Medicon Medical Sciences
Volume 9 Issue 4 October 2025
Article Type: Review Article
ISSN: 2972-2721

A Scoping Review (To 31 August 2025) of Compartmental Epidemic Models for H1N1 and H3N2 Seasonal Influenza

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Received: September 06, 2025; **Published:** September 30, 2025

DOI: 10.55162/MCMS.09.317

Abstract

H1N1 and H3N2 Influenza remains a persistent threat to global health, with annual seasonal outbreaks causing a sizeable number to be severely ill and dead. To address this public health issue, mathematical modelling, particularly epidemic compartmental models are used to understand disease dynamics and guide public health policy. However, there are no systematic review to-date examining the epidemiological models for H1N1 and H3N2. Hence, this study is a scoping review of epidemic compartmental models of H1N1 and H3N2 seasonal influenza strains, using studies indexed in PubMed to 31 August 2025, inclusive. Of the 370 studies obtained, 81 studies are included and analysed to identify and characterize common trends in viral strains, methodological approach, thematic applications, and structural complexity. The results show the focus on the H1N1 viral strain (83.9% of studies), which reflects the impact of the 2009 H1N1 pandemic to the global and scientific community. Simultaneously, 13.6% of research studies is focused on both H1N1 and H3N2 strains, indicating an interest towards understanding complex multi-strain interactions. From a methodological perspective, Ordinary Differential Equations (ODEs) continue to be the leading framework (80.3%), due to their ability to provide clear evaluation of population-level trends and effectiveness of interventions. However, the deliberate use of Stochastic Differential Equations (SDEs) and other models demonstrates a versatile approach to include uncertainty and subtle dynamics. Thematic analysis reveals a dual emphasis in the research field: a sizeable portion of studies is centred on Intervention and Policy Assessment (37.0%), whereas another key theme is Core Epidemiological Dynamics (33.3%), highlighting the need to translate theoretical knowledge into practical policy. Additionally, increased model complexity (i.e., more compartments) is directly correlated to detailed, policy-focused insights. The overall trend shows a shift from generic theoretical frameworks to advanced, "fit-for-purpose" methodologies that deliver prompt and reliable insights to support public health policies.

Introduction

Every year, seasonal influenza outbreaks affect people all over the world, resulting in it being a widespread and persistent public health concern. Although frequently thought of as a common illness, the annual burden of seasonal influenza is extremely significant, with an estimated one billion cases worldwide, up to five million cases of severe illness, and approximately 290000 to 650000 influenza-related respiratory deaths each year [1]; highlighting the ongoing threat of influenza, which disproportionately impacts susceptible populations like young children, the elderly and people with chronic medical conditions (see https://www.cdc.gov/flu/about/

viruses-types.html). The influenza A virus and these two subtypes are the main causes of seasonal epidemics worldwide that are circulating among the human population [2]. The 2009 H1N1 pandemic led to a surge in research and an ongoing effort to understand its viral epidemiology and dynamics [3], while the H3N2 virus exists as a co-circulating strain, bringing about its own set of unique epidemiological challenges.

One of the key tools that public health officials use when trying to control and mitigate the effects of infectious disease, is to use mathematical modelling, particularly with compartmental frameworks. Compartmental models are the basic standard of quantitative epidemiology to track an individual's movement between distinct health states; such as, Susceptible (S), Infectious (I), Recovered (R) in the SIR model, to simulate disease progression [4]. Such modelling techniques provide an organized and user-friendly method to represent complex population dynamics, so as to understand the mechanics of disease spread, predict epidemic trajectories, and evaluate the possible effects of public health interventions [5, 6]. The development and use of these models offer a scientific justification for policy choices, which ranges from planning for the demands of healthcare resources during a pandemic to optimizing vaccination strategies [7-9].

However, there has not been a systematic review to-date to consolidate compartment-based epidemiological models for H1N1 and H3N2. Therefore, this study presents a scoping review on compartmental epidemic models for H1N1 and H3N2 viral strains.

Methods

This study follows the Preferred Reporting Items for Systematic Review and Meta-Analyses Extension for Scoping Reviews (PRISMA-ScR) guidelines and checklist [10]. A scoping review methodology was employed due to the broad spectrum of modelling techniques applicable to this research area. This approach enables the swift identification and mapping of the core conceptual framework and identification of the principal sources and types of available evidence [11].

Search Strategy

PubMed searches for relevant literature were conducted on February 26, 2025, with final updates performed on September 01, 2025. The search methodology employed a Boolean combination of terms representing influenza strains and modelling approaches. Specifically, the query combined keywords such as 'H1N1' and 'H3N2' with terms like 'mathematics', 'epidemic', 'epidemiology', 'transmission', and 'model'. The exact search syntax, applied universally across all fields, was (H1N1 OR H3N2) AND ("math* model*" OR "transmi* model*" OR "epidemi* model*"), resulting in the following search URL: https://pubmed.ncbi.nlm.nih.gov/?term=(h1n1[All+Fields]+OR+h3n2[All+fields])+AND+("math*+model*"[All+Fields]+OR+"transmi*+model*"[All+Fields]+OR+"epidemi*+model*"[All+Fields])&filter=dates.1000/1/1-2025/8/31. The use of Boolean operators enhanced the accuracy of search results, thereby ensuring all relevant studies were included [12].

Exclusion Criteria

Studies were excluded if they involved non-human subjects or genome studies, did not specifically investigate H1N1 or H3N2 viral strains, or lacked mathematical modelling. For example, studies that referred to animals used as biological 'models' for human influenza, where the 'model' referred to the animal species itself, were excluded as this differs from the mathematical definition of 'model' (i.e., a system described using mathematical concepts) [13, 14]. Studies that were based on other types of models, e.g. agent-based model, statistical model, stochastic models, were excluded, as well as transmission models that were not specifically epidemic models.

Results and Discussion

The search returned 370 studies. Following which, only 357 English full-text articles were found, with six duplicates removed. Full-text analysis was conducted and only 81 articles met the selection criteria and were included for analysis, as shown in Figure 1. In-depth analysis of 81 papers was conducted, and model characteristics of the papers were tabulated in Table 1.

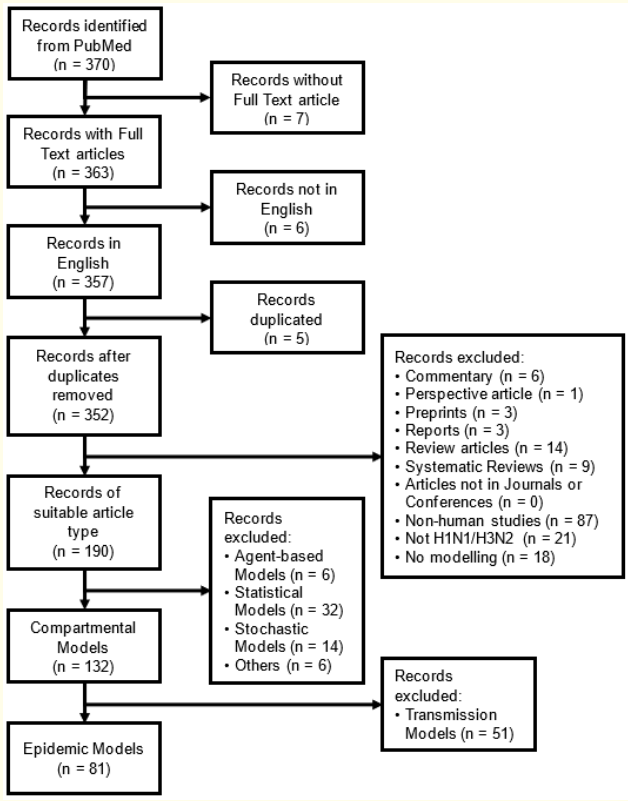

Figure 1: PRISMA diagram of study selection processes.

