COVID-19 SEVBIRDS Modelling using Cadmium Cell-DEVS

Muhammad Salman
Department of Electrical and
Computer Engineering
Carleton University
Ottawa, ON Canada
muhammadbsalman@cmail.carleton.ca

ABSTRACT

This project was undertaken using Cell-DEVS, cellular automata theory based on DEVS formalisms, and was implemented using the Cadmium library. The repository that was added to is called *Geography-Based-SEIRDS-Vaccine-Booster* [1], which before our implementation, included modelling the spread of COVID-19 in Public Health Units (PHU) across Ontario, outputting data on state variables, such as the current amount of susceptible, vaccinated (first and second dose), exposed, individuals per PHU, etc. The task assigned was to continue modelling the spread of COVID-19 with the effects of an additional booster shot, and simulate the output results. This would also include allowing individuals who have received both shots to become susceptible once again to COVID-19, and then allowing the booster to drive down the total susceptible cases down again. For simplicity, it is assumed that once the booster shot has been received, an individual can no longer become susceptible.

KEYWORDS

COVID-19, Vaccine-Booster, Cadmium Cell-DEVS Modelling

1 Introduction

DEVS, or Discrete-Event Simulation, is a formalism that allows us to simulate discrete events based on time or other state triggers, while also providing the capability to define different DEVS atomic models, a model that monitors the values of different states, state variables, inputs/outputs to the model, and state transformation functions along with a provided time advance. Coupled models under the DEVS formalism allow the combining of other atomic models with input/output ports.

Cell-DEVS uses the same DEVS formalisms, while combining them with cellular automata theory, where cells are automated based on their adjacent cells' state values (neighbouring cells), on a grid-like surface.

The project on hand deals with pandemic modelling over a given geographical field, as explained by Zhong et al. in [2]. The model on hand was structured from the original *SIRD* (Susceptible, Infected, Recovered, Deceased) model, where a proportion of a population can fall into one of these four states during a pandemic. The model was later expanded to include exposed individuals to the virus as an extra state, and then individuals who have received one or two doses of the COVID-19 vaccine, bringing the most up to date model to the SEVIRDS model. This project took the simulation one step ahead and added the booster shot after the two vaccines, then simulated the state variables across the different PHUs in Ontario.

Additionally, the specific type of modelling is different from typical cell-based modelling, rather it is referred to as agent-based modelling. This is because unlike in cell-based modelling, where all cells are the same in terms of size and the relative cell neighborhood, agent-based modelling allows cells to be different in size and in neighbourhood, where each agent defines its own cellular borders. This is helpful in our case, since each PHU in Ontario will be unique, with different set borders with other PHUs.

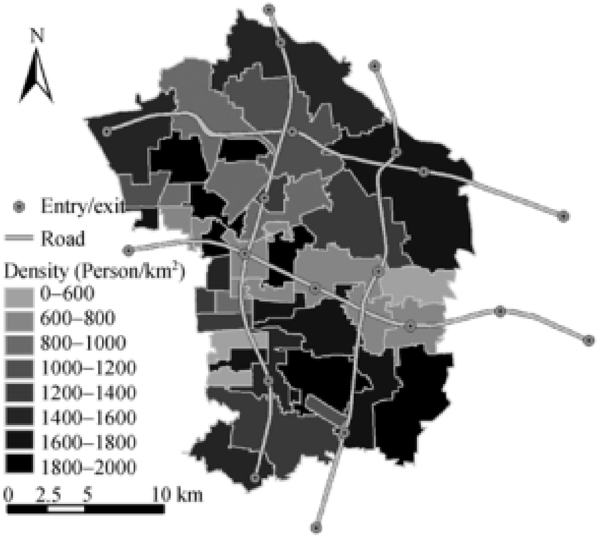


Figure 1: An Example of Agents as Provinces in a Country

Contributions:

The main contribution of this project was to add the booster vaccine equations to the existing *Geography-Based-SEIRDS-Vaccine-Booster* repository on GitHub. Once complete, we simulated our model over 500 days across Ontario to visualize the effects of COVID-19 on the different state variables.

