Towards a simplified solution of COVID spread in buildings for use in coupled models.

Lucas Heighington and Derek Groen

Brunel University London, Kingston Lane, London UB8 3PH, UK
2052561@brunel.ac.uk
Derek.Groen@brunel.ac.uk

Abstract
We present a prototype agent-based simulation tool, Flu And Coronavirus Simulation inside Buildings (FACS-iB), for SARS-Cov2 to be used in an enclosed environment such as a supermarket. Our model simulates both the movement and breathing patterns of agents, to better understand the likelihood of infection within a confined space, given agent behaviours and room layout. We provide an overview of the conceptual model, its implementation, and showcase it in a modelled supermarket environment. In addition, we demonstrate how the model can be coupled to the Flu and Coronavirus Simulator (FACS), which is currently used to model the spread of SARS-CoV2 in cities and larger regions.

Keywords: Agent-based Modelling, Covid-19 Transmission, Breathing Modelling

1 Introduction

For the past 3 years, Covid-19 has had a profound effect on society, infecting 678,000,000 people and leading to the deaths of 6,800,000 lives [1]. These numbers are directly related to the policies introduced in each country, as their governments and officials try to determine what their best options are. Computational models played an important role in the decision making for many governmental strategies, from social and behavioural impacts to epidemic forecasting, along with the scale of these simulations from countries to counties [2]. The results these models produce are vital in predicting where hotspots may arise, where extra resources need to be sent and to get an insight into how the virus is spreading throughout a population.

Current simulation models were produced to try and understand the SARS-Cov-2 virus as it spreads, in the hopes of being able to predict where and how it works. As a result, the current models tend to focus on two main functions. Some models focus on large scale areas, modelling the transmission of the virus throughout a population. These areas can range from small towns all the way to countries or globally. The other type of model simulates the fluid dynamics of particulates around an individual, and how those droplets travel.

These models do have limitations in what they are able to simulate. Larger scale population models tend to drastically simplify the scenario they are trying to replicate [3], with the agents usually moving set intervals and infection rates being limited to just

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a simple percentage. On the other hand, fluid dynamic models only focus on the immediate surroundings of 1-2 individuals [4], drastically limiting its ability to provide information on scenarios involving several people, along with the simulation itself being very computationally intensive [5].

In this work, we aim to implement ideas from both large-scale population models and fluid dynamics in a simplified manner, to produce a model that can simulate enclosed environments, whilst being resource friendly, in the hope that it will fill the gap that exists between current models.

2 Conceptual Model

Our model attempts to replicate the movement and interactions that may occur within a room or building by making use of independent agents that move around the environment by randomly selecting a direction to travel in and designing the outcome of potential interactions.

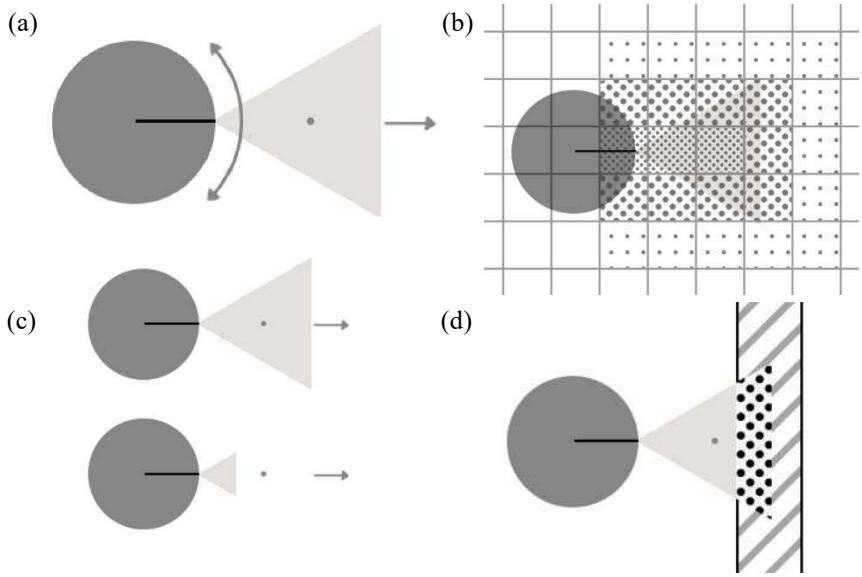

Figure 1 - Agent Model

Agent Movement

As a first step, we decided to use a modified version of the Random Walk algorithm, however, instead of using variables of orientation (N, E, S, W, etc.) we have implemented a randomized degree of rotation. Using the current direction of the agent, it will randomly select to turn either 5° to the left or right before moving forward. This model for the movement of the agent produces, in our opinion, a more fluid and realistic movement, as people tend to turn before they walk.