Model Theme 1 (T1) is Modelling Methodologies & Data Utilization. Model Theme 2 (T2) is Core Epidemiological Dynamics. Model Theme (T3) is Contextual & Influencing Factors. Model Theme (T4) is Intervention & Policy Assessment. Model Sub-Theme 1 (S1) is Model Construction & Parameterization. Model Sub-Theme 2 (S2) is Spatiotemporal & Predictive Modelling. Model Sub-Theme 3 (S3) is Transmission Dynamics & Progression. Model Sub-Theme 4 (S4) is Disease Characteristics & Biology. Model Sub-Theme 5 (S5) is External & Environmental Factors. Model Sub-Theme 6 (S6) is Human & Social Context. Model Sub-Theme 7 (S7) is Impact & Evaluation. Model Sub-Theme 8 (S8) is Intervention Strategies. Model Sub-Theme 9 (S9) is Parameter Estimation and Model Calibration. Model Sub-Theme 10 (S10) is Pattern Recognition and Algorithmic Modelling. Model Sub-Theme 11 (S11) is Forecasting and Real-Time Monitoring. Model Sub-Theme 12 (S12) is Spatiotemporal and Environmental Modelling. Model Sub-Theme 13 (S13) is Epidemic Wave Dynamics. Model Sub-Theme 14 (S14) is Transmission Dynamics and Epidemic Spread. Model Sub-Theme 15 (S15) is Evolution, Immunity, and Cross-Strain Dynamics. Model Sub-Theme 16 (S16) is Comparative Infectivity and Fatality. Model Sub-Theme 17 (S17) is Environmental and Ecological Impact. Model Sub-Theme 18 (S18) is Behavioural and Social Dynamics. Model Sub-Theme 19 (S19) is Economic and Policy Evaluation. Model Sub-Theme 20 (S20) is Healthcare Resource Planning. Model Sub-Theme 21 (S21) is Vaccination Strategy and Impact. Model Sub-Theme 22 (S22) is Drug Resistance and Strategic Interaction.

Study	*Strain*	*Type of DE*	*No. of Compartments*	*Model Theme*	*Model Sub-Theme*
[3]	H1N1	SDE	3	T1	S1, S9
[15]	H1N1	ODE	3 x (age group)	T1	S1, S9
[16]	H1N1	ODE	SIR : 3 SEIR : 4	T1	S1, S9
[17]	H1N1	SDE	4	T1	S1, S9, S10
[18]	H1N1	SDE	4	T1	S2, S11
[19]	H1N1	ODE	4	T1	S2, S12
[20]	H1N1	ODE	12 x (age group)	T1	S2, S11
[21]	H1N1	ODE	3	T1	S2, S11
[22]	Both	ODE	3	T1	S2, S11
[23]	Both	SDE	4	T1	S2, S12
[24]	H3N2	ODE	4 x (region in country)	T1	S2, S12
[25]	Both	ODE	5	T1	S2, S11
[26]	H1N1	ODE	4	T1	S2, S11
[27]	H1N1	ODE	5 x (age group)	T1	S2, S11
[28]	H1N1	Others (DE)	3	T1	S2, S11
[29]	H1N1	ODE	4 x (city)	T1, T2	S2, S3, S12, S13
[30]	H1N1	SDE	3 x (age group)	T2	S3, S14
[31]	H1N1	ODE	5 x (groups within population)	T2	S3, S13
[32]	H1N1	SDE	3 x (age group)	T2	S3, S14
[33]	H1N1	ODE	5 x (traveller's originating country)	T2	S3, S14
[34]	H1N1	ODE	5	T2	S3, S14
[35]	H1N1	ODE	4	T2	S3, S14
[36]	H1N1	SDE	6 x (mobility flows) x (distinct census areas)	T2	S3, S14
[37]	H1N1	ODE	Isolation : 5 Vaccination : 7 Antivirals : 5 School Closure : 4 Combination : 11	T2	S3, S14
[38]	H1N1	ODE	6	T2	S3, S14
[39]	H1N1	ODE	First Wave : 12 Second Wave : 10	T2	S3, S14
[40]	H1N1	ODE	3	T2	S3, S14
[41]	H1N1	ODE	4	T2	S3, S14
[42]	H1N1	ODE	4	T2	S3, S14
[43]	H1N1	ODE	4	T2	S3, S14
[44]	H1N1	ODE	3 x (individual within population)	T2	S3, S14
[45]	H1N1	ODE	4	T2	S3, S14

[46]	H1N1	Others (DDE)	8 x (dummy groups)	T2	S3, S14
[47]	H1N1	ODE	4 4 x (presence of cross immunity)	T2	S4, S15
[48]	Both	ODE	10	T2	S4, S15
[49]	H1N1	ODE	3	T2	S4, S15
[50]	Both	ODE	4	T2	S4, S15
[51]	Both	ODE	44 x (age groups) x (viral strain)	T2	S4, S15
[52]	H1N1	ODE	7	T2	S4, S16
[53]	H3N2	ODE	4 x (transmission route) x (age group)	T2	S4, S15
[54]	H1N1	ODE	7 x (type of prior or acquired immunity) x (immunisation dose)	T2	S4, S15
[55]	H1N1	ODE	3 x (age group) x (antibody titre level)	T2	S4, S15
[56]	H1N1	ODE	18	T3	S5, S17
[57]	H1N1	ODE	4 x (states in country)	T3	S5, S12
[58]	H1N1	Others (DE)	4	T3	S6, S18
[59]	H1N1	ODE	3	T3	S6, S18
[60]	H1N1	ODE	3	T3	S6, S18
[61]	H1N1	ODE	3 x (age group) x (site) x (household)	T3	S6, S18
[62]	H1N1	ODE	3 x (colleges in a campus)	T3	S6, S18
[63]	H1N1	ODE	5 x (cities)	T3	S6, S18
[64]	H1N1	ODE	6	T3	S6, S18
[65]	H1N1	SDE	4	T4	S7, S19
[66]	H1N1	ODE	9	T4	S7, S19
[67]	H1N1	ODE	4	T4	S7, S19
[68]	H1N1	SDE	4 x (age group)	T4	S7, S19
[9]	H1N1	SDE	10 x (travel mode) x (countries)	T4	S7, S20
[69]	H1N1	SDE	5 x (between-city transmission)	T4	S7, S19
[7]	H1N1	ODE	3	T4	S7, S19
[70]	H1N1	ODE	12 x (age group) x (complication risk)	T4	S7, S19
[71]	H1N1	ODE	5 x (age group) x (gender)	T4	S7, S20
[72]	H1N1	ODE	7 x (age group) x (level of pandemic severity)	T4	S7, S20
[73]	H1N1	ODE	17	T4	S7, S19
[74]	H1N1	ODE	12	T4	S7, S20
[75]	Both	ODE	23 x (population from different hemispheres)	T4	S8, S21
[76]	H1N1	ODE	8 x (age group)	T4	S8, S21
[77]	Both	ODE	6 x (age group)	T4	S8, S21
[8]	Both	ODE	22	T4	S8, S21
[78]	H1N1	ODE	7 x (age group) x (district in a country)	T4	S8, S21

