Infectious Disease Prediction Model: A Systematic Review

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Abstract: Predictive modeling for infectious diseases plays a vital role in guiding global public health strategies, supporting epidemic containment, assessing pathogen severity, and optimizing healthcare resource allocation. The COVID-19 pandemic has spurred extensive research in epidemic forecasting, offering valuable insights for public health decision-making. This article systematically reviews studies up to 2025, focusing on dynamic models, time series models, machine learning models, and hybrid models. It examines their theoretical foundations, applications, and evolution in COVID-19 prediction, and critically compares their performance, limitations, and suitability across different scenarios-such as short-term case forecasting, long-term trend simulation, and medical resource demand warning. The review aims to outline future research directions and provide guidance for researchers in model selection and integration.

Keywords: Infectious Disease Prediction; Dynamic Models; Systematic Review; COVID-19

1. Introduction

Infectious diseases have become one of the main causes of human death: Over the past decade or so, major epidemics caused by the Ebola virus, the Middle East Respiratory Syndrome Coronavirus (MERS-CoV), and the 2019 novel coronavirus (COVID-19) pandemic have demonstrated how prevalent pathogens can spread rapidly in healthcare institutions[1]. Every year, millions of people die from infectious diseases. The pandemic has exerted profound impacts on population health, reducing global life expectancy by 1.8 years between 2019 and 2021-the sharpest decline in recent history-and eroding gains in health achieved over the preceding decade. Rising levels of anxiety and depression linked to the pandemic have shortened global healthy life expectancy by approximately six weeks, counteracting improvements in non-communicable disease mortality during the same period[2]. To design effective interventions against infectious diseases, it is essential to identify determinants of transmission. Understanding these factors enables more accurate forecasting, which in turn informs policy decisions such as vaccine procurement, public awareness initiatives, and training programs for healthcare personnel Essentially, infectious disease prediction is a time prediction task[3]. It involves various samples over a certain period of time and different influencing parameters to predict the trend of infectious disease infections in the future.

Up to now, numerous approaches have been developed for infectious disease prediction. Kermack and Mckendrick proposed the SIR compartment model in their paper on infectious disease modeling, which is recognized as the most classic infectious disease dynamic model based on the single-population method. Initially, this model was constructed to describe the spread of plague and the Black Death. The advent of the SIR model spurred extensive research on compartment models. Bailey published “Mathematical Epidemiology”, marking the flourishing development of infectious disease dynamics research. Subsequently, extended compartment models such as SEIR were developed, which together with the SIR model form the two classic frameworks in the field of infectious disease dynamics. Time series analysis is an effective method for modeling data arranged in chronological order[4][5].

Among them, ARIMA and Prophet are currently popular time series prediction models. The ARIMA model decomposes a time series into trend, seasonality, and residual components through differencing, and predicts future values based on statistical relationships between historical data using autoregressive and moving average mechanisms. Its parameters can be optimized to minimize prediction errors, and it has been widely applied in finance, business, and weather forecasting, among other fields. Prophet is a Bayesian time series model with an additive structure developed by Facebook, specifically designed for scenarios with strong seasonality, holiday effects, and missing data. It can automatically identify trend change points and separately estimate trend terms, periodic components (such as daily, weekly, and annual cycles), and the impact of outliers, thereby achieving robust prediction of complex time series.

In infectious disease prediction, Machine learning techniques have also shown considerable promise in capturing spatial and temporal transmission dynamics. Their ability to process high-dimensional, nonlinear data allows the identification of subtle patterns that may elude traditional statistical methods, leveraging diverse data sources such as electronic health records, genomic data, and social media. However, the acquisition of high-quality data remains a key challenge restricting its application: real-world data often has incompleteness, bias, or noise, and some infectious diseases have long incubation periods, making historical epidemic data difficult to accurately reflect the current epidemic situation. To address these issues, researchers have adopted various machine learning methods including decision trees, random forests, support vector machines, and deep neural networks. In addition, to improve prediction performance, hybrid approaches that combine mechanistic models with data-driven techniques are gaining attention for their potential to balance interpretability with predictive power.

