

A Review of Construction Methods Based on Agent Modeling in the Field of Public Health Control

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Abstract

Public health control involves complex and dynamic processes shaped by individual heterogeneity, social interaction, spatial context, and policy intervention. Traditional aggregate models often have limited capacity to represent these micro-level mechanisms and their emergent population-level effects. Against this background, agent-based modeling (ABM) has become an important methodological approach in public health research. This review systematically examines the construction methods of ABM in the field of public health control, with a focus on its conceptual foundations, core modeling procedures, major methodological choices, and their implications for public health decision-making. The review shows that public health ABMs are commonly structured around four key components: agent and population specification, environment and spatial structure design, contact mechanism and social network construction, and disease state transition modeling. These construction choices directly shape the model's explanatory capacity, realism, and policy relevance. The study further finds that, despite the flexibility and analytical strengths of ABM, current research still faces challenges in reporting transparency, data support, calibration, and validation. Overall, examining ABM from the perspective of construction methods can strengthen methodological rigor and improve its value for public health policy design and decision support.

Keywords

agent-based modeling, public health control, infectious disease modeling, decision support

1. Introduction

Public health control problems are rarely simple linear processes of transmission. Instead, they usually involve multiple interacting mechanisms, including individual heterogeneity, social interaction, spatial mobility, institutional constraints, and policy interventions. Traditional approaches that focus mainly on average effects and static relationships often fail to capture the dynamic mechanisms through which public health interventions operate in real social settings [1]. Against this background, agent-based modeling (ABM) has gradually become an important tool in public health research because it can represent heterogeneity, behavioral rules, and local interactions at the individual level, and thereby simulate how macro-level health outcomes emerge over time.

This review aims to provide a systematic overview of ABM construction methods in the field of public health control. Specifically, it examines the basic conceptual foundations of ABM, the main steps involved in

model construction, the key methodological choices made during that process, and the ways in which these choices influence the value of ABM for public health decision-making.

At the theoretical level, this paper helps to deepen the understanding of the logical framework of the ABM method from the perspective of “construction approach”, enrich the methodological research on the modeling of complex public health systems, and encourage researchers to shift from focusing on the model results to the formation mechanism of the model. At the practical level, this paper helps to provide methodological references for public health policy simulation and decision support, offers applicable experiences for the design, development, verification and application of ABMs, and also helps to enhance the transparency, interpretability and practical transformation value of model research.

2. The Theoretical Foundation of ABM in Public Health

2.1 Definition

Agent-based modeling (ABM) is a computational approach for simulating complex systems composed of heterogeneous entities interacting over time within specific environments. In ABM, individuals, organizations, or other relevant entities are represented as agents with defined attributes, behavioral rules, and decision-making capacities. Through interactions among agents and between agents and their environment, the model generates system-level outcomes over time. The core strength of ABM does not lie in directly assuming macro-level outcomes; rather, it starts from micro-level behavioral rules and examines how aggregate patterns emerge from local interactions. By simulating the concurrent actions and interactions of multiple agents, ABM can be used to represent and predict complex collective dynamics [2, 3]. For this reason, ABM is often regarded as a valuable method for understanding complex social and health problems through the lens of micro-level mechanisms and macro-level outcomes.

2.2 Basic Characteristics

In terms of the characteristics, ABM primarily emphasizes individual heterogeneity. ABM can depict the differences in attributes, risk exposure, contact patterns, and behavioral responses among different agents, thereby avoiding simplifying the population into a completely homogeneous entity. Therefore, ABM is particularly suitable for analyzing issues such as stratified risks, super-spreading, and differentiated interventions in public health [4]. Secondly, ABM is characterized by local interaction and macro-level emergence. By simulating repeated local contacts and interactions among individuals, ABM explains how population-level transmission dynamics or broader system outcomes gradually emerge from micro-level behavior [5]. This feature enables ABM to account for the formation of macro-level public health phenomena on the basis of underlying behavioral mechanisms. Thirdly, ABM is rule-driven and behavior-configurable. In ABM, agents act according to pre-defined rules, and researchers can flexibly set individual behaviors, adaptive mechanisms, and policy response methods based on research objectives [6]. Therefore, ABM is well suited to exploring how changes in individual behavior under different scenarios may affect public health outcomes. Fourthly, ABM commonly incorporates spatiality, networkness and dynamic randomness. ABM can incorporate specific spaces such as households, schools, workplaces, and communities, as well as social network structures into the model, thereby more realistically representing the transmission pathways of public health [7]. At the same time, the model usually progresses over time and introduces random mechanisms during contact, exposure, and infection processes to reflect the uncertainty in the actual transmission process [8].