[79]	H1N1	SDE	7 x (population of different country)	T4	S8, S22
[80]	H1N1	ODE	9 x (age group)	T4	S8, S21
[81]	H1N1	SDE	M1 : 3 M2 : 3 x (different schools) M3 : 3 x (different schools) x (residential district)	T4	S8, S21
[82]	H1N1	ODE	9 x (age group)	T4	S8, S21
[83]	H1N1	ODE	4 x (age group) x (complication risk)	T4	S8, S21
[84]	H1N1	ODE	5 x (children vs adults) x (risk level) x (vaccination status)	T4	S8, S21
[85]	H1N1	ODE	5 x (age group)	T4	S8, S21
[86]	Both	ODE	8 x (viral strain) x (age group)	T4	S8, S21
[87]	H1N1	ODE	3	T4	S8, S21
[88]	H1N1	ODE	18 x (age group)	T4	S8, S21
[89]	H1N1	ODE	14 x (age group) x (number of weekly contacts)	T4	S8, S21
[90]	H1N1	ODE	3	T4	S8, S21
[91]	Both	ODE	8 x (season)	T4	S8, S21

Table 1: Model characteristics of all included studies.

Distribution of Studies by Viral Strain

The articles were first characterised by the viral strain (H1N1 or H3N2 or both) studied with the model. Among the papers included, 68 articles (83.9%) were based on only H1N1 viral data [3, 15-21, 26-47, 49, 52, 54-66, 68, 9, 69, 7, 70-74, 76, 78-85, 87-90], 2 papers (2.5%) were based on only H3N2 viral data [24, 53], and 11 papers (13.6%) utilised viral data of both H1N1 and H3N2 strains [75, 77, 8, 86, 91, 23, 22, 25, 48, 50, 51] as described in Table 1.

A substantial portion of the studies, 83.9%, focused on the H1N1 viral strain, which is likely a result of the extensive impact of the 2009 H1N1 pandemic on the world, causing a surge in research in virus epidemiology and response measures. Major public health crises, such as pandemics, tend to cause such sudden waves in scientific research and funding directed to the study of the pathogen, resulting in a disproportionate representation in scientific literature, as seen in our results. While the focus on H1N1 research has likely resulted in more mature and varied modelling techniques and methodologies, this also highlights the lack of attention towards other pandemic-relevant strains, such as H3N2, which has only 2.5% of studies solely dedicated to it. Knowledge gaps or lack of variation in modelling approaches for other such strains exist as a result.

Additionally, 13.6% of the studies modelled both H1N1 and H3N2 viral strains, pointing to an interest in understanding multi-strain dynamics within the field. This indicates a shift in influenza modelling from single-epidemic analyses towards more complex models that study the ecological and immunological interactions between different influenza strains over multiple epidemic waves. For instance, some research specifically evaluate the impact of vaccine mismatch between strains during large-scale events like the Hajj pilgrimage [75], or model multiple viral strains to understand the complex relationship between influenza virus characteristics, which include antigenic drift and shift, and the resulting cross-immunity dynamics [47]. This highlights the need for more detailed, ecologically sensitive models to capture the complex dynamics of influenza development and transmission in the real world.

Distribution of Studies by Type of Differential Equation

65 of the 81 articles included were based on ordinary differential equation (ODE) modelling (80.3%) [7, 8, 15, 16, 19-22, 24-27, 29, 31, 33-35, 37-45, 47-57, 59-64, 66, 67, 70-78, 80, 82-91], 13 utilised stochastic differential equation (SDE) models (16.0%) [3, 9, 17, 18, 23, 30, 32, 36, 65, 68, 69, 79, 81], and the remaining papers (3.7%) were classified as others - 2 were difference equation (DE) models [28, 58], and the remaining utilised delayed differential equation (DDE) models [46], as seen in Figure 2.

With 80.3% of studies utilizing ODEs as the primary modelling framework, this shows that ODEs are the preferred mathematical framework in epidemiological modelling. As ODEs are relatively simple, they are especially useful in capturing how populations change over time. This corresponds with compartmental models, which groups people into health states and track their movement between these states. As ODEs simulate continuous shifts in population compartments over time, they can be used to understand the typical course of a disease, such as peak incidence or total cases, or assess the efficacy of interventions. The simplicity and reliability of ODEs makes them a crucial tool in generating insights for resource allocation and strategic planning, in guiding public health policy.

In order to fully understand epidemic dynamics, SDEs were used instead of ODEs, as seen in 16.0% of the studies, which aimed to capture time-varying drivers of an epidemic [18]. SDEs are used when it is important to capture the random fluctuations and variability which naturally occur in real-world epidemics. These are especially crucial during early outbreak phases or in smaller populations [92], where unpredictable fluctuations can have a huge impact on transmission dynamics. With SDEs accounting for a sizeable portion of the studies, this reflects the importance of capturing variability in infectious diseases modelling, to provide more reliable and refined estimates to support risk assessment and develop adaptive public health interventions.

The remaining 3 studies, accounting for 3.7% of the total, fall into the "Others" category, with 2 studies utilizing DEs [28, 58] and 1 study employing DDEs [46]. Thus, researchers are increasingly turning to other frameworks, apart from ODEs, to capture individual-level interactions or extract insights from complex datasets. By strategically using a variety of modelling frameworks that is well-suited to the unique challenges of each study, more complex research problems can be studied, driven by access to extensive data, increased computational power, and the need for more precise models of disease dynamics.

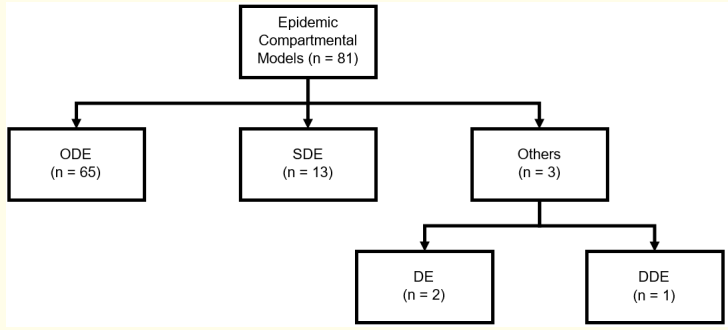

Figure 2: Type of equation used in epidemic compartmental models (Consolidated from Table 1).

Distribution of Studies by Model Themes

As illustrated in Table 1, these studies were classified into 4 major themes: Modelling Methodologies and Data Utilization, Core Epidemiological Dynamics, Contextual and Influencing Factors, and Intervention and Policy Assessment, and shown in Figure 3.

