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Optimizing Vaccine Distribution Using Sine Cosine Algorithm with Mutation

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Abstract – **Vaccination is the best approach in curbing the spread of a pandemic. However, during pandemic one of the challenge is limited number of vaccine due to limited manufacturing capacity and high demand. Therefore, optimal vaccine distribution is needed to ensure maximum effectiveness in decreasing the total infections in the population. In this paper, the vaccine distribution is optimized using sine cosine algorithm improved with mutation (SCAmut). The SEIR model of H1N1 pandemic in 2009 is used as the case problem here. The effectiveness of SCAmut vaccine deployment is studied using two factors, which are vaccine coverage percentage and vaccine releasing time. The algorithm's result is compared with three traditional methods and original SCA without mutation. The findings suggested that the proposed SCAmut is able to provide more effective vaccination distributions better than the three traditional methods and also the original SCA.**

Keywords— Vaccine deployment, H1N1, SEIR, Sine cosine Algorithm, Mutation

I. INTRODUCTION

Recent global Covid-19 pandemic outbreak has affected worldwide population with the rapid spread of the highly infectious and deadly SARS-CoV-2 virus. The Covid-19 pandemic is a wakeup call for all of us that pandemic is not something from the relics of history or exist only in a sci-fi movie. Pandemic is a real threat to mankind and could happen at any time.

Pandemic is referred to spread of infectious disease across international boundaries, frequently on worldwide scale. It could be caused by a novel virus/ bacteria/ fungus or a strain that has not affected people for a long time. Humans have little to no immunity to it in most cases. Infectious disease can be a deadly threat to humanity as it claims the lives of millions of people when the spread of it cannot be controlled. In the case of Covid-19, the virus spreads rapidly from person to person throughout the world. The infectious disease is caused by a novel virus which is called as SARS-CoV-2 virus. It has the characteristics of person-to-person transmission and 7-14 days incubation period, which brings a great difficulties for epidemic prevention and control [1]. As of February 25, 2022, the novel coronavirus illness (COVID-19) had caused a major public health crisis, with more than 431 million confirmed infections and 5.93 million deaths worldwide.

The impact of COVID-19 shows how important is pandemic preparedness. One of the worrying factors during a pandemic is the limited resources in hospitals to handle the number of patients need to be treated. To lessen the hospitalization, mortality and morbidity burden, a variety of non-pharmaceutical measures are enforced, such as the use of facemasks, handwashing, shelter-in-place orders, remote schooling, workplace closures, cancellation of public meetings, and travel restrictions [2]. However, these approaches may have negative consequences due to the psychosocial changes that result in isolation, contact limitations, and an economic closure. The changes lead to the rise of mental health issues such as anxiety and stress, increase of domestic violence, child abuse and suicidal cases [3, 4].

Vaccination on the other hand is an effective method in preventing and curbing the spread of viral deceases. Vaccination reduces the number of people who are at risk of contracting a disease by boosting the immune system to protect them. As a result, immunisation can limit the disease's infection to a smaller population of susceptible individuals. The vaccines are expected to be given to the population to achieve herd immunity so that life can return to normalcy prior to the respective outbreak. But, vaccine production is frequently costly, and time-consuming causing limited supply [5]. Therefore, the distribution of vaccines to susceptible persons must be optimised in order to achieve the optimum effects [6].

The optimal vaccine distribution is a complex nonlinear operational research problem. The distribution planning can be guided by SEIR model of the disease. Therefore, this study

focuses on the optimization of vaccine distribution using a metaheuristic algorithm, namely sine cosine algorithm with mutation (SCAmut). The study is carried using vaccination data from the 2009 Hong Kong H1N1 influenza pandemic [7]. Some influenza strains wander genetically from year to year as seasonal flu [8]. Similarly, the H1N1 strain also continues to circulate as seasonal flu virus.