2.3 The Main Application Scenarios in the Field of Public Health Control

In public health control, ABM is primarily applied to problems characterized by substantial heterogeneity, dynamic transmission, and complex local interactions. Based on the existing literature, three major application areas can be identified.

The simulation of infectious disease transmission is the most typical and well-established application scenario of ABM in public health [9]. Transmission processes depend strongly on interpersonal contact patterns, environmental conditions, and behavioral differences. By integrating synthetic populations, environmental settings, contact networks, and disease-state transition rules, ABM can represent disease transmission pathways in society with a relatively high degree of realism [9, 10]. Consequently, ABM has

been widely used to simulate the spread of infectious diseases such as COVID-19 and tuberculosis and to evaluate interventions including social distancing, lockdowns, testing, vaccination, and contact tracing.

Another important application direction of ABM is population health research. Compared with models that focus only on the transmission of pathogens, this type of research pays more attention to how health outcomes are jointly influenced by individual behaviors, social networks, environmental exposures, and policies. Silverman et al. argue that ABM is particularly suitable for handling “complex issues” in population health research because these issues usually involve interactions of multiple factors, long-term feedback, and emotional dependencies, and traditional epidemiological tools often have difficulty fully expressing them [1]. At the same time, ABM has also made an important contribution to research on health inequalities [11].

ABM is increasingly used for policy design and policy evaluation. The effectiveness of public health policy depends not only on the formal design of the policy itself but also on individuals' willingness to comply, their adaptive responses, and the constraints of their lived circumstances [12]. A major strength of ABM is that it can incorporate factors such as emotions, risk aversion, social norms, vaccine hesitancy, and information diffusion within a unified analytical framework, thereby making it possible to examine the two-way interaction between policy measures and human behavior.

3. The Basic Construction Process of ABM in Public Health

3.1 Construction of Agents and the Overall Population

During the construction of the public health ABM, the setting of agents and the overall population forms the basis of the model, because subsequent contact processes, spatial transformations, and disease transmission are all based on the actors in the mode and the characteristics of these actors. One of the defining features of ABM is its attempt to explain population-level public health outcomes on the basis of individual-level heterogeneity. Population construction should therefore not be treated as a simple initialization step; rather, it is a crucial component that shapes the model's representational scope and explanatory capacity [7].

From the perspective of agent types, the public health ABM mostly uses individual agents as the basic unit, as behaviors such as disease exposure, infection, and recovery typically occur at the individual level [7]. At the same time, to represent the transmission environment more realistically, many studies also introduce specific environments such as families, schools, workplaces, and hospitals, so that individual contacts occur in specific spaces. EpiPredict simultaneously models individuals and places, and links individual behaviors with the transmission environment through individual schedules driving movement and through place rules forming contacts [6].

With respect to agent attributes, existing studies typically include three broad categories of variables. The first consists of demographic attributes, such as age, sex, occupation, household size, and geographic location. The second includes health-related attributes, such as infection status, susceptibility, vaccination status, and symptom profile. The third comprises behavioral attributes, such as travel patterns, policy compliance, risk perception, and protective behavior. Together, these attributes shape individual contact patterns, transmission risks, and responses to interventions. As Bissett et al. note, one important advantage of ABM over homogeneous population models is its capacity to represent such differences explicitly [7].

To make the overall model more realistic, public health ABMs usually also construct synthetic populations [13]. A synthetic population is an artificial population generated from empirical data and statistical procedures so that it resembles the real population in key characteristics [14]. However, many existing synthetic population datasets do not include social network information and are not easily transferable across different modeling contexts [10]. In geographically explicit ABMs, the integration of social networks is often necessary to represent interactions among agents more accurately across settings [10].