This article aims to conduct a comprehensive and systematic review and summary of the research on infectious disease prediction based on dynamic models, time series analysis, machine learning, and hybrid methods. Through analysis of the construction principles, application scenarios, and performance in actual epidemic prediction of various models, it is ultimately hoped that this review will provide direction references for future research and offer suggestions in terms of model selection, integration strategies, and policy support, thereby enhancing the global prediction and response capabilities for COVID-19 and other emerging infectious diseases.At the same time, this article is also the first one to comprehensively discuss both the single model and the hybrid model.

As shown in Figure 1, this review will discuss and summarize each of the model categories classified in the figure one by one.

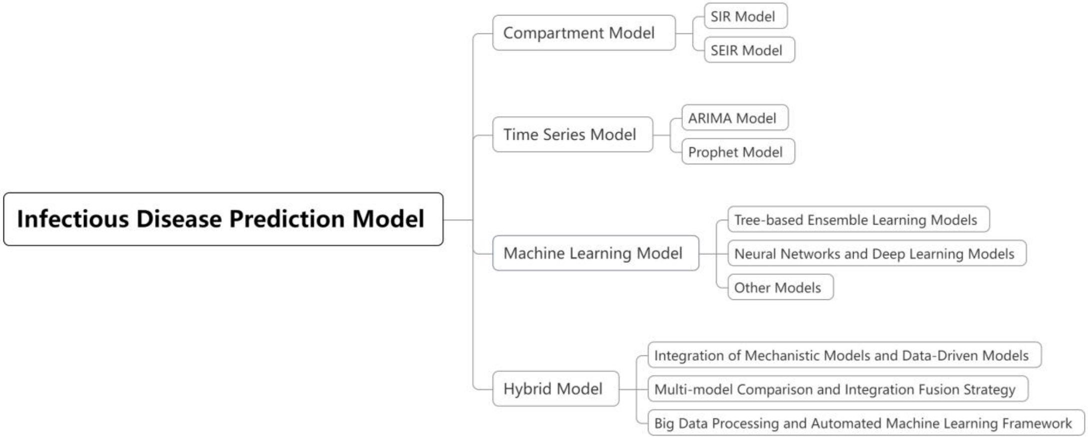

Figure 1. Classification of The Model

As shown in Figure 1, this review will discuss and summarize each of the model categories classified in the figure one by one.

2. Dynamical Models Of Infectious Diseases

The SIR model and the SEIR model are two classic models in the field of infectious disease dynamics. To better align with the actual situation of the epidemic, researchers have established a modified SEIR model by adding multiple parameters and modules. Currently, there are many research projects that use these three models to predict the trend of infectious disease incidence[6].

2.1 SIR Model

The demand for the application of transmission dynamics models in predicting the development trend of epidemics is high, and they are widely used in the modeling and analysis of various infectious diseases. The SIR model is the most common model among population-based models.The SIR model divides the population into three categories:

A. Susceptible: Individuals in the population who have not yet contracted the infectious disease but are at risk of infection.

B. Infectious: Individuals who are infected with the infectious disease virus and are contagious.

C. Recovered: Individuals who have contracted the infectious disease but have recovered and gained immunity.

The SIR model is based on three assumptions:(1) Demographic processes such as births, deaths, and migration are neglected; (2) Contact between infectious and susceptible individuals leads to new infections at a rate proportional to the product S(t)I(t). (3) Recovery occurs at a rate proportional to the number of infectious individuals.

Based on the above three states, the basic SIR model equations can be established as follows:

$$\frac{dS(t)}{dt}=-\beta S(t)I(t) \tag{1}$$

$$\frac{dI(t)}{dt}=\beta S(t)I(t)-\gamma I(t) \tag{2}$$

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

In the above equation: β denotes the transmission rate and γ the recovery rate. Initial conditions are specified as $S(0),I(0),R(0)$. The recovery term at time t equals $\gamma I(t)$. The value of β can be solved by fitting I(t) using methods such as the least squares method, maximum likelihood function method, Markov chain Monte Carlo method (MCMC), and Runge-Kutta methods[7].

Researchers have conducted targeted model enhancements by focusing on specific stages of epidemic progression and critical external confounding factors. In[8], He et al. proposed a fractional-order SIR epidemic model that accounts for parameter seasonality and external noise, and designed a hard limiter control system to fit the early-stage trends of infectious disease outbreaks. In [9], Cooper et al. augmented the classic SIR model to accommodate the surge in susceptible individuals during the COVID-19 outbreak, enabling it to adapt to rapid increases in the susceptible population. They further estimated key epidemiological parameters for disease transmission across diverse communities .

