Research and Analysis of Epidemic Prevention and Control Based on BP Neural Network

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Abstract: The continuous spread of COVID-19, especially the emergence and spread of a series of mutant strains, has brought new challenges to the development of human society, and the emergence of sewage epidemiology has provided a new idea for the early warning and detection of COVID-19 in countries around the world. By analyzing the rationality and optimal site selection of sewage sampling sites in the United States, early warning of the local epidemic development trend was conducted, and corresponding measures were proposed for epidemic prevention and control by the local government. The BP neural network prediction method is adopted to carry out deep learning and prediction of the changes in the number of infected persons in the next 5 weeks in each state of the United States based on the data related to the number of infected persons in the recent 18 weeks in the United States with 70% training ratio, 15% verification ratio and 15% rationality ratio. In addition, the epidemic development trend of each state in the United States is visualized in the form of the top ten regions in the United States. The threshold of epidemic development in each state of the United States was calculated by using SIR epidemic model, and the prediction results of BP neural network model were used to obtain the areas likely to break out large-scale epidemic, and based on the results, prevention and control suggestions were put forward for the areas likely to break out large-scale epidemic.

1. Introduction

1.1. Problem background

The emergence and continuous development of COVID-19 has posed a threat to human health and economic and social development of the world at the same time. Therefore, it has been identified as a global pandemic by the World Health Organization, and countries around the world are facing challenges. Now, a kind of sewage water quality situation of a certain area by method to detect the virus and its RNA that sewage disease research method for the new crown of early warning and detection provides a new train of thought, it can make up for nucleic acid detection and

the weakness of the antibody detection[1], for the relevant departments to provide timely warning outbreak of relevant information.

2. Problem Analysis

Early warning of the development of the epidemic situation in each region is required, so this article makes predictions based on the data on the number of people infected with the new coronavirus in each state in the United States in the last 18 weeks. Considering that the changes in the number of new coronavirus infections are intricate, this paper uses BP neural network prediction, and uses 70% of the training ratio to perform deep learning on the number of new coronavirus infections in US states in the last 18 weeks, so as to predict US states[2]. The number of infections in the next 5 weeks, and the SIR infectious disease model is used to determine the threshold for a large-scale outbreak of the new crown epidemic, and then to warn states in the United States that may experience a large-scale epidemic.

3. Model Assumptions

Assumption 1: It is assumed that the evaluation indicators selected by the model are independent of each other and have no correlational impact on the results.

Hypothesis 2: When selecting evaluation indicators, only important indicators that reflect the evaluation object are considered, and other secondary factors are ignored.

Hypothesis 3: The probability of recovery in the SIR model used does not affect the evolutionary timescale during infection.

4. Model establishment and solution

4.1. Construction of epidemic early warning model based on BP neural network and SIR infectious disease model

It is necessary to give early warning to the epidemic situation in various states of the United States, so this paper uses a basic three-layer BP neural network to judge the development of the epidemic situation. The BP neural network can learn and process the training set by simulating the activity process of the neurons in the human brain, and continuously input, process, and output the data of the training set to make the final decision. The network layer of the BP neural network consists of an input layer I, several input layers H and an output layer, and the input layer I, input layer H and output layer of the neural network are all connected to each other[3].

In order to improve the calculation accuracy of the BP neural network, the input training set can be normalized, so that the function of the BP neural network can be fully utilized. At the same time, the determination of the number of nodes in the input layer H and the output layer plays a critical role in the accuracy of the deep learning results. Too few node values will lead to too many minimum values of the local environment of the neural network, and too many node values will also lead to a relatively long learning time for deep learning of BP neural network and easily lead to errors that are not optimal[4]. The determination of the number of nodes in the input layer H and the output layer can be determined by (representing the number of nodes in the input layer H of the BP neural network, representing the number of samples in the training set).

4.1.1. Threshold Calculation Based on SIR Infectious Disease Model

In order to better determine the critical value for the transformation of the new coronary pneumonia epidemic into a large-scale epidemic, this paper assumes that the transmission mode of

the new coronary pneumonia epidemic obeys the Poisson distribution, and sets C_a as a variable of the infection cycle of the new coronary pneumonia, and assumes that C_a and the sampling point have a relationship between them. The serving population ρ is independent of each other[5]. Then the Wald equation can be obtained, which is $E\left[C_\rho^q\right] = E\left[C_a\right]E\left[P_r^*\right]$ (where P_ρ^* represents the number of service populations in the elimination phase during the infection phase, and C_ρ^q represents the total infection cycle from the beginning of the epidemic to the final extinction of the epidemic). Let $\varphi_\rho = E\left[P_\rho^*\right]$, then φ_ρ can be expressed as:

$$\varphi_\rho = \rho - \sum_{b=0}^{\rho-1}\binom{\rho-1}{b}\tau_b \gamma(b\xi), b = 1, 2, \cdots \qquad (1)$$

