Optimizing Vaccine Distribution for Different Age Groups of Population Using DE Algorithm

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***Abstract*—Vaccination is one of the most promising methods to control the epidemic spread by protecting the most vulnerable population and reducing the number of susceptible population who are exposed to the virus. However, the vaccine doses are usually limited and can only be supplied during the epidemic outbreak. How to distribute the vaccines to different populations to reduce the total number of infectious people is important to the public health. In this paper, a DE algorithm is proposed to solve the problem by searching for the optimal strategy to distribute the limited vaccines to different age groups of population. The performance of the algorithm is compared with three strategies in the literature. The results show that the proposed algorithm can offer more effective vaccine distributions significantly.**

Keywords- Differential evolution, optimization, vaccine distribution

I. INTRODUCTION

According to the statistics from the Health & Disease Control Center, millions of people lose their lives because of infectious diseases [1]. When the outbreak of an infectious disease emerged, people often use protection means to avoid infection. Isolation and vaccination are the two most used means. Isolation can reduce the contacts of crowds but influence routine activities. Vaccination, which is regarded as an effective way for reducing the diffusion of an epidemic disease, is highly recommended [2][3]. After vaccinated, one will be immune to a disease for a period of time which is supposed to cover the whole epidemic of the disease or even a whole life. However, the production of vaccination is sometimes limited and costly at the initial outbreak of a disease. How to design a vaccine distribution strategy for minimizing the infected population is highly demanding.

At present, a vaccination scheme for distribution mainly concentrates on the people who appear to be the most vulnerable to the disease, such as children aged between six months and less than six years, or the elderly over 65 years with chronic illnesses, healthcare workers, etc. However, if we can estimate the infectious feature of the disease and the activities of the people, a better vaccination scheme can be designed. Mossong et al. [4] pointed out that social contacts between different groups are relevant to the spread of infectious disease, thus a population is divided into groups according to their ages. People in different age groups have different vulnerability to a disease [5]. In this paper, we will analyze the data from history and build an optimization model of the vaccine distribution for each age group of people.

The objective of the optimization problem is to minimize the total infectious population since the outbreak of the disease until the epidemic seized. In the literature, vaccine distribution mainly focuses on the transmissibility and infection risk of the disease and the vulnerability of people [6]-[8]. Longini and Halloran [9] proposed a strategy for the distribution of influenza vaccine to high-risk groups. Patel et al. [10] proposed a genetic algorithm to find the optimal vaccine distributions to minimize the number of illnesses or deaths in the population. Tuite and his partners [11] used a transmission model to explain spatial spread of disease and identify optimal control interventions.

For solving the vaccine distribution optimization problem, we propose to use the differential evolution (DE) algorithm [12][13] to enhance the effectiveness of vaccine protection. DE is a type of evolutionary algorithms which are inspired by the natural evolution of the survival of the fittest. DE has shown promising performance in searching nonlinear and multimodal space. In this paper, a DE algorithm for optimizing the vaccine distribution strategy is proposed and a series of simulations have been made for analyzing the performance of the algorithm.

The rest of the paper is constructed as follows. Section II introduces the epidemic transmission model of the infectious disease. The implementation of the proposed algorithm is presented in Section III. Numerical experiments are shown in Section IV. Conclusions are made in Section V.

II. BACKGROUND

In this section, the epidemic transmission model considered in this paper will be introduced. The composition

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of the population who are susceptible to the disease will then be analyzed.

A. Epidemic Transmission Model

In the literature, various epidemic transmission models have been proposed based on the features of the disease. We only focus on the transmission model of H1N1 influenza [1][14] in this paper for analyzing the performance of the proposed vaccine distribution algorithm. Note that the algorithm can also be applied in the other transmission models.

Fig. 1 illustrates a schematic of the transmission model of influenza pandemic with time-dependent vaccination. Suppose the vaccinated individuals will be immune to the disease during the pandemic. The stage progression of the individuals can be classified as follows. The subscript i indicates the group of population to which the individuals belong.

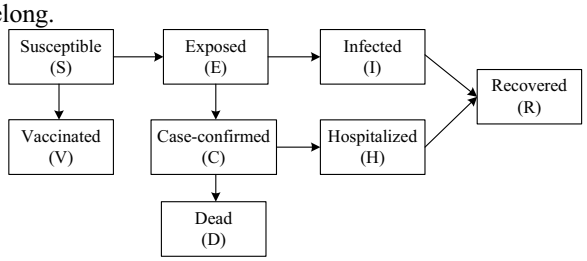

Figure 1. Schematic illustration of the epidemic transmission model.