Objective: COVID-19 began in late 2019 and was soon labelled as a pandemic based on its high magnitude spread around the world, prompting sudden lockdowns and rising infections leading to fatalities. Through the help of modelling, researchers can predict the amount of active cases and projected infections, helping lawmakers to better understand the extent of restrictions that need to be placed on a given population.

Survey Outline: The remainder of the paper is divided as follows: *Section 2* presents the background of the existing repository where the booster equations were added, as well as some general theory on how the simulation is performed. *Section 3* explains the atomic and coupled models used within the simulation, as well as the original and modified vaccination equations used to simulate the population getting their three doses and its remaining effects. *Section 4* explains the results gathered from the simulations and provides a discussion to compare the new results with those from the previous repository before the booster shot was added. Section 5 presents some room for future work to grow the simulation and make it more accurate in terms of comparing it with real life situations. Finally, Section 6 provides a brief conclusion for the paper, followed by acknowledgements and references.

2 Background

The current repository supports a two vaccine model following the SEVIRDS specifications. When we analyze the results from this, we assume that once someone has received two doses, they can no longer become susceptible to the disease. An individual will go from first being Susceptible to the disease, to Exposed or getting the first dose of the vaccine. If exposed, they will eventually recover after the infection stage and become re-susceptible again with some built immunity, or become deceased. If they got the first dose of the vaccine, then they can either get the second right away, or go through the susceptible process before getting fully vaccinated. Once fully vaccinated and the immunity time has passed for the second dose of the vaccine, as aforementioned, they cannot become susceptible according to the current model. The sum of all these states when combined must equal one, or 100% of the population.

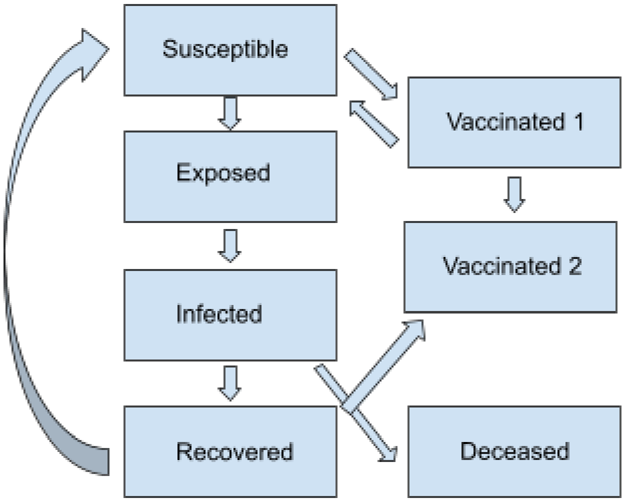


Figure 2: SEVIRDS Flow Chart

The different PHUs in the province are linked together by a calculated correlation or connection factor (*c*), as referred to by Zhong [2]. This essentially describes how likely it is that the virus in one cell carries over to another cell. Variables i, j can be understood as the two adjacent cells, with shared borders, while the weight *w*, increases based on how long a shared border is. When the cells are adjacent, the weight and correlation factor are set equal to each other. The border is represented as *z*, while the total perimeter of a cell is *l*, as seen in the equation below.

$$w_{ij} = w_{ji} = (z_{ij} / l_i + z_{ji} / l_j) / 2.$$

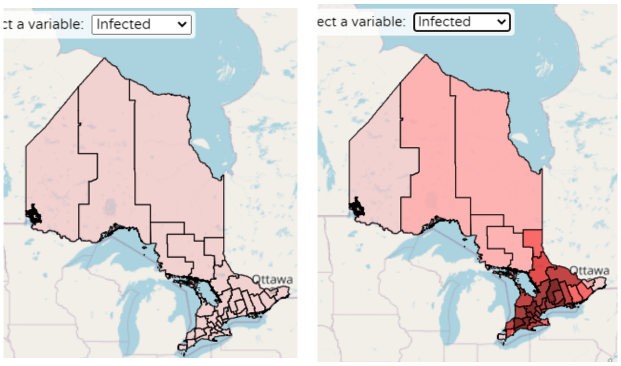
Equation (i): Weight Equation Based on Shared Borders

Aside from direct adjacency, other connections between different cells in reality, such as common major highways, connecting bus routes, etc., could increase the correlation factor between two regions as well.

