. Simplified equations for H and IU are provided in Eq. (6) and (7):

$$\frac{dH}{dt} = \xi I + \wedge IU - \eta H - \gamma H \quad (6)$$

$$\frac{dIU}{dt} = \eta H - \wedge IU - \eta H \quad (7)$$

where ξ represents the hospitalization rate of infectious individuals, $\wedge$ is the transition rate from compartment IU to H , and η is the reverse transition rate. Γ denotes the removal rate. There is no removal rate from the IU compartment, as individuals can only exit from the hospitalized (H) compartment.

Jarumaneroj et al. (2022) utilized the SIQRV model to describe the transmission dynamics of infection in the context of the COVID-19 Vaccine Allocation Problem (CVAP). This model divides the population in each region into seven compartments based on health states: Susceptible (S), Infectious (I), Quarantined (Q), Recovered (R), Dead (D), vaccinated with immunity (V), and vaccinated without immunity ($\bar{V}$). Similarly, Saha and Samanta (2021) divided the population $N(t)$ at time t into six groups: the susceptible population (S), asymptomatic individuals exposed to the virus who have not yet shown clinical symptoms of COVID-19 (A), quarantined individuals (Q), symptomatically infectious individuals (I), hospitalized and isolated individuals (H), and the recovered population (R).

The SEUACRD-VP model proposed by Zhan et al. (2023) represents a significant advancement in understanding the multi-directional mutation process of SARS-CoV-2 and the spread of COVID-19, particularly in the context of multiple variants. This model evaluates the impact of various public health interventions in the presence of these mutations. More detailed information about this model can be found in Zhan et al. (2022). Table 3 lists some references that use combined models.

Liu et al. (2024) introduced a hybrid model that combines the SEIR and SEI frameworks to study the prevalence of dengue fever in humans and mosquitoes, respectively. In Rajasekar et al. (2024), the total vulnerable population, represented by a constant size (N), is divided into eight epidemiological compartments: susceptible (S), exposed (E), symptomatic and infectious (I), hyper spreaders (P), infectious but asymptomatic (A), hospitalized (H), recovered (R), and fatalities (F). The inclusion of the hyper spreaders class (P) is particularly important for understanding the dynamics of disease transmission.

4 Analysis of assumptions

In this section, the assumptions within the reviewed models are categorized based on the associated population, interventions, and epidemiological factors, as detailed in Table 4. Each category is examined in a separate subsection.

4.1 Population factors

Population factors, including socio-demographic and regional elements, are critical for defining population characteristics in SIR models. The SIR model requires that the sum of all groups equal the population size in all phases (Qundus et al., 2023; Shringi et al., 2021; Yaladanda et al., 2022). Population size influences disease spread dynamics (Erkayman et al., 2023). Birth and death rates, apart from disease-related factors, can enhance model realism. In some cases, birth and death rates are assumed negligible for model simplification or short outbreak durations. Equal birth and death rates can offset each other, maintaining a constant population size. However, for extended epidemics, model validity decreases, requiring adjustments to transitions considering births and natural deaths (Hethcote, 2000).

Table 3 Extended models

Reference	Purpose	Model	Description of added components
Kühn et al. (2021)	Assess the effectiveness of the sets of non-pharmaceutical interventions	SECIHUDR	<i>C</i> : Carriers: Who carry the virus and are infectious to others but do not yet show symptoms (they may be pre- or asymptomatic); Hospitalized (<i>H</i>): Who experience a severe development of the disease; In Intensive Care Unit (<i>U</i>)
Parolini et al. (2022)	Investigation of new species and the effect of vaccination on the course of the disease	SUIHTEV	<i>U</i> : Undetected (both asymptomatic and symptomatic) infectious individuals; <i>I</i> : Individuals isolated at home; <i>H</i> : Number of infected hospitalized individuals; <i>T</i> : Infected threatened individuals hosted in ICUs; <i>E</i> : Extinct individuals; <i>V1</i> : Individuals partially vaccinated with only one dose; <i>V2</i> : Individuals fully vaccinated with two doses; <i>VR</i> : Recovered individuals who have been vaccinated,
Bertsimas et al., (2021)	Forecast the progression of COVID-19 and evaluate the impact of various social distancing policies	DELPHI	<i>UR</i> : Undetected people who will recover; <i>UD</i> : Undetected people who will decrease; <i>DHR</i> : Detected hospitalized people who will recover; <i>DHD</i> : Detected hospitalized people who will decrease; <i>DQR</i> : Detected quarantined people who will recover; <i>DQR</i> : Detected quarantined people who will decrease; <i>DT</i> : Total Detected Cases; <i>DD</i> : Total Detected Deaths
Robinson et al. (2022)	Model more complex disease dynamics and to capture clinically relevant quantities of interest	22-compartment model	<i>Q</i> : Exposed (quarantined); <i>A</i> : Infectious (pre-symptomatic); <i>W</i> : Infectious (pre-symptomatic, isolated); <i>B</i> : Infectious (mild-to-moderate symptoms); <i>N</i> : No access to hospital care; <i>H1</i> : Admitted to hospital (pre-ICU); <i>I</i> : Admitted to hospital (ICU); <i>H2</i> : Admitted to hospital (post-ICU) etc
Kemp et al. (2021)	Consider the interplay between vaccinations and social measures and estimate the vaccination rate to achieve herd immunity	16- compartment model	<i>NI</i> : Recovering at home; <i>H</i> : Hospitalized; <i>H₁</i> : Long stayed hospitalized; <i>ICU</i> : Admitted to hospital (ICU); <i>AICU</i> : Back to hospital after ICU
O'Dea and Drake (2022)	Forecasts of COVID-19 cases, hospital admissions and deaths	9- compartment model	<i>Z_r</i> : number of cases reported each day; <i>A</i> : new hospital admissions; <i>D_r</i> : The number of newly reported deaths each day
Pang et al. (2022)	Consider the impact of asymptomatic COVID-19 carriers on pandemic policy outcomes	SEOAR	<i>O</i> : Ordinary carriers; <i>A</i> : Asymptomatic carriers

Incorporating migrating individuals into birth and death processes improves the model's representation of human mobility (Bhadauria et al., 2021). Some models assume a constant recruitment rate in the susceptible class (Saha et al., 2022). Newborns' conditions and placement in specific compartments depend on disease characteristics. For example, newborns may be vaccinated immediately and recover from certain virus types (Chang et al., 2020), while in diseases like COVID-19 with age-limited vaccinations, newborns are placed in the susceptible compartment (Batistela et al., 2021). In cases such as diphtheria, some newborns are vaccinated and enter the recovered compartment, while others remain in the susceptible compartment (Fauzi et al., 2024).

Table 4 Classification of papers studying the SIR model based on their assumptions

Reference	Epidemiological factors				Population factors				Intervention factors								
	RT	IM	IC	MP	MS	BD	NB	CO	MG	MI	MR	SO	MD	NPI	PI	N-MD	
Iranzo and Pérez-González (2021)	Constant	Permanent						Homogenous									General
Storlie et al. (2021a)	Variable				*												
Batis-tela et al. (2021)		Permanent				Equal	Susceptible						Hesitancy			MDMT	
Dias et al. (2022)	Variable															SDST	Social distancing
Al et al. (2022)				*				Homogenous	Age								Social distancing
Goodkin-Gold et al. (2022)		Permanent				Equal		Homogenous								SDST	General
Zhang et al. (2023)	Variable						Recovered									SDST	Social distancing
Gros and Gros (2022)	Constant																General
Safan (2019)	Variable				*		Susceptible	Homogenous	Age-Gender						Hospital		General
Hwang et al. (2020)	Constant															SDST	
Deka et al. (2020)	Constant	Waning		*				Homogenous	Age							SDST	

Table 4 (continued)

Reference	Epidemiological factors			Population factors					Intervention factors						
	RT	IM	IC	MP	MS	BD	NB	CO	MG	MI	MR	SO	MD	NPI	N-MD
De Miguel-Arribas et al. (2022)	Variable-Constant	Waning		*				Heterogenous			Age		Hesitancy		
Nepomuceno et al. (2021)	Constant	Permanent				Equal	Susceptible								SDST
O'Regan et al. (2020)						Equal	Susceptible-Recovered								SDST
Deng et al. (2021)	Constant	Delayed			*										SDST
Loertscher and Muir (2021)	Variable							Homogenous			Age				SDST
Nguyen et al. (2022)	Constant	Permanent	*										Be-tween regions		Quarantine / Isolation
Sharov (2020)	Variable		*												Lockdown
Kozyreff (2021)	Constant			*									Hospital		Lockdown
Chang et al. (2020)	Constant						Susceptible-Recovered	Homogenous							SDST