The term "metaheuristics" refers to a class of approximate optimization algorithms. Approximate optimization techniques are used to solve problems intelligently by picking the best option from a larger collection of possibilities under some computational constraints. They were frequently adopted to solve complicated optimization problems when standard or classical optimization approaches were ineffective and inefficient. "To investigate or to find via trial and error" and other terms are used to describe the subordinate heuristic, which is referred to as a metaheuristic. Metaheuristics are more advanced than ordinary heuristics, and this might translate into better performance. Metaheuristics have become more popular than exact approaches in solving optimization problems because of its potential to be used across a wide variety of fields, including engineering, business, transportation, and even the social sciences. New approaches, applications, and performance evaluations have been developed by the metaheuristic community. There are numerous metaheuristic algorithms that take their cues from nature while others from physics or mathematical field like the sine cosine algorithm (SCA) [9]. SCA is chosen here due to its strength in solving nonlinear optimization problem. However, SCA suffers from poor convergence rate and global search [10] – [12]. Hence, differential evolution-based mutation operator is proposed here to improve the performance of SCA.

This paper is arranged as follows. Section 2 introduces the literature's models of infectious illness transmission and control. The implementation of the suggested method is discussed in Section 3. Detailed simulations and analysis are carried out in Section 4. Section 5 is where the conclusions are drawn.

II. Infectious Disease Transmission And Control Modelling

The spread of epidemics is one of society's most dangerous challenges. Given that humanity has previously experienced devastating pandemics such as the Spanish flu in 1917, the Hong Kong virus (H3N2) in 1968, and the swine flu (H1N1) in 2009, forecasting epidemic evolution appears to be one of the most pressing issues faced by our civilizations [8]. The isolation of a new coronavirus by a team of Chinese scientists on January 7, 2020 (later designated coronavirus disease 2019 (Covid-19) by the World Health Organization), which causes severe acute respiratory syndrome in patients infected with this virus (later designated coronavirus disease 2019 (Covid-19) by the World Health Organization), shed new light on this issue.

Mathematical models in epidemiology have become key tools in analysing the spread and control of infectious diseases in recent decades [8]. On the basis of infectious diseases characteristics, many epidemic transmissions are modelled using SEIR model. The SEIR models divide the population into four compartments based on the epidemic [8]. The 4 compartmental models are:

- Susceptible (S)
- Exposed (E)
- Infectious (I)
- Recovered (R)

Given a number of individuals in a population, initially all are vulnerable (or susceptible) to contracting the disease and grouped in the S compartment. As the pandemic progresses and vaccine becomes available, some susceptible individuals will be vaccinated removing them from the potentially contagious population. In the meantime, some people will be exposed to the disease as a result of their contact and social activities with infectious population. The group of population exposed to the disease are in, E. Those who are exposed and infectious are in the I compartment, whereas those who are infectious but already recovered are in the R compartment.

The SEIR model can be extended to include more elaborate state of the population, like hospitalization, vaccinated, dead, etc. Additionally, different disease have different SEIR model like the SEIR model for Covid-19 [1] and H1N1 [7]. SEIR models are also tailored to specific region or location of the outbreak [13, 14].

A. Hong Kong H1N1 SEIR

The Hong Kong H1N1 SEIR model in [7] is applied in this work. This model is suitable because the model incorporates the vaccination efficacy. The researchers represent the SEIR model using the following Eqs. (1) to (5);

$$dS_i/dt = (-\lambda_i) \cdot [S_i - \Delta v_i] + (-\Delta v_i) \tag{1}$$

$$dE_i/dt = (-\gamma) \cdot E_i + \lambda_i \cdot [S_i - \Delta v_i] \tag{2}$$

$$dI_i/dt = (-\tau) \cdot I_i + \gamma \cdot E_i \tag{3}$$

$$dR_i/dt = \tau \cdot I_i \tag{4}$$

$$dV_i/dt = \Delta v_i \tag{5}$$

, where i represents the age group. There are five age groups ($n = 5$) of population considered in the experiment where (1) individuals of 5-14 years, (2) 15-24 years, (3) 25-44 years, (4) 45-64 years, and (5) 65 years or above. Chowell *et al.* [15] claimed that separating the entire population into numerous groups can provide better assess of the individual's risk of becoming infected. This is because people of different ages have varied rates of social contact, therefore, their chances of becoming infected are varied. When vaccine doses are limited, an effective vaccine distribution approach that takes age factor and the social contact into consideration will lower the number of infected people during the pandemic better than the strategy that does not take this into consideration.