Another pivotal direction for improvement involves integrating macroscopic epidemiological models with microscopic individual behavioral decisions, using stochasticity to simulate population behavioral heterogeneity and its impact on transmission dynamics. Karako et al. developed a stochastic transmission model[10] that additionally simulates individual decisions to avoid crowded areas. This work links macroscopic epidemiological parameters to microscopic behavioral choices and enriching modeling frameworks. Their conclusions indicate that reducing individuals' daily time spent in crowded areas to less than 4 hours could effectively curb the spread of the epidemic in Japan.

Given that fixed parameters fail to capture dynamic changes in epidemics driven by interventions and behavioral shifts, a core breakthrough in subsequent research has been the formulation of key parameters as time-varying functions or history-dependent variables, followed by data-driven high-precision calibration via inverse engineering. Dos Santos et al.[11] modeled the critical epidemiological parameters-transmission rate and recovery rate-as time-varying dynamic parameters instead of fixed constants, allowing the model to automatically adapt to changes in transmission characteristics induced by control measures and population behavioral modifications during epidemic progression. Alshomrani and Ullah[12] constructed a fractional-order SIR model based on the Caputo derivative, introducing fractional calculus to describe the historical dependence of epidemic transmission and determining the optimal fractional order via optimization algorithms. Chen and Lu[13] developed a time-varying parameter SIR model, whose core contribution lies in the explicit division of the total infected population into two heterogeneous subgroups-“detectable” and “undetectable”-for the first time.

2.2 SEIR Model

The SEIR model is currently the most representative fixed-population infectious disease dynamics model. This model is mainly aimed at infectious diseases with a long incubation period. It adds the latent population (E) on the basis of the SIR model. The basic assumptions of the model are as follows: (1) Population changes are not considered, that is, the total population in this area is a fixed value, and the total number of the four populations (N) remains unchanged at any time, N = S(t) + E(t) +

I(t) + R(t). (2) The traditional SEIR model assumes that the incubation period is not contagious. After a certain incubation period, it transforms into an infected person. The probability that one infected person infects one susceptible person per unit time is β, which is also known as the infection coefficient. (3) The rate at which pathogen carriers transform into infected individuals is α, and α is the reciprocal of the average incubation period. (4) The rate at which individuals from the infected population leave is γ. It is assumed that the removed population R no longer has contagiousness or the ability to be reinfected, and γ is the cure rate, 1/γ is the average cure period length.

The basic SEIR model equations can be established as follows:

$$\frac{dS(t)}{dt}=-\beta S(t)I(t) \tag{4}$$

$$\frac{dE(t)}{dt}=\beta S(t)I(t)-\alpha E(t) \tag{5}$$

$$\frac{dI(t)}{dt}=\alpha E(t)-\gamma I(t) \tag{6}$$

$$\frac{dR(t)}{dt}=\gamma I(t) \tag{7}$$

$$N=S(t)+E(t)+I(t)+R(t) \tag{8}$$

To provide a clear visual representation of the structure and flow of the SEIR model, Figure 2 illustrates the transition dynamics among the four compartments. As shown in the figure, susceptible individuals (S) become exposed (E) upon effective contact with infectious individuals (I) at a rate governed by the transmission coefficient β. Following the average incubation period, exposed individuals progress to the infectious compartment (I) at a rate α. Subsequently, infectious individuals transition to the recovered compartment (R) at a rate γ, after which they are assumed to be immune and no longer contribute to transmission. This compartmental structure forms the basis for the system of ordinary differential equations presented in Equations (4)–(8).