Table 4 (continued)

Reference	Epidemiological factors		Population factors							Intervention factors								
	RT	IM	IC	MP	MS	BD	NB	CO	MG	MI	MR	SO	MD	NPI	PI	N-MD		
Marinov and Marinova (2020)	Variable	Permanent						Homogenous										General
Duan et al. (2023)	Constant																Quarantine / Isolation	
Vattiatio et al. (2022)	Variable	Waning	*	*	*			Homogenous	Age					Hospital	MDST	Quarantine / Isolation		
Huang et al. (2021)	Variable-Con-stant	Permanent		*	*				Geographic-Demo-graphic Age	*						General		
Alanazi et al. (2020)	Constant															General		
Betti et al. (2021)	Constant	Permanent	*												SDMT	General		
Erkayman et al. (2023)	Constant	Delayed		*								Hesitancy			MDST			
Qundus et al. (2023)	Constant	Permanent												Medicine	SDST			
Hussien and Mohammad (2022)	Constant	Permanent			*		Susceptible-Recovered								SDST			

Table 4 (continued)

Reference	Epidemiological factors							Population factors				Intervention factors				
	RT	IM	IC	MP	MS	BD	NB	CO	MG	MI	MR	SO	MD		N-MD	
													NPI	PI		
Lai et al. (2021)	Constant		*					Heterogenous	Gender							Social distancing— Lockdown
Feng et al. (2020)	Variable		*					Susceptible-Recovered	Gender							SDST
Aldila et al. (2020)	Variable-Constant	Waning	*							Homogenous					Hospital-Test	
Zhang et al. (2022b)	Variable	Permanent	*							Between regions	*		Hospital		Quarantine / Isolation	
León et al. (2022)		Waning	*					Homogenous								MDST
Zhang et al. (2022a)	Variable	Waning	*									*		Hospital		
Caldwell et al. (2021)		Waning	*		*											MDST
Demon-geot et al. (2022)	Variable-Constant	Permanent	*													MDST
Pey et al. (2022)	Variable	Waning-Delayed	*		*						*					Quarantine / Isolation
Parolini et al. (2022)	Constant	Permanent	*		*			Homogenous	Age				Hospital		General	
Du et al. (2023)		Waning	*												Hospital	

Table 4 (continued)

Reference	Epidemiological factors		Population factors							Intervention factors						
	RT	IM	IC	MP	MS	BD	NB	CO	MG	MI	MR	SO	MD	PI	N-MD	
Dagpunar and Wu (2023)	Constant	Waning													MDST	General
Robinson et al. (2022)	Variable	Waning	*					Heterogenous	Age				Hospital	SDST		Quarantine / Isolation
Tuite et al. (2020)	Variable		*										Hospital			Social distancing – Quarantine / Isolation
Zhan et al. (2023)	Constant		*	*				Homogenous			*			SDST	General	General
Tzamalali et al. (2023)	Variable-Constant	Waning	*					Homogenous						SDST	General	General
Jarumanee et al. (2022)				*					Age		*			SDMT		Social distancing—Quarantine / Isolation
Vahdani et al. (2023)		Permanent	*	*		*			Age				Test	SDMT		Quarantine / Isolation
Bertsimas et al. (2021)	Variable	Permanent	*						Demog., Geog., Comorbidity ...		*		Hospital			Social distancing
Boon et al. (2021)	Constant			*					Age				Hospital	SDMT		General

Table 4 (continued)

Reference			Epidemiological factors					Population factors				Intervention factors			
RT	IM	IC	MP	MS	BD	NB	CO	MG	MI	MR	SO	MD	NPI	PI	N-MD
Kühn et al. (2021)	Constant	*	*	*			Heterogenous	Age	Be- tween regions	*		Hospital			General
Deo and Grover (2022)	Variable	Permanent													General
Rodiah et al. (2023)	Variable	Waning	*	*	*	Susceptible	Heterogenous	Age				Hospital	SDST		General
Polcz et al. (2023)	Variable	Waning-Delayed	*	*	*							Hospital	MDST		
Saad-Roy et al. (2021)	Variable	Waning			*		Heterogenous						MDST	Mask, Lockdown-Social distancing	General
Harari and Monteiro (2022)	Constant	Waning			*	Susceptible-Recovered	Homogenous		Be- tween groups		Anti-vacc		SDST		
Gollier (2021)		Delayed	*				Heterogenous	Age			Anti-vacc		SDST		Lock-down—Social distancing
Ruiz et al. (2023)		Waning	*		*			Age						SDST	Lockdown
Fudolig (2023)	Constant	Waning		*										SDST	

Table 4 (continued)

Reference	Epidemiological factors			Population factors							Intervention factors					
	RT	IM	IC	MP	MS	BD	NB	CO	MG	MI	MR	SO	MD	NPI	PI	N-MD
Fudolig and Howard (2020)	Constant	Waning			*											SDST
Tamassiga et al. (2023)		Permanent	*					Homogenous								SDST
Neofotistos et al. (2022)		Waning						Homogenous								SDST
Angeli et al. (2022)		Permanent			*							Hesitancy -Anti-vacc				SDST
Mesa et al. (2022)		Waning-Delayed						Homogenous	Age			Hesitancy	Hospital		MDMT	General
Wali et al. (2022)	Constant	Waning	*			*										SDST
Hawkes and Good (2022)						*			Age				Hospital		SDST	General
Chen and Stanciu (2021)		Waning														SDST
Malinzi and Juma (2023)		Waning	*		*	*										SDST
General																General
Ahumada et al. (2023)	Constant	Waning-Delayed			*	*		Homogenous								SDST
Quarantine / Isolation																Quarantine / Isolation

Table 4 (continued)

Reference	Epidemiological factors		Population factors							Intervention factors		
	RT	IM	IC	MP	MS	BD	NB	CO	MG	MI	MR	SO
											MD	N-MD
											NPI	PI
Turky-ilmazoglu (2022)		Waning										SDST
Kain et al. (2021)	Variable										Hospital	General
Kabir and Tanimoto (2020)	Constant	Waning		*							Hospital	SDST
Caulkins et al. (2023)	Variable					Equal		Heterogenous	Age		Hospital	SDST
Yaladanda et al. (2022)	Constant	Waning		*				Homogenous				SDST
Gorji et al. (2023)		Waning		*					Age		Hospital	SDST
Filho et al. (2021)		Waning										SDST
Al-bani et al. (2021a)	Variable								Age		Hospital	SDST
Al-bani et al. (2021b)	Variable								Age		Hospital	SDST
Song et al. (2020)	Constant	Waning		*	*		Susceptible-Recovered					SDST

Table 4 (continued)

Reference	Epidemiological factors			Population factors							Intervention factors				
	RT	IM	IC	MP	MS	BD	NB	CO	MG	MI	MR	SO	MD	N-MD	PI
Barua and Dénes (2023)	Variable	Waning	*				*	Susceptible-Recovered							SDST
Markovic et al. (2021)	Variable-Constant	Waning	*					Heterogenous		*			Hospital	SDST	General
Engelbrecht and Scholes (2021)	Constant	Permanent						Homogenous							Social distancing—Lockdown
Rao and Brandeau (2021a)	Variable		*						Age						SDMT
Rao and Brandeau (2021b)	Variable		*						Age						SDST
Rao and Brandeau (2022)	Variable		*						Age						SDST
Shringi et al. (2021)	Variable			*											General
Šušteršič et al. (2021)	Variable		*					Homogenous							Quarantine / Isolation
Geoffroy et al. (2022)	Constant	Immediate	*												MDST

Table 4 (continued)

Reference	Epidemiological factors							Population factors				Intervention factors			
	RT	IM	IC	MP	MS	BD	NB	CO	MG	MI	MR	SO	MD		N-MD
													NPI	PI	
Hieu et al. (2024)	Variable	Waning													SDST
Khalifi and Britton (2024)	Constant	Waning			*			Heterogenous	Immunity						MDST
Mara-ver et al. (2024)	Variable	Waning	*	*	*				Immunity		*			Hospital	MDST
Khan and Tanimoto (2024)	Variable	Waning			*										SDMT
Tuong et al. (2024)	Variable	Waning				*	Susceptible-Recovered		General						SDST
Gökçet al. (2024)	Constant	Delay	*			*									SDST
Li et al. (2024)	Variable	Waning	*										Hospital	MDST	General
Vio-laris et al. (2023)	Variable	Waning	*	*					Age						SDST
Park et al. (2024)	Variable			*		*									General
Wang et al. (2023)	Variable	Permanent			*	*	Susceptible		Immunity	*			Hospital	MDST	