The λ_i, γ, τ, and v_i are infection risk, probability of exposed individual to get infected, recovery rate and number of individuals vaccinated in group i. The probabilities of the exposed individuals to be infected by the disease and the recovery rates are set at $\tau = 0.25$, $\gamma = 0.334$. These values are the same for the five age groups. The infection risk of the group is calculated using Eq. (6)
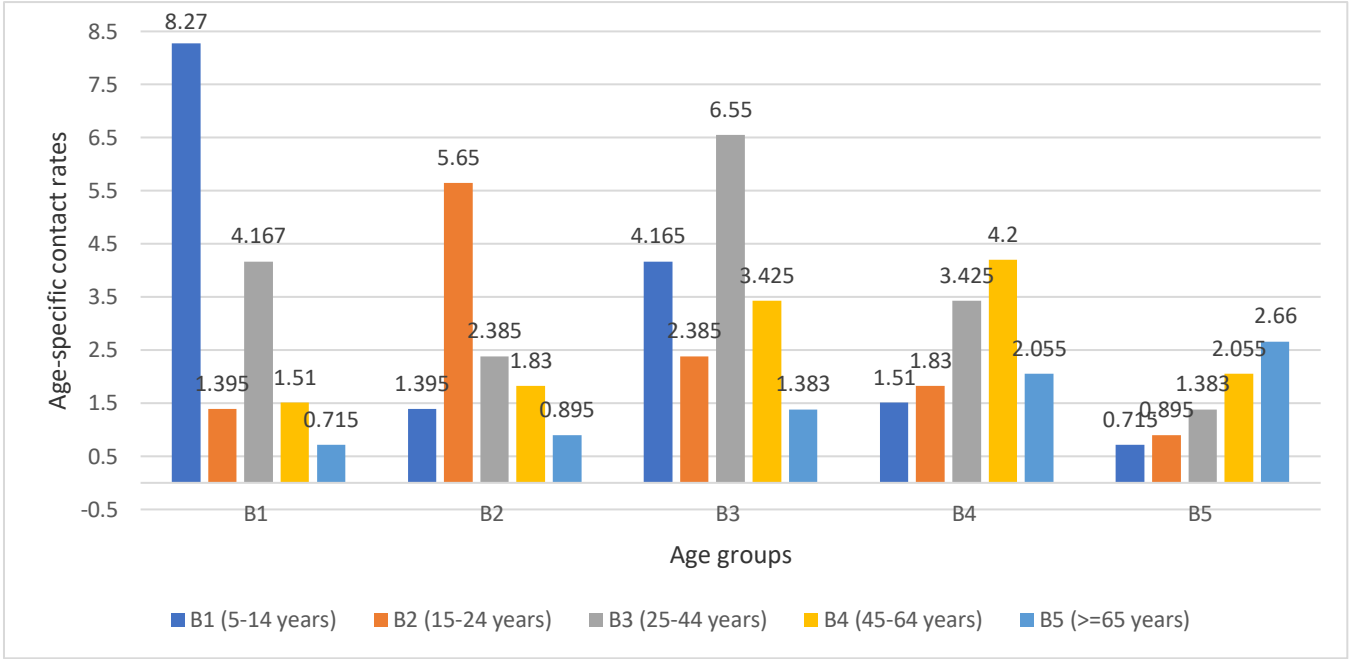
Fig. 1. Illustration of the contact rates between age group.

$$\lambda_i = \frac{1}{n} \cdot \left(\sum_{j=1}^{n} \left(c_{ij} \cdot \frac{I_j}{P_j} \right) \right) \cdot \frac{S_i}{P_i} \cdot \beta_I \quad (6)$$

In the H1N1 SEIR model defined by [7], the vulnerability values of the population are $\beta_1 = 0.434$, $\beta_2 = 0.158$, $\beta_3 = 0.118$, $\beta_4 = 0.046$, and $\beta_5 = 0.046$. The number of individuals in population i is presented as p_i, while c_{ij} is the numbers of contacts between different age groups. These numbers are determined based on the demographical statistics of 2006 Hong Kong Population By-census and a survey on contact pattern conducted in [16]. The population size of each age group are as follow; $p_1 = 0.94m$, $p_2 = 0.91m$, $p_3 = 2.30m$, $p_4 = 1.86m$, and $p_5 = 0.85m$. Meanwhile, the contact rates of the groups are illustrated in Fig. 1. It can be observed that the individuals within the same group have more frequently contact with each other than those in the other groups. Youngsters in group B_1 have the highest contact frequency within same age group and the individuals in B_3 have the highest total contact frequency.