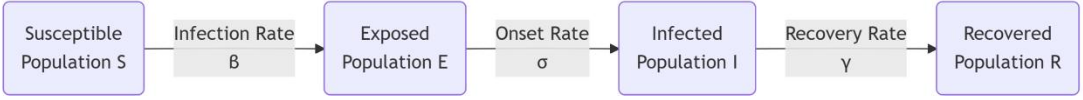

Figure 2. Principle of SEIR Model

To better align with the biological characteristics of COVID-19, which has an incubation period, many studies have adopted SEIR models that incorporate an "exposed" compartment. These models significantly enhance the accuracy of depicting the early dynamics of the epidemic by distinguishing between "infected but not yet infectious" individuals and have become powerful tools for evaluating the immediate effects of non-pharmaceutical interventions (NPIs). The work by He and Peng [14] is a representative example in this regard. They applied the SEIR model to analyze the early epidemic in China and successfully quantified the immediate effects of measures such as the "lockdown of Wuhan". The research by Hou et al.[15] is representative of this stage. They based their analysis on the classical well-mixed SEIR model and quantified the effect of the Wuhan lockdown as a reduction in the contact rate of individuals in the incubation period to 6-18 times per day.

With the advent of vaccines, the research focus of the SEIR model has naturally shifted from simple transmission prediction and NPI evaluation to integrating the vaccination process, aiming to provide theoretical guidance and quantitative benchmarks for long-term strategies to establish herd immunity. The work by Wintachai and Prathom[16] incorporated the vaccination process into the SEIR model and conducted in-depth dynamical stability analysis. Their theoretical proof indicated that when the control reproduction number, which includes vaccine parameters, is suppressed below 1, the system will tend towards a globally stable disease-free equilibrium point. Li et al.[17] developed a time-dependent SEIR model that simultaneously incorporated the effects of NPIs (reflected as time-varying transmission rates) and the vaccination process into a unified framework. Through scenario simulations, the model dynamically quantified the relative weights and synergistic effects of the two measures at different stages of the epidemic.

The development of the epidemic in the real world is not only governed by the biological characteristics of the virus and external interventions but also profoundly influenced by adaptive changes in population contact behaviors due to risk perception or resource constraints. To capture this complex feedback, researchers have introduced nonlinear incidence functions or explicit behavioral feedback mechanisms into the SEIR model. Mandal et al.[18] introduced a saturated incidence function $\beta SI/1+\alpha I$ into the SEIR model to describe the "saturation effect" where the transmission efficiency decreases as the number of infected individuals increases due to behavioral changes or strained medical resources. Kim et al.[19] developed a model that explicitly incorporates behavioral feedback mechanisms due to risk perception. In this model, the effective contact rate or transmission rate dynamically decreases as the scale of infection increases, simulating the public's spontaneous protective behaviors.

One of the important functions of mathematical models is to provide early warnings for the medical system to deal with the impact of the epidemic. The stochastic SEIR model constructed by Chatterjee et al.[20] for India not only predicted the trajectory of the epidemic but more importantly quantitatively assessed its impact on the medical system, indicating that the demand for ICU beds at the peak could be as high as 102,000. Foy et al.[21] used an age-structured transmission model to systematically compare three vaccine distribution strategies in the Indian context.

3. Time Series Prediction Models

Time series models predict possible future outcomes based on existing historical information. This review will focus on summarizing the research of ARIMA and Prophet on infectious disease prediction.

3.1 Autoregressive Integrated Moving Average Model

The ARIMA model combines autoregressive (AR), differencing (I), and moving average (MA) components.For series with seasonal patterns, a seasonal multiplicative ARIMA(p,d,q)(P,D,Q)_s is often used[22]. In this framework, the parameters p, d, and q denote the orders of the non-seasonal autoregressive, differencing, and moving average components, respectively, while their seasonal counterparts (often denoted as P, D, and Q capture the analogous seasonal dynamics[23].

As a purely data-driven predictive tool, the classic ARIMA model, with its simplicity and efficiency, was widely used in different countries and regions for short-term trend extrapolation and risk assessment in the early stage of the pandemic. Its universal applicability has been verified by multiple independent studies. Roy et al.[24] directly applied the ARIMA model to the cumulative case data series of various Indian states for short-term prediction and drew a spatial distribution map of epidemic risks based on this. Alzahrani et al.[25] constructed an ARIMA(2,2,0) model for Saudi Arabia for short-term prediction. The prediction showed that the cumulative case curve was monotonically increasing but with a slowing growth rate. Kufel[26] systematically established ARIMA models for multiple European countries including Poland, Germany, and France. This work not only predicted the number of cases but also simultaneously calculated the changing trends of infection rates and fatality rates, and pointed out that the latter could serve as an early warning indicator of medical risks.

