

# Solving Mobility Intervention of Epidemics using Genetic Algorithm

Rong Zhou  
rong.zhou@siat.ac.cn  
SIAT, CAS  
Shenzhen, China

Kaidong Zhao  
kd.zhao@siat.ac.cn  
SIAT, CAS  
UCAS  
Shenzhen, China

Li Ning  
li.ning@siat.ac.cn  
SIAT, CAS  
Shenzhen, China

## ABSTRACT

As the coronavirus disease 2019 (COVID-19) has become a pandemic in a global scale, it is urgent to take effective interventions to suppress the spread of the epidemic. A challenge to design mobility intervention strategies is held by Workshop of Prescriptive Analytics for the Physical World (PAPW 2020). The task is to look for effective human mobility intervention policies during an epidemic outbreak. Generally, its goal is to minimize the total number of infected people and minimize the intervention on human mobility. In this paper, we present our winning solution to the challenge where a genetic algorithm (GA) is used to solve the problem and won the 2nd place of the challenge.

## CCS CONCEPTS

• **Applied computing** → **Health informatics; Multi-criterion optimization and decision-making.**

## KEYWORDS

prescriptive analytics, epidemic intervention, genetic algorithms

## 1 INTRODUCTION

On 30-th January 2020, the epidemic of coronavirus disease 2019 (COVID-19) is declared by the World Health Organization (WHO) as a public health emergency of international concerned, the highest level emergency response for infectious disease. The number of infected cases is still accelerating in the whole wide world. In order to end the global pandemic, multiple intervene strategies can be applied, such as social distancing, contact tracing and so on. Thus, it is critical to assess the effects of these measures on the epidemic progression. Under such a circumstance, Workshop of Prescriptive Analytics for the Physical World (PAPW 2020) hosted a challenge to design mobility intervention strategies to contain an epidemic[1]. The challenge aims to look for effective human mobility intervention policies to minimize the spread of the virus during an epidemic outbreak. Generally, the goal is to minimize the

total number of infected people and minimize the intervention on human mobility at the same time.

## 2 SIMULATOR MODELING

The simulator used in the competition simulates individual mobility in a city of 3 categorical areas (working, residential, and commercial) with 10000 people for 60 days. It employs the susceptible-infectious-recovered (SIR) model [6] for spread of disease, and runs the individual-level epidemic simulation according to the intervention strategy. According to the SIR model, an individual's health status includes 5 stages: **susceptible, pre-symptomatic, symptomatic, critical and recovered**. And there are 5 levels of mobility intervention: **No intervene, Confine, Quarantine, Isolate and Hospitalize**.

In the following part we will briefly introduce the models and scenarios used in the simulator. For more details about the simulator, please refer to its official documentation [2].

### 2.1 Human mobility model

The simulator simulates the human mobility with one simulation step corresponding with one hour in the real world. An individual has different modes of mobility during weekdays and weekends. On weekdays, an individual will start from residential area to working area at a certain time  $T_{start}^d$ , and stay there for  $T_{work}$  hours. After work, they may visit a nearby commercial area with probability  $P_{com}^d$  and stay there for  $T_{com}^d$  hours. Then, they will return to residential area. On weekends, people may visit a random commercial area at a certain time  $T_{start}^e$  with probability  $P_{com}^e$  and stay there for  $T_{com}^e$  hours. After that, they will return to residential area.

### 2.2 Disease transmission model

The disease can transmit from an infected individual through two kinds of contacts:

**Acquaintance contacts:** An individual has a fixed small group of acquaintance contacts. At each time step, there is a probability  $P_c$  for an individual to get infected from an infected acquaintance contact.

**Stranger contacts:** An individual could be in contact with strangers visiting the same area at the same time. At each timestamp, there is probability 0.005 for an individual to get infected from an infected stranger contact.

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## 2.3 Competition scenarios

5 scenarios are provided with the following specified parameters:

**Scenario 1 - default:** default parameters are specified in the previous section.

**Scenario 2 - higher infection rate:** infection rate from both acquaintance and stranger contacts are higher.

**Scenario 3 - More areas in the city:** there will be much more areas in the city.

**Scenario 4 - larger initial infected population:** there is a large infected population at the beginning of the simulation.