16 papers [3, 15-29] (19.8%) looked into Modelling Methodologies and Data Utilization, with 4 papers exploring "Model Construction and Parameterization" [3, 15-17], and 12 papers exploring "Spatiotemporal and Predictive Modelling" [18-29]. Within "Model Construction and Parameterization", this was broken down into *Parameter Estimation and Model Calibration* (4 papers) [3, 15-17], and *Pattern Recognition and Algorithmic Modelling* (1 paper) [17]. Within "Spatiotemporal and Predictive Modelling", this was broken down into *Forecasting and Real-Time Monitoring* (8 papers) [18, 20-22, 25-28], and *Spatiotemporal and Environmental Modelling* (4 papers) [19, 23, 24, 29]. Studies within this theme focused on improving the accuracy of basic parameters through rigorous estimation and calibration. In doing so, this can generate accurate predictions and real-time insights, which makes frameworks more dependable, adaptable and data-driven to keep up with the challenges of public health. Using this method, researchers can uncover complex relationships in how diseases spread across time and space, and identify environmental factors that influence disease transmission.

27 papers (33.3%) focused on Core Epidemiological Dynamics [29-55], which is the second major theme in this review. Within this, 9 papers focused on "Disease Characteristics and Biology" [47-55], and 18 papers focused on "Transmission Dynamics and Progression" [29-46], and these can be further broken down into *Comparative Infectivity and Fatality* (1 paper) [52], *Evolution, Immunity and Cross-Strain Dynamics* (8 papers) [47-50, 53-55], *Epidemic Wave Dynamics* (2 papers) [29, 31], and *Transmission Dynamics and Epidemic Spread* (16 papers) [30, 32-46]. The primary focus within this theme are *Transmission Dynamics and Epidemic Spread*, which accounts for 19.8% of all papers, and *Evolution, Immunity and Cross-Strain Dynamics*, which accounts for 9.9% of all papers. These sub-themes account for a sizeable portion of all papers, demonstrating a strong research interest towards deepening the understanding of disease transmission and viral evolution, while also developing practical public health tools.

9 papers (11.1%) focused on Contextual and Influencing Factors [56-64] impacting viral transmission, with 7 papers studying "Human and Social Contexts" [58-64], and 2 papers exploring "External and Environmental factors" [56, 57]. This can be further broken down into *Behavioural and Social Dynamics* (7 papers) [58-64], *Environmental and Ecological Impact* (1 paper) [56], and *Spatiotemporal and Environmental Modelling* (1 paper) [57]. These papers show that epidemics are not only impacted by the biological aspects of the disease, but also by human behaviour, social structures, and environmental conditions (termed non-biological elements). With most of the papers within this theme arising from the sub-theme of *Behavioural and Social Dynamics* (7 papers, 8.6%), and with research highlighting the impact of "voluntary avoidance behaviour" on disease transmission [61, 64], this emphasizes the need for more comprehensive models that include the biological aspect of the disease and account for the intricate effects of the non-biological elements, to support effective public health strategies.

30 papers [7-9, 65-91] (37.0%) focused on Interventions and Policy Assessments, with 18 papers focused on "Intervention Strategies" [8, 75-91], and 12 papers focused on "Impact and Evaluation" [7, 9, 65-74]. These can be further broken down into *Vaccination Strategy and Impact* (17 papers) [8, 75-78, 80-91], *Drug Resistance and Strategic Interaction* (1 paper) [79], *Economic and Policy Planning* (8 papers) [7, 65-70, 73], and *Healthcare Resource Planning* (4 papers) [9, 71, 72, 74]. Of the four themes, this is the largest theme accounting for 37.0% of studies and within this theme, *Vaccination Strategy and Impact*, and *Economic and Policy Planning*, are the most prominent sub-themes that accounted for 21.0% and 9.9% of studies, respectively. These highlight a key objective of modelling research - to provide practical insights for public health officials to make informed decisions, particularly in resource allocation and strategic planning during pandemics. Another sub-theme, *Healthcare Resource Planning* (4.9%), highlights the tangible, operational benefits of epidemiological models. During pandemics, accurate forecasting of resources, such as ICU beds or antiviral medications, are essential [9, 71]. This highlights how epidemiological models are utilized for crisis management during pandemics, making this area of research extremely relevant and necessary to current operational needs in public health. Thus, models within this theme aim to provide actionable insights for public health decisions.

The distribution of papers across the two main themes, Core Epidemiological Dynamics, and Interventions and Policy Assessments, highlights the need to establish a robust scientific foundation that can be effectively applied to public health, to solve real-world problems and guide policy research.

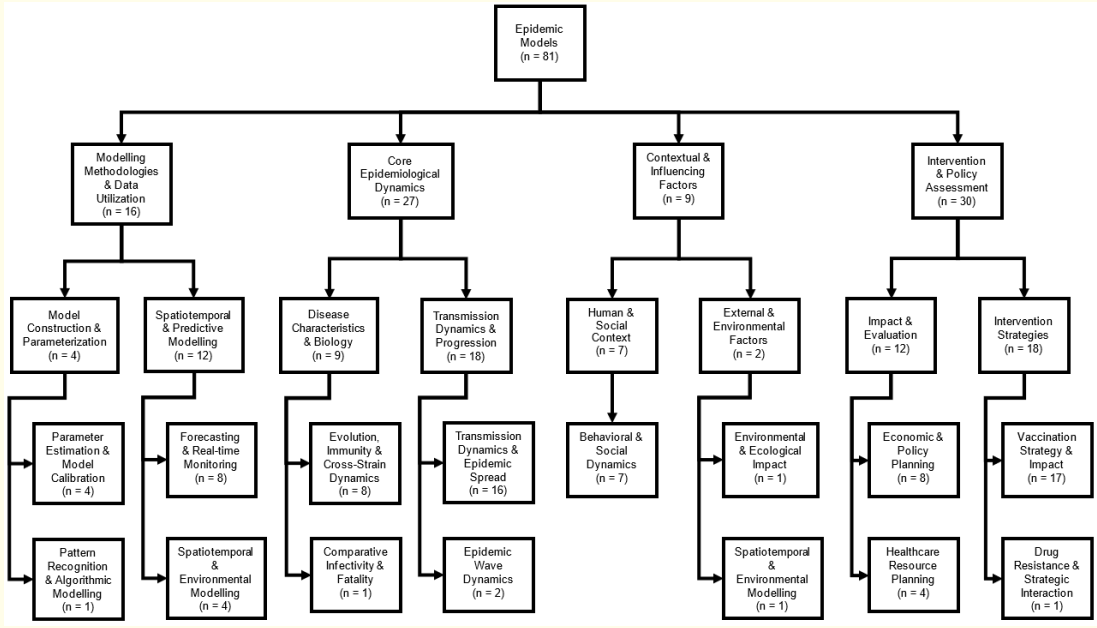

Figure 3: Epidemic Compartmental Models Classified by Themes and Subthemes (Consolidated from Table 1).

Distribution of Studies by Number of Compartments

The papers were characterised by the number of compartments in their models, as an indicator of its structural complexity and the level of detail it captured, and the results in Table 1 was summarised and provided in Table 2.

From Table 2, models with 3 to 4 compartments are the most common, representing 51.9% of studies [3, 7, 15-19, 21-24, 26, 28-30, 32, 35, 37, 40-45, 47, 49, 50, 53, 55, 57-62, 65, 67, 68, 81, 83, 87, 90], where these simple models would be used to investigate the basic epidemiological concepts or general trends at the population level. However, a huge portion of studies (50.6%), utilize models with 5 or more compartments, indicating the prevalence of complex and highly stratified models. Specifically, complex models with 5 to 11 compartments take up 37.0% of studies [9, 25, 27, 31, 33, 34, 36-39, 46, 48, 52, 54, 63, 64, 66, 69, 71, 72, 76-80, 82, 84-86, 91], and highly stratified models take up 13.6% of studies [8, 20, 39, 51, 56, 70, 73-75, 88, 89].