3.2 Prophet Model

Taylor et al.[27] proposed Prophet, which employs multiple nonlinear and linear methods as components and takes time as a regression variable. This model ignores the time dependence of the data, and the training is only set to the exercises of curve fitting. Therefore, irregular observations are also allowed in the dataset. The main idea is to decompose the time series into multiple parts such as trends (such as linear growth, saturated growth or segmented trends), seasonality (annual, weekly, daily, etc.) and holidays (or other special events), and fit the data through additive models. It is simple, fast and efficient to use, and can better predict future trends, especially when dealing with data with outliers. It has a good effect and is widely used in trend prediction in the medical field.

The model structure is as follows:

$$y(t)=g(t)+s(t)+\mathrm{h}(t)+\varepsilon(t) \tag{9}$$

Where $g(t)$ captures the underlying trend component-modeling long-term, non-repeating movements in the series. $s(t)$ accounts for the seasonal component, reflecting regular, repeating fluctuations tied to fixed calendar intervals. $\mathrm{h}(t)$ encodes holiday-related effects, capturing transient, event-driven deviations associated with specific dates or periods (such as festivals or public holidays). and $\varepsilon(t)$ denotes the residual or innovation term, embodying unexplained variability.

Xie et al.[28] applied the Prophet model developed by Facebook to predict the incidence of hand-foot-mouth disease. Such models have unique advantages in handling infectious disease data with strong seasonality and cyclical fluctuations. Mahanty et al.[29] empirically tested this, directly applying the Prophet model to global COVID-19 case data. The results showed that Prophet not only effectively fitted the growth trend of the epidemic but also outperformed the traditional ARIMA model in terms of prediction accuracy.

4. Machine Learning Model

Machine learning algorithms have demonstrated strong potential in predicting the spread and emergence of infectious diseases, often matching or exceeding the performance of traditional statistical approaches. There are numerous algorithm models in machine learning. In this section, these models will be classified by category without being listed one by one.

4.1 Tree-based Ensemble Learning Models

The tree-based ensemble learning model accomplishes prediction tasks by constructing and combining multiple decision trees. Its core idea is "pooling wisdom", which combines multiple weak learners (usually shallow-depth decision trees) to form a strong learner. This type of method effectively overcomes the shortcomings of single decision trees, such as easy overfitting and poor stability. By introducing randomness and adopting weighted average or voting mechanisms, it significantly enhances the generalization ability, prediction accuracy and robustness of the model.

In the field of infectious disease prediction, data often have characteristics such as high dimensionality, nonlinearity, interaction and missing values. The tree-based ensemble model has advantages such as loose requirements for data distribution assumptions, the ability to automatically handle feature interactions, and the combination of predictive performance and interpretability. It has become one of the core tools for predicting the trend of disease transmission, identifying high-risk areas and populations, and evaluating the effectiveness of intervention measures.

As the core predictor, these models demonstrate robust and outstanding performance when dealing with multivariate and high-dimensional feature data. They can automatically handle the interactions between features without the need for complex preprocessing, making them powerful tools for predicting various infectious diseases. Meng et al.[30] systematically applied and compared two algorithms, namely Random Forest and XGBoost, for predicting the incidence of hand-foot-mouth disease in China. Guo et al.[31] in the study of predicting hepatitis E, compared various machine learning models and found that Random Forest performed the best in prediction performance, demonstrating its applicability in the field of viral hepatitis prediction. Chumachenko et al.[32] specifically explored the use of the Random Forest method to predict the course of the COVID-19 pandemic, further verifying the practicality and effectiveness of such models in responding to acute pandemics.

Tree-based models not only predict but also provide the intrinsic "feature importance" output, which can help researchers identify key risk factors and deepen the understanding of the disease driving mechanism. Pickering et al.[33] research did not focus on achieving ultimate prediction accuracy but rather on identifying various factors that affect the AI prediction of COVID-19 cases. Ahmad et al.[34] in the research of improving COVID-19 prediction, explored the use of various machine learning algorithms such as Random Forest to optimize the output of infectious disease dynamics models.