**Scenario 5 - larger range of start-working time:** each individual have a larger range of time to go to work.

## 2.4 Evaluation metrics

The total number of infected people and the intervention on human mobility are both considered in the score calculation for the competition:

$$score = \exp\left(\frac{I}{500}\right) + \exp\left(\frac{Q}{10000}\right)$$

where  $I$  is the accumulated number of infected people, and  $Q$  is the weighted sum of  $N_o$  ( $vin\{hospitalized, isolated, quarantined, confined\}$ ) which is the number of the intervention actions for one day.

## 3 METHOD DESCRIPTION

In this section, we first introduce the framework of our algorithm, and then explain the further improvements in detail.

### 3.1 Solution framework

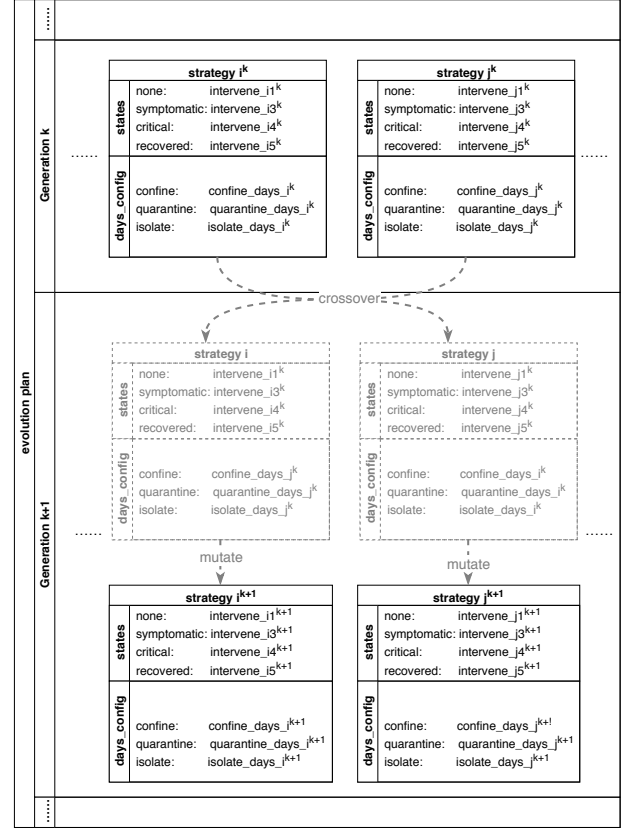
To generate our solutions, we used genetic algorithm (GA) [4] to find the intervention strategies. GA are a family of computational models inspired by evolution. They are robust search and optimization techniques due to their capacity to locate the global optimum. Thus, GAs are often used to find complex, non-obvious solutions to algorithmic optimization and search problems [3, 5].

Generally speaking, a basic GA contains the following procedures:

- Initialization: some initial solutions are created, either random or “blank”
- Evaluation: measure the performance of different solutions
- Evolution: crossover and mutate from the current solutions to generate better solutions.

We apply the above algorithm and use a template for strategies based on the variant versions the strategy model proposed for the quick test. The procedures of GA and details about the variant version of the strategy template can be found in 1.

As shown in Fig. 1, we consider each strategy as a joint of two gene segments. In the first segment, it consists of the intervene operations for different infection states, and the second segment consists of the intervention days for the confine, quarantine and isolate operations, respectively. The intervene options is enlarged to include all types of operations (no intervene, confine, quarantine, isolate and hospitalized) for each state, and the range of confine/quarantine/isolate days are enlarged to  $\{3, \dots, 30\}$ . In the iteration steps of the strategy evolution, one generation is broken down into a crossover phase and mutation phase. In the crossover