III. THE PROPOSED SOLUTION

The implementation of the SCAmut for vaccines distribution is discussed in this section. Initialization of population, fitness evaluation, updating the best solution, and modify the population procedures are all part of the SCA optimization process.

For stochastic population-based optimization strategies like SCA, a random collection of solutions is used to begin the process of finding the best solution. Using an objective function and a set of rules, the optimization technique evaluates and improves the solutions [9]. There is no guarantee that a solution will be found in a single run. However, the likelihood of discovering the global optimum grows as the number of random solutions and optimization steps (iterations) increases. All stochastic population-based optimization requires two important phases: exploration and exploitation. For exploration of SCA, a random solution set is combined with high rate of randomization to locate interesting parts of the search space [9]. There are, however, subtle shifts in the random solutions in the exploitation phase, and the random variations are far lower than in the exploration phase. The solutions of SCA are following position update equations shown in Eqs. (7) and (8):

$$X_i^{t+1} = X_i^t + r_1 \times sin\,(r_2) \times |r_3 P_i^t - X_i^t| \quad (7)$$

$$X_i^{t+1} = X_i^t + r_1 \times cos\,(r_2) \times |r_3 P_i^t - X_i^t| \quad (8)$$

, where X_i^t is the current solution's location in the i-th dimension at the t-th iteration, r_2 and r_3 are random values, P_i is the destination point's position in the i-th dimension, and $\|$ is the absolute value. P_i is selected based on the solutions fitness value, which is a problem dependent function. In this research the fitness function is the total number of infection.

These two equations are combined to form the following formula

$$X_i^{t+1} = \begin{cases} X_i^t + r_1 \times sin\,(r_2) \times |r_3 P_i^t - X_i^t|, & r_4 < 0.5 \\ X_i^t + r_1 \times cos\,(r_2) \times |r_3 P_i^t - X_i^t|, & r_4 \geq 0.5 \end{cases} \quad (9)$$

, where r_4 is a random number in the range of [0,1] and used to determine whether the solution is updated using either Eqs. (7) or (8).

Four primary SCA parameters may be seen in the equations above: r_1, r_2, r_3 and r_4. To determine the next position (or movement direction), r_1 specifies the area (or space) in which the next position (or movement direction) can occur using Eq. (10):

$$r_1 = a - t\,\frac{a}{T} \quad (10)$$

, where *t* represents the current iteration, *T* is the maximum number of iterations, and a is a constant. Movement in or out of a given direction is determined by the r_2 parameter, which is a random value within the range of $[0, 2\pi]$. The random weight r_3, highlight or de-emphasis the influence of destination on distance definition stochastically. This is

followed by the changeover between the sine and cosine components based on the random parameter r_4.
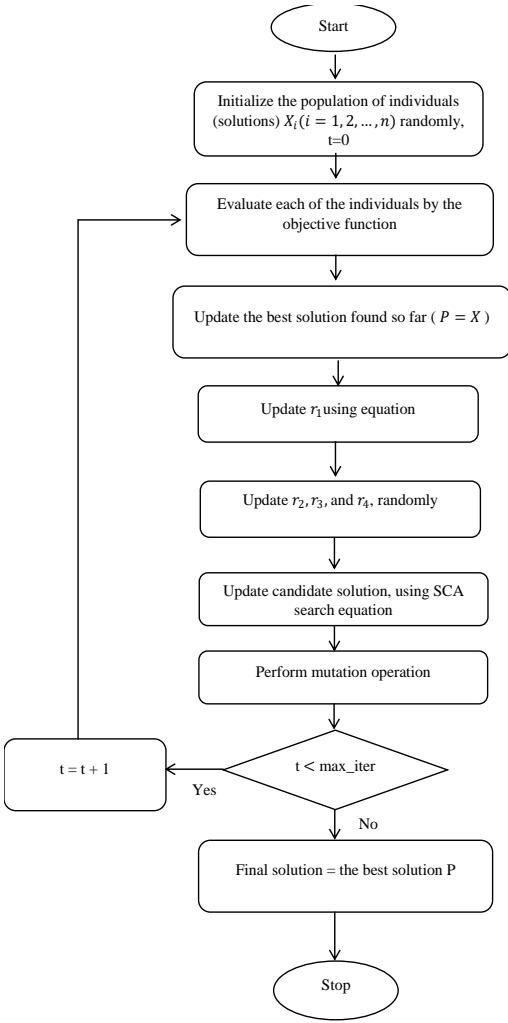