- Susceptible (S): Initially all individuals in the population are susceptible to the disease. During the progress of the epidemic, some susceptible individuals will be vaccinated, who are excluded from the potential infectious population. Some individuals will be exposed to the disease due to their contact activities with the infectious exposures, i.e., they will experience a period of latency under the risk of virus infection denoted by λ_i.
- Exposed (E): The individuals exposed to the disease have the probability to be confirmed in clinics or hospitals, or they are infected without being noticed. The probability of the exposed individuals to be infected by the disease is denoted by τ_i.
- Case-confirmed (C): The cases-confirmed rate of the exposed individuals is σ_i.
- Hospitalized (H): Some of the infectious confirmed individuals will be hospitalized by the rate η_i.
- Dead (D): Case-confirmed individuals have the rate κ_i to be dead.
- Infected (I): The rate of the exposed individuals developed to the infectious stage without being confirmed is $(1-\sigma_i)$.
- Recovered (R): Some of the infectious individuals will self-recover with the rate γ_i.
- Vaccinated (V): The vaccinated individuals $\Delta v_i(t)$ at each time t are supposed to be immune to the disease immediately.

The above epidemic transmission model can also be described by the following system of nonlinear differential equations.

$$\dot{S}_i(t) = -\lambda_i(S_i(t) - \Delta v_i(t)) - \Delta v_i(t) \quad (1)$$

$$\dot{E}_i(t) = \lambda_i(S_i(t) - \Delta v_i(t)) - \tau_i E_i(t) \quad (2)$$

$$\dot{C}_i(t) = \tau_i \sigma_i E_i(t) - (\eta_i + \kappa_i) C_i(t) \quad (3)$$

$$\dot{H}_i(t) = \eta_i C_i(t) \quad (4)$$

$$\dot{D}_i(t) = \kappa_i C_i(t) \quad (5)$$

$$\dot{I}_i(t) = \tau_i(1-\sigma_i) E_{i-1}(t) - \gamma_i I_i(t) \quad (6)$$

$$\dot{R}_i(t) = \gamma_i I_i(t) \quad (7)$$

The infection rate λ_i for group i relates to the virus transmission variable μ, the vulnerability of the population β_i, the average number c_{ij} of contacts between different age groups i and j, the number I_j of infectious individuals and the number P_j of individuals in group j [14]. The computation of λ_i is

$$\lambda_i = \mu \beta_i \sum_{j=1}^{n} c_{ij} \frac{I_j}{P_j} \quad (8)$$

where n is the number of age groups.

B. Age Groups of Population

According to Chowell et al. [15], the whole population can be divided into several groups for better evaluating their risk to be infected by the epidemic disease. For example, 0-5 yr, 6-12 yr, 13-19 yr, 20-39 yr, 40-59 yr, >=60 yr. Because individuals in different age groups have different contact rates, their risk to be infected are statistically different.

Since the supply of vaccine doses is limited, a good vaccine distribution strategy is to distribute vaccine doses to the individuals with the highest risk in order to reduce the number of infected individuals during the pandemic. In the following sections, we will propose a DE algorithm to search for the optimal vaccine distribution strategy to control the epidemic.

III. The Proposed DE Algorithm

In this section, the implementation of the proposed DE algorithm to address the vaccine distribution problem will be described. Fig. 2 shows the flowchart of the DE algorithm, which includes initialization, mutation, crossover, and selection operations. The variable G represents the counter of generations of the algorithm.

A. Initialization

Each individual in the DE algorithm is encoded as the relative percentages of the vaccine for the n age groups respectively, i.e., $X_k^G = \{x_{k1}^G, x_{k2}^G, ..., x_{kn}^G\}$, k=1,2,…,m, where m is the number of individuals in the population. Note that we have

$$\sum_{i=1}^{n} x_{ki}^G = 1 \quad (9)$$

and $x_{ki}^G \in [0,1]$. The individuals in the initial population are randomly generated and they satisfy the above constraint.