Table 4 (continued)

Reference	Epidemiological factors		Population factors						Intervention factors							
	RT	IM	IC	MP	MS	BD	NB	CO	MG	MI	MR	SO	MD	NPI	PI	N-MD
Aronna and Moschen (2024)	Variable	Permanent	*	*			*			*	*					SDST
Zhou et al. (2024)	Variable		*	*	*	Equal		Homogenous	Gender, age, occupation, location							MDST General

RT: Rate of Transmission; IM: Immunity; IC: Incubation time; MP: Multi-period; MS: Multi-Strain/Wave; BD: Birth & Death Rate; NB: Newborns; CO: Composition; MG: Multi-grouping; MI: Migration; MR: Multi-Region; SO: Social; MD: Medical; N-MD: Non-Medical; SDST: Single-Dose Single-Type; SDMT: Single-Dose Multi-Type; MDMT: Multi-Dose Single-Type; MDMT: Multi-Dose Multi-Type;

RT: Rate of Transmission; IM: Immunity; IC: Incubation time; MP: Multi-period; MS: Multi-Strain/Wave; BD: Birth & Death Rate; NB: Newborns; CO: Composition; MG: Multi-grouping; MI: Migration; MR: Multi-Region; SO: Social; MD: Medical; N-MD: Non-Medical; SDST: Single-Dose Single-Type; SDMT: Single-Dose Multi-Type; MDST: Multi-Dose Single-Type; MDMT: Multi-Dose Multi-Type;

Population studies can collectively examine or segment populations based on demographics, geography, infection risk, and social factors. While homogeneity assumptions are common in well-mixed populations, even when subdividing, heterogeneity is crucial for accuracy, as shown in studies accounting for variations across countries, demographics, income levels, and seasons (Lai et al., 2021). In SIRD models, factors such as age and seasonal effects significantly influence mortality rates and transmission dynamics (Engelbrecht & Scholes, 2021; Rao & Brandeau, 2021a, 2022). Several elements impact inter-compartment transmission, including time-dependent rates, hospitalization, and varying infection severities (Albani et al., 2021a).

Recognizing demographic heterogeneity and government interventions, modeling confined areas may lack accuracy, requiring a nationwide system approach (Robinson et al., 2022). A multi-regional perspective that considers inter-regional population movements and factors such as infection status and travel restrictions based on health conditions is more logical (Jarumaneeroj et al., 2022; Kühn et al., 2021). For further reference, readers may consult Zhang et al. (2022b), Hong et al. (2024), and Han et al. (2023) for equations in multi-regional disease transmission.

Beyond health or disease states, combining social, economic, and geographical dimensions—such as social structure, socioeconomic status, social interactions (both direct and virtual), adaptive or maladaptive behaviors, and population density—can enhance model accuracy (Blasioli et al., 2023; Davies et al., 2020). De Miguel-Arribas et al. (2022) developed an age-structured SIR model using age-contact matrices from Mistry et al. (2021) tailored to the 2019 population structure (Arregui et al., 2018). Table 5 outlines the impact of population factors on epidemiological equations, including birth rates, death rates, and newborn vaccination statistics. If we assume a given birth rate, the analysis must also account for the proportion of newborns receiving vaccinations, which directly affects the susceptible and recovered compartments in the model. Understanding this vaccination percentage is critical, as it determines how many newborns move directly into the recovered group versus remaining susceptible. Factors such as vaccination campaigns, healthcare accessibility, and vaccine acceptance play pivotal roles in these dynamics. The table aims to capture these parameters for various scenarios, enabling a more accurate prediction of disease spread and control strategies.

Another important assumption in SIR models concerns vaccine hesitancy. Several studies have explored its effects on vaccination uptake (de Miguel-Angeli et al., 2022; Arribas et al., 2022; Banerjee et al., 2023). This factor is mainly applied as an index of the vaccination rate and is sometimes adjusted based on factors such as age. For instance, de Miguel-Arribas et al. (2022) highlight the impact of hesitancy on COVID-19 mortality rates and emphasize the need to boost vaccine acceptance, particularly among older age groups, while stressing the role of younger groups. Some individuals are also classified as anti-vaccine, meaning those who are fully against vaccination. Table 5 illustrates how anti-vaccine individuals can be integrated into the model.

4.2 Epidemiological factors

Assumptions regarding epidemiological conditions and change processes, such as transmission and recovery rates, can vary across epidemiological models (Marinov & Marinova, 2020). Infection and recovery rates, which are essential parameters in epidemiology, can

Table 5 Population factors and related equations

Factor	Equations		
	Updated SIR compartments	Other affected compartments	
	$\frac{dS}{dt}$	$\frac{dI}{dt}$	$\frac{dR}{dt}$
Birth and death rate	$-\frac{\beta SI}{N} + \theta N - \mu S$	$-\gamma I - \mu I$	$\gamma I - \mu R$
Newborns	$-\frac{\beta SI}{N} + \rho \theta$	$\frac{\beta SI}{N} - \gamma I$	γI
Anti-vaccine	Divided into P and AV	$\frac{\beta SI}{N} - \gamma I$	$\gamma I + \omega P(t)$
		$+\beta (AV(t) + P(t)) I(t)$	$\frac{dV}{dt} = (1 - \rho) \theta$ $\frac{dP}{dt} = -\beta P(t) I(t)$ $\frac{dAV}{dt} = -\beta AV(t) I(t) - \omega P(t) + \pi AV(t) - \sigma P(t)$

θ : Birth rate; μ : Death rate; ρ : Fraction of unvaccinated at birth; β : Transmission rate; ω : Vaccination rate; π : rate of migration from the AV -group to the P -group; σ : rate of migration from the P -group to the AV -group

be known or unknown (Marinov & Marinova, 2020), as well as constant (Iranzo & Pérez González, 2021) or variable. Huang et al. (2021) considered a variable transmission rate while keeping other rates constant, whereas Betti et al. (2021) assumed a relatively constant testing and reporting rate in the population. Factors such as age, underlying diseases, and location can lead to varying rates among individuals (Prem et al., 2020), necessitating group segmentation based on these characteristics (Dias et al., 2022). Barua and Dénes (2023) examined infectious transmission from deceased individuals, while van Boven et al. (2024) assessed age- and time-dependent household introduction hazards, alongside within-household transmission rates, utilizing data from a prospective household study conducted in the Netherlands.

Recovery and mortality rates in related studies assume long-term immunity following recovery (Zhang et al., 2022b). The possibility of re-infection or secondary infection is another crucial consideration. While some models assumed no co-infection or super-infection (Betti et al., 2021), others explored the potential for re-infection due to new virus variants or waning immunity (Ginting et al., 2024; Marinov & Marinova, 2020). However, some papers argue that it is not possible to return from the recovery compartment to the infection compartment (Goodkin-Gold et al., 2022) due to acquired permanent immunity (Batistela et al., 2021; Iranzo & Pérez González, 2021) or because the acquired immunity lasts longer than the outbreak (Betti et al., 2021). Fisman et al. (2024) examined the impact of immune evasion, waning immunity, and booster effects on the dynamics of population mixing between unvaccinated minorities and vaccinated majorities.

The duration of the epidemic and state transitions are also vital considerations. The incubation period, assumed to be zero in some models (Iranzo & Pérez González, 2021), is acknowledged as having potential infectiousness in other research (Chen et al., 2020b; Saharan & Tee, 2023; Yang et al., 2020). Models now consider that exposed individuals can infect susceptible ones before symptoms appear (Zhang et al., 2022b).

As mentioned in the previous subsection, the type of immunity generated depends on the nature of the disease and the vaccine used. Therefore, the effects of different types of immunity and the re-infection rate are presented in Table 6. Various types of immunity include:

- *Permanent Immunity*: In the case of permanent immunity, it is assumed that immunity lasts for a lifetime or remains effective throughout the duration of the simulation.
- *Waning Immunity*: This term refers to the gradual decrease in the effectiveness of an immune response over time following vaccination or natural infection, particularly in the context of a virus with emerging variants.
- *Weak/Loss Immunity*: This term describes a more severe scenario where the immune system fails to provide adequate protection against a pathogen.
- *Delayed Immunity*: Delayed immunity contrasts with immediate immunity. In this scenario, which more closely resembles real-world situations, there is a temporal gap between vaccination and complete recovery. This time delay increases the risk of infection in vaccinated individuals before they achieve full immunity.