Among the studies with greater model complexity, 27 studies [9, 20, 27, 31, 33, 36, 46, 51, 54, 63, 69-72, 75-80, 82, 84-86, 88, 89, 91] (33.3%) were stratified by age groups, geographical units, or social contexts, highlighting the need for real-world heterogeneity to be included in the models to provide meaningful and applicable insights. While simple models with fewer compartments can provide a general overview, they are not be able to provide a deep understanding of the complex transmission dynamics in disease epidemiology or for comprehensive policy evaluations. Thus, number of compartments in the models researched upon have increased and included greater stratification, to obtain more accurate and effective models.

Although some models can be extremely complex, for example, involving 23 compartments across populations from North and South hemispheres [75], or 44 compartments across age groups across viral strains [51], there is a clear balance between levels of model complexity - highly stratified models (13.6%) are less common and much fewer than complex models (37.0%). While increased complexity provides for more accurate models, practical limitations with regards to the parameterization viability, computational

efficiency, and the interpretability of results for public health authorities, must be considered as well. Thus, the distribution of studies that is described in this segment is reflective of the compromise between realism and ease of utility of the model.

Model Complexity	*No. of Studies*	*% of Studies*
Simple Model (3 – 4 compartments)	42	51.9%
Complex Model (5 – 11 compartments)	30	37.0%
Highly Stratified Models (≥12 compartments)	11	13.6%

Table 2: Epidemic Compartmental Models by Complexity (Consolidated from Table 1).

Breakdown of Model Themes with Equation Type

A further analysis of the relationship between themes and type of equation was undertaken and illustrated in Table 3. Within Modelling Methodologies and Data Utilization, 11 papers utilised the ODE framework [15, 16, 19-22, 24-27, 29], 4 used SDE [3, 17, 18, 23], and 1 used DE [28]. Within Core Epidemiological Dynamics, 23 papers employed ODEs [29, 31, 33-35, 37-45, 47-55], 3 used SDEs [30, 32, 36], and 1 paper utilised DDEs [46]. Within Contextual and Influencing Factors, 8 papers employed ODEs [56, 57, 59-64], and 1 utilised DEs [58]. Within Intervention and Policy Assessments, 24 papers utilised ODEs [7, 8, 66, 67, 70-78, 80, 82-91], 6 used SDEs [9, 65, 68, 69, 79, 81].

Model Theme	*ODE*	*SDE*	*Others*
Modelling Methodologies and Data Utilization	11	4	1 (DE)
Core Epidemiological Dynamics	23	3	1 (DDE)
Contextual and Influencing Factors	8	0	1 (DE)
Interventions and Policy Assessments	24	6	0

Table 3: Model Theme by Equation Type (Consolidated from Table 1).

Breakdown of Model Theme with Model Complexity

Analysis of model theme was conducted alongside the number of compartments included in the model to identify possible correlations between the two, as seen in Table 4. Within the theme of Modelling Methodologies and Data Utilization, 13 papers used simple models [3, 15-19, 21-24, 26, 28, 29], 2 papers used a complex model [25, 27], and only 1 paper used a highly stratified model [20]. Within the theme of Core Epidemiological Dynamics, 16 papers contained simple models [29, 30, 32, 35, 37, 40-45, 47, 49, 50, 53, 55], 11 papers contained complex models [31, 33, 34, 36-39, 46, 48, 52, 54], and 2 papers contained highly stratified models [39, 51]. Within the theme of Contextual and Influencing Factors, 6 papers utilised a simple model [57-62], 2 papers were complex models [63, 64], and 1 paper was a highly stratified model [56]. While most used a simple model, these were mostly stratified models [57, 61, 62]. Within the theme of Interventions and Policy Assessments, 8 papers used simple models [7, 65, 67, 68, 81, 83, 87, 90], 15 papers used complex models [9, 66, 69, 71, 72, 76-80, 82, 84-86, 91], and 7 papers used highly stratified models [8, 70, 73-75, 88, 89]. Within this theme, complex models were more commonly used, and it was also noted that 21 papers utilized a stratified model [9, 68-72, 75-86, 88, 89, 91].

Theme	*Simple Model (3 - 4 compartments)*	*Complex Model (5 – 11 compartments)*	*Highly Stratified Model (12 – 44 compartments)*
Modelling Methodologies and Data Utilization	13	2	1
Core Epidemiological Dynamics	16	11	2
Contextual and Influencing Factors	6	2	1
Interventions and Policy Assessments	8	15	7

Table 4: Model Complexity by Theme (Consolidated from Table 1).

Relationship between Model Themes, Methodologies and Complexity

Considering modelling methodologies and data utilization, ODEs and simpler models are most common. ODEs can provide straightforward results that are easily interpretable, to understand fundamental patterns in disease progression. SDEs are also used, particularly in the sub-theme *Forecasting and Real-Time Monitoring* [18], to quantify uncertainty, and deduce parameters from noisy or incomplete data. Within the same sub-theme, Difference Equations were also used [28], suggesting that the modelling framework selected should be based on data availability and forecasting goals. Other sub-themes such as *Parameter Estimation and Model Calibration* and *Pattern Recognition and Algorithmic Modelling* highlight the importance of improving model reliability and integrating advanced techniques like machine learning. Simple models are typically used to isolate and understand the impact of individual variables towards disease transmission dynamics, increasing their ease of use.

In terms of core epidemiological dynamics, studies show a wide spectrum of modelling complexity, dependent on the research question and the granularity required. Simpler models, like the basic SIR or SEIR structures, can be used to explore theoretical investigations of basic mechanisms. On the other hand, more complex models can be used to capture complex populations structures, like human mobility networks or intricate biological processes, such as multi-strain interactions and detailed immune responses, as seen in [31, 33, 37, 38]. Various modelling frameworks are also employed within this theme, most notably ODEs, due to their ease of use. However, SDEs and DDEs are also used, particularly to include randomness and uncertainty, or time-lagged effects, within the model.

Most employed the ODE framework to consider contextual and influencing factors, and used stratified models, whether by age, geography, household, or site. Stratification helps to better understand the minute differences in human behaviour and transmission patterns across sub-populations. Even though most studies used ODEs and simple models with few compartments, multiplicative stratification allowed the models greater complexity by incorporating tiny differences in subpopulations into the model. SDEs and DEs were also employed in some studies to include randomness and uncertainty in real-world data.

In terms of intervention and policy assessment, models tend to be more complex, highlighting the importance of capturing differences at the population-level and scenario-specific intervention effects. This granularity is essential for evidence-based policy formulation. Most studies used ODEs, but SDEs also accounted for a substantial number of studies. SDEs can capture uncertainty and deduce parameters from noisy or incomplete data, which is particularly useful in risk assessment and resource management. Many of the studies were complex models, with 5 or more compartments, and majority of the papers included used multiplicative stratification. This allows minute differences between subpopulations to be included in the models.