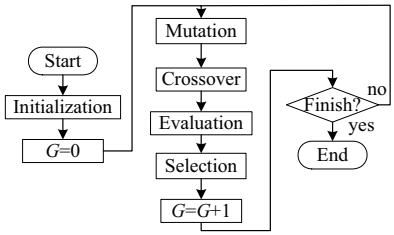

Figure 2. Flowchart of the DE algorithm.

The objective function is the total number of the infectious population since the outbreak of the disease until the epidemic seizes. The smaller the total number of the infectious population, the better the individual is.

B. The Mutation Operation

After initialization, the mutation operation will be used to produce a mutant vector V_k^G with respect to each individual X_k^G in the current population in the Gth generation, and X_k^G is called the target vector, k=1,2,…,m. V_k^G is generated via a mutation strategy. In this paper, V_k^G is computed by

$$V_k^G = X_{kr_1}^G + F \cdot (X_{kr_2}^G - X_{kr_3}^G) + F \cdot (X_{kr_4}^G - X_{kr_5}^G) \qquad (10)$$

The indices r_1, r_2, r_3, r_4, r_5 are different uniform random integer numbers generated in the range [1, m]. The scaling factor F is a positive predefined parameter for scaling the different vector.

C. The Crossover Operation

After the mutation operation, each pair of target vector X_k^G and its corresponding mutant vector V_k^G will be used to generate a trial vector $U_k^G = (u_{k1}^G, u_{k2}^G, ..., u_{kn}^G)$, and the process is called crossover. The uniform crossover is defined as

$$u_{ki}^G = \begin{cases} v_{ki}^G, & \text{if } (rand(0,1) \le CR) \text{ or } (j = k) \\ x_{ki}^G, & \text{otherwise} \end{cases} \qquad (11)$$

where rand(0,1) is a uniform random value in the range (0,1), k=1,2,…,m, i=1,2,…,n. The crossover rate CR is a predefined parameter in the range [0,1).

D. The Selection Operation

After mutation and crossover, the newly generated individuals will be evaluated. DE compares the objective value of each trial vector and its corresponding target vector in the current population. Since the objective of the problem is to minimize the total number of the infectious population, if the objective function value of the trial vector satisfies $f(U_k^G) \le f(X_k^G)$, the target vector will be replaced by the trial vector and join in the population of the next generation. Otherwise, the target vector will be reserved in the next generation. The selection operation is defined by

$$X_k^{G+1} = \begin{cases} U_k^G, & \text{if } f(U_k^G) \le f(X_k^G) \\ X_k^G, & \text{otherwise} \end{cases} \qquad (12)$$

IV. Experiments

In the experimental section, the performance of the proposed DE algorithm will be compared with some vaccine distribution strategies in the literature. The 2009 Hong Kong H1N1 influenza pandemic data [1][16] will be used in the simulation. The age groups of population considered in the experiment are A_1(5-14 yr), A_2(15-19 yr), A_3(20-29 yr), A_4(30-39 yr), A_5(40-49 yr), and A_6(50-59 yr). The virus transmission variable μ =0.015841. Fig. 3 illustrates the number of population in each age group, and the parameter values β_i, σ_i , η_i, κ_i for each age group in the epidemic transmission model, i=1,2,…,6. The parameters τ_i =0.25, γ_i =0.17 are the same for the six age groups.

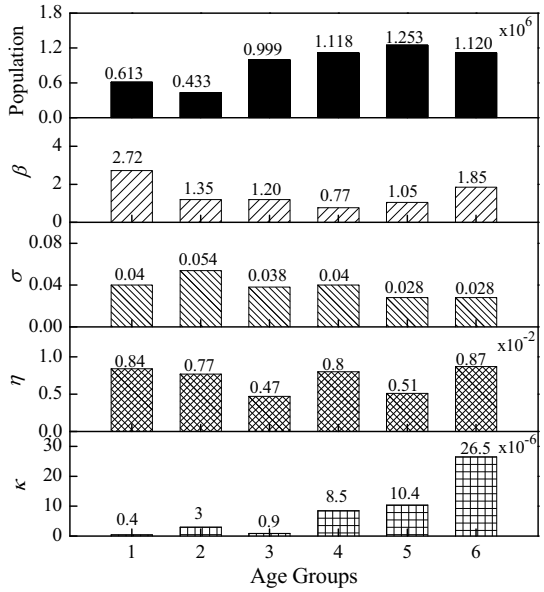

Figure 3. Illustration of the parameter values in the six age groups.

