

# **An Agent-Based Model to Study the Spread and Control of Infectious Diseases: Combining the Advantages of Agent-Based and Compartmental Models in Epidemiology**

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Date: 22<sup>nd</sup> August 2022

Module Title: MSc Spatial Data Science & Visualisation

Module Code: CASA0004

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Word Count: 11,555

This dissertation is submitted in part requirement for the MSc in the Centre for Advanced Spatial Analysis, Bartlett Faculty of the Build Environment, UCL.

# Abstract

In recent years, the world has been affected by the massive spread of COVID-19 without knowing when it will end. By the time COVID-19 broke out, most countries did not have proper preparedness when the number of infected cases had started rising.

This research combined an agent-based model with a compartmental model known as the SIRV to study the spread and control of epidemics. The model is used to study the effectiveness of different vaccination rates, infectious periods, immunity periods and social distancing levels in controlling epidemics during the first year of the outbreak.

This research's primary analysis and learning methods include the NSGAII for parameter optimisation, Saltelli global sensitivity analysis for impact assessment of the input parameters, linear regression, and a random forest for forecasting the parameter outcomes. Also, the random sampling methods used in the analysis involve the LHS and Direct Sampling.

As a result, all the model's target input parameters significantly impacted the overall infected cases. Among the input parameters, the infectious period had the most impact on the spread of infectious diseases. A longer infectious period greatly stimulated the spread of infectious diseases. In contrast, the rest of the input parameters, including the vaccination rate, immunity period and social distancing level, indicated that the higher the values, the better the suppression of epidemics.

## **Declaration**

I, Jeonghwa Kang (student number: 21044456), hereby declare that this dissertation is all my own original work and that all sources have been acknowledged. It is 11,555 words in length from the introduction to conclusion inclusive.

Signed: Jeonghwa Kang

Date: 22<sup>nd</sup> August 2022

# Acknowledgements

Firstly, I would like to express the deepest appreciation for my supervisor, Dr. Juste Raimbault for his continual supervision and valuable feedback regarding my dissertation which took place over the summer of 2022.

Secondly, I would also like to thank all the staff including the PhD students in the Centre for Advanced Spatial Analysis of the Built Environment, University College London, for their endless support throughout my academic life at UCL.

Lastly, I would like to thank my friends and family who are supporting me both academically and personally throughout my life.

# 1. Introduction

## ***1.1 Context and Motivation***

The impact of one of the fatal epidemics in history, the Black Death, has led to the death of almost one-third of the population of Europe (Editors, 2010), and the most recent epidemic in the world today, COVID-19, is currently costing millions of valuable human lives. Before the introduction of mathematical and computational modelling, humans had little knowledge of effectively controlling and minimising the spread of infectious diseases. Monitoring and analysing the impacts of preventive measures on the spread of epidemics had to be utterly dependent on assessing the aftermath, which is the damage done to a population. Due to this, developing and applying the countermeasures often took a tremendous amount of time. However, recent advances in mathematical and computational modelling began to play an essential role in forecasting epidemics by hypothetically simulating agents' interactions to understand complex spatial behaviours. Forecasting disease transmission dynamics provides ways for humans to develop and apply appropriate preventive measures and ensure the adequate use and distribution of limited material and human resources. Furthermore, the importance of forecasting the spread of diseases in recent years has become even more crucial as the world is rapidly globalising and becoming closer with ever-advancing technologies that make it easier for humans to travel faster and further around the globe.

Modelling of diseases began in the 17th century by John Graunt. He conducted an empirical study on infections affecting individuals in various regions in Britain (Morabia, 2013). Daniel Bernoullie, in the 18th century, developed a more sophisticated model, which is more of a data-driven and equation-based approach to studying the outbreak of the smallpox epidemic that happened in Europe (Dietz and Heesterbeek, 2002). In the 19th century, various mathematical equational models were further developed for modelling the complex spread of infectious diseases. The well-known equational models include the Ordinary Differential Equations (ODEs), Partial Differential Equations (PDEs) and Differential Equations. In recent years, Agent-Based Modeling (ABMs) has combined traditional equational models to study complex spatial dynamics of epidemics. After several devastating epidemic outbreaks, particularly the SARS, MERS, and COVID-19, in the recent 21st century, many models have played a vital role in developing essential government policies to counter the epidemic