Among them, $\gamma(b) = E\left[e^{-bC_a}\right]$ represents the reference function of the infection cycle C_a, ξ represents the infection probability between people infected with new coronary pneumonia and people who are not infected with new coronary pneumonia, and τ_b is defined by the following formula:

$$\sum_{j=0}^{b}\binom{b}{j}\tau_j \gamma(j\xi) = b, b = 0, 1, \cdots \qquad (2)$$

Finally, based on the infection cycle and infection probability of the new crown epidemic, the epidemic threshold g_j of the new crown pneumonia epidemic is calculated. The specific formula is as follows:

$$g_j = \sum_{\rho=1}^{\infty}\sigma_\rho \varphi_\rho = \sum_{\rho=1}^{\infty}\sigma_\rho \xi E\left[C_\rho^q\right] \qquad (3)$$

Among them, σ_ρ represents the probability of infection between the sampling point with ρ person and other sampling points. φ_ρ can be represented by the following formula:

$$\varphi_\rho = \xi E\left[C_\rho^q\right] \qquad (4)$$

4.1.2. Model solution

In order to predict the development trend of the epidemic situation in US states for a period of time in the future, this paper uses Matlab, based on the relevant data of the number of infected people in US states in the past 18 weeks, using 70% of the training ratio, 15% of the verification ratio and 15% of the rationality ratio Compare, conduct deep learning and forecast changes in the number of infections in US states in the next 5 weeks. Then, according to the distribution of 10 regions in the United States, this paper visualizes the development trend of the epidemic in each state in the United States in the form of regions. The preliminary prediction results based on the BP neural network model are: Connecticut, Alabama, Kansas, Michigan and Alaska are more likely to have large-scale outbreaks. The threshold of , and then the above results are revised to make more accurate predictions for areas where large-scale outbreaks are likely to occur.

In order to obtain a more accurate prediction result, this paper defines R_0 to represent the basic reproduction number generated in the process of single-point contact scenario, which represents that

each time an infected individual interacts with others in a well-mixed S-state population The number of individuals that can be infected at the time of contact, and the average basic reproduction number $R_0 = \dfrac{\langle N \rangle \xi}{\chi}$ according to the model in the network structure (where $\langle N \rangle$ represents the average degree of nodes between susceptible, infected and dead states). Through this basic concept, it can be preliminarily believed that the new coronary pneumonia will continue to grow on a large scale when $R_0 > 1$, and $R_0 < 1$ indicates that the new coronary pneumonia may decrease or die out. In this research scenario, the steady-state COVID-19 transmission model will only be in two states, S and R, and the following assumptions are made based on the above formula:

$$R(\rho_1) = \chi \sum_{\rho=0}^{\rho_1} I_\rho \approx \chi \int_0^{\rho_1} I(\rho) d\rho \qquad (5)$$

Therefore, the density function $S(\rho_1)$ of uninfected nodes can be obtained as:

$$S(\rho_1) = e^{-\xi \langle N \rangle \int_{\rho=1}^{\rho_1} I(\rho) d\rho} = e^{\frac{-\xi \langle N \rangle R(\rho_1)}{\chi}} \qquad (6)$$

To investigate whether the new crown pneumonia will break out in a certain time span, you can directly analyze the steady state model situation when the transmission process ends:

$$R_\infty = 1 - S_\infty = 1 - e^{-\xi \langle N \rangle R_\infty} \qquad (7)$$

where $R_\infty = 0$ always satisfies the equation, and R_∞ represents the spread of the novel coronavirus under study at steady state. If the equation has a non-zero solution, then the non-zero solution function satisfies:

$$F(R_\infty) = 1 - e^{-\xi \langle N \rangle R_\infty} - R_\infty \qquad (8)$$

According to $F(1) < 0$, it can be seen that when there is a non-zero solution: $\xi \langle N \rangle - 1 > 0, \xi > \dfrac{1}{\langle N \rangle}$ finally obtains the threshold of propagation as:

$$g = \frac{1}{\langle N \rangle} \qquad (9)$$

This formula is used to calculate the epidemic threshold of each state, and combined with the prediction results of BP neural network model, the regions with large-scale epidemic can be obtained.

References

[1] Liu Sifeng. Grey System Theory and Its Application (5th edition) [M]. Beijing: Science Press, 2010:62.
[2] Yang Shue, Huang Li. System engineering-theory & practice,2005,25(1):12-18,26.
[3] Liu Y. Research on epidemic and vaccine efficacy model based on basic regeneration rate [D]. Sichuan: University of Electronic Science and Technology of China,2010.
[4] Li Changkun, Wang Xiuhai. Research on supply chain knowledge sharing risk early warning system based on BP neural network [J]. Science and Technology Management Research, 2009,29(4):191-193.
[5] Li Ruiqi, Wang Wei, Shu Panpan, Yang Hui, Pan Liming, Cui Aixiang, Tang Ming. A review of outbreak threshold analysis of epidemic transmission dynamics on complex networks [J]. Complex Systems and Complexity Science, 2016,13 (01):1-39.