Fig. 2. Flowchart of SCAmut algorithm.

Here, mutation is proposed to improve the performance of SCA in lowering the total infection. The position update with mutation is shown in Eq. (11).

$$V_k^i = X_{kn}^i + F \cdot (U_1^i - U_2^i) \qquad (11)$$

The mutation operator used here is inspired by differential evolution's mutation. It is used to create a trial vector V_k^G for each solution in the current population of ith iteration. It is done by mutating a target vector X_{kn}^i. U_1^i and U_2^i are also randomly selected solution and different with the target vector and parent vector. Scale factor F is a user defined parameter.

The mutation is introduced to delay convergence of SCA to that the population can explore better solution. To balance the exploration and exploitation, the mutation is carried by one agent only. Specifically, the mutation is performed on the worst agent, i.e.; target vector is the worst agent. The worst agent is identified and the mutation is done after the candidate solution is updated using SCA search equation and the fitness evaluation will be done after the mutation process.

The proposed SCA with mutation (SCAmut) algorithm's flowchart is shown in Fig. 2. Here, the algorithm is looped till maximum number of iterations is reached.

B. Implementation of the Proposed Algorithm

The dimension of the SCAmut's solution follows the number of the age group. Since the H1N1 model adopted here divided the population to 5 age groups, the dimension of the solutions is also equal to 5. Each of the SCAmut solution represents the proposed percentage of total vaccine given for the respective age group. Therefore, the following equations need to be satisfied.

$$\sum_{G=1}^{5} X_i^{t,G} = 1 \qquad (12)$$
$$V^G = X_i^{t,G} V_{max} \qquad (13)$$
$$\sum_{G=1}^{5} V^G = V_{max} \qquad (14)$$

, where G represent the group number, V^G is the total vaccine allocated to group G and V_{max} is the total vaccine available.

The fitness of a solution is evaluated here based on the SEIR model's total number of infection. The objective here is to minimize the infection value.

$$f(X_i^t) = \sum_{d=1}^{dmax} \sum_{G=1}^{5} I_G(d) \qquad (15)$$

, where d is the day starting from the pandemic outbreak till the end at *dmax*. *I* is calculated using the SEIR model shown in Eqs. (1) – (5).

IV. SIMULATION AND ANALYSIS

In the experimental section, the performance of the proposed SCAmut will be compared with some traditional vaccine deployment strategies. First, the settings of the simulations are described.

A. Settings of the Simulation

The vaccine coverage and releasing time influence the total number of infection within the population. The composition of the population in each age group is $p_1 = 0.94 \times 10^6$, $p_2 = 0.91 \times 10^6$, $p_3 = 2.30 \times 10^6$, $p_4 = 1.86 \times 10^6$, and $p_5 = 0.85 \times 10^6$. Initially 30 individuals in p are set exposed to the disease this is similar to [6]. Various vaccine coverage and the releasing time are used in the experiment according to [7] and the duration of the pandemic is T = 300. The parameters in the SCAmut are set as follows; the search population is 20, and F = 0.5. The maximum number of SCAmut's iteration is 1000.

B. Traditional Deployment Methods for Comparison

In the literature [7], the vaccine deployment strategy is generally made according to the transmissibility of the disease (S1), the vulnerability of the population (S2), or the infection risk of the disease (S3). Therefore, the SCAmut's performance is compared with the three traditional strategies (S1 to S3) in this work.