4.2 Neural Networks and Deep Learning Models

Neural networks and deep learning models simulate the connections and signal processing mechanisms of human brain neurons to construct computational networks with multi-level abstract learning capabilities. Unlike tree-based models that focus on structured feature analysis and integrated decision-making, the core advantage of deep learning lies in its ability to automatically learn deep representations and complex patterns from raw or high-dimensional data, especially excelling in handling unstructured or spatiotemporal data such as images, sequences, and graph structures. In the field of infectious disease prediction, the spread of epidemics is essentially a dynamic process with spatiotemporal dependence and complex nonlinear driving factors. Deep learning models provide a powerful modeling framework for depicting the temporal evolution of case curves, spatial diffusion networks, and the fusion of multiple heterogeneous data sources.

Recurrent neural networks (RNNs), especially Long Short-Term Memory (LSTM) networks, are widely used for temporal forecasting. Absar et al.[35] conducted a systematic evaluation of deep learning models based on LSTM in predicting the outbreak of infectious diseases (such as dengue fever, influenza). Their research showed that LSTM can effectively learn the long-term dependencies and temporal patterns in case data. Chimmula and Zhang[36] specifically used LSTM networks to conduct time series prediction of the COVID-19 spread in Canada, confirming the model's ability to capture the complex transmission trajectory of this epidemic. Additionally, Ardabili et al.[37] in their early COVID-19 prediction research, also systematically compared various machine learning models including artificial neural networks (ANN), verifying the effectiveness of neural network models in trend prediction during the initial stage of the epidemic outbreak.

As applications deepen, research focus has shifted from validating the basic LSTM model to exploring more advanced neural network architectures to address more complex prediction challenges, including handling multi-variable inputs, capturing spatio-temporal correlations, and optimizing attention mechanisms. Kamana et al.[38] adopted a more advanced LSTM-Seq2Seq (sequence-to-sequence) architecture to predict the impact of climate change on the risk of malaria resurgence in China. This model can handle multi-variable input sequences and output predictions for future time steps. Nguyen et al.[39] compared the performance of LSTM, ConvLSTM (convolutional LSTM), and Transformer models in predicting dengue fever in Vietnam using climate data, showcasing the potential of cutting-edge deep learning architectures in linking environmental factors with disease dynamics. Verma et al.[40] proposed a specialized temporal deep learning architecture for predicting COVID-19 cases in India, further enhancing the ability to capture complex epidemic time series patterns. Zhang et al.[41] further proposed an attention-oriented model, optimizing the attention mechanism to predict infectious disease cases more accurately, highlighting the targeted application of attention mechanisms in this field.

To further enhance model interpretability and data utilization efficiency, cutting-edge research has explored hybrid paradigms that integrate epidemiological mechanisms with deep learning, as well as innovative methods using generative models to create synthetic data or simulate epidemic trajectories. Wang et al.[42] innovatively combined generative adversarial networks (GANs) with epidemiological principles, proposing epidemiology-based generative adversarial networks (Epi-GANs) to predict the epidemic trend of COVID-19. Additionally, deep learning has been used to reveal the intrinsic mechanisms of transmission. Murphy et al.[43] utilized deep learning techniques to directly learn the transmission dynamics on complex contact networks, providing a new paradigm for understanding the spread of diseases in structured populations.

Facing the core practical challenges in infectious disease prediction, such as spatiotemporal heterogeneity and the scarcity of data on emerging diseases, researchers have developed specialized spatiotemporal prediction models and introduced transfer learning strategies, significantly enhancing the applicability of deep learning in public health practice. Shen et al.[44] specifically employed a convolutional long short-term memory network (ConvLSTM) to predict the spatiotemporal distribution of human brucellosis in Europe. This architecture can simultaneously extract spatial features and temporal dependencies. Xu et al.[45] used deep learning to forecast dengue cases across 20 Chinese cities. Additionally, to address the challenge of scarce data on emerging infectious diseases, Roster et al.[46] explored transfer learning strategies, using models pre-trained on existing disease data to quickly adapt and predict the spread of new diseases.

4.3 Other Models

In addition, there are other machine learning models used for predicting infectious diseases, such as regularized linear models, Bayesian machine learning methods.

4.3.1 Regularized linear model

These models are essentially an extension of linear regression, by adding regularization terms such as L1 (LASSO), L2 (ridge regression), or a combination of both (Elastic Net) to perform feature selection or handle multicollinearity during the fitting process. Their greatest advantage lies in their efficiency, strong interpretability, and suitability for high-dimensional small-sample data, enabling automatic selection of the most relevant few variables from a large number of potential predictors.