It is also important for the agent to recognize the boundaries of the simulation, and so if the agent finds itself within a fixed range from the boundary of the simulation

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(indicated by the circular point placed in front of it shown in figure 1.A), it will again randomly choose to turn between 45° to 180°, before checking again if its heading towards the boundary. If it is, it will perform the randomization again, if not, it will continue moving forward.

We are aware that this implementation is limited, as humans tend to have destinations and will take the shortest path possible to get to them. It may be possible to improve this using a routing algorithm, which make the agents movements more meaningful.

Breathing, Coughing and Sneezing

To keep the simulation simplified, we represent the volume of air produced by the agent through a cone as this is the most accurate shape for a simplified exhale [6]. To model the action of breathing, we resize this cone every 2 seconds to represent the rate of breathing [7]. The smaller cone models the act of breathing in, whilst the larger cone represents breathing out, with the breath travelling up to 1 metre away.

This can be seen in Figure 1.C, with the two smaller diagrams showing the agent breathing out and the agent breathing in. As for the agent coughing or sneezing, we simply extend the cone a set distance, two metres for coughing and six metres for sneezing [8], which represent the immediate shape of the exhale, with a cloud of infectious particles forming via the diffusion model.

Walls

To make our simulation environment more accurate, we introduce the concept of walls which can be used to represent any physical barrier to divide rooms or act as aisles in a supermarket. Obviously, walls make up a large part of our constructed environment, and so it's important to model dividers that determine different spaces.

Implementing these allows us to model a more accurate environment, along with more agent interactions, and dividing the room into separate spaces means that we restrict the distance an infected agent's exhalation can travel. Highlighted in Figure 1.D.

Grid Diffusion Model

One of the most important findings made during the pandemic was the length of time Covid-19 could linger in the air. Early studies suggesting minutes, later studies revealed viral copies remained airborne for up to three hours [9]. Our opinion is that this should be factored into any room scale simulation, so we designed and implemented a simplified diffusion model using a grid-based system on top of the agent simulation, shown in Figure 1.B.

In this model, we increase the number of droplets per cell in the grid by factoring in the method of exhale and the distance from the agent, with breathing producing fewer droplets than a sneeze or cough and dividing that by the cell's distance to the agent. We then use this value to influence the probability of an agent getting infected, with the simple concept that a higher number of droplets equates to a higher chance of infection, through lingering particles.

It should be noted that the design for our diffusion model is limited by the features we have chosen to simulate, as it does not factor in two variables that may impact the results. Those being aerosol dynamics and varying viral load, which can influence

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infection rates by the movement of aerosolised particles and the number of particles within the air, respectively, as elaborated on by Clifford K. Ho [10].

3 Establishing a realistic base infection probability

Before we could simulate anything, it was important for the model to use a more accurate infection probability. To do this, we calculated the given probability of an individual getting infected within a fixed environment. We calculated that the chance of infection for an individual in a two metre by two metre area, over 24 hours is around seven percent [Evidence.1 & 2] Using this information, we can recalculate the probability that an individual gets infected within one hour [8]:

$$(1\text{-}0.07)^{(1/12)} \approx 0.994 = (1\text{-}0.006)$$

With the value of 0.006 calculated, we then needed to try to get as close to that value with the simulation. To do this, we first calculated the scale our simulation would be working at, using the average width of male (41.50cm) and female (36.50cm) shoulders [7] and taking the average between the two and then dividing that by the number of pixels in the diametre of our agents.

$$39\text{cm} / 20\text{pixels} = 1.95\text{cm/pixels}$$

Using that value, we can calculate the number of pixels needed to represent any object, including the size of the boundaries of our simulation. As mentioned in the research behind the chance of infection in 24 hours, we remodelled that space as a two metre by two metre window for the agents to randomly walk around in. With the environment established, we then ran the simulation for 1 hour of simulated time and repeated this 100 times, each time altering the infection probability until the results reflected our calculated per-hour chance.