Overall, variation in model complexity across the themes reflects the diverse research questions being studied, from high-level analysis of population dynamics to more granular studies of specific demographic or biological factors. The preference for models of increased complexity or stratification highlights the importance of capturing heterogeneity between subgroups to accurately reflect the dynamism of real-world scenarios, which are essential for contextual modelling and evidence-based policy formulation. However, this is dependent on data accessibility and processing power. As computation power and data collection technology improves, such as

through digital surveillance and comprehensive demographic surveys, it is then possible to build and evaluate increasingly complex models. The specific modelling framework is chosen depending on the complexity of the research question, and the specific thematic area to be investigated. The different model themes that are encapsulated in this study demonstrates the interdisciplinary nature of modern-day epidemiological modelling, integrating knowledge from different fields such as computer science, statistics, and social sciences.

Implications for the Future

The findings above highlight the importance of compartmental models in influenza epidemiology, which shows their adaptability and increasing complexity to meet the demands for granular insights. This signifies a shift from theoretical research to evidence-based research for practical applications. The use of multiplicative compartmentalization - stratifying by age, geography, or other factors - across various themes, reveals an advanced method in integrating real-world heterogeneity. Advances in methodological frameworks have made it possible for models to provide more realistic depictions of disease systems, improving their use in policy development. The constant improvement and diversification of these approaches reflects the need for models that can answer more complex epidemiological questions with greater accuracy and adaptability.

Limitations and Future Research

With compartmental models becoming more complex to better reflect real-world dynamics, this also brings about new challenges. One such challenge is that of increased data requirements, where extensive and high-quality data is required for parameter estimation and validation. This can be challenging to provide in resource-constrained settings or for emerging pathogens where data remains scarce. Another challenge is the computational demands of increasingly complex models. For such models, the computational burden of running and analysing the data can be substantial, resulting in limited utility for rapid, real-time decision-making. Furthermore, the identifiability of parameters in complex models can be challenging, impacting the reliability of their predictions, as previously discussed [16].

To address these challenges, future research should focus on several key areas. First, more efficient computational methods and statistical techniques need to be developed to manage the increased data requirements and computational burden of complex models, especially for real-time applications. Second, further investigation into H3N2-specific dynamics using more complex models must be conducted to bridge the identified research gap. Third, diverse data sources, including behavioural, environmental, and genomic data, need to be integrated to further improve model realism and predictive power. Fourth, expanding the research to include alternative modelling frameworks, such as Agent-Based Models, Stochastic Models, to provide more insights into individual-level interactions and behaviours. Lastly, fostering "Communities of Practice" between public health professionals and mathematics modellers, as suggested by existing literature [93], can help ensure that modelling advancements are effectively translated into actionable public health policy. This collaborative approach will help bridge the gap between theoretical modelling and practical application, ensuring that future models are not only scientifically robust, but also directly relevant to the challenges of influenza control and prevention.

Conclusion

This scoping review describes a dynamic and evolving research landscape of compartmental models for seasonal influenza (A/H1N1 and A/H3N2) in which model structure and methodology are intricately linked to the specific research question, reflecting a shift from theoretical models to those focused on practical applications for public health preparedness and response.

While most modelling efforts have been focused on H1N1 viral strain, there is increased interest in modelling both H1N1 and H3N2 viral strains together, by accounting for interactions between both strains, so to have a more comprehensive understanding of the influenza virus. While ODEs are generally preferred due to their ease of use, they are unable to account for uncertainty, social behavioural dynamics and time-lagged effects as compared to SDEs, DDEs and DEs. Thus, the methodological framework selected is to

be considered against the purpose of the model. The result of thematic analysis indicates focus on Intervention and Policy Assessment and Core Epidemiological Dynamics, indicating researchers remain committed to deepening their understanding of disease transmission, and translating this knowledge into actionable insights for public health officials. The direct correlation between increased compartmentalization and need for granular insights supports the finding that model complexity is driven by the need for more realistic and practical models.

Overall, what initially began as descriptive modelling in the classic SIR model [4], has evolved into prescriptive models with highly stratified designs. This reflects the increasing complexity of research questions and the need for the field of public health to take on a more proactive approach. Although challenges of data scarcity, computational burden and parameterization remain, researchers continue to push for advancements in the field of modelling. With the findings of this paper, we hope to provide public health officials with the information needed to reduce the social impact of influenza and create a robust infrastructure to manage future threats.

Supplementary Materials

Supplementary materials can be downloaded from https://bit.ly/Influenza_Models.

Conflict of Interest

The authors declare no conflict of interest.

Acknowledgement

The authors wish to thank the institution, Management Development Institute of Singapore, for morally supporting this work, as the financial cost of publication fees were borne by the authors.

References

1. Mackenzie L. "The burden of Influenza". World Health Organization (2024). https://www.who.int/news-room/feature-stories/detail/the-burden-of-influenza
2. Peteranderl C, Herold S and Schmoldt C. "Human Influenza Virus Infections". Seminars in Respiratory and Critical Care Medicine 37.04 (2016): 487-500.
3. Schwartz EJ, Choi B and Rempala GA. "Estimating epidemic parameters: Application to H1N1 pandemic data". Mathematical Biosciences 270.Pt B (2015): 198-203.
4. Kermack WO and McKendrick AG. "A contribution to the mathematical theory of epidemics". Proceedings of the Royal Society of London Series A, Containing Papers of a Mathematical and Physical Character 115.772 (1927): 700-721.
5. Elveback L and Varma A. "Simulation of mathematical models for public health problems". Public Health Reports (Washington, DC: 1896) 80.12 (1965): 1067-1076.
6. Briggs A, Scarborough P and Smith A. "Modelling in Public Health". Public Health Intelligence, eds Regmi K, Gee I (Springer International Publishing, Cham) (2016): 67-90.
7. Arino J., et al. "Pandemic influenza: Modelling and public health perspectives". Mathematical biosciences and engineering: MBE 8.1 (2011): 1-20.
8. Wenzel NS., et al. "Cost-effectiveness of live-attenuated influenza vaccination among school-age children". Vaccine 39.2 (2021): 447-456.
9. Balcan D., et al. "Modeling the critical care demand and antibiotics resources needed during the Fall 2009 wave of influenza A(H1N1) pandemic". PLoS currents 1 (2009): RRN1133.
10. Tricco AC., et al. "PRISMA Extension for Scoping Reviews (PRISMA-ScR): Checklist and Explanation". Annals of Internal Medicine 169.7 (2018): 467-473.
11. Arksey H and O'Malley L. "Scoping studies: towards a methodological framework". International Journal of Social Research Meth-

odology 8.1 (2005): 19-32.