Application in infectious disease prediction: They are often used for real-time prediction and identification of key drivers. For instance, Chen et al.[47] cross-national comparative study demonstrated that LASSO performed robustly in real-time predictions of endemic infectious diseases such as influenza and dengue fever, with practicality comparable to complex models . Katragadda et al. [48] used elastic net to analyze the relationship between the growth rate of COVID-19 cases in the United States and the mobility of different types of populations, effectively identifying key predictors . Nsoesie et al.[49] utilized LASSO to correlate Google search data with the trend of influenza-like diseases, demonstrating its applicability in digital stream data modeling .

4.3.2 Bayesian machine learning methods

These methods combine Bayesian statistical principles with machine learning models. The core of these methods is to integrate prior knowledge (such as epidemiological assumptions) into the model in the form of probabilities and output predictions along with their uncertainties in the form of posterior distributions. This provides a natural probabilistic framework and the ability to quantify uncertainty.

They are applicable to scenarios that require risk assessment, spatial prediction, and the incorporation of domain knowledge. Ak et al. [50] used Bayesian networks to predict Crimean-Congo hemorrhagic fever and identified the probabilistic relationships among key risk factors . Niraula et al. [51] proposed a Bayesian machine learning method for spatio-temporal prediction of COVID-19, combining the flexibility of Bayesian inference with the data fitting ability of machine learning.

4.4 Hybrid Model

A single model does have unique advantages in a certain aspect, but its drawbacks are also obvious. Meanwhile, the hybrid model, by integrating the advantages of different models, aims to enhance the accuracy, robustness or interpretability of the predictions. It is currently the forefront and mainstream direction of research. This review classifies the hybrid models into the following three categories

4.4.1 Integration of mechanistic models and data-driven models

The integration of mechanistic models and data-driven models involves using data-driven methods to calibrate, enhance, or supplement theoretical epidemiological models, in order to achieve complementary advantages of mechanistic insights and data fitting capabilities. Such studies typically use classic compartmental models (such as SIR, SEIR) as theoretical frameworks, and employ machine learning methods to estimate key parameters (such as transmission rates) from real-time data, simulate the impact of intervention measures, or compare and synthesize the outputs of both.

The most direct application of hybrid modeling is to use machine learning algorithms to infer or optimize the key time-varying parameters (such as transmission rates) in the mechanistic model from real-time data, thereby improving the simulation accuracy of the model under complex intervention conditions. Alsmadi[52] proposed a hybrid framework that combines the classic SEIR (Susceptible-Exposed-Infectious-Recovered) compartment model with machine learning predictions to analyze the COVID-19 epidemic in Jordan. Similarly, Ahmad et al.[53] also explored the use of multiple machine learning algorithms (such as random forests, gradient boosting) to optimize and improve the prediction output of infectious disease dynamics models, thereby enhancing the prediction accuracy of COVID-19 cases.

Another integration approach is to concurrently construct and compare mechanistic models and machine learning models, through mutual verification and complementarity, to form a more comprehensive and robust judgment of the epidemic trend. Haq et al.[54] proposed a "dual application" framework when predicting the COVID-19 epidemic in Bangladesh: on the one hand, using the SIR model for theoretical simulation, and on the other hand, applying multiple machine learning algorithms (such as linear regression, support vector regression) for data-driven prediction, and comparing and complementing the results of both to provide a more comprehensive perspective. Kumar et al. and Lmater et al.[55, 56] also followed a similar approach, with the former constructing a prediction model from a statistical modeling perspective and the latter using machine learning combined with intervention relaxation scenarios to predict the spread of COVID-19.

