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Enhanced SEIARN Infectious Disease Modeling with Adaptive Parameter Estimation Using Sparrow Search Algorithm

Bryson Caldwell
University of Nebraska–Lincoln, Lincoln, USA
brysonc92@unl.edu

Abstract: Infectious diseases pose a significant threat to global public health, impacting both human well-being and socio-economic development. The SEIARN model is a widely used epidemiological framework for predicting disease transmission by categorizing individuals into different states. However, accurate parameter estimation remains a major challenge, as traditional methods relying on empirical and statistical approaches often suffer from limitations in precision and stability. To address this issue, this paper proposes an adaptive parameter estimation model, SSA-SEIARN, which leverages the Sparrow Search Algorithm (SSA) to dynamically optimize SEIARN parameters.Compared to conventional approaches, SSA-SEIARN enhances model accuracy and stability by adaptively adjusting key parameters, including the latency infection rate (α), infection recovery rates (γ_1 and γ_2), and the probability of secondary infection (θ). Simulation experiments demonstrate that SSA-SEIARN significantly improves the fitting performance of the model, making it a more reliable tool for infectious disease prediction. The findings of this study provide valuable insights into the application of optimization algorithms in epidemiological modeling and offer a novel approach to refining disease transmission predictions.

Keywords: SEIARN; SSA; Parameter Optimization; Epidemic Prediction.

1. Introduction

Infectious diseases are global public health problems, and their seriousness is not only reflected in the direct threat to human health, but also in the serious negative impact they bring to social and economic development. With the continuous development of science and technology, more and more scholars have begun to use mathematical modeling and computer simulation methods to study the transmission mechanism of infectious diseases, and have made important contributions in predicting and controlling infectious diseases.

The SEIARN model is a classic epidemiological model, whose basic assumption is that each individual in a population is in one of the states of susceptibility, latency, infection, isolation, rehabilitation, or death. Through mathematical modeling of these states, the transmission trend of infectious diseases in the population can be predicted. However, the parameter estimation of the SEIARN model has always been one of the difficulties in the study of infectious disease transmission. Currently, the traditional SEIARN model parameter estimation methods mainly rely on empirical and statistical methods, which have certain limitations in accuracy and stability. To this end, we previously constructed a new model SEIARN: Intelligent early warning model of episodic spread based on LSTM trajectory prediction [1]. This model uses LSTM to predict patient trajectories, thereby achieving real-time calculation and update of contact rates, and optimizing the parameters of SEIARN to a certain extent. However, this is only an optimization of a single parameter, and the optimal estimation of other parameters remains unresolved.

In order to solve the limitations of other parameter estimation methods in our previous model, this paper proposes a SEARN parameter adaptive model SSA-SEARN based on Sparrow Search Algorithm (SSA). The model adaptively adjusts model parameters through SSA algorithm to optimize the fitting effect of the model. Compared to the original methods, the method proposed in this paper has higher accuracy and stability in predicting the transmission trend of infectious diseases. The main contributions of this article include the following three aspects:

1) A parameter adaptive model SSA-SEIARN based on SSA algorithm is proposed, which provides a new idea and method for the study of infectious disease transmission.

2) Experiments have proved that the method proposed in this paper has higher accuracy and stability in predicting the transmission trend of infectious diseases.

3) It provides a reference for further exploring the application of optimization algorithms in the study of infectious disease transmission.

The structure of this article is as follows: In the second section, the principle of SSA algorithm, the principle of SEIARN model, and relevant literature research are introduced. In the third section, the algorithm idea and establishment process of SSA-SEIARN are introduced. In the fourth section, VSO-SEIARN is used for simulation and comparative experiments, and the results are analyzed. In section 5, conclusions are drawn.

2. Related Foundations

2.1 Sparrow Search Algorithm

Sparrow Search Algorithm (SSA) is a swarm intelligent optimization algorithm proposed by Xue et al. [2] based on a series of behaviors of sparrow populations during the foraging process. The sparrow search algorithm can quickly converge near the optimal value, and has efficient global optimization ability and high stability. The sparrow search algorithm consists of three parts: a finder who is responsible for foraging and providing direction for the group, a follower who joins the finder, and a watcher who is always alert to predators. The discoverer is the best located and closest part of the sparrow population to the food; Participants will update the location based on the discoverer to improve the probability of obtaining food; When an alert person detects a predator, they alert the sparrow population, and the sparrows in the population will approach each other to reduce the probability of being preyed on and engage in anti predatory behavior.