Strategy 1 (S1): Based on Transmissibility

According to the transmissibility strategy, more vaccine doses are given to the individuals with a higher contact frequency. The vaccination proportion v_i for each age group p_i at time t_{vacc} is

$$v_i(t) = \frac{\sum_{k=1}^{n} c_{ik}}{\sum_{j=1}^{n} \sum_{k=1}^{n} c_{jk}}, \quad i = 1,2,\dots,n. \qquad (16)$$

Strategy 2 (S2): Based on Vulnerability

This 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 v_i for each age group p_i at time t_{vacc} is

$$v_i(t) = \frac{\beta_i}{\sum_{j=1}^n \beta_j}, \quad i = 1, 2, \dots, n. \tag{17}$$

Strategy 3 (S3): Based on Infection Risk

The vaccination proportion v_i for each age group p_i at time t_{vacc} is based on the value of the time-dependent infection risk $\lambda_i(t)$; thus

$$v_i(t) = \frac{\lambda_i(t)}{\sum_{j=1}^n \lambda_i(t)}, \quad i = 1, 2, \dots, n. \tag{18}$$

C. Findings

i.   *Vaccine releasing time*

Four vaccination release days are investigated here; day 1, day 50, day 75 and day 100. The total number of vaccine available is 5% of the total population. This setting is following the experimental setting in [6]. The findings are illustrated in Figs. 3 to 6.

From the figures, it is clear that different days of vaccine deployment have huge impact in controlling the total infections during epidemic. As we can see from the result, day 1 and day 50 give better result than day 75 and day 100. Where the peak of infection can be significantly lowered with earlier vaccination program.

The contribution of SCAmut is significantly noticeable when the vaccine is released on day 1 and 50. The total infection of the population using vaccination percentage given by SCAmut is the lowest for the two cases. Interestingly, the infection curve of vaccination distribution on day 1 shows that different distribution according to the different strategy effect the day of the peak. The vaccine distribution of SCAmut delayed the peak the most.

Vacinnation program that begins at later day; day 75 and 100, did not give good result, the peaks of the infection case regardless of the vaccination strategy are similar to without vaccination. Nonetheless, the vaccination smoothen the curve faster than without vaccination and SCAmut is the fastest.

From the findings here, it is observed that with early deployment of vaccine during pandemic, we can efficiently control the infection risk of the virus, lower the total infection and even delay the peak. This would allow health provider to have better preparation and not stressing the health facilities. Most importantly SCAmut gives the best distribution percentage, better than the distribution of SCA and the three traditional strategies.
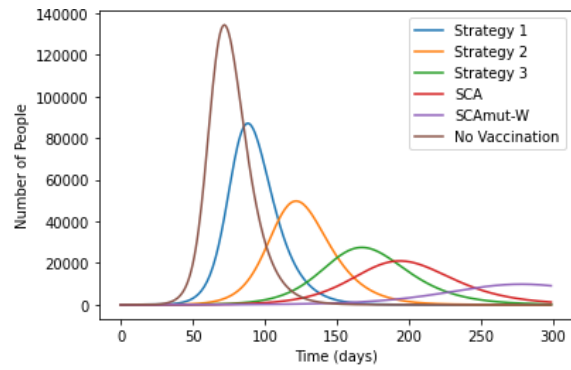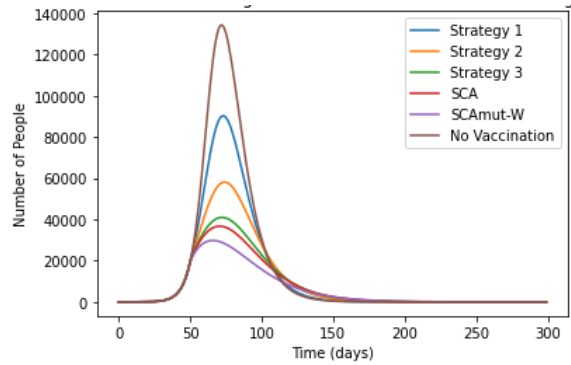

Fig. 3. Day 1 vaccine released.