Further research is dedicated to developing a systematic methodology that integrates the advantages of different models into a unified prediction framework, even incorporating more dimensions of real-world constraints (such as age structure, medical resources) and higher-order data into the fusion framework, in pursuit of higher prediction robustness and policy evaluation capabilities. For example, González-Bandala et al.[57] developed a comprehensive computational prediction methodology for acute respiratory infectious disease dynamics modeling, with the core idea being to integrate the advantages of different models to generate robust predictions. Wang et al.[58] further advanced their research by using models to predict the dynamics of COVID-19 under imperfect vaccination assumptions, demonstrating a comprehensive assessment approach from prevention policies to epidemic prediction. Yang et al.[59] conducted a representative study in the early stage of the COVID-19 pandemic, using an improved SEIR model combined with artificial intelligence (AI) prediction to assess the epidemic trend under public health intervention in China. Kumari and Toshniwal[60] explored real-time COVID-19 case estimation via machine learning and mathematical models in India. Mei et al.[61] further incorporated dynamic age structure and medical resources into the calculation of infectious disease transmission rates, demonstrating the advantages of hybrid models in integrating complex real-world constraints.

4.4.2 Multi-model comparison and integration fusion strategy

Multi-model Comparison and Integration Fusion Strategy is to obtain a more robust and reliable prediction output by systematically comparing or integrating the prediction results of multiple models.

Adiga et al.[62] proposed a Bayesian ensemble framework for the high-resolution COVID-19 prediction problem. This framework does not build a single optimal model but instead performs Bayesian averaging of the prediction results from multiple different types of sub-models. Ardabili et al. [63] conducted a systematic comparison of models such as adaptive neuro-fuzzy inference system (ANFIS), multi-layer perceptron (MLP), and random forest (RF) in COVID-19 prediction performance, providing empirical evidence for model selection. Benedum et al.[64] provided weekly forecasts for dengue fever in Iquitos, San Juan, and Singapore, integrating multiple forecasting methods including seasonal autoregressive models, demonstrating the potential of an operational ensemble forecasting system. Dixon et al.[65] conducted a large-scale cross-sectional study, systematically comparing various forecasting methods including autoregressive models, machine learning models (such as random forest) and ensemble methods in the performance of different locations, diseases (such as influenza, dengue fever, etc.) and time periods. Chaurasia and Pal[66] research also focused on applying and comparing various machine learning time series analysis methods (possibly including ARIMA, Prophet, LSTM, etc.) to predict the COVID-19 pandemic. Masum et al.[67] applied ARIMA and LSTM simultaneously when predicting the daily increase in COVID-19 cases in Bangladesh, and compared their performances, demonstrating the contrast and combination of traditional time series models and deep learning models. Xu et al.[68] explored earlier the method of combining Google search queries with statistical models for predicting influenza activity in Hong Kong, demonstrating the value of multi-source data and model integration. Fan et al.[69] explicitly adopted the stacking ensemble (Stacking) meta-learning framework, integrating the prediction results of infectious disease dynamics models and traditional machine learning models to improve the prediction performance of the COVID-19 pandemic.

4.4.3 Big data processing and automated machine learning framework

Big Data Processing and Automated Machine Learning Framework lies in addressing the computational challenges posed by massive and multi-source data, and reducing the technical barriers to professional modeling to achieve efficient and reproducible predictions. As the volume of data increases, new computing architectures are required; at the same time, in order to respond quickly to the epidemic, automated tools have become crucial.

Dash et al.[70] proposed a big data-driven intelligent prediction model (BIFM) for COVID-19 prediction. This model is likely to integrate big data processing technologies and advanced machine learning algorithms to address the challenges brought by massive and multi-source epidemic data. Asfahan et al.[71] used an open-source AutoML algorithm to predict the spread of COVID-19. This study demonstrated that even with a relatively simple AutoML process, a prediction model with certain accuracy could be quickly generated. Goo et al.[72] research on the prediction of the COVID-19 situation in South Korea may have also applied similar automated or standardized modeling processes to ensure the timeliness and repeatability of the predictions.

5. Conclusion

Infectious disease prediction has advanced significantly, driven by global public health needs, especially during COVID-19. Each modeling class has distinct strengths: dynamic models provide theoretical insights into transmission and interventions; time series models offer efficient short-term forecasts; machine learning captures complex nonlinear relationships; and hybrid frameworks combine interpretability with predictive power. However, all models depend heavily on data quality and timeliness. Challenges remain in model interpretability, real-time calibration under non-stationary conditions, and deeper integration of mechanistic and data-driven approaches. Future work should focus on developing transparent, robust, and standardized modeling platforms, while fostering interdisciplinary collaboration to ensure practical relevance in epidemic preparedness and response.

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