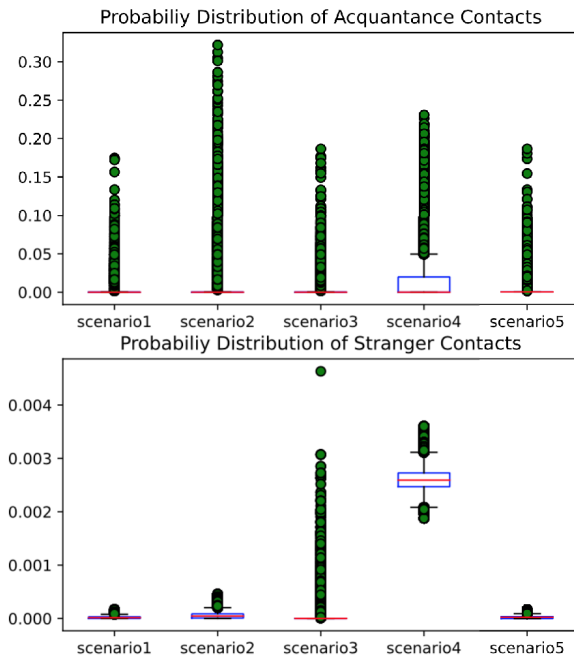


**Figure 1: Procedures of GA: one generation is broken down into a crossover phase and mutation phase.**

phase, we execute the partial exchange of strategies using a fixed cross site with probability  $P_{cx}$ . The cross site separates two gene segments in the strategy. In the mutation phase, we carry out independent mutation for each element in the strategy with probability  $P_{mut}$  and  $P_{ind}$  to generate the off-springs. Finally, in the resulting off-springs,  $k$  randomly selected children are replaced by the top  $k$  strategies from the parent generation. In most of our submissions,  $k$  is set to 5.

### 3.2 Further improvement: distinguish the scenarios and refine strategy

According to the configuration, scenario 2, 3, 4 can be easily distinguished according to some characteristics on the first day under the test environment (scenario “submit”), so the strategies were calculated according to each of the scenarios. Soon we realized that an optimal solution was found in the mentioned strategy space, which is suitable for all the 5 scenarios. By applying the strategy, scenario 1, 2, 3 and 5 can achieve a score around 2.5, while the score of scenario 4 is about 6.7. Naturally, we wondered if there is any room for further improvement in scenario 4. It is noticed that we only use the information of individual’s infection state, while the information of “probability from infected” is left.



**Figure 2: Probability Distribution of Acquaintance / Stranger Contacts under Different Scenarios.**

Fig. 2 demonstrates that the probability distribution of acquaintance / stranger contacts in scenario 4 is significantly different from other scenarios.

Consequently, to further improve the intervention result, the situations of both “acquaintance contact” and “stranger contact” are substituted by two sub-situations respectively, which are distinguished with the aggregated probability of contacts, i.e. one with the probability larger than a threshold and one with the probability smaller than the threshold.

The proper threshold is determined according to the quantitative analysis of the statistics of the experiment processes and a grid search in the candidate value range.

### 3.3 Results

The strategy used in our best submission (total score 21) is , and the detailed scores for the five scenarios are: scenario 1: 2.42; scenario 2: 2.64; scenario 3: 2.44; scenario 4: 5.76; scenario 5: 2.43.

For scenario 4, by applying the refined strategy, the scores are improved to around 5.7 according to our evaluations in running the submit processes.

## 4 CONCLUSION AND DISCUSSION

In this paper, we present our solution algorithm and tricks for improvement, which is capable to effectively contain the epidemic. A simple genetic algorithm is developed to provide solutions, with a variant version of strategy template proposed for the quick test by official. In order to minimize the evaluation metric of some scenarios, we extended the strategy template based on the analysis results. We do hope these findings may inform public health policy

for countries and regions to combat the global pandemic of COVID-19.

Nevertheless, it remains a lot work to do for the study of epidemic control. For example, from a modeling perspective, the number of people, areas and activities in each scenario is too small, and we omit the probability rate of death and becoming susceptible again. In the long run, in order to better evaluate the intervene strategy, on the one hand, we hope to improve the above cons of the simulator, on the other hand, we are particular interested in prediction over trends of epidemic transmission in a relatively short horizon. And we believe these will better guide the implementation of intervention strategies.

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