Finally, for the overall population, researchers usually need to decide whether to model static population or dynamic population. Static population typically assumes that the population size and structure remain unchanged during the simulation period, and is more suitable for simulating short-term epidemic spread, thereby enabling the assessment of immediate policies. On the other hand, dynamic population incorporates processes such as birth, death, migration, and aging into the system, and is more suitable for long-term disease transmission studies [15].

3.2 Construction of the Environment and Spatial Structure

The environment and spatial structure serve as a crucial link between individuals and the transmission of diseases. ABM usually requires the understanding of the environmental conditions in which agents are located, knowledge of their preferred places on a daily basis, and clarification of how these spatial conditions directly or indirectly affect the contact opportunities between diseases and individuals. Existing studies have pointed out that public health issues often exhibit significant spatial heterogeneity, thus the spatial structure in a specific environment is of great importance for the accuracy of the model [16].

In practical modeling, places are usually the core elements of environmental construction. Public health ABMs often treat households, schools, workplaces, communities, and hospitals as the major nodes of daily activity. These places matter because they shape where individuals stay, how they move, and how frequently and intensely they come into contact with others. For example, the INFEKTA model proposed by Gomez et al. represents urban space as a complex network embedded in Euclidean space and composed of residences, public transport stations, and points of interest such as schools, workplaces, and markets. The model simulates movement among these locations through individual daily schedules and models exposure and transmission within places [9]. In this way, disease transmission is not treated as a uniformly occurring process, but as one linked to routine spatial behavior such as commuting, schooling, shopping, and healthcare seeking.

Spatial resolution also affects the model validity. Different studies adopt different levels of spatial granularity: some use countries, states, or counties as the basic spatial units and are therefore more suitable for evaluating regional policies, whereas others use communities, blocks, or even rooms and are thus better suited to analyzing highly localized transmission. Higher spatial resolution allows the model to represent variation across environments more precisely, but it also increases data requirements and computational costs [6, 7].

3.3 Construction of Social Networks

In the construction of ABM, the contact mechanism and the construction of social networks often determine how, where, and at what frequency the disease spreads. High-resolution representations of human contact are a key component of infectious disease ABM. If the contact structure is oversimplified, the model may still function computationally, but it will often struggle to reproduce transmission pathways with sufficient realism [17]. Based on the existing literature, contact mechanisms in public health ABM can be broadly divided into three types.

The first type is based on the construction of contact through co-presence in places. These models typically do not pre-set the premise of interpersonal relationships but rather form contact opportunities based on the overlapping of individuals' time and space presence in different places. In this section, we consider the EpiPredict model. This model arranges individuals' movements between different locations through schedules, and then contact is realized by the rules of each place. It sets up family contact layer, school contact layer, workplace and social contact layer respectively. This approach directly links the transmission process with daily activities such as commuting, going to school, shopping and staying at home [6].

The second type can be categorized as explicit social network-based contact construction. In this type of research, the contact relationships between individuals are directly represented as a network structure, with nodes corresponding to individuals and edges corresponding to social connections such as family, friendship, school, work, or sexual partners. In contrast, this contact pattern is more suitable for expressing long-term stable relationship structures and can more accurately simulate contact heterogeneity. In a study evaluating a COVID-19 contact tracing application, the researchers explicitly placed all subjects within a multi-layer social network including family, school, friendship, work, etc., thereby enabling the virus's contact transmission to function within the real relationship structure [18].

The third type is the implicit probability mixed-contact construction. This contact structure is typically used in studies where data is scarce or large-scale simulations are required. This approach does not explicitly describe social relationships but determines whether infection contacts occur based on group attributes, spatial units, or activity categories. This modeling method is commonly used in infectious disease ABM because it has a lower implementation cost, higher computational efficiency, and is suitable for large-scale population simulations and rapid policy evaluation. However, it is relatively limited in depicting repeated contacts, local clustering, and network structural inequality [19].

3.4 Construction of the State Transition Mechanism

For the dynamics of epidemics, setting different disease states and establishing transitions between these states can effectively simulate this dynamic process. The agents, spatial environment, and contact structure previously defined determine “whether different entities come into contact”, while the state transition mechanism further answers “whether infection occurs after contact, how the infection develops after infection, and when an individual enters a new healthy state”.