The mathematical model of the discoverer is shown in (1):

$$X_i^{t+1} = \begin{cases} X_i^t \times \exp\left(\dfrac{-i}{a \times iter_{\max}}\right), R_2 < ST \\ X_i^t + Q \times L, R_2 \geq ST \end{cases}$$

Where, X_i^t represents the position of the i-th sparrow at iteration t; $iter_{\max}$ is the maximum number of iterations; a is a random number of, $a \in (0,1)$; R_2 is the early warning value, while $R_2 \in [0,1]$ indicates that the sparrow population is safe if the early warning value is not reached; ST is the safety value, $ST \in [0.5,1]$, and sparrows within the safety range can only be active; Q is a random number that follows a global distribution.

The update model for the participant's location is shown in (2):

$$X_i^{t+1} = \begin{cases} Q \times \exp\left(\dfrac{X_{worst}^t - X_i^t}{i^2}\right), i > \dfrac{n}{2} \\ X_P^{t+1} + \left|X_i^t - X_P^{t+1}\right| \times A^{+} \times L, i \leq \dfrac{n}{2} \end{cases}$$

A is a matrix of $1 \times d$, in which each element is randomly assigned a value of 1 or -1, and has an $A^{+} = A^{T}\left(AA^{T}\right)^{-1}$.

The location update model for the vigilante is shown in (3):

$$X_i^{t+1} = \begin{cases} X_{best}^{t} + Q \times \left|X_i^t - X_{best}^t\right|, f_i > f_g \\ X_i^t + K \times \left(\dfrac{\left|X_i^t + X_{worst}^t\right|}{f_i - f_w + \varepsilon}\right), f_i = f_g \end{cases}$$

f_i is the fitness value of the current sparrow individual; f_g is the optimal fitness value for the global sparrow; f_w is the current global worst fitness value; ε is an infinitesimal constant.

2.2 SEIARN Model

The SEIARN model is a mathematical model based on the spread of infectious diseases, which is used to describe the changes in the number of different groups in a population. The population is divided into five compartments: susceptible (S), latent (E), asymptomatic (A), symptomatic (I), and convalescent (R). The dead can be calculated based on other compartments. In this model, susceptible individuals will become infected and become latent after contacting infected individuals; A latent person becomes an infected person after a period of incubation; An infected person can be quarantined and treated as a person who recovers or dies. Neither the convalescent nor the deceased will be infected again. In addition, the SEIARN model we constructed [1] also takes into account the secondary infection of convalescents.

The dynamic propagation equation of the SEIARN model is shown in (4):

$$\begin{cases} \dfrac{dS}{dt} = \theta R - \dfrac{\lambda_1 \beta_1 SI}{N} - \dfrac{\lambda_2 \beta_2 SA}{N} \\ \dfrac{dE}{dt} = \dfrac{n_1 \lambda_1 SI}{N} + \dfrac{n_2 \lambda_2 SA}{N} - \alpha(1-m)E - \alpha m E \\ \dfrac{dA}{dt} = \alpha(1-m)E - \gamma_1 A \\ \dfrac{dI}{dt} = \alpha m E - \gamma_2 I \\ \dfrac{dR}{dt} = \gamma_1 A + \gamma_2 I - \theta R \end{cases}$$

Where β_1 represents the probability of S contacting I and becoming ill; λ_1 represents the contact rate between S and I; β_2 represents the probability of S contacting I and becoming ill; λ_2 represents the contact rate between S and I; α represents the latent infection rate; m represents the proportion of symptomatic infections among infected persons; γ_1 represents the recovery rate of asymptomatic infected persons; γ_2 represents the recovery rate of asymptomatic infected persons; θ represents the probability of secondary infection in the rehabilitated person.