In Turkiylmazoglu (2022) and Angeli et al. (2022), individuals in the vaccinated component can become infected. However, in Angeli et al. (2022), individuals are transitioned from the recovered component back to the infected component. Vattiatio et al. (2022) explored a model for COVID-19 that accounted for waning immunity resulting from vaccination and

Table 6 Epidemiological factors and related equations

Factor	Equations			Other affected components
	Updated SIR components			
	$\frac{dS}{dt}$	$\frac{dI}{dt}$	$\frac{dR}{dt}$	
Re-infection	$-\frac{\beta SI}{N} - \omega S$	$\frac{\beta SI}{N} - \gamma I$	γI	$\frac{dV}{dt} = \omega S$
Waning immunity	$-\frac{\beta SI}{N} + \delta R$	$\frac{\beta SI}{N} - \gamma I$	$\gamma I - \delta R$	$-\ddot{v}VI$
Delayed immunity	$-\frac{\beta SI}{N} - \frac{\omega S}{N}$	$\frac{\beta SI}{N} - \gamma I$	$\gamma I + \epsilon 3V$	$\frac{dV}{dt} = \omega S/N$
	$+ (1 - \epsilon) 3V$	$+ \xi IV/N$		$-\xi IV/N - 3V$

$\ddot{v}$: Parameter of re-infection disease transmits via weak or lost immune host in contact with the infected population; ω : Vaccination rate; δ : Rate of disappearance of temporal immunity; ϵ : Vaccine effectiveness, 3^{-1} : The amount of time an individual spends in the vaccinated compartment before reaching immunity and moving to the removed compartment, ξ : The rate at which a vaccinated (but still not immune) individual enters into contact with an infected

prior infection, considering various levels of behavioral changes compared to the initial Omicron wave. The durability of immunity from previous infection remains a significant uncertainty in epidemiological models. In Yaladanda et al. (2022), equations are like Turkyilmazoglu (2022) but use $(1 - V_{eff})\beta$ for the parameter of re-infection, where β and V_{eff} are the transmission rate and vaccine effectiveness, respectively.

4.3 Intervention factors

Implementing medical and non-medical interventions plays a crucial role in epidemic control (Goodkin-Gold et al., 2022). Non-medical interventions are typically employed at the onset of unknown epidemics when vaccines are unavailable. These interventions, such as isolation measures, aim to curb the spread of the disease (Melis & Littera, 2021). The effectiveness of these interventions is essential for managing epidemic peaks (Dias et al., 2022).

Vaccination assumptions vary in epidemiological models based on factors such as vaccine effectiveness, dosage requirements, and target populations (Goodkin-Gold et al., 2022). Some studies emphasize the protective effects of vaccines, including a reduced likelihood of infection, lower mortality rates, and decreased transmission rates among vaccinated individuals (Erkayman et al., 2023). However, contrasting views exist; some researchers suggest that vaccination does not significantly influence transmission or recovery rates (Rao & Brandeau, 2021a, 2021b, 2022).

Rizvi (2016) investigated the dynamics of multi-dose vaccines for diseases like pertussis, utilizing a modeling approach for analysis. Similarly, Gao et al. (2007) examined a repeated vaccination strategy across different age groups aimed at eradicating diseases, concluding that sufficient vaccination levels for each age group are necessary to prevent disease persistence. Liu et al. (2008) employed the SVIR model to assess the number and timing of required doses, emphasizing the necessity of considering non-epidemiological factors to optimize vaccination strategies. The effectiveness of vaccines is a debated topic, influenced by factors such as vaccine types, dosages, and population characteristics (Jarumaneeroj et al., 2022). Models may incorporate multiple vaccine doses or booster shots to enhance effectiveness (Dagpunar & Wu, 2023; Du et al., 2023). Vaccination models often account

for varying levels of protection against infection and severe outcomes (Mesa et al., 2022), and the vaccinated compartment has been expanded in models based on different types of immunity (Pérez-Alós et al., 2022).

The emergence of new virus strains and concerns regarding vaccine effectiveness underscore the need for ongoing research (Li et al., 2021). Assumptions about vaccine risks and efficacy can significantly impact vaccination strategies and coverage (Deka et al., 2020; De Miguel-Arribas et al., 2022; Andreu-Vilarroig et al., 2024). The literature also emphasizes the importance of considering delays in vaccine rollout and the impact of quarantine measures on disease transmission (Booton et al., 2021; Zhang et al., 2022b). Social challenges, such as willingness to vaccinate and adherence to preventive measures like social distancing, further influence epidemic control strategies (Caulkins et al., 2023; Choi & Shim, 2020). Overall, understanding the dynamics of interventions, vaccination strategies, and societal behaviors is essential for effectively managing infectious disease outbreaks.

Some studies have incorporated intervention factors into their models and updated the equations accordingly (Table 7). The revised equations are simplified and focus on the changes made. For instance, while Caulkins et al. (2023) denote the compartment for vaccinated individuals as R_2 , this analysis uses V for easier model comparison. Although birth and natural death rates are part of the original models, they are excluded here to concentrate on vaccination aspects. When the vaccine's effectiveness is known, it is factored into the model by multiplying the effectiveness by the vaccination rate. Additionally, the impact of vaccination assumptions on the equations is highlighted, including Vahdani et al.'s (2023) approach, which involves testing and quarantining positive cases.

5 Parameters uncertainty

Uncertainty is a significant factor in compartmental models, which have proven valuable for analyzing pandemic behavior, particularly when dealing with imperfect data (Cauchemez et al., 2019). Therefore, forecasting various parameters, such as time-varying reproduction numbers or mortality rates, can be crucial (Cori et al., 2013; Duijzer et al., 2018; Ghostine et al., 2021). However, it is essential to prioritize the assessment of relevant approaches based on the nature of the uncertainty, especially for emerging viruses with limited historical data. In general, data-driven probabilistic approaches are recommended for pandemic models and scenarios to address these uncertainties (Ardesch et al., 2023). Flaig and Houy (2024) examined an emerging disease (referred to as disease X) within a closed population using both a stochastic SIR model and its deterministic approximation.

Managing uncertainty during a pandemic is further complicated by the diversity in disease characteristics and sampling methods. For instance, in the context of COVID-19, data from reputable organizations like the Statistical Office and the World Health Organization (WHO) show that reaching a consensus on key parameters, such as infectivity and fatality rates, is challenging. Section 4.1 on population factors highlights how geodemographic elements, such as population density and regional characteristics, influence pandemic parameters and trajectories (Davies et al., 2020). Additionally, epidemiological factors like transmission and recovery rates may remain unknown (Marinov & Marinova, 2020). The effectiveness of vaccination as an intervention factor is often uncertain (Goodkin-Gold et al., 2022).

Table 7 Intervention factors and related equations

Factor	Equations			Other affected components
	Updated SIR components			
	$\frac{dS}{dt}$	$\frac{dI}{dt}$	$\frac{dR}{dt}$	
Vaccination	$-\frac{\beta SI}{N} - \omega S$	$\frac{\beta SI}{N} - \gamma I$	$\gamma I + \omega \varepsilon S$	
Testing and quarantine	$-(\beta_1 I + \beta_2 Q + \beta_3 U) S$	$\frac{\beta SI}{N} - \gamma I + (\beta_1 I + \beta_2 Q + \beta_3 U) S - \kappa I$	$\gamma I + (\beta_1 I + \beta_2 Q + \beta_3 U) S - \kappa I$	$\frac{dQ}{dt} = k\tau IQ$ $\frac{dQ}{dt} = k\tau IQ$ $+ k(1 - \tau) I$
		$(\beta_1 I + \beta_2 Q + \beta_3 U) S - \kappa I$		

ω : Vaccination rate; ϵ : Vaccine effectiveness; K : Information interaction rate through which individuals admit to taking a test; τ : The probability of a test being positive, $\beta_1/\beta_2/\beta_3$: The transmission rate of infectious from infected/quarantined/unquarantined individuals

One potential solution is to employ statistical or machine learning techniques; however, using learning algorithms in public health can encounter issues related to trustworthiness and explainability, especially in complex, multi-parameter scenarios (Farhat et al., 2023). In crisis management, while parameters like the transmission rate (β) and mean spontaneous recovery time (t_R) are essential for modeling, predicting the expected number of hospital beds and their occupancy duration is often more critical (Chen et al., 2020a; Chowdhury et al., 2020; Li et al., 2020; Richardson et al., 2020; Wu et al., 2020; Zhou et al., 2020).