According to the existing research, the construction of the state transition mechanism should first be set up based on different disease state systems. The most basic approach is to use state divisions similar to SIR or SEIR, dividing individuals into susceptible (S), exposed (E), infected (I), and recovered (R) stages [20]. In specific public health applications, however, researchers often further refine the states based on disease characteristics, such as adding asymptomatic infection, symptomatic infection, mild case, severe case, hospitalization, death, isolation, and post-vaccination protection. The INFEKTA model, for instance, extends the SEIR framework by introducing additional states such as asymptomatic infection (IA), severe infection (IS), critical infection (IC), death (D), and immunity (M), thereby offering a richer representation of how age, sex, route preference, comorbidity, and social isolation policies affect disease progression [10].

After the state system is determined, the model needs to further specify the state transition rules, which determine under what conditions and with what probability an individual will enter another state from one state within a certain period of time. Müller et al. in their modeling of predicting the effects of COVID-19-related interventions set similar age-dependent transition probabilities based on existing literature, and based on clinical research incorporated the corresponding infectivity and susceptibility of different age groups, as well as the infection probability of individuals [21]. This rule-setting pattern that combines state transitions with the parameters of the natural history of the disease is also the most commonly used method at present.

In addition, the disease transmission mechanism usually also needs to take into account the differences of the disease at different stages and individual heterogeneity. The infectiousness of an infected person at the end of the incubation period, the asymptomatic infection period, and the symptomatic period is usually different [20], and the infection probability and disease outcome of individuals of different ages, occupations, health conditions or vaccination statuses may also be different. In recent years, more and more public health ABMs no longer adopt the simplified assumptions of ‘all infected individuals having the same transmission ability’ and ‘all susceptible individuals having the same risk of illness’, but incorporate age, symptom type, vaccine protection and underlying disease risk into the state transition and transmission rules. The platform models such as HPVsim and Covasim in recent years reflect this trend: the former fine-tunes the differences in disease progression of different infected individuals through individual effect parameters, while the latter characterizes the changes in infectivity of different entities through individual disease course, state duration and viral load differences [22, 23].

4. Discussion

4.1 Research Finding

This article reviews the construction methods of agent-based modeling (ABM) in the field of public health control and conducts a comparative analysis of different ABM models. It is found that the value of ABM is not limited to its ability to simulate disease transmission and intervention effects. More importantly, it provides a methodological path for integrating individual heterogeneity, social contact, spatial environment, disease status, and policy responses into a single framework model. Unlike traditional overall models that mainly focus on average benefits and overall trend changes, ABM places greater emphasis on starting from the individual level to explain the formation process of macro public health outcomes.

Firstly, public health ABMs display clear modular and layered characteristics. The construction of agents and populations, environmental and spatial settings, contact mechanisms and social networks, and state transition rules are not isolated components; rather, they form an interdependent system. Put simply, agents and populations provide the heterogeneous units of analysis, environmental and spatial structures define the contexts in which agents act, social networks and contact mechanisms determine routes of transmission, and

state transition mechanisms convert contact into dynamic disease processes such as infection, illness, recovery, and death.

Secondly, one of the major strengths of ABM is its ability to represent the complexity of real public health scenarios, including heterogeneity across individuals, places, and social relationships. As mentioned earlier, public health issues are not uniformly distributed throughout the population and society; instead, they involve multiple layers of social-spatial environments such as families, schools, workplaces, hospitals, and communities. Moreover, individuals also have significant differences in terms of health status, social attributes, risk perception, behavioral preferences, and policy compliance. ABM can precisely reveal the mechanisms of local transmission, clustered infections, behavioral feedback, and stratified intervention by constructing agents with differentiated attributes, specific environmental structures, and diverse contact mechanisms.

