

## **HYBRID SIMULATION MODEL FOR VIRUS TRANSMISSION ON THE DIAMOND PRINCESS CRUISE SHIP**

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### **ABSTRACT**

We propose a hybrid simulation model structure for accurate prediction of the COVID-19 transmission on the Diamond Princess cruise ship where a fixed population mixes and has transmissible contacts among different types of small-scale facilities such as restaurants or dorms. We use the agent-based model (ABM) and discrete-event simulation (DES) to predict the infected population in enclosed facilities and the overall transmission dynamics, respectively. The actual infection data fall into the 95% confidence interval of this hybrid model output with the basic reproduction number  $R_0=2.38$ .

### **1 INTRODUCTION**

Interventions that prevent the spread of COVID-19 disease are of great importance to the reopening of operations in public places. Accurate prediction of virus spreading plays a supportive role in making the policies. Most previous works have applied the SEIR model to calculate  $R_0$  mathematically (Noakes et al. 2006), but works that predict infectious data in enclosed systems with dynamic activity patterns are lacking. To overcome these barriers, we propose a simulation model combining the agent-based model (ABM) and discrete-event simulation (DES) for accurate prediction of the virus spreading in those enclosed systems. The hybrid model is flexible enough to be adapted into different scenarios under different policy restrictions. In this article, we briefly discuss the establishment of the hybrid model and validation of it on the confined system of Diamond Princess cruise ship.

### **2 METHOD**

The 2-phase simulation model combines ABM and DES to predict virus transmission in an enclosed system consisting of small-scale functional units, such as the cruise ship. The structure diagram is shown in Figure 1. On a cruise ship, these small-scale units can be cabins, restaurants, etc., in which a mixture of the population has physical transmissible contacts and virus transmissions happen. We call these units Contact Nodes (CN). The layout of CNs is adapted from Diamond Princess's deck plan and the specific parameters of CN are location area and moving frequency of agents in each CN. Agents, e.g. guests and crew on the cruise ship, move freely among CNs given certain schedules and routines based on the opening time of each CN. The combined network system of the CNs and the temporal dynamics of agents within the network are simulated with the DES. The transmission in a CN is determined through a predefined infection probability function. The infection probability function is estimated as a function of the contact factor, determined by the predictive regression model, infectious factors, determined by the SEIR model, and adjustment factors, such as age factors. The ABM simulates the physical dynamics of a certain number of agents under different

layout settings of CN and outputs the expected number of transmissible contacts experienced by the agents given a time range. We train the predictive regression model by a sufficient number of inputs from the ABM and predict the contact factor in a CN during the runtime of the DES.

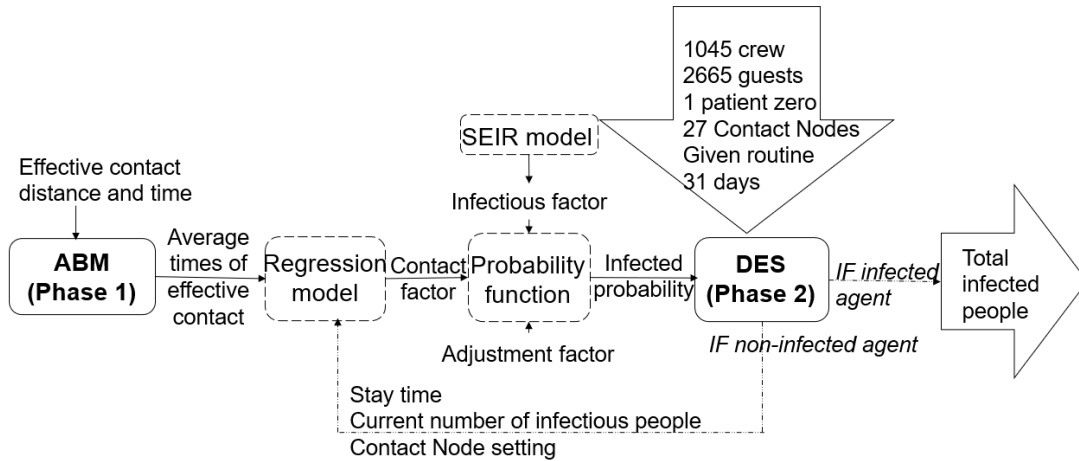


Figure 1: Structure of the hybrid model in the context of a cruise ship.

The simulation model takes advantage of both ABM and DES. The dynamics of daily activities of agents and the structure of the aggregate system can be well captured by the DES; while the ABM enables better simulation of the physical dynamics and social mixture settings within a confined space. Besides, computational resources are saved since the two simulations are connected through a flexible regression model instead of running in parallel.

### 3 RESULTS AND DISCUSSIONS

We constructed the ABM in Python 3, DES in ProModel (Harrell and Tumay 1992), and regression model in R for implementation. We calibrated the model with actual infection data, including the infected people, the initial number of crew and guests, and the cruise ship duration, as reported by National Institute of Infectious Diseases, Japan (2020), and with the basic reproduction number,  $R_0$ , by running the model for various  $R_0$  values between 1.5 and 3.0 (Liu et al. 2020). Choosing  $R_0=2.38$  as the calibrated value by linear interpolation with 5 replicates for each scenario, we further validated the value by running 10 replicates. The actual reported total number of infected people, 619, was within the 95% confidence interval, 581.02-649.98, of the predicted infected number. Therefore,  $R_0=2.38$  passed the validation.

The calibrated model can be used to perform analysis on the effectiveness of various interventions and reopening policies. It can be further adapted to more complex and unconfined systems such as schools or nursing homes, with locations and routing settings in DES adjusted to control the interactions with the outside world, and with ABM parameters changed to reflect agents' moving patterns.

### REFERENCES

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