# Summary of the Dynamic Model of Infectious Disease Transmission and its Application

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## Abstract

**The epidemic of infectious diseases has brought harm to society, so the study of the epidemic trend of viruses has been widely concerned by researchers. In this paper, by analyzing the current research status at home and abroad, the prediction models of infectious diseases are classified, and the principle and application of each model are introduced respectively. It mainly includes differential equation model, mainly introduces SIR, SEIR model, time series model ARIMA model and BP neural network model, compares the advantages and disadvantages of each model, helps readers quickly understand the main tasks and common methods of current model research. Finally, the methods and progress of infectious disease research models are summarized, the existing problems are analyzed, and the future research directions are prospected.**

## Keywords

**Infectious Disease, Prediction, Dynamical Model, Neural Network.**

## 1. Introduction

The outbreak of COVID-19 broke out in Hubei Province of China at the end of 2019. The virus spread widely in many regions within a short period of time, and the epidemic spread rapidly to other regions. In terms of the global epidemic situation, the number of infected people in the United States, India and other countries also rose sharply. Early in order to suppress the illness spread quickly, China is quickly implement a series of emergency control measures, including sealing city of Hubei province, delay in all cities in China to return to work, school, the open level emergency response, home quarantine, etc. In the short term, these measures played an obvious inhibiting communication effect, in just a few months at home, add in the number of cases, however, Long-term prevention and control measures will have a huge negative impact on the country's economy and people's lives, so it is very important to make effective and optimal decisions at the national level.

The transmission time has been nearly two years, no matter from the aspects of time or infections are much more than 2003 of SARS, it can be seen that there are many uncertain factors in the unknown field is temporarily unable to solve the human existing technology, new viruses harm have been, in the face of severe complex trend of infectious diseases. The model plays a crucial role in the application of all kinds of virus prediction. The prediction and analysis of the model will help to formulate prevention and control policies, and reduce the human and economic losses caused by the spread of the virus and the fight against the epidemic. The main contribution of this paper is to classify and summarize the dynamics models commonly used in the prediction of the spread of infectious

diseases, and at the same time discuss the practical application cases, and finally put forward conclusions and prospects.

## 2. Research Method

### 2.1 Literature Sources

Reference literature study, this article USES the representative articles related to this propagation dynamics model research, this article through two kinds of literature search, the first is through the CNKI database retrieval, time limit for 2000 to 2021, retrieval methods for search "epidemic" and contains "predict" or "model" for precise retrieval, The second method is to search the literature through literature tracing and study the initial modeling methods of infectious disease models. Through the above two methods, 34 relevant representative articles were finally determined.

### 2.2 Model Classification

At present, there are many methods used in the prediction model of infectious diseases. Through reading the research articles in related fields, this paper summarizes the widely used models and divides them into the following three categories:

(1) Differential equation model;

(2) Model based on time series;

(3) Artificial neural network model;

Among them, the classical forms of differential equation model are SIS model and SIR model, which are optimized to form SEIR model based on the basic SIR model. Among the propagation methods of time series model, ARIMA model is commonly used in infectious diseases, and the technology in the field of artificial intelligence is very suitable for modeling nonlinear systems. BP neural network model was also introduced into the medical field earlier.

## 3. Research Progress of the Model

### 3.1 Differential Equation Model

Differential equation model is a closed system, its main principle is to use differential equations describe the change in the number of relationship between several groups, reveal the natural development process of infectious diseases, but the model does not consider the artificial constraints, when to take effective control measures of infectious diseases, model predicted results and actual results may be there is a big gap. Classical models include SI model, SIR model, SIS model, SEIR model, etc. SI model applies to the situation of only susceptible and infected persons, and only considers the outbreak and transmission process of infectious diseases, while SIS considers the situation of repeated outbreaks of diseases. From the current research content, more studies are optimized based on SIR and SEIR.

#### 3.1.1 SIR Model

SIR model is a classic infectious disease model, which was first proposed by W.O. Kelmack and A.G.McKendrick[1][2] in 1927. This model includes susceptible S, infected I and removed R. It is assumed that the total number of people in the region is constant, and susceptible and infected persons are completely immune after recovery. The mathematical expression of this model is as follows:

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

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

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

Where, the total population N=S+I+R, S(t), I(t) and R(t) respectively represent the number of susceptible infected persons, infected persons and displaced persons at time t, β represents the infection rate (the probability of conversion from susceptible infected persons to infected persons), γ represents the cure rate (the probability of conversion from infected persons to displaced persons).