Furthermore, this study also found that the construction process of the public health ABM is always accompanied by a series of important method choices and realistic trade-offs. As discussed in the third section: when constructing agents and the overall population, researchers need to balance between simplifying the population and highly realistic synthetic populations; in the setting of environment and spatial structure, they need to make a choice between abstract environment, place-based environment, and geographically explicit environment; in the construction of contact mechanisms, they need to consider different contact patterns such as place coexistence type, explicit social network type, and implicit probability mixture type; for the state transition mechanism, they often need to make a trade-off between simple SIR/SEIR state classification and more detailed complex states such as symptoms, hospitalization, isolation, and vaccine protection. In my opinion, these choices do not often have a single correct answer; they are influenced by various factors such as disease type, data availability, disease development process, and policy requirements. In other words, ABM has strong flexibility, but this flexibility also means that its construction process is highly dependent on the subjective theoretical judgment and method judgment of the researchers.

4.2 Limitations of the Current Study

There are still some relatively prominent common issues in the current ABM research in the field of public health:

The current literature on the calibration, validation and uncertainty analysis of ABM models is still insufficient. Public health decisions often heavily rely on the credibility of model results, but many ABM studies still remain at the level of setting based on literature parameters or limited historical fitting, and the handling of actual verification and sensitivity analysis is relatively inadequate. For example, in the ABM of tuberculosis, independent verification of the model is still rare [24], and Belfrage et al.'s research on the application of ABM policies also points out that most experiments currently have a generally low level of formal verification of the model, unable to fully reflect the model's capabilities and limitations [25].

The second issue is the standardization of the description of the model construction methods. Although many studies have developed complex agent rules, contact structures, and state transition mechanisms, they often provide inadequate detail on parameter sources, key assumptions, relationships among modules, and implementation choices. Moreover, limitations in code availability, reporting standards, and transparency continue to constrain comparability and reproducibility across models.

Furthermore, data availability and data quality limitations still significantly affect model construction. Although growing attention has been paid to synthetic populations, social networks, behavioral attributes, and dynamic populations, researchers often lack sufficient empirical data to support these components and therefore must rely on simplifying assumptions. At the same time, data quality directly affects model performance. These constraints influence not only simulation outcomes but also the reliability of subsequent risk assessment and policy analysis.

4.3 Future Research Direction

Based on the above analysis, future development direction of Public Health ABM should not solely focus on achieving higher technical complexity, but rather should place greater emphasis on constructing transparent structures, reasonable parameter settings, sufficient model validation, and matching with actual decision-making requirements. It should also further promote the integration of synthetic populations, social networks,

disease dynamic transmission, and different spatial environments to enhance the model's ability to depict real public health scenarios. At the same time, there is a clear need to strengthen reporting standards, code sharing, parameter documentation, and process validation so as to improve reproducibility and the credibility of model-based evidence and research should incorporate more real epidemiological data, field investigation data, and healthcare service data to calibrate and externally validate the model parameters and output results, and conduct sensitivity analysis and uncertainty analysis to identify the impact effects of different parameters or assumptions on the model outcomes, thereby enhancing the robustness of the model conclusions. On this basis, it is also necessary to further enhance the connection ability between ABM and actual public health decision-making. In the future model design, it should start from specific decision-making issues, clearly define the policy scenarios to which the model serves, such as vaccine distribution, isolation strategies, school closures, medical resource allocation, or targeted population intervention, etc. The model output should not only stop at indicators such as the number of infections, incidence rate or mortality rate, but also further incorporate dimensions such as cost, health equity, medical system pressure and policy acceptability, in order to enhance its support value for real decision-making.

5. Conclusion

This article provides a comprehensive review of ABM in the field of public health control, systematically analyzing its basic concepts, main characteristics, application scenarios, and model construction processes. The study reveals that the construction of public health ABMs generally involves four core components: the specification of agents and populations, the design of environmental and spatial structures, the construction of contact mechanisms and social networks, and the formulation of disease state transition mechanisms. Different construction methods will directly affect the model's ability to represent real mechanisms, and further influence its disease explanation ability, risk prediction ability, and policy support ability. Furthermore, this article also points out that current public health ABM research still has issues such as insufficient reporting transparency, inadequate calibration and validation, strong data dependence, and limited decision-making transformation. Future research should place greater emphasis on the transparency of model construction logic, the standardization of validation procedures, and the connection with decision-making practices. In general, understanding ABM from the perspective of construction methods not only helps deepen the understanding of modeling complex systems in public health, but also provides valuable references for future model design and public health decision support.

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