2.3 Related Literature Research

Epidemic transmission models are one of the important tools for predicting the trend of epidemic development. Some scholars have begun to explore the use of optimization algorithms to optimize the parameters of epidemic transmission models. Some researchers use genetic algorithms to optimize the parameters of infectious disease models to improve the prediction accuracy of the models. For example, Wang et al. proposed an optimized SEIHR infectious disease model based on genetic algorithms, successfully predicting the spread of influenza A (H1N1) [3]. In addition, Pan et al. applied genetic algorithms to the SIRS model to optimize vaccination strategies and improve the prediction accuracy and efficiency of the model [4]. In addition to genetic algorithms, particle swarm optimization is also a common optimization algorithm that can be applied to the optimization of infectious disease models. Wang et al. used particle swarm optimization to optimize the parameters of the H7N9 avian influenza model based on the infectious source, improving the prediction accuracy of the model [5]. At the same time, Zhou et al. also proposed an optimization method based on particle swarm optimization to improve the prediction effect of the SEIQR infectious disease model [6]. In addition, in recent years, deep learning algorithms have gradually been applied to the optimization of infectious disease models. For example, Qian et al. proposed an infectious disease prediction model based on convolutional neural networks, which can accurately predict the development trend of the epidemic [7]. At the same time, Zeng et al. also applied deep learning algorithms to SIR models to predict and analyze the propagation of COVID-19 [8].

In summary, the combination of optimization algorithms and infectious disease models has become a research field of great concern. In future research, more optimization algorithms will be applied to the optimization of infectious disease models to help us better understand and control the spread of infectious diseases.

3. Establishment of SSA-SEIARN Model

3.1 Model Ideas

There are many parameters in the SEIARN model that have a significant impact on the results of the model. We have previously used LSTM models to predict patient trajectories, thus enabling real-time updates of contact rates, which have been effectively resolved [1]. However, for the four parameters of latent infection rate (α), infection recovery rate (γ_1 and γ_2), and probability of secondary infection of convalescents (θ), conclusions based on experience and statistical methods may not make the results of SEIARN optimal. For this reason, we use the SSA algorithm to find the optimal values of latent infection rate, infection recovery rate and asymptomatic infection incidence in the SEIARN model, so that the model fits well.

3.2 Modeling Process

In our SEIARN model, the four parameters, latency infection rate (α), infection recovery rate (γ_1 and γ_2), and the probability of secondary infection of the rehabilitated person (θ), have a significant impact on the final fitting result of the model. Therefore, in order to achieve the optimal selection of parameters, we use the SSA algorithm to optimize the parameters and establish the SSA-SEIARN model. The specific establishment process of the algorithm is as follows:

Step 1 Initialize the sparrow population and related parameters: Set the sparrow population number to 300; The number of iterations is set to 100; The value range of α is $[0.01, 0.1]$; The value range of γ_1 and γ_2 is $[0.05, 0.2]$; The value range of θ is $[0.01, 0.05]$.

Step 2 calculates the fitness values of all sparrows using the mean square error (MSE) as the fitness value.

Step 3 updates the discoverer location according to (1) to determine the optimal discoverer.

Step 4 updates the position of the enrollee according to (2).

Step 5 Randomly select sparrows from the discoverers and participants as the watchers, and use (3) to update them.

Step 6 determines whether the algorithm has reached the maximum number of iterations, and if it reaches the end of the loop, execute Step 7; If the cycle is not reached, continue to execute Step 2.

Step 7 outputs the optimal position, which is the optimal parameter combination. By substituting the optimal parameters into the SEIARN model, the SSA-SEIARN model is successfully constructed.

The overall process of the model is shown in **Fig 1**.

4. Simulation and Analysis

4.1 Experimental Environment and Data

In order to verify the fitting performance of SSA-SEIARN, epidemic data from Hebei, Tianjin, and Xi'an in January and February 2022 were obtained using reptile technology for simulation experiments. The running environment of each experiment is the same, and it is obtained using Python language programming under the Intel (R) Core (TM) i7-10750H CPU @ 2.60 GHz 2.59 GHz, and RAM 16GB environment.