For this model, we landed on a value of 0.0005%, which within an hour simulation gives us only 0 or 1 infected. This value will continue being tested as other parts of the model are added, but we feel that this value is accurate enough for the sake of our current testing.

4 Multiscale simulation approach

In previous sections we presented a design and prototype implementation of FACS-iB, and how it can be used to approximate the spread of infectious diseases through the air and droplets (using simplified cone shapes). One of the main motivators to develop FACS-iB is the wish to add additional detail in the disease transmission dynamics of Flu And Coronavirus Simulator (FACS) code [11]. We have previously coupled FACS with the CHARM hospital model [12] to model hospital load resulting from infection patterns generated by FACS. As of now, however, there is no explicit coupling between FACS and actual in-building infection models, and the infection in buildings in FACS itself is only resolved using a single simplified equation.

In Figure 2 we present a graphical overview of a multiscale simulation approach that extends FACS with infectious predictions using FACSiB.

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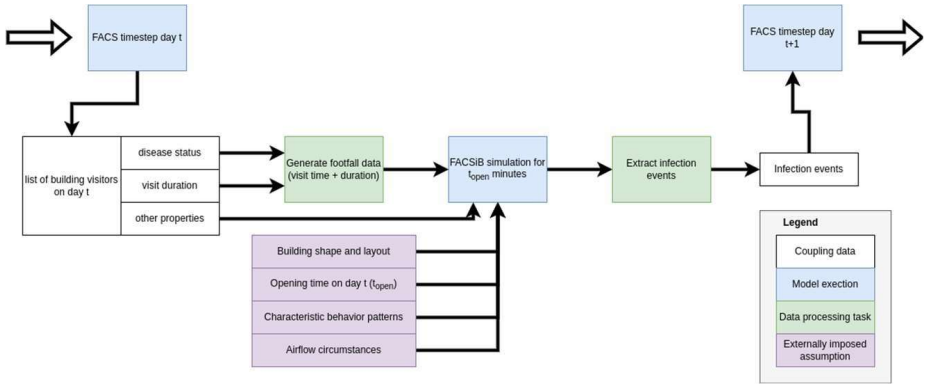

Figure 2: Schematic overview of a coupled interaction between FACS and FACSiB

Here, the FACSiB model is started every day for each relevant building in the FACS model and run for the full period that the building is open that day. The FACSiB simulation then takes in a footfall profile, which is generated from the visiting information that we can extract from FACS. In addition, FACSiB requires a range of assumptions relating to the properties of the building, the opening times, the typical movement behaviour of people in such buildings, and airflow-related characteristics. After FACSiB has been run, we then use a post-processing script to extract infection events which are then passed back to FACS. The multiscale simulation approach we present here is currently under development, with the aim of obtaining preliminary results later this year.

5 Showcase

After finding an acceptable infection probability we ran some simulations to see what results we could get, using a small population of agents within the room, with 1-2 agents starting off infected.

Figure 3 shows our simulation's seven-point moving average when changing the scale of the environment, and having one agent spawned as infected, over a period of 6 hours. The general trend the simulation produced, is that with a smaller room, a higher rate of infection occurs, a trend we would believe to be accurate. The graph shows how in a larger room (10m x 10m) the infection rate is slower, taking longer to reach higher levels. Whereas, in the smaller rooms (1m x 1m and 3m x 3m), the infection rate is much faster. However, we do want to mention that six people in a 1m x 1m room is an unrealistic scenario and we would expect its results to be more dramatic. The average produced by the 5m x 5m room, however, experiences an anomalous trend where more infections were recorded near the four-hour interval than the five-hour interval, and so the line creates a small wave pattern. In Figure 4, we change the minimum infectious dose required to trigger the probability function to run, ranging between a diffusion cell value of 0 to 250. Again, the overall trend is to be expected, a lower minimum dosage requirement leads to a higher infection rate. However, the results for dosages of 200 and 250 seem to be faster than predicted, this is potentially due to the way the number of droplets within a cell influences the infection rates, but this may need some further investigating.