12. Atkinson LZ and Cipriani A. "How to carry out a literature search for a systematic review: a practical guide". BJPsych Advances 24.2 (2018): 74-82.
13. Huppert A and Katriel G. "Mathematical modelling and prediction in infectious disease epidemiology". Clinical Microbiology and Infection 19.11 (2013): 999-1005.
14. Molla J., et al. "Mathematical modeling of mpox: A scoping review". One Health 16 (2023): 100540.
15. Yaari R., et al. "Model-based reconstruction of an epidemic using multiple datasets: understanding influenza A/H1N1 pandemic dynamics in Israel". Journal of the Royal Society, Interface 13.116 (2016): 20160099.
16. Bilge AH, Samanlioglu F and Ergonul O. "On the uniqueness of epidemic models fitting a normalized curve of removed individuals". Journal of Mathematical Biology 71.4 (2015): 767-794.
17. Tessmer HL, Ito K and Omori R. "Can Machines Learn Respiratory Virus Epidemiology?: A Comparative Study of Likelihood-Free Methods for the Estimation of Epidemiological Dynamics". Frontiers in Microbiology 9 (2018): 343.
18. Dureau J, Kalogeropoulos K and Baguelin M. "Capturing the time-varying drivers of an epidemic using stochastic dynamical systems". Biostatistics (Oxford, England) 14.3 (2013): 541-555.
19. Chowell G., et al. "Characterizing the epidemiology of the 2009 influenza A/H1N1 pandemic in Mexico". PLoS medicine 8.5 (2011): e1000436.
20. Birrell PJ., et al. "Efficient Real-Time Monitoring of an Emerging Influenza Pandemic: How Feasible?". The Annals of Applied Statistics 14.1 (2020): 74-93.
21. Roberts MG. "Epidemic models with uncertainty in the reproduction number". Journal of Mathematical Biology 66.7 (2013): 1463-1474.
22. Yang W., et al. "Forecasting Influenza Epidemics in Hong Kong". PLoS computational biology 11.7 (2015): e1004383.
23. He D., et al. "Global Spatio-temporal Patterns of Influenza in the Post-pandemic Era". Scientific Reports 5 (2015): 11013.
24. Zhang B., et al. "Mechanisms for the circulation of influenza A(H3N2) in China: A spatiotemporal modelling study". PLoS pathogens 18.12 (2022): e1011046.
25. Chlif S., et al. "Modelling of seasonal influenza and estimation of the burden in Tunisia". Eastern Mediterranean Health Journal 22.7 (2016): 460-467.
26. Dukic V, Lopes HF and Polson NG. "Tracking Epidemics with Google Flu Trends Data and a State-Space SEIR Model". Journal of the American Statistical Association 107.500 (2012): 1410-1426.
27. Haw DJ., et al. "Using real-time data to guide decision-making during an influenza pandemic: A modelling analysis". PLoS computational biology 19.2 (2023): e1010893.
28. Fisman DN., et al. "An IDEA for short term outbreak projection: nearcasting using the basic reproduction number". PloS One 8.12 (2013): e83622.
29. Eggo RM, Cauchemez S and Ferguson NM. "Spatial dynamics of the 1918 influenza pandemic in England, Wales and the United States". Journal of the Royal Society, Interface 8.55 (2011): 233-243.
30. Liccardo A and Fierro A. "A lattice model for influenza spreading". PloS One 8.5 (2013): e63935.
31. Mummert A., et al. "A perspective on multiple waves of influenza pandemics". PloS One 8.4 (2013): e60343.
32. Fierro A and Liccardo A. "A simple stochastic lattice gas model for H1N1 pandemic. Application to the Italian epidemiological data". The European Physical Journal E, Soft Matter 34.2 (2011): 11.
33. Wang X., et al. "An Epidemic Patchy Model with Entry-Exit Screening". Bulletin of Mathematical Biology 77.7 (2015): 1237-1255.
34. Zhou X and Guo Z. "Analysis of an influenza A (H1N1) epidemic model with vaccination". Arabian Journal of Mathematics 1.2 (2012): 267-282.
35. Earn DJD., et al. "Effects of school closure on incidence of pandemic influenza in Alberta, Canada". Annals of Internal Medicine 156.3 (2012): 173-181.
36. Colizza V., et al. "Estimate of Novel Influenza A/H1N1 cases in Mexico at the early stage of the pandemic with a spatially struc-

tured epidemic model". PLoS currents 1 (2009): RRN1129.

37. Chen T., et al. "Evaluating the effects of common control measures for influenza A (H1N1) outbreak at school in China: A modeling study". PloS One 12.5 (2017): e0177672.
38. Liu L, Cai W and Wu Y. "Global dynamics for an SIR patchy model with susceptibles dispersal". Advances in Difference Equations 2012.1 (2012): 131.
39. Ghosh S and Heffernan J. "Influenza pandemic waves under various mitigation strategies with 2009 H1N1 as a case study". PloS One 5.12 (2010): e14307.
40. Gupta SD., et al. "Modeling of H1N1 Outbreak in Rajasthan: Methods and Approaches". Indian Journal of Community Medicine: Official Publication of Indian Association of Preventive & Social Medicine 36.1 (2011): 36-38.
41. González-Parra G., et al. "Modeling the epidemic waves of AH1N1/09 influenza around the world". Spatial and Spatio-Temporal Epidemiology 2.4 (2011): 219-226.
42. Vaidya NK., et al. "Modelling the epidemic spread of an H1N1 influenza outbreak in a rural university town". Epidemiology and Infection 143.8 (2015): 1610-1620.
43. Wang L., et al. "New global dynamical results and application of several SVEIS epidemic models with temporary immunity". Applied Mathematics and Computation 390 (2021): 125648.
44. KhudaBukhsh WR., et al. "Survival dynamical systems: individual-level survival analysis from population-level epidemic models". Interface Focus 10.1 (2020): 20190048.
45. Massad E., et al. "The 1918 influenza A epidemic in the city of São Paulo, Brazil". Medical Hypotheses 68.2 (2007): 442-445.
46. Avilov KK., et al. "The 1978 English boarding school influenza outbreak: where the classic SEIR model fails". Journal of the Royal Society, Interface 21.220 (2024): 20240394.
47. Sachak-Patwa R, Byrne HM and Thompson RN. "Accounting for cross-immunity can improve forecast accuracy during influenza epidemics". Epidemics 34 (2021): 100432.
48. Borchering RK., et al. "Anomalous influenza seasonality in the United States and the emergence of novel influenza B viruses". Proceedings of the National Academy of Sciences of the United States of America 118.5 (2021): e2012327118.
49. Dang UJ and Bauch CT. "Can interactions between timing of vaccine-altered influenza pandemic waves and seasonality in influenza complications lead to more severe outcomes?". PloS One 6.8 (2011): e23580.
50. Du X., et al. "Evolution-informed forecasting of seasonal influenza A (H3N2)". Science Translational Medicine 9.413 (2017): eaan5325.
51. Thommes EW., et al. "Examining Ontario's universal influenza immunization program with a multi-strain dynamic model". Vaccine 32.39 (2014): 5098-5117.
52. Xue L., et al. "Infectivity versus fatality of SARS-CoV-2 mutations and influenza". International journal of infectious diseases: IJID: official publication of the International Society for Infectious Diseases 121 (2022): 195-202.
53. Gambhir M., et al. "Multiple contributory factors to the age distribution of disease cases: a modeling study in the context of influenza A(H3N2v)". Clinical Infectious Diseases: An Official Publication of the Infectious Diseases Society of America 57 (2013): S23-27.
54. Bolton KJ., et al. "The influence of changing host immunity on 1918-19 pandemic dynamics". Epidemics 8 (2014): 18-27.
55. Yuan H-Y., et al. "The impact of stratified immunity on the transmission dynamics of influenza". Epidemics 20 (2017): 84-93.
56. Singer AC., et al. "Assessing the ecotoxicologic hazards of a pandemic influenza medical response". Environmental Health Perspectives 119.8 (2011): 1084-1090.
57. Tamerius J., et al. "Impact of School Cycles and Environmental Forcing on the Timing of Pandemic Influenza Activity in Mexican States, May-December 2009". PLoS computational biology 11.8 (2015): e1004337.
58. Springborn M., et al. "Accounting for behavioral responses during a flu epidemic using home television viewing". BMC infectious diseases 15 (2015): 21.
59. Chen SC., et al. "Behavioural response in educated young adults towards influenza A(H1N1)pdm09". Epidemiology and Infection

143.9 (2015): 1846-1857.