The simulation is based on data gathered from the Canadian census of 2016 that can be used to form the age proportions per PHU. For example, the simulation assigns five age group proportions, with a certain age group falling under each, as well as an associated percentage of how much each group makes up of the total population in a PHU.

The simulation is performed with input data stored in a default.json file, which holds different state and configuration values required to perform the simulation. Upon receiving a vaccine dose, the time to become fully vaccinated depends on the length of the vaccine array. There are also parameters to decide rates of immunity, time between doses, time to receive a dose if recovered from COVID-19, etc.

The initial infection of a COVID-19 outbreak begins from predefined cells, which later spreads to other cells as the days pass. This can be seen in an example from the simulation in Figure 3.



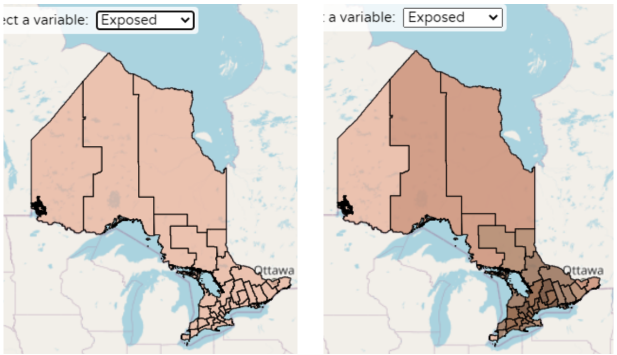


Figure 3: Top) Growth of Infected Individuals, Bottom) Growth of Exposed Individuals

The simulation is performed based on equations and variables that are also predefined, which will be explained in detail in Section 3.

Once the simulation has completed, the Cadmium tool allows a log file to be generated after each simulation, with the value of state variables every time unit. Using a provided .jar application, we can convert our data to be seen as a day-by-day simulation on the GIS Viewer, which allows the user to see the evolution of state variables over a given geographical region. The GIS viewer also requires other files, such as the .geojson for the Ontario region and other .json files to define the output display on the map.

3 Model Definitions and Equations

The models for this simulation can be understood as atomic and coupled, as explained in Section 1. The Cell-DEVS models did not change from the last repository, rather we added extra state variables and equations to simulate the addition of a booster shot. One individual cell, or PHU in our case, can be understood as an instantiation of an atomic model, known as a geographical_cell. The individual cell is initialized using a cell id which is a string, a given neighbourhood (vicinity), state variables known as *sevirds*, and a time constant. The coupled model is simply just the combination of all geographical_cells combined, Ontario being the top model. Simply put, each atomic model in Ontario can be understood as M = {M_{PHU_A}, M_{PHU_B}…}, A and B are PHU IDs. The couplings for the different models are defined using vicinity as mentioned above.

Atomic Model Definition:

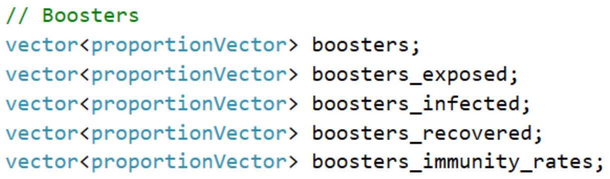
Geographical_cell (PHU) = < T, C, S, V = N >

C = Cell ID as a string, representing the PHU

S = {vaccinated, exposed, recovered…} //defined in *sevirds.hpp*

V = Neighbourhood definitions, unique to each cell, defined in *vicinity.hpp*

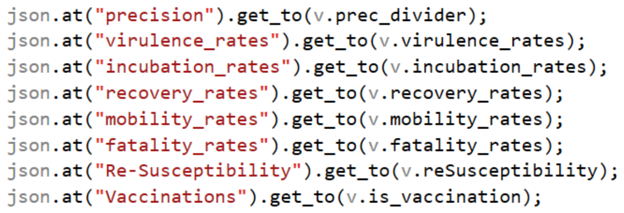
The *sevirds* state variables hold all information required for the current state of the geographical_cell. This is where we added state variables required for the booster shot. Every time a