Yunlong Guo et al. [3] took buses and small private cars as the scenarios, introduced the virus transmission density, constructed SIR transmission models with different parameters and simulated the models, and analyzed the influence of different driving time, ventilation conditions and disinfection conditions on virus transmission. Wentao Wu et al. [4][5] constructed SIR model based on the official statistical data of Guangdong province and predicted the basic regeneration number of Guangdong province with exponential smoothing method, which showed that R0=1.65 on February 8 and continued to decline, and the inflection point appeared around February 21, indicating that the prevention and control measures in Guangdong province had a good effect on epidemic control. Vishal Deo et al. [6] introduced the concept of isolated and not isolated infected persons into SIR model and proposed SI(Q/F)RD model, which was used to predict the transmission situation in California and Florida. As for the characteristics of this pneumonia epidemic, SIR model did not consider the latent patients, which had certain limitations in prediction.

### 3.1.2 SEIR Model

SEIR model introduces cabin E into the basic SIR model, which represents the population in the incubation period. The model assumes that the total number of people is constant N, and they will get permanent immunity after recovery. The susceptible people will be infected when they contact with the infected people. To describe the spread of the virus, let the probability of infection be β, the probability of onset be λ, and the probability of transformation from class I cure or death to class R be γ (Figure 1).



**Figure 1**. SEIR model

Without considering any measures, the differential equations of this model can be expressed as:

$$\frac{dS(t)}{dt} = -\beta\, IS$$

$$\frac{dE(t)}{dt} = \beta\, IS - \lambda\, E$$

$$\frac{dI(t)}{dt} = \lambda\, E - \gamma\, I$$

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

Where S(t), E(t), I(t) and R(t) respectively represent the number of susceptible, latent, infectious and emigrated persons at time t.

Regarding the rapid spread of the new coronavirus, many scholars have devoted themselves to the study of the disease situation, and a large number of documents have been optimized based on the SEIR model. In the sudden outbreak of new coronary pneumonia, a large number of literatures used the SEIR model to predict the inflection point of the disease. Based on the complex network, the SEIR model was established to predict the spread of the virus and the inflection point. Ruguo Fan[7] and others analyzed the epidemic data in Wuhan. Set up three models with different incubation period scenarios to predict the inflection point. After comparing the epidemic situation in different incubation periods, they gave suggestions on epidemic prevention and control. Hui Geng et al. [8] predicted the epidemic under different intervention measures and explained prevention and control in detail. The impact of the measures on the epidemic pointed out the trend of outbreaks under the suspension of work and school and travel restrictions. The modified model proposed by Shengli Cao et al. [9] introduced the H cabin on the basis of which represents hospitalized patients. Junfeng Lin[10] introduced invisible communicators in the model. The literature pointed out that the definition of the SEIR model for the E model is too rough, and it is divided into Exposed and Undiscovered, which represent people in medical observation and suspected states, respectively.

### 3.1.3 SEIR Optimization

The SEIR model is currently the most commonly used model to study infectious diseases. According to the different characteristics of each virus, the basic model will be optimized accordingly, such as adding cabins, classifying cabins, considering control measures, changing assumptions, etc., and then The various optimization models described above are obtained. The effect of the optimization model can more simulate the actual virus transmission process, and the prediction accuracy is higher. In the past relatively major infectious disease transmission, such as the SARS virus transmission, some optimization models were generated. The following summarizes the classic optimization model.

G. Chowell [11] used the model to predict outbreaks in Hong Kong, Singapore and other places; the BloComp (2,7) model proposed by Juan Zhang et al. [12] is the optimization of a typical SEIR model, and the model is divided into 2 With independent areas and 7 cabins, the model divides the overall population into free and isolated areas, imitating the control strategy implemented in China, and the conclusion shows that isolation measures greatly reduce the basic reproductive number; SEIUR is a typical five-cabin model. It was proposed in 2004 that Glenn F. Webb et al. [13] used to study the spread of SARS in the Toronto area, and pointed out the role of hospitals in the process of spreading. After implementing the methods of hospital control and community isolation, it effectively reduced the secondary incidence. Infection rate, this model proposes two models corresponding to the SARS outbreak stage. Model 1 is the previous model including SEIUR, and the U cabin is proposed on the SEIR model, which represents direct contact with the infection environment in the hospital environment, which may be infected but not cause the public Threatened populations, each of which is divided into the public (g) and medical care and patients (h). In Model 2, second-generation infection cases are introduced. These cases have been quarantined before being sent to the hospital. The public has only low risk; Marc Lipsitch et al. introduced cabin D on the basic model in the SEIDR model, and the population in this cabin is an isolated infected person [14].