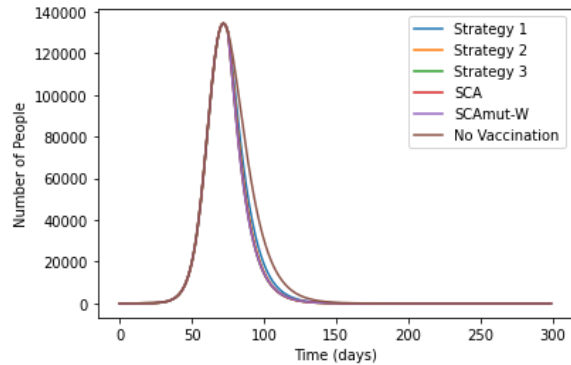Fig. 4. Day 50 vaccine released.
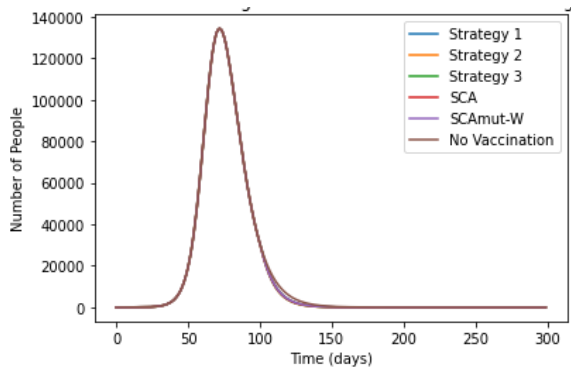

Fig. 5. Day 75 vaccine released.

Fig. 6. Day 100 vaccine released.

ii.   *Vaccine coverage doses*

In this test, the vaccination doses supply for the population are varied; 5%, and 10%, while the release day is fixed at day 50. The results are shown in Figs. 7 and 8.
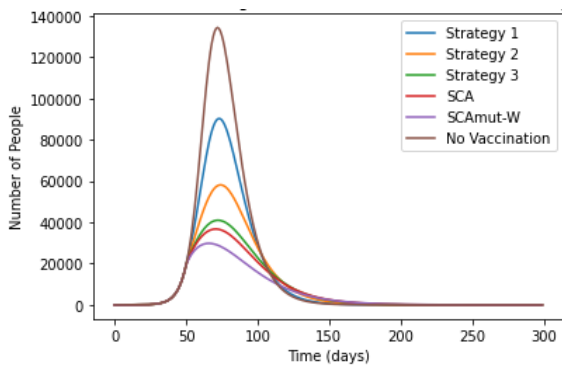

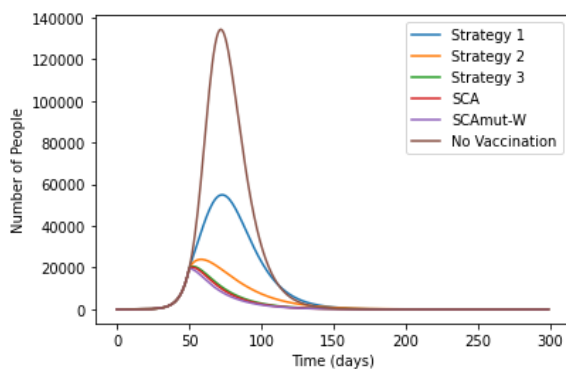
Fig. 7. Vaccine coverage for 5%.

Fig. 8. Vaccine coverage 10%.

As expected, the greater the number of available vaccine, the lower the infection rate and its peak. The total infection using SCAmut vaccination distribution with vaccine coverage of 10% have better result in reducing the infection during the epidemic which only around 20000 maximum daily cases, compared to 5% vaccine coverage that have near 40000 daily infections. The SCAmut always outperformed strategy 1 and 2.

V. CONCLUSION

This project was aimed to study the optimization of vaccine distribution to minimize the total infections. Hong Kong H1N1 SEIR is adopted in this study. An improved version of SCA, SCAmut is proposed to better distribute the vaccine among several age groups so that the total infections is minimized. The SCAmut is compared with three traditional vaccine deployment strategies and original SCA. The SCAmut is found to contribute to better handling of the vaccine, where the infection peak is better lowered and delayed. The performance is better than traditional strategies and performance of original SCA.

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