60. Deng J, Tang S and Shu H. "Joint impacts of media, vaccination and treatment on an epidemic Filippov model with application to COVID-19". Journal of Theoretical Biology 523 (2021): 110698.
61. Bayham J., et al. "Measured voluntary avoidance behaviour during the 2009 A/H1N1 epidemic.". Proceedings Biological Sciences 282.1818 (2015): 20150814.
62. Palin K and Greer ML. "The effect of mixing events on the dynamics of pH1N1 outbreaks at small residential colleges". Journal of American college health: J of ACH 60.6 (2012): 485-489.
63. Bootsma MCJ and Ferguson NM. "The effect of public health measures on the 1918 influenza pandemic in U.S. cities". Proceedings of the National Academy of Sciences of the United States of America 104.18 (2007): 7588-7593.
64. Poletti P, Ajelli M and Merler S. "The effect of risk perception on the 2009 H1N1 pandemic influenza dynamics". PloS One 6.2 (2011): e16460.
65. Park H. "A real option analysis for stochastic disease control and vaccine stockpile policy: An application to H1N1 in Korea". Economic Modelling 53 (2016): 187-194.
66. Tracht SM, Del Valle SY and Edwards BK. "Economic analysis of the use of facemasks during pandemic (H1N1) 2009". Journal of Theoretical Biology 300 (2012): 161-172.
67. Khazeni N., et al. "Effectiveness and cost-effectiveness of vaccination against pandemic influenza (H1N1) 2009". Annals of Internal Medicine 151.12 (2009): 829-839.
68. Xiao Y., et al. "Estimated impact of aggressive empirical antiviral treatment in containing an outbreak of pandemic influenza H1N1 in an isolated First Nations community". Influenza and Other Respiratory Viruses 7.6 (2013): 1409-1415.
69. Dimitrov N., et al. "Optimizing tactics for use of the U.S. Antiviral Strategic National Stockpile for Pandemic (H1N1) Influenza, 2009". PLoS currents 1 (2009): RRN1127.
70. Dover DC., et al. "Pandemic Risk Assessment Model (PRAM): a mathematical modeling approach to pandemic influenza planning". Epidemiology and Infection 144.16 (2016): 3400-3411.
71. Smetanin P., et al. "Potential intensive care unit ventilator demand/capacity mismatch due to novel swine-origin H1N1 in Canada". The Canadian Journal of Infectious Diseases & Medical Microbiology = Journal Canadien Des Maladies Infectieuses Et De La Microbiologie Medicale 20.4 (2009): e115-123.
72. Araz OM., et al. "Simulating school closure policies for cost effective pandemic decision making". BMC public health 12 (2012): 449.
73. Hansen E., et al. "Strategies for the use of oseltamivir and zanamivir during pandemic outbreaks". The Canadian Journal of Infectious Diseases & Medical Microbiology 21.1 (2010): e28-63.
74. Adisasmito W., et al. "Pandemic influenza and health system resource gaps in Bali: an analysis through a resource transmission dynamics model". Asia-Pacific Journal of Public Health 27.2 (2015): NP713-733.
75. Alharbi MH and Kribs CM. "A Mathematical Modeling Study: Assessing Impact of Mismatch Between Influenza Vaccine Strains and Circulating Strains in Hajj". Bulletin of Mathematical Biology 83.1 (2021): 7.
76. Chowell G., et al. "Adaptive vaccination strategies to mitigate pandemic influenza: Mexico as a case study". PloS One 4.12 (2009): e8164.
77. Thorrington D., et al. "Assessing optimal use of the standard dose adjuvanted trivalent seasonal influenza vaccine in the elderly". Vaccine 37.15 (2019): 2051-2056.
78. Yu Z., et al. "Efficient Vaccine Distribution Based on a Hybrid Compartmental Model". PloS One 11.5 (2016): e0155416.
79. Jnawali K., et al. "Emergence and spread of drug resistant influenza: A two-population game theoretical model". Infectious Disease Modelling 1.1 (2016): 40-51.
80. Arinaminpathy N., et al. "Estimating Direct and Indirect Protective Effect of Influenza Vaccination in the United States". American Journal of Epidemiology 186.1 (2017): 92-100.
81. Sato T, Akita T and Tanaka J. "Evaluation of strategies for control and prevention of pandemic influenza (H1N1pdm) in Japanese

children attending school in a rural town". Nihon Koshu Eisei Zassh 60.4 (2013): 204-211.

82. Lee S, Golinski M and Chowell G. "Modeling optimal age-specific vaccination strategies against pandemic influenza". Bulletin of Mathematical Biology 74.4 (2012): 958-980.
83. Medlock J, Meyers LA and Galvani A. "Optimizing allocation for a delayed influenza vaccination campaign". PLoS currents 1 (2009): RRN1134.
84. Matrajt L and Longini IM. "Optimizing vaccine allocation at different points in time during an epidemic". PloS One 5.11 (2010): e13767.
85. Kim S and Jung E. "Prioritization of vaccine strategy using an age-dependent mathematical model for 2009 A/H1N1 influenza in the Republic of Korea". Journal of Theoretical Biology 479 (2019): 97-105.
86. Nguyen VH, Hilsky Y and Mould-Quevedo J. "The Epidemiological and Economic Impact of a Cell-Based Quadrivalent Influenza Vaccine in Adults in the US: A Dynamic Modeling Approach". Vaccines 9.10 (2021): 1095.
87. Omori R and Nishiura H. "Theoretical basis to measure the impact of short-lasting control of an infectious disease on the epidemic peak". Theoretical Biology & Medical Modelling 8 (2011): 2.
88. Van Effelterre T, Dos Santos G and Shinde V. "Twin Peaks: A/H1N1 Pandemic Influenza Virus Infection and Vaccination in Norway, 2009-2010". PloS One 11.3 (2016): e0151575.
89. Conway JM., et al. "Vaccination against 2009 pandemic H1N1 in a population dynamical model of Vancouver, Canada: timing is everything". BMC public health 11 (2011): 932.
90. Cohen MJ., et al. "Vaccination, herd behavior, and herd immunity". Medical Decision Making: An International Journal of the Society for Medical Decision Making 33.8 (2013): 1026-1038.
91. Lee K., et al. "The Potential Benefits of Delaying Seasonal Influenza Vaccine Selections for the Northern Hemisphere: A Retrospective Modeling Study in the United States". The Journal of Infectious Diseases 230.1 (2024): 131-140.
92. Ndanguza D, Mbalawata IS and Nsabimana JP. "Analysis of SDEs Applied to SEIR Epidemic Models by Extended Kalman Filter Method". Applied Mathematics 07.17 (2016): 2195-2211.
93. Driedger SM, Cooper EJ and Moghadas SM. "Developing model-based public health policy through knowledge translation: the need for a 'Communities of Practice'". Public Health 128.6 (2014): 561-567.

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