Y.Zhou[15] proposed a discrete mathematical model to study the spread of SARS and its basic reproductive number. The model contains six cabins called SEIQJR. The Q cabin has been added to the basic SEIR model. People who are infected and quarantined but have not yet been diagnosed, the newly added J compartment represents the people who are infectious, have been diagnosed and have been quarantined. This model is used to predict the spread of the SARS virus, and it is mentioned that it is assumed that the E-category population is also certain Infectiousness; Wendi Wang et al. [16] used the model to simulate the SARS outbreak in Beijing, proposed the SEQSPR model, and divided the general model into two simple models, the two-compartment susceptible model and the single-compartment-possible model. Of course, it is also used in the characteristics of other infectious diseases. Huang Huang[17] used the SEIR model to study the small-scale outbreak of norovirus in hospitals, and compared and analyzed the natural transmission and the spread of the virus after

prevention and control measures were taken at different points in time. The effect of isolation time is evaluated, and the prediction effect of the model is compared with the actual data to reach a conclusion that the model predicts well.

## 3.2 Time Series Model

Time series prediction model belongs to quantitative prediction, which assumes that the change of the predicted object is only related to time, and predicts its future state based on the principle of inertia according to its change characteristics. Deterministic time series models include exponential curve model, quadratic curve model and so on. Random time series models are suitable for the prediction of data without some typical trend characteristics. The commonly used random time series models include ARIMA model, exponential smoothing model and so on.

### 3.2.1 Autoregressive Moving Average Model

ARIMA is a model for the prediction of infectious diseases, which is suitable for the prediction of infectious diseases with seasonal trends. The model structure is:

$$ARIMA(P,D,Q) \times (P,D,Q) \ S.$$

Where, P is the order of autoregression, q is the order of moving average, D is the difference operation to extract the deterministic information of the original sequence, P and Q are the order of seasonal autoregression and seasonal moving average, D is the number of seasonal difference, and S is the seasonal period and cycle length. Zhaohua Shi et al.[18] applied ARIMA model to the prediction of 6 common respiratory infectious diseases, and the results were satisfactory. Moreover, the study showed that ARIMA model had higher accuracy by comparing the prediction of uniform data between exponential curve model, gray model and ARIMA model[[19],[20]]. However, ARIMA model is not suitable for the prediction of infectious diseases with large data fluctuations. If there is no obvious cyclical or seasonal trend of infectious diseases, the model is difficult to predict accurately[21].

There are also many studies that combine ARIMA with other technologies. Lu Yu[22] proposed that since most infectious diseases have the characteristics of small samples, considering the advantages of SVR in processing small sample data, SVR should be combined with ARIMA, and time series model should be applied and combined with neural network. For example, ARIMA-GRNN[23] predicted that the accuracy was higher than ARIMA model. At present most of the research still use the spread of infectious diseases of the dynamic model of forecasting, time sequence model of autoregressive moving average model (ARIMA model) with time sequence to study the regularity of virus [19], the main rules suitable for time, relatively stable data for virus research, has great limitations of the application of [[18], [22]].

### 3.2.2 Exponential Smoothing Model

Exponential smoothing method is widely used in the prediction of infectious diseases. Xuyan Wang et al. [24] used quadratic smoothing method to predict and analyze the COVID-19 epidemic in Hubei Province and fitted three quadratic exponential smoothing models: Holt linear model, Brown linear model and Damped trend model, Damped model was selected according to the maximum determination coefficient, and the model fitting effect was better according to the value of standardized Bayesian information criterion, square root of mean square error and mean absolute error percentage.

## 3.3 Neural Network Model

In recent years, the research of artificial intelligence has developed rapidly, and the application field of this technology has gradually expanded. During the SARS virus outbreak in China in 2003, most of the prediction models at that time were modeled by traditional mathematical models. Many scholars have published the results of using artificial intelligence to build predictive models of

infectious diseases. The research on the use of neural network models in infectious diseases is not deep enough, but there have been papers that have proved its feasibility and the predictive effect in certain specific situations. Will be more accurate than traditional models[[25],[26]]. Among them, the BP neural network was first introduced in medical research, and it has been proven to have a good ability to solve nonlinear problems, and can make reasonable judgments on complex problems based on the learned knowledge and experience in handling problems [25].

