

Development of adaptable pandemic simulation models

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KEY MESSAGES

1. A pandemic simulation programme was developed with three components: an adaptable population generator that creates synthetic populations with various structures; a disease simulator that handles combinations of reactive intervention strategies; and a user interface that offers flexible input and graphical output for analysis.
2. Simulation experiments of different reactive strategy combinations were carried out over the regional synthetic populations.
3. The effectiveness of various practical schooling strategies under a realistic demographic situation and movement dynamics were modelled. Limiting contact amongst students in more schools can

reduce the overall attack rate. Increasing the duration of school closures can reduce the overall infection attack rate.

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Introduction

It is important to protect healthcare workers and patients from infection during pandemics, especially in a densely populated city such as Hong Kong. A simulation-based model mimicking realistic population structures can simulate possible scenarios in a timely manner.

This study aimed to develop an adaptable disease-spread simulation model with a user-friendly platform and interface that can accurately and reliably mimic regional community structures, including demographic dynamics and healthcare facilities. Simulation efficiency and robustness can be improved through appropriate probability and statistical approximation methods.

Methods

We developed a susceptible-exposed-infected-removed compartmental model, a stochastic agent-based heterogeneous model, and a stochastic simulation model with two major improvements to the Longini model.¹ First, the input synthetic population was based on Hong Kong demographic properties to reflect person-to-person contact patterns, especially in the educational and healthcare sectors. Second, extra refinements were made to intervention strategies to provide more reactive strategy combinations. We used C++ Qt programming to develop a visual simulation platform for the disease-spread simulation model.

Results

We calibrated the model using the 2009 H1N1 outbreak in Hong Kong in two major workable models: one based on the Hong Kong regional structure (HKmodel) and another comprising both Hong Kong's regional structure and the partial design of the high cycle fatigue (HK_HCFmodel). The simulators were calibrated to match the documented illness attack rate and basic reproductive number. We calibrated the age-group-specific cumulative infection attack rate at day 180 to match an independent study in Hong Kong. The basic reproduction number of the calibrated model was 1.5 which fell within the range of estimates between 1.1 and 2.1 of 2009 H1N1 pandemic influenza.

The effectiveness of various reactive strategies was examined using the Hong Kong regional structure model. With 10% antiviral coverage alone, the attack rate reduced to 8.56%. With school closure and social distancing, the attack rate significantly reduced to 0.96% for scenarios without antiviral coverage and to 0.24% for scenarios with antiviral coverage. The attack rate reduced to 3.19% when school closure (individual schools) was adopted and to 5.05% when social distancing was adopted. In general, for containing the spread of a disease, closing more types of schools was more effective than increased school closure length. The overall attack rate of closing all school types is lower than that for closing kindergartens and primary schools or closing kindergartens only.

Four alternative algorithms (ie, the Longini, Longini+S, Tai-S, and algorithms) were reviewed from the viewpoint of either infectious or susceptible individuals. Through theoretical analysis and simulation experiments, some standards for selecting the most efficient algorithm were identified. In addition, methods for applying the algorithms to real applications and potential directions for further studies were indicated. Algorithm efficiency was examined with respect to the changing factors of infectious individuals, transmission probabilities magnitude, and population size. The performance measure was based on the computational time of a 1-day simulation setting. A computationally efficient algorithm for a population with heterogeneous transmission rates was presented. Based on a heterogeneous subset sampling method,^{2,3} our combined algorithm is more efficient than other algorithms for sampling disease transmission in a subset of a heterogeneous population.

Discussion

Current simulation models for infectious diseases often overlook regional variations when constructing detailed community structures. Simulation with more detailed community dynamics provides a better opportunity to contain potential pandemic influenza strains at the source. We developed a population-generation algorithm for Hong Kong-based simulations and a disease transmission simulation model taking into consideration the healthcare facilities.

We used C++ Qt programming to develop a visual simulation platform to facilitate graphical user interface-based displays and advanced modelling of pandemic disease transmission. It enables programming of the complicated dependencies between modules from the local community perspective. It also displays visual outputs and data analysis to facilitate effective decision-making. The platform allows users to analyse the disease transmission results. By simulating various scenarios, the impact and effectiveness of interventions can be studied prior to their implementation.

We proposed to rebuild the daily contact model from the perspective of infectious individuals to track each susceptible individual, which is different from the Longini model.⁴ Such an approach has been reported by Tsai et al.^{2,3} In summary, the approach from the infectiousness perspective is not as efficient as we expected. Accordingly, the Longini model from the susceptibility perspective may still have its advantages compared with the Tsai model. A reference guideline for selecting an efficient algorithm of disease transmission under various model settings is summarised.

Our simulation models allow epidemiologists, public health professionals, and policy makers

to evaluate the impact of pandemic outbreaks and associated mitigation strategies, to develop effective countermeasures to minimise the impact of pandemics, to improve the performance of regional medical operation and public health systems in the face of pandemic outbreaks, and to prepare action, prophylaxis, and intervention strategies. Nonetheless, further development of the healthcare component of the model is needed to represent a more realistic situation. For instance, a fever clinic, an emergency department, and an infectious disease centre will be added in future, as well as realistic dynamics among various healthcare units. Furthermore, district-specific demographics for hospital components may be taken into account.

Bernoulli trials are time-consuming from the infectiousness perspective and susceptibility perspective. Binomial or normal approximation methods may reduce the time on Bernoulli trials and increase algorithm efficiency. Although we have not reached this stage, the idea should be applicable in developing a new and more efficient algorithms for disease transmission models. In addition, computational epidemiology approaches such as disease detection surveillance, simulation studies, and microbiological informatics¹ can play complementary roles to enable more comprehensive outbreak detection and tracking the spread of infectious disease at its origin. Exploring the interoperability among different methods for disease detection can justify optimal data-sharing for effective containment of infectious diseases. The development of a more robust model will require collaboration and understanding among statisticians, simulation modellers, epidemiologists, microbiologists, practitioners, and public health policy makers.⁵

Conclusions

A pandemic simulation programme was developed with three components: an adaptable population generator that creates synthetic populations with various structures; a disease simulator that handles combinations of reactive intervention strategies; and a user interface that offers flexible input and graphical output for analysis. Simulation experiments showed that the overall attack rate can be reduced by limiting contact amongst students in more schools and increasing the duration of school closures. However, school closure incurs high costs as parents have to stay at home to look after their children. Reference guidelines for selecting an efficient algorithm of disease transmission under various model settings were summarised.

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