outbreaks from their emergence in a particular country to the current global pandemic. For example, the early spread of the COVID-19 pandemic has led to travel restrictions and closures of the countries' borders. Monitoring the impact of various preventive measures, such as social distancing or movement policies, has been crucial in evaluating these decisions. However, strict long-term restriction policies had other devastating impacts on local and global economies. Economic evaluations and government policies have combined both economic and epidemic models to assess the economic consequences of COVID-19, informing policy calls for easing restrictions on a situational basis. At the same time, the models for social contact and mobility, have provided practical ways to evaluate appropriate pathways to reduce regulations for mobility and distancing measures safely. Finally, the advancement in agent-based modellings has provided flexibility in evaluating the dynamics of epidemics under various complex scenarios. These include examples of how governments can achieve mass immunisation or suppression of rapidly growing epidemics by introducing different vaccination strategies. Today, the methods of infectious morbidity forecasting were able to advance quickly due to the recent deployment of information supervision systems and a vast volume of statistics available for analysis. Out of all, human interaction is the most crucial factor which plays a significant role in transmitting the virus from one to the other. Interestingly, its dynamic can be modelled via a combination of ABM and compartmental model representing Spatio-temporal features in different stages of the agents during the infection process, e.g., an ABM composed of the Susceptible-Infected-Recovered (SIR) or the Susceptible-Exposed-Infected-Recovered models (SEIR) compartmental model, to name a few.

## ***1.2 Research Question and Objectives***

The main objective in keeping humans safe against fatal disease outbreaks is to control the spread of infectious diseases successfully. The first step to successfully controlling the spread of diseases would be to identify which factors are likely to impact the dynamics of the epidemics. For instance, we might be interested in the effects of social distancing and wearing masks since they are well-known preventive measures that effectively mitigate the virus's spread (Kwon *et al.*, 2021). Furthermore, we might also be interested in the effects of vaccination since the high rate of immunisation is known to successfully control the spread of diseases and even achieve herd immunity by mass immunisation (Bicher *et al.*, 2022). This research is generic and stylized for studying the spread and control of contagious respiratory

illnesses such as COVID-19 and Influenza. Because the model is rather generic, it is flexible in simulating various scenarios that consider different types of infectious diseases with particular social and geographical contexts.

This leaves us with several important research questions to answer.

- What factors affect the spread of infectious diseases, and how can we estimate the impacts of those factors?
- To what extent do different preventive measures protect humans against the spread of infectious diseases?
- To what extent do different longevity of immunity and infectious periods of the human body affect the spread of infectious diseases?
- To what extent do the optimal values of the chosen factors control the spread of infectious diseases during the first year of the outbreak?

Questions like these are worth considering as they often come into play when recognising the importance of modelling epidemics. Guided by these research questions, there are several objectives which we list according to the analytical steps in this research:

1. Implement an ABM that adapts the compartmental model's dynamics to monitor and track the spread of infectious diseases in a hypothetical scenario.
2. By using the LHS for generating random values of the model's input parameters, explore the output space of the model by analysing the statistical distributions.
3. Using the Grid Sampling to evaluate every possible combination of the model's input parameter values, identify which combination results in the highest and the lowest proportional numbers of sick agents.
4. Using the Saltelli sensitivity analysis, calculate sensitivity indices for each model input parameter.
5. By using NSGAII multi-criteria calibration method, optimise the model input parameter values relative to the proportional number of sick agents.

### ***1.3 Project Scope***

This work aims to analyse and quantify the impacts of the chosen input parameters of the model on the spread of infectious diseases. The simulation projects a real-life situation where agents commute from home to their designated workplaces via different modes of transportation on a fixed daily schedule. At the beginning of the simulation, the entire

population is set to susceptible. Then, an infected agent is introduced daily for the first 30 days because if none of the infected agents gets introduced into the environment, the infection process does not happen. The model's output parameters include the number of agents associated within each state of the compartmental model upon which the ABM is based. Since the ABM is based on the SIRV compartmental model, proportional numbers of susceptible, infected, recovered, and vaccinated agents have been collected accordingly. Several analysis methods used in this research include the NGSAll for parameter optimisation (Pareto Front) and the Saltelli global sensitivity analysis for calculating sensitivity indices for the model's input parameters. The LHS and Direct Sampling methods based on the uniform distribution are used for randomised sample selection.

### ***1.4 Ethical Consideration***

This work does not handle any real-life data available to the public. There will be no data concerning a real person's identity, nor does the 2D environment depict confidential areas. All the data and predictions are obtained after the completion of the simulation. Since data and predictions generated from this work can be used for the public good to design choices that may facilitate more effective control of epidemics, the data analysis process must be as transparent as possible without any bias.