The numbers of contacts in Equation (8) are shown in Fig. 4. It can be observed that the diagonal values are always larger than those in the same row or column, which means that the people in the same groups contact very frequently.

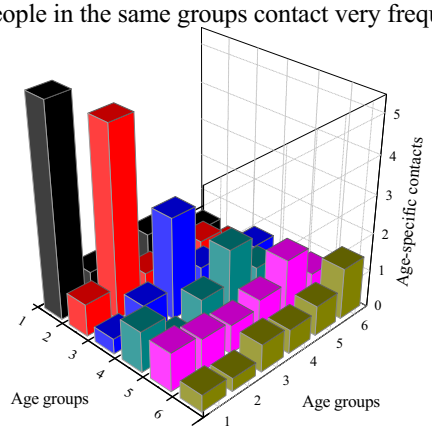

Figure 4. Illustration of the contact rates between the six age groups.

A. Algorithms for Comparison

In the literature, the vaccine distribution strategy is generally made according to the vulnerability of the population, the transmissibility of the disease, or the hospitalization and mortality rate of the disease. The vaccinate distribution proportion for each age group for the three strategies (S1 to S3) are introduced.

- Strategy 1 (S1): Based on Vulnerability

The vaccine distribution strategy focuses on the infectious vulnerability β_i. The number of vaccine doses for each population group is proportional to their infectious vulnerabilities. The vaccination proportion p_i for each age group A_i is

$$p_i(t) = \frac{\beta_i}{\sum_{j=1}^{6} \beta_j}, \; i = 1,2,...,6 \tag{13}$$

- Strategy 2 (S2): Based on Transmissibility

More vaccine doses will be given to the individuals with a higher contact frequency. The vaccination proportion p_i for each age group A_i is

$$p_i(t) = \frac{\sum_{k=1}^{6} c_{ik}}{\sum_{j=1}^{6}\sum_{k=1}^{6} c_{jk}}, \; i = 1,2,...,6 \tag{14}$$

It can be observed that the above two strategies do not depend on the time of the epidemic development.

- Strategy 3 (S3): Based on Hospitalization and Mortality

This strategy considers the number of the hospitalized infection cases $H_i(t)$ and the dead cases $D_i(t)$ at time t. The vaccination proportion p_i for each age group A_i is

$$p_i(t) = \frac{H_i(t) + D_i(t)}{\sum_{j=1}^{6} (H_j(t) + D_j(t))}, \; i = 1,2,...,6 \tag{15}$$

B. Experimental Settings

Besides the features of the virus infection that would affect epidemic spreading, the vaccine coverage and releasing time can also influence the total number of infectious population. For the purpose of evaluation, we choose four releasing days to simulate vaccine distributions to control the epidemic. They are

- after 1 day of an infection outbreak (T=1)
- after 50 days of an infection outbreak (T=50)
- after 100 days of an infection outbreak (T=100)
- after 150 days of an infection outbreak (T=150)

The number of vaccination doses is 500,000. Suppose they are all successfully injected to the susceptible individuals on the same day and the vaccinated people are immune to the disease immediately.

Four sets of initial values are tested in the experiment for analyzing the performance of the algorithms.

Simulation 1: $S_i(0)$ = 99.94%, $E_i(0)$ = 0.06%
Simulation 2: $S_i(0)$ = 99.96%, $E_i(0)$ = 0.04%
Simulation 3: $S_i(0)$ = 99.98%, $E_i(0)$ = 0.02%
Simulation 4: $S_i(0)$ = 99.96%, $I_i(0)$ = 0.04%

The other values are initially set as 0%. The population size in the proposed DE algorithm is 20, and the function evaluations before termination is 1000. The default parameter values F and CR are set as F=0.5, CR=0.4.

C. Results and Analysis

The proposed DE algorithm is compared with the other three vaccine distribution strategies S1, S2, S3 in the four simulations with different vaccination dates. Fig. 5 to Fig. 8 illustrate the infection dynamic curves. Without vaccination, the development of the epidemic is similar to a Gaussian distribution curve and the peak of infectious population appears in the range of 150 to 200 days.