The transmission rate (β) represents the average number of contacts per unit of time that result in disease transmission (Nepomuceno et al., 2021). This rate can vary by age group (Dias et al., 2022; De Miguel-Arribas et al., 2022) or gender subgroup (Safan, 2019). Table 8 provides examples of the estimation of these parameters. Some parameters are essential in modeling, including the transmission rate (β) and the mean spontaneous recovery time (t_R). However, from the perspective of crisis management, it is more critical to predict the expected number of hospital beds and the duration of their occupancy (Chen et al., 2020a; Chowdhury et al., 2020; Li et al., 2020; Richardson et al., 2020; Wu et al., 2020; Zhou et al., 2020).

Lai et al. (2021) utilized accurate data based on reported cases and mobile phone data to calculate travel and contact rates in each country, rather than relying solely on transmission rates. In Demongeot et al. (2022), the transmission rate is determined by various parameters, including the fraction of unreported symptomatic infectious individuals capable of transmitting the pathogen (k), the fraction of reported symptomatic infectious individuals (f), the number of susceptible individuals at time t_0 (S_0), the number of exposed individuals at time t_0 (E_0), the number of asymptomatic infectious individuals at time t_0 (I_0), the number of symptomatic infectious individuals who are not reported at time t_0 (U_0), and the transition rates between different compartments. According to Aldila et al. (2020), isolation at home or in a hospital reduces the transmission rate. Additionally, Grass et al. (2024) considered the severity of the lockdown when calculating the transmission rate.

According to the reviewed papers, in addition to using real data (Khan et al., 2024; Kozyreff, 2021; Papageorgiou & Tsaklidis, 2024), there are various approaches to estimating the parameters, including the inverse modeling problem (Libotte et al., 2020; Marinov & Marinova, 2020), brute force methods (Ahmetolan et al., 2020), the Particle Swarm Optimization (PSO) algorithm (Ai et al., 2022), and least squares techniques (Ai et al., 2022; Andreu-Villarroig et al., 2024; Husniah et al., 2021; Ji et al., 2021). Solving the inverse problem is essential for model calibration and controlling model parameters. Inverse problem methodologies can be effectively applied in a wide range of critical processes, such as spreading infectious diseases, enabling epidemiologists and public health professionals to forecast epidemics (Bauch et al., 2009).

6 Optimization using epidemiological models

Several of the reviewed studies highlight the importance of optimizing epidemic control interventions by utilizing a range of techniques to determine the most effective strategies. Often guided by SIR (Susceptible-Infected-Recovered) models, these methods assess the current state of disease spread to inform targeted responses. Epidemics are inherently dynamic, with factors such as infection prevalence, age-related susceptibility, and govern-

Table 8 Estimation of parameters

Parameter	Effective factor	Equations	References
Transmission rate (β)	Original	$a * b$	Erkayman et al. (2023)
Different waves and interventions		$\beta(t) = \begin{cases} \beta_1 t^{-\sigma_1} t_0 < t \leq t_1 \\ \gamma & t_1 < t \leq t_2 \\ \beta_2 t^{-\sigma_2} t_2 < t \end{cases}$	Huang et al., (2021)
Temperature		$M[1 - c1(1 - \exp(-kt))ms] + \xi(t)$ $(1 - \psi) \cdot (\beta_i + \beta_j + \beta_k)$ $sk(t) \beta_0$	Ai et al. (2022)
Isolation		$sk(t) \sim 1 + k \sin\left(\pi\left(\frac{t}{182.5} + \frac{1}{2}\right)\right)$	Šušteršič et al. (2021)
Season			Kühn et al. (2021)
Undetected individuals		$(I_X/I + \tilde{\beta}(I_H + I_R)/I)$	Kühn et al. (2021)
Age and lockdown		$\alpha_{ij}(\beta q(1 - \kappa) + (\underline{\beta} b_{jt} + \tilde{\beta}(1 - b_{jt}))\kappa)(1 - b_{jt})$	Gollier (2021)
Different efficacies against different strains		$\beta_i(1 - \eta_i)$	Ahumada et al. (2023)
Severity of infection			
Death rate (μ)		$\mu = \frac{\gamma}{d}$ $d = dm + \alpha ds$ $\gamma = \frac{1}{d} - \mu$	Rao and Brandeau (2021a)
			Rao and Brandeau (2021a)

a : Average number of individuals in contact with each person per unit of time, b : The possibility of transmitting the disease, $\beta_1(\beta_2)$: Transmission rate for the first (second) outbreaks, σ : Intervention parameter reflecting the force of intervention in the epidemic control, m , c_1 , k , and ms : Influence of temperature on the transmission rate, ξ : The Gaussian white noise with the intensity of $\sqrt{2D}$, which can be understood as the difference of transmission rate among different individuals, γ : Fraction of infectious individuals die, dm : Average duration of a mild infection, ds : Average duration of a severe infection, α : fraction of infections in group i that are severe, ψ : Effect of isolation, β_j : Transmission rate of mild cases, β_i : Transmission rate of severe cases (hospitalized cases), β_i : Transmission rate of critical cases (ICU cases), β_0 : Transmission rate without season effect, k : Season effect, $\tilde{\beta}$: Risk of infection from the detected and infected symptomatic patients not yet effectively isolated, I_X : Undetected Infected, I_H : Hospitalized infected, I_R : Infected that recover on their own, κ : A proportion of infected people are asymptomatic, b_{jt} : Intensity of the lockdown imposed to age class j , α_{ij} : Interactions between age classes i and j , β : Contagion index, $\tilde{\beta}$: Daily contagion rate of confined persons, β : Daily contagion rate of working persons, β_i : Transmission coefficient for the i th strain class, η_i : Efficiency of the vaccine against strains from the i th class

ment policies—like school closures and travel restrictions—affecting transmission risks (Dings et al., 2024). As the severity of the outbreak escalates, individuals may adopt more rigorous social distancing practices. Therefore, evaluating optimal personal strategies requires considering key state variables such as vaccination rates and levels of social distancing (Choi & Shim, 2020). This enables the identification of the most effective blend of medical and non-medical measures for controlling the epidemic.

Human behavior is pivotal in efforts to curb COVID-19 transmission, as the success of mitigation strategies largely depends on public compliance with non-pharmaceutical interventions (NPIs) and vaccine acceptance (Molla et al., 2023). In low-resource settings, particularly rural areas in developing countries, the shortage of medical infrastructure poses a major challenge. Allocating limited healthcare resources efficiently is essential for meaningful control of disease spread (Deng et al., 2021). For instance, Holleran (2024) used simulation models based on COVID-19 transmission dynamics to evaluate different vaccine donation policies. The results suggest that vaccine sharing between countries is not a zero-sum game—donor nations can derive local health benefits while fulfilling a moral imperative.

Therefore, in pursuit of effective epidemic control, it is vital to go beyond epidemic modeling alone. Since multiple variables influence disease transmission and intervention efficacy, some studies advocate for integrating epidemic models with optimization frameworks. This combined approach offers a more robust strategy for designing and evaluating epidemic response measures, as further discussed below.