The BP neural network model is a one-way multi-layer feedforward network model consisting of an input layer, a hidden layer and an output layer. The number of nodes in the input layer is the number of input variables, such as factors affecting infectious diseases. The hidden layer is the main processing unit. The function of its nodes in the network is to extract and store its internal laws from the sample data. The weights in each hidden layer node are parameters to improve the mapping ability of the BP network. The parameters of model design mainly include the number of layers of the model, the number of input vectors, the number of hidden nodes and the function. In the current infectious disease prediction models, most of the proposed models are three-layered, and the Sigmoid function is commonly used as the functional function, and the input parameters and the number of hidden nodes are designed according to the characteristics of the disease [[26], [27]]. The learning principle of the BP algorithm mainly includes forward and reverse transmission. The information is passed to the network through the input vector, the result is compared with the expected, and the weight and threshold of the network are continuously adjusted through backpropagation, and finally the error is squared. The sum reaches the minimum, and the fitting of the mapping relationship is completed. In actual use, the training data is used to train the neural network, and the structure and parameters of the model are constantly modified in the process. The output vector of the network is required to be as close to the expected vector as possible, and the weight and deviation of the network at this time are saved. After the parameters are determined, the final research model is formed [28].

Jianxun Zhang et al. [29] used data from Beijing and Hong Kong during SARS to make predictions and pointed out that the parameters that determine the spread of the disease include the number of cases in the previous 7 days and the number of new cases. They determined that the neural model contains 14 input vectors, and 1 output vector is the number of new cases in a day. Jing Zhu et al. [26] indicated that the prediction of the BP model can accurately approximate the spread of infectious diseases. The model takes three days of daily infection data as input and an output vector as the predicted value, taking into account the media propaganda and government The intensity of control measures such as the intensity of isolation and the degree of disinfection in public places will change with the development of the epidemic. The results show that the use of BP for forecasting can more truly reflect the actual situation. Dongyang Shi et al. [30] proposed a method of approximating the spread law function of infectious diseases with ELMAN neural network. The BP neural network is still the most commonly used neural network model in medical research. However, due to the local optimization problem of the BP network, the training speed is slow and the efficiency is low, the RBF neural network model overcomes these problems to a certain extent[23] . Radial basis function (RBF) neural network is a forward network with a single hidden layer proposed by Moody and Darken in the late 1980s, based on function approximation theory. The author proposed the results of RBF model and ARIMA-GRNN are better than the ARIMA time series model, which is also a researchable direction. Peng Huang[31] used the ARIMA model and the LSTM model to conduct comparative experiments on Type B infectious diseases, verifying that the LSTM model is more accurate than the ARIMA model, and also proposed the use of machine learning algorithms to solve the method of predicting the trend of infectious diseases.

At present, many statistical methods and models have been used for early prediction of infectious diseases, but each model has its applicable diseases and data types, and no statistical technique can ideally adapt to each virus [32]. In practical applications, it is necessary to comprehensively consider disease characteristics, data types, model characteristics, etc., to select the most appropriate prediction model. The spread of infectious diseases is a complex issue, and we should consider more factors to develop more accurate models. Classical mathematical models are still widely used in the field of

infectious disease prediction, but their mathematical formulas are more complicated. When constructing nonlinear equations, there will be situations that are difficult to describe using differential equations[9], and the model does not consider human factors, etc. Both are the limitations of the model, because the basic model cannot show all the characteristics of infectious diseases. The time series model is very advantageous for virus research with time rules, but it is not accurate for other irregular viruses and has certain application limitations. The neural network has a simple structure and strong simulation capabilities. The model's back-generation and prediction capabilities are good. Studies have shown that the prediction effect of the neural network model is better than the gray theoretical model in several infectious diseases. They all use the actual epidemic data of infectious diseases and using neural network prediction to draw conclusions [[24], [33]], compared with traditional methods, neural network methods do not need to establish a complex mathematical model, and the modeling method is simpler.

## 4. Conclusion

With the development of the Internet and the impact of different infectious diseases that have emerged in recent years on the world, the model of epidemiology has attracted more and more attention from the public. This article first gives the background and research progress of the propagation dynamics model, and then summarizes the principles and application scenarios of the mathematical model, time series model, and neural network model, and compares the advantages and disadvantages of each model. It can be seen that the current domestic and foreign research on it mainly uses mathematical models, time series models are used for the research of characteristic diseases, and the research of neural network models is still in the ascendant stage. The use of models to predict future epidemic trends of diseases is extremely important, and it is also helpful to recommend prevention and control measures, but there are still some unsolved problems. First of all, in the prevention and control of the new coronavirus disease, in the future model optimization can be based on the spread of the new coronavirus, taking into account special characteristics such as "asymptomatic infections" and "prevention and control measures" into the model. Secondly, in the future research in this field, other deep learning algorithms can be introduced, which is also the future development trend.

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