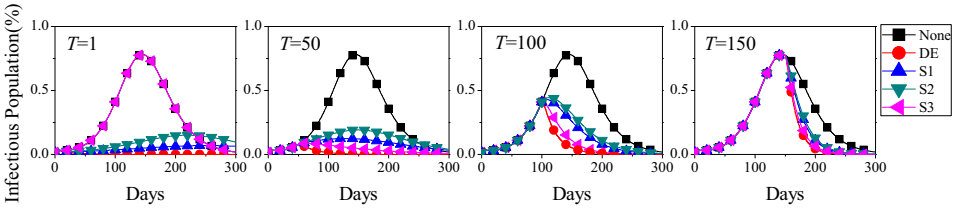

Figure 5. Infection dynamics curves for Simulation 1.

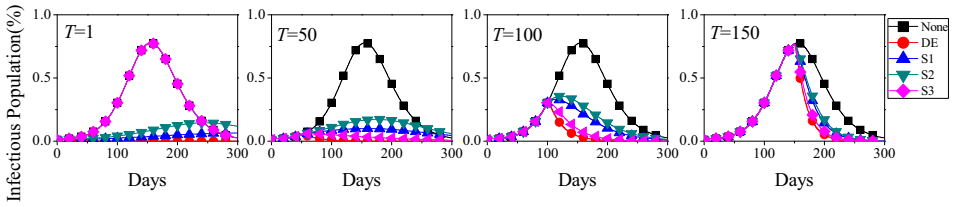

Figure 6. Infection dynamics curves for Simulation 2.

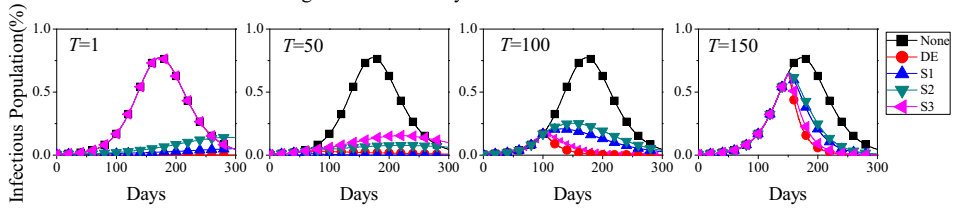

Figure 7. Infection dynamics curves for Simulation 3.

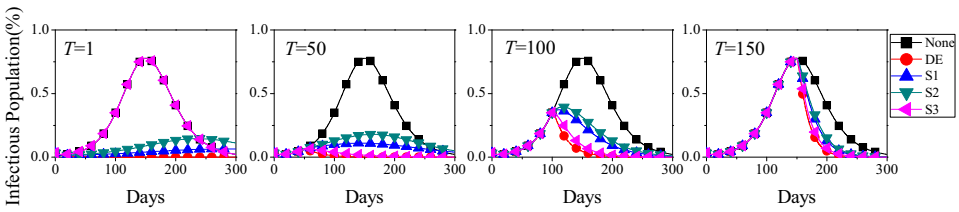

Figure 8. Infection dynamics curves for Simulation 4.

According to the figures, it is obvious that vaccination can ameliorate epidemic spreading by reducing the total infectious population at the peak of an infection outbreak. Generally speaking, the vaccination programs started on the earlier days of epidemic spreading can delay the appearance of the infection peaks. No matter in which simulation, the proposed DE algorithm has the best result compared to the other three methods. DE also has the lowest peak and the peak appears the latest.

In the case of the vaccination started on day 1, there are no obvious infection outbreaks for all the prioritization strategies. The case on day 50 has a similar result as on day1. However, in the cases of the vaccination started on day 100 and day 150, there are obvious infection outbreaks, and the latest day has the highest peak. Especially for the case of the vaccine releasing time set to day 150, the effect of the epidemic control by vaccination is not as effective as the other cases. Nevertheless, it still has a better outcome by the proposed DE algorithm in reducing the total infection population.

V. CONCLUSIONS

In this paper, the problem of finding the optimal distribution strategy to determine the number of vaccine doses to different age groups of population is considered. The objective of the problem is to minimize the infection population during the pandemic. Although there are several prioritization strategies in the literature to solve the problem, the proposed DE algorithm can obtain the best results. A series of simulations have been used to test the performance of the DE algorithm. The results show that the DE algorithm is very promising in solving the vaccine distribution problem.

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