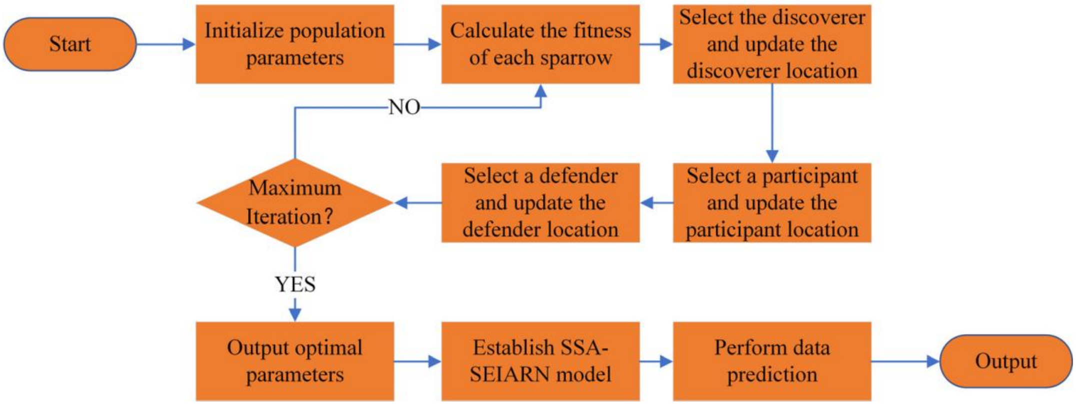

Fig 1. SSA-SEIARN Algorithm Flowchart

From the results, it can be seen that SSA-SEIARN has successfully improved the fitting effect of the model on the original basis by setting parameters. On the data from Hebei, where the original model performed poorly, the average improvement value of MSE for SSA-SEIARN reached 483.95315, the average improvement value of MAPE reached 483.95315, and the average improvement value of MSE reached 483.95315. The forecast for Beijing and Tianjin has improved in all aspects compared to the original indicators.

In addition, we took Beijing as an example to draw a comparison diagram between the real situation and the SSA-SEIARN prediction, as shown in **Fig 2** and **Fig 3**.

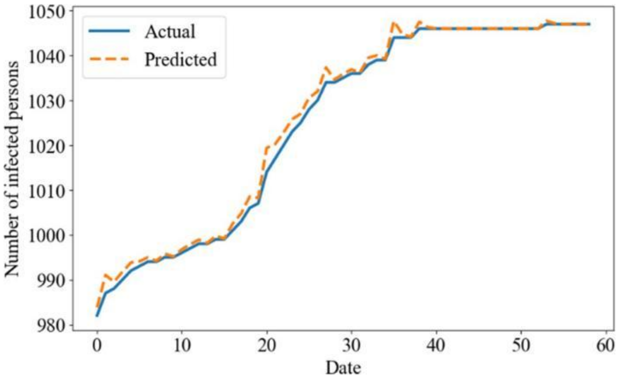

Fig 2. Comparison Figure 1

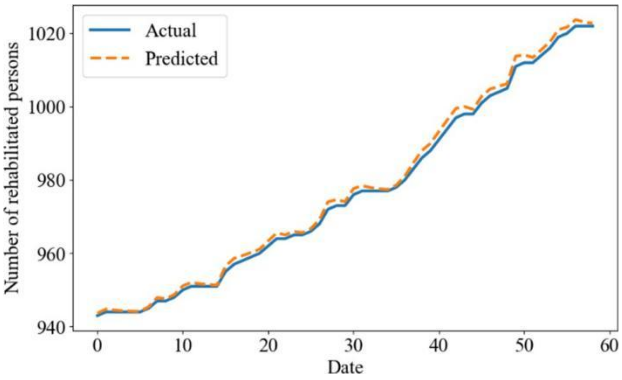

Fig 3. Comparison Figure 2

From the fitting results in **Fig 2** and **Fig 3**, the predicted situation of SSA-SEIARN is relatively similar to the actual situation, with a high coincidence degree. Therefore, the model successfully predicted the infected and rehabilitated persons during the period from January 1, 2021 to February 28, 20211, and achieved good results. To some extent, it can provide a reference for the management of epidemic situations in real life.

5. Conclusion

Based on the model SEIARN Based on LSTM Trajectory Prediction, this paper uses the SSA algorithm to optimize the four parameters of SEIARN, namely, the latency infection rate (α), the infection recovery rate (γ_1 and γ_2), and the probability of secondary infection of the rehabilitated person (θ). Through simulation experiments and analysis, the SSA-SEIARN model has achieved good results in the final fitting effect because it can better estimate parameters.

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