6.1 Game theory

Game theory is one approach to this problem, applied in different areas of epidemic control. Kabir and Tanimoto (2020) developed an epidemic model integrated with evolutionary game theory to assess the cost-efficiency of voluntary vaccination programs for multi-serotype diseases influenced by antibody-dependent enhancement (ADE), highlighting the superiority of primary vaccination while emphasizing the critical role of a high-efficacy secondary vaccine during cyclical outbreaks. Choi and Shim (2020) presented a game-theoretic epidemiological model evaluating individual decision-making regarding vaccination and social distancing, especially when both interventions incur costs. Under the assumption that individuals act to maximize personal payoffs, the model identified Nash equilibrium strategies when both or only one intervention is available. It also determined cost thresholds at which individuals shift preferences between vaccination and social distancing, highlighting how relative costs shape behavioral responses during epidemics. Jing et al. (2023) developed a hybrid epidemiological-game theoretic model to investigate how individual vaccination behavior influences the emergence of vaccine-resistant SARS-CoV-2 variants. Simulations revealed that reducing vaccine hesitancy—by lowering perceived vaccination costs and raising perceived infection risks—significantly decreased the likelihood of mutant strain establishment. Conversely, high vaccine hesitancy increased both wild-type cases and the risk of variant emergence. The study also demonstrated that rapid vaccination, when combined with non-pharmaceutical interventions, was the most effective strategy for preventing new variants, highlighting the importance of integrating behavioral policy tools with epidemic control measures. Marca et al. (2024) developed a two-timescale epidemic model by coupling a classical SIR framework with an evolutionary vaccination game, where

individual decisions to adopt pro-vaccine behavior depended on disease incidence. Recognizing that opinion shifts may occur faster than epidemic spread, the model incorporated Geometrical Singular Perturbation Theory (GSPT) to analyze rapid behavioral dynamics. The authors demonstrated that GSPT offered more realistic insight than the Quasi-Steady-State Approximation (QSSA), especially for medium-to-large strategy-switching rates, and revealed critical features of the system near repelling branches of the critical manifold.

Marca and Menale (2024) modeled voluntary vaccination behavior in a population exposed to a preventable infectious disease by integrating imitation game dynamics with opinion flexibility—defined as the tendency to change vaccination attitudes. Using a Susceptible–Infected–Removed (SIR) framework and kinetic theory across multiple scales, the authors demonstrated through simulations that opinion flexibility significantly influenced individual transitions between pro- and anti-vaccine groups during an epidemic. Vilota Miranda & Rodríguez Ibeas (2024) analyzed individual vaccination decisions using a game-theoretic model coupled with an SIR epidemiological framework and found that the equilibrium vaccination rate fell below the herd immunity threshold due to uninternalized externalities. It evaluated three public policy instruments—informational campaigns, monetary incentives, and penalties for non-vaccination—and concluded that monetary incentives were necessary to achieve herd immunity when used alone. When multiple policies were allowed, the optimal strategy involved effective informational campaigns alone or combined with monetary rewards, while coercive measures such as vaccine passports were deemed suboptimal. Table 9 shows summarize of related article to game theory.

6.2 Machine learning (ML) and evolutionary algorithms

Evolutionary algorithms and machine learning approaches are increasingly utilized to enhance epidemic modeling and intervention planning. For example, Alkhamis and Hosny (2022) implemented the Controlled Elitism Non-Dominated Sorting Genetic Algorithm (CENSGA) to evaluate impulsive vaccination strategies. Haq et al. (2022) explored the predictive power of machine learning techniques in comparison to traditional SIR models for forecasting pandemic trajectories and informing intervention strategies. Wang et al. (2022) proposed the T-SIRGAN framework, which synergizes epidemiological modeling with deep learning to capture intricate epidemic dynamics, thereby improving the accuracy of COVID-19 growth predictions. Mishra et al. (2024) emphasized short-term forecasting of cumulative infection and mortality figures using advanced multivariate time series techniques, including an extended SEIR model, long short-term memory (LSTM) networks, and vector autoregression (VAR). Details of the studies employing machine learning to optimize epidemic models are summarized in Table 10.

6.3 Optimal control and OR modeling

Accurate estimation of model parameters is a fundamental component of optimal control methodologies, including model predictive control. Nonetheless, the inherent complexities of non-linear systems pose significant challenges to the development of reliable state estimators (Isidori, 1995). To address these challenges, integrating compartmental epidemiological models with optimal control problems (OCs) provides a robust framework for dynamic optimization (Castilho, 2006), with the potential to achieve endemic equilibrium in

Table 9 Integration of epidemic model to game theory

References	Problem/focus	Disease	Region	Key insights
Kabir and Tanimoto (2020)	Cost-efficiency of voluntary vaccination	N-serovar diseases	Japan	Voluntary vaccination influenced by cost- infection risk tradeoff; modeling reinforcement by antibody effects
Choi and Shim (2020)	Optimization of vaccination and social distancing	COVID-19	South Korea	Joint vaccination and distancing strategies reduce disease burden effectively
Jing et al. (2023)	Vaccine hesitancy and new variants emergence	COVID-19	China	Managing opposition crucial to prevent variant emergence; balancing varied interventions needed
Marca and Menale (2024)	Impact of opinion flexibility on vaccine choices	COVID-19	Italy	Public opinion flexibility significantly affects vaccination decisions during epidemics
Marca et al. (2024)	switching from vaccine refusal to vaccine acceptance	COVID-19	Italy	Switching dynamics influence long-term vaccination equilibria and strategy stability
Villota Miranda and Rodríguez Ibeas (2024)	Economics of vaccination: policies and incentives	COVID-19	–	Economic incentives and public policy directly impact individual vaccination decisions

Table 10 Integration of epidemic model to ML and evolutionary algorithms

Reference	Problem/focus	Epidemiological model/techniques	Disease	Key findings
Alkhamis and Hosny (2022)	Pulse influenza vaccination policy synthesis	SIR model+ Genetic Algorithm	Influenza	CENSGA effectively synthesizes vaccination policies to reduce epidemic impact
Haq et al. (2022)	COVID-19 prediction in Bangladesh	SIR model and ML techniques	COVID-19	Combined SIR and ML improves forecasting accuracy for intervention planning
Wang et al. (2022)	Epidemic trend forecasting	SIR + Deep Learning (GAN)	COVID-19	T-SIRGAN outperforms traditional models in forecasting COVID-19 growth
Mishra et al. (2024)	Short-term multi-variate time series forecasting	Extended SEIR + ML (LSTM, VAR)	COVID-19	Advanced ML models enhance short-term forecasting accuracy of COVID-19 cases and deaths

the context of diseases such as COVID-19 (Gaff & Schaefer, 2009). Despite their potential, the technical complexity of implementing such models has hindered their widespread adoption (Vahdani et al., 2023).

Hwang et al. (2020) proposed an OCP aimed at minimizing infection rates and vaccination costs, introducing a feedback control mechanism based on the Hamilton–Jacobi–Bellman (HJB) equation. To approximate the HJB solution, the authors applied a viscosity solution approach, supported by a successive approximation method and the upwind finite difference scheme. Their numerical simulations revealed that feedback control could dynamically guide vaccination strategies based on real-time variations in susceptible and infected populations, enabling swift adjustments to epidemic progression.

Several studies have employed linear and non-linear programming techniques in epidemic control. For instance, Loertscher and Muir (2021) incorporated dynamically evolving lockdown strategies, considering healthcare capacity constraints to identify optimal inter-

vention policies. Similarly, López et al. (2022) applied non-linear programming to fit epidemiological models and determine minimum estimates for constrained non-linear functions.

In the domain of vaccine allocation, many approaches leverage epidemiological models to assess disease status—specifically the proportions of susceptible, infected, and recovered individuals. Vahdani et al. (2023) developed a dynamic model within an optimal control framework to address multi-vaccine, multi-depot location-inventory-routing problems, facilitating local equilibrium through demand estimation. Erdoğan et al. (2024) introduced an equitable and efficient vaccine distribution model, spanning multiple population centers and time periods during a pandemic. Other works, including those by Jarumaneeroj et al. (2022) and Hazard-Valdés and Montero (2023), incorporate epidemiological data—such as vaccine demand projections—as operational constraints within mathematical programming models.

Governments worldwide have implemented vaccination campaigns and policy restrictions based on individuals' vaccination status to control disease transmission. Maintaining a stable vaccine supply under fluctuating demand—amplified by seasonal patterns and virus mutations—remains a significant challenge due to variability in vaccine efficacy (Kim et al., 2024). Gomes et al. (2023) introduced a comprehensive two-stage framework for optimizing vaccine supply chain strategies. The first stage utilizes Mixed Integer Programming (MIP) to enhance distribution networks across various disruption scenarios, promoting rapid rollouts and reducing morbidity and mortality. The second stage couples system dynamics simulation with the SEIR model to evaluate the broader public health impact of vaccination initiatives.

Lastly, Federico et al. (2024) explored an optimal vaccination policy within a SIR model framework that allows reinfection. Their work focused on minimizing the number of susceptible individuals while balancing social and economic costs, thereby supporting evidence-based decision-making by public health planners. Table 11 provides examples of papers that apply OR modelling and optimal control.

7 Epidemiological models in the supply chains

The global health crises caused by pandemics, such as COVID-19, have profoundly disrupted supply chains worldwide, exacerbating issues like hoarding and panic buying, which have intensified downstream bottlenecks. The imposition of travel restrictions and lockdowns has further skewed supply and demand balances, making short-term forecasting essential for effective management and informed policy-making decisions (Nikolopoulos et al., 2021).

The COVID-19 pandemic has redefined the concept of resilient supply chains, revealing vulnerabilities that led to sharp declines in productivity and a significant contraction in global GDP (Harris, 2020). The disruptions to labor markets were severe, with estimates suggesting that labor demand decreased by 16.24% due to the combined effects of travel and trade restrictions, along with widespread workplace closures (Baveja et al., 2020; Castro et al., 2020; Nikolopoulos et al., 2021). These economic shocks underscore the need for supply chains to incorporate adaptive strategies that address both short-term disruptions and long-term resilience, ensuring continuity and stability in the face of future global crises. In this context, future research should focus on enhancing predictive models for supply chain

resilience, particularly those that integrate real-time data with adaptive planning methodologies, to mitigate the risks posed by global pandemics and other large-scale disruptions.

Araz et al. (2020) identified COVID-19 as one of the most significant global supply chain disruptions in the last decade, prompting extensive research into the pandemic's far-reaching effects. Numerous studies have simulated the pandemic's impact on supply chains (Ivanov, 2020), assessed the stress placed on healthcare systems (Team & Murray, 2020a), and analyzed disruptions in food supply chains (Hobbs, 2020). Solutions proposed include increasing critical product stockpiles (Team & Murray, 2020b) and optimizing healthcare supply management through Fuzzy Inference Systems (FIS) (Govindan et al., 2020), highlighting the need for adaptable strategies during crises.

Epidemiological models, especially the widely-used SIR model, are proving useful not only for understanding disease transmission but also for evaluating and predicting risks to supply chains (Liang et al., 2022; Yu et al., 2022a, b; Chen & Yin, 2023). These models shift the focus from infection rates to risk transmission, applying similar methodologies to assess vulnerabilities in supply chain networks. Optimal control methods are increasingly being used to model the interplay between epidemic dynamics and supply chain processes. This enables production managers to balance operational costs and fluctuating demand (Brusset et al., 2022a), analyze the ripple effects of disruptions on supplier production capacities (Brusset et al., 2022b), and take proactive measures to mitigate these effects over time (Brusset et al., 2023b).

The discussion that follows will delve into the application of epidemiological models to forecast disease trends and vaccine demand, illustrating how these models can inform and enhance supply chain resilience during pandemics. This integration of epidemiology and supply chain management underscores the evolving need for interdisciplinary approaches to crisis management in a globalized world.

7.1 Vaccine supply chain

Azam et al. (2021) proposed a comprehensive modeling framework that integrates a vaccine supply chain model with an SEIR epidemiological model to evaluate critical factors in vaccination campaigns. Their model assesses the preparation time needed to launch campaigns, the level of vaccine coverage achieved, and the dynamics of outbreaks that occur simultaneously. This integration enables more precise planning and management of vaccine distribution during pandemics. Similarly, Vahdani et al. (2023) developed an innovative model to tackle the multi-vaccine, multi-depot location-inventory-routing problem. By incorporating an epidemiological model, their approach dynamically assesses vaccine demand across different locations, optimizing both logistics and healthcare responses.

Enayati and Ozaltin (2020) focused on influenza, using a compartmental transmission model to design a mathematical program to minimize the number of vaccine doses required to contain outbreaks at early stages. Their work highlights the importance of timely interventions and efficient resource allocation in the face of emerging health crises. Building on this, Gomes et al. (2023) proposed a two-stage method for optimizing vaccine distribution networks using a combination of Mixed Integer Programming (MIP) and an SEIR model. Their approach supports agile and lean supply chain operations, optimizing the distribution network while evaluating vaccination's impact on public health.

Table 11 Details of optimization in compartmental models

Study	Problem	Optimization model		Context		
		Objective	Technique	Decisions/optimal variable	Key constraints	Solution approach
Hwang et al. (2020)	Vaccination strategy optimization	Minimize the number of infected people, number of administered vaccines, and vaccination cost	Optimal control	Vaccination rate	Epidemiological constraints	Viscosity Solution
						SIR
Rao and Brandeau (2021a)	Vaccine allocation	Minimize new infections, deaths, or life years lost, or quality-adjusted life years lost due to death	Linear programming	Proportion of the vaccinated population	Limited supply of vaccine, proportion of eligible people, equity	Exhaustive search
						SIRD
Jarumneeroj et al. (2022)	Vaccine allocation	Minimize total weighted strain on the whole healthcare systems	Nonlinear programming	Vaccine doses, remaining doses of vaccine, and the number of vaccinated, susceptible, infected, recovered, and deceased individuals	Flow balancing, vaccine administration capacity, Equity, allowed number of vaccinations, odes	Proposed iterative approach by Lsq- <i>IntGen</i>
						SIQRV
						COVID-19
						COVID-19
						Thailand
						Early vaccination to reduce the number of infectious individuals

7.2 Other supply chains

Gutierrez et al. (2021) developed a comprehensive framework for designing and optimizing an end-to-end antibody strategy to address clinical needs during the COVID-19 pandemic and prepare for future health crises. Their approach integrates multiple aspects, including product design, epidemiology, demand forecasting, and supply chain optimization, providing a holistic solution for meeting critical healthcare demands. In a similar vein, Nikolopoulos et al. (2021) presented predictive analytics tools that forecast pandemic growth rates and product demand surges. By utilizing statistical, epidemiological, and machine learning models, they developed a hybrid forecasting method capable of anticipating both COVID-19 trends and excess demand for essential products, improving response times and resource planning.

Sharif et al. (2022) extended the traditional SEIR model by incorporating four sub-models that simulate the effects of non-pharmaceutical interventions (NPIs), such as social distancing and lockdowns, on disease spread and healthcare system demand. Their enhanced model offers more detailed predictions of how NPIs can mitigate disease transmission while addressing sudden healthcare demand surges. Meanwhile, Brusset et al. (2023a) proposed a dynamic framework that integrates an optimal control model with supply chain reconfiguration strategies, allowing for the analysis of ripple effects caused by pandemics. By coupling epidemic dynamics with supply chain management, this approach enables decision-makers to adapt swiftly to disruptions, optimize resource allocation, and mitigate risks in real-time.

These studies underscore the critical role of integrating epidemiological models with advanced supply chain optimization techniques, particularly during vaccine distribution efforts. By integrating disease dynamics, forecasting methods, and supply chain logistics/management, these models offer more effective and resilient strategies for resource allocation and public health interventions during pandemics.

8 Discussion

This study reviews epidemiological modeling by analyzing its components, assumptions, variables, uncertainties, parameters, and optimization techniques. It offers theoretical and practical insights across various sections, including compartments, population factors, epidemiological assumptions, intervention factors, and optimization methods.

8.1 Compartments

Theoretical Insights: The SIR model is widely recognized for its simplicity and efficacy in modeling the spread of infectious diseases through differential equations. This model segments the population into key compartments – Susceptible (S), Infected (I), and Recovered (R)—which evolve dynamically as the epidemic progresses. An extension of this model, the SEIR model, incorporates an additional Exposed (E) compartment to account for the disease's incubation period. However, this model often shows limitations in alignment with confirmed case data, as noted by Nakamura et al. (2021).

Further extensions of these models, which may include compartments for vaccinated, quarantined, or asymptomatic individuals, provide enhanced granularity and improve pre-

dictive accuracy based on the epidemic's stage and nature. These models allow for a more nuanced understanding of the disease dynamics and the various factors influencing its spread.

Practical Insights: The integration of extended models significantly improves the capacity for real-time intervention by facilitating the tracking of additional population groups, such as vaccinated individuals and those under quarantine. Public health measures, including vaccination campaigns, actively reduce the susceptible population, while fluctuations in hospitalizations directly impact the infected group. Models incorporating these intervention strategies yield more reliable predictions of disease dynamics and control outcomes.

Future research should prioritize integrating demographic factors such as birth and death rates into these models. This approach will enable a more comprehensive understanding of the long-term effects of diseases like COVID-19, which are frequently overlooked in short-term analyses. By doing so, we can better inform public health policies and interventions to manage infectious diseases over extended periods.

8.2 Population factors

Theoretical Insights: Population dynamics, including birth and death rates, are critical in shaping epidemic models. Many basic models operate under the assumption of homogeneity, which significantly oversimplifies the complexities of real-world scenarios. Individuals exhibit diverse susceptibility to infectious diseases based on various factors, including age, occupation, and pre-existing health conditions (Pomar et al., 2022; Rose et al., 2022). This variability necessitates a more nuanced approach to modeling epidemic dynamics.

Practical Insights: In practice, it is essential for models to incorporate subgroups that reflect differences in susceptibility due to age, occupation, and health status. For instance, healthcare workers and individuals with chronic conditions are at a higher risk of severe disease outcomes, and this heightened risk must be accurately represented in model predictions. By adjusting for these subgroups, along with accounting for migration patterns between regions, researchers can enhance the precision of disease spread estimates and the effectiveness of intervention strategies.

Future research should delve deeper into the implications of population heterogeneity, particularly regarding its impact on vaccine demand and the formulation of targeted intervention strategies. Understanding these dynamics will be instrumental in developing more effective public health responses to epidemic outbreaks.

8.3 Model assumptions

Theoretical Insights: Assumptions related to population dynamics, such as homogeneous mixing and fixed population characteristics, can lead to significant inaccuracies in epidemic models. Many existing models fail to account for factors such as individual mobility and the implementation of quarantine measures, which can distort predictive outcomes (Alanazi et al., 2020; Anderson & May, 1979). By neglecting these dynamics, models may not accurately reflect the complexities of disease transmission within populations.

Practical Insights: To enhance the accuracy of epidemic models, it is crucial to adapt assumptions to better mirror real-world conditions, particularly concerning mobility patterns and occupation-based risks. For diseases like COVID-19, incorporating factors such

as occupational exposure and the effects of quarantine measures can lead to more realistic and reliable predictions. Future modeling efforts should aim to refine these assumptions, ensuring they adequately account for the impact of migration patterns on vaccine demand and the overall effectiveness of interventions. This approach will provide a more comprehensive understanding of disease dynamics, ultimately guiding more effective public health responses.

8.4 Epidemiological factors

Theoretical Insights: Immunity—temporary or permanent—is fundamental in epidemiological modeling. Models must accurately represent immunity conditions and the potential for re-infection. Some existing models simplify this complexity by allowing direct transitions from recovered to susceptible compartments or from vaccinated to infected individuals due to vaccine failure. This oversimplification may hinder the models' ability to reflect disease transmission and control dynamics.

Practical Insights: In real-world applications, it is imperative to account for the dynamics of immunity, including the waning of immune responses and the potential for re-infection. Accurate modeling of these factors is essential for effectively planning booster vaccination campaigns and anticipating future outbreaks. Future research should explore how immunity variations influence epidemic trajectories and intervention strategies. This includes considering factors such as secondary infections, the duration of vaccine effectiveness, and the implications of differing immune responses across populations. By addressing these aspects, public health efforts can be better informed and more adaptive to evolving epidemic scenarios.

8.5 Intervention factors

Theoretical Insights: Interventions, including vaccination, hospitalization, and social distancing, are crucial in shaping epidemic dynamics. These interventions can be integrated into transmission rate equations or represented as separate compartments within epidemiological models. By incorporating these elements, models can more accurately reflect the complex interactions between disease spread and public health measures.

Practical Insights: Implementing effective intervention strategies necessitates access to real-time data to dynamically adjust models and refine public health strategies. Key factors, such as vaccine coverage rates and the timeliness of interventions like quarantine or hospitalization, significantly influence the outcomes of epidemics. Future research should focus on developing methodologies for integrating various types of interventions into models while addressing the uncertainties associated with their effectiveness. This includes examining the roles of tracing, screening, and the potential for secondary infections in influencing disease transmission. By enhancing our understanding of these dynamics, we can improve the efficacy of public health responses to future epidemics.

8.6 Parameter uncertainty

Theoretical Insights: Parameter uncertainty represents a critical challenge in the dynamic modeling of epidemics. Accurate estimation of essential parameters, such as transmission

and recovery rates, is fundamental for reliably predicting epidemic outcomes. Techniques like inverse modeling and optimization algorithms play a vital role in refining these estimates, thereby enhancing the overall robustness of the model.

Practical Insights: In practical applications, forecasting epidemic trends can be complicated by parameter uncertainties. Continuous model calibration and precise estimation of parameters—including transmission rates and vaccine efficacy—are essential for effective resource allocation and timely public health interventions. By actively addressing parameter uncertainty and integrating real-world data into the modeling process, researchers can significantly enhance the validity of models and improve the accuracy of predictions, ultimately leading to more effective epidemic management strategies.

8.7 Optimization and simulation techniques

Theoretical Insights: Optimal control theory introduces control variables into epidemic models, facilitating the identification of the most effective strategies for disease management. Integrating advanced methodologies, such as game theory, evolutionary algorithms, and machine learning techniques—exemplified by models like T-SIRGAN—can significantly enhance prediction accuracy by effectively capturing the complexities of epidemic dynamics.

Practical Insights: Optimization is crucial in resource allocation and public health planning, particularly in regions with constrained resources. By integrating OR models with traditional SIR frameworks, it is possible to optimize intervention strategies to minimize infection rates and associated costs. Future research should prioritize refining optimization techniques while incorporating assumptions related to multiple regions and population movement, enabling real-time decision-making in response to evolving epidemic scenarios.

8.8 Epidemiological model in supply chains

Theoretical Insights: The COVID-19 pandemic has underscored the critical need for reevaluating supply chain resilience, exposing key vulnerabilities and complex interdependencies in global logistics. Epidemiological models, particularly the SIR framework, present a novel approach to predicting and managing risks within supply chains, offering a connection between health crises and supply dynamics. By integrating public health data with supply chain logistics, predictive analytics, and optimal control methods, these models enhance the accuracy of forecasts and facilitate more effective, proactive responses to future disruptions. This interdisciplinary approach strengthens the ability to anticipate supply chain disruptions triggered by pandemics or other health-related crises.

Practical Insights: Travel restrictions, lockdowns, and other pandemic-related measures have severely impacted labor demand and productivity, highlighting the need for strategic workforce management and supply chain adaptability. The crisis has accelerated the demand for robust short-term forecasting and agile response systems to support more effective management and policy-making in real-time. Models that integrate vaccine supply chains with epidemiological models, such as SEIR, have proven essential for managing healthcare demand surges. These models emphasize the need for coordinated logistics and flexibility, demonstrating how agile strategies can support the rapid distribution of vaccines and essential goods during a pandemic. The lessons learned during the COVID-19 crisis

underscore the importance of integrating health data with supply chain management to better prepare for future global health emergencies.

9 Conclusion

This review provides a thorough examination of the intersection between compartmental epidemic models and operations research optimization techniques, demonstrating their combined potential to enhance epidemic control strategies and improve supply chain resilience in the face of uncertainty. By systematically reviewing recent literature—particularly the surge of studies following the COVID-19 pandemic—this paper synthesizes foundational modeling approaches with modern optimization frameworks, showing how these methods work together to improve decision-making during public health emergencies.

Compartmental models, such as the classic SIR model and its expanded variants, remain essential for modeling infectious disease transmission and guiding intervention strategies. However, the integration of OR methods adds a vital layer of optimization, enabling more precise allocation of resources, better scheduling of interventions, and the balancing of competing priorities under various constraints. This review emphasizes how optimization techniques enhance the reliability of epidemic models, particularly in managing uncertainties related to epidemiological parameters, intervention effectiveness, and changing human behaviors.

A key aspect of this review is the growing role of epidemiological modeling within the field of supply chain management—an area significantly impacted during pandemics. The combination of disease dynamics and supply chain optimization allows for better management of disruptions, enabling more flexible and responsive resource distribution and logistics planning. These capabilities are crucial for maintaining healthcare capacity and ensuring the availability of essential goods during crises.

Despite these advancements, there are still notable research gaps that need to be addressed. Future works should focus on refining model details to account for different population structures, integrating variations over time and space, and utilizing real-time data to implement adaptive intervention strategies. Additionally, there is a clear need for scalable, computationally efficient optimization algorithms capable of managing the complexity of connected epidemic and supply chain systems.

In conclusion, this review underscores the importance of interdisciplinary collaboration between epidemiologists, operations researchers, and public health professionals. By advancing integrated epidemic-OR frameworks, the research community can provide policymakers with more effective decision-support tools, ultimately improving preparedness, response efficiency, and resilience in the face of future infectious disease outbreaks.

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Declarations

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

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