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6 Discussion

In this paper, we have presented our current work on a simplified model for the spread of COVID-19 in an enclosed environment using agent-based simulation. We have highlighted the design for our model, using individual agents which are able to randomly move around whilst representing their breathing through a visual cone, and how they are able to infect each other. We have also highlighted our plans for implementing this model into a larger simulation, such as FACS, with the aim to produce more accurate results. The model in its current form, publicly available on Github [13], we believe, highlights the potential for agent-based modelling to simulate viral spread within an enclosed environment, and its potential to simulate viruses other than COVID-19 through differing infection rates. We are aware of the current implementation's limitations, which does not include features such as physical dividers, aerosol dynamics or varying viral load and resistance, which we believe can be future additions to the model.

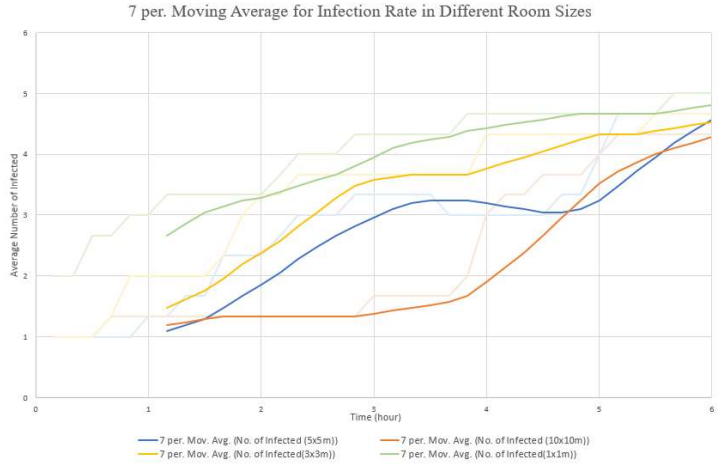

Figure 3 – Comparison of room size on infection rates over 24 hours

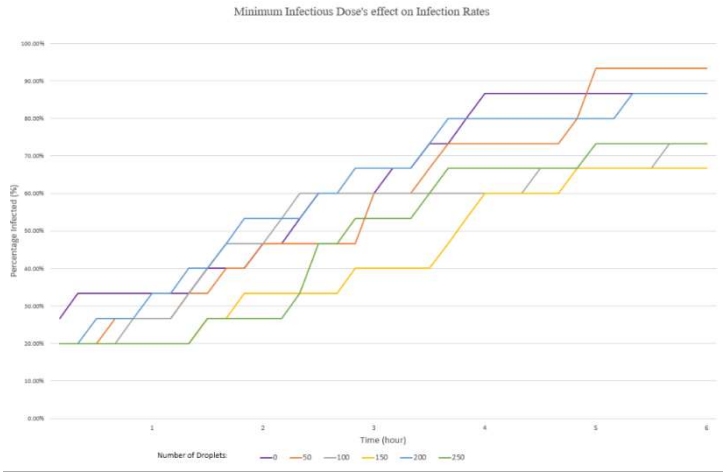

Figure 4 – Comparison of room shape on infection rates over 24 hours

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Summary of evidence:
1: 11.2% secondary attack rate in house holds: 1.112^(1/8.5)=1.012568 -> 1.2568% infection chance per day.# We assume that 20% of the time is spent within 2 metres in the household -> 1.2568% / 20% = 6.284% or 0.06284# Qifang Bhi et al., Lancet, 2020. DOI: https://doi.org/10.1016/S1473-3099(20)30287-5#
2: Source paper: https://www.sciencedirect.com/science/article/pii/S2468042720300063# This paper reports a peak value of R ~ 8 among the crew of the Diamond Princess (who are probably subject to similar confinement levels).# Deriving from that: 8**(1 / 8.5)= 1.277 -> infection rate of 0.277 in a heavily confined cruiseship setting with little precautions and awareness.# 13.8% secondary attack rate in house holds: 1.138^(1/8.5)= 1.015325 -> 1.5325% infections chance per day.# We assume that 20% of the time is spent within 2 metres in the household -> 1.5325% / 20% = 7.6625% or 0.076625# Wei Li et al., clinical Infectious Diseases 2020. Source paper: https://doi.org/10.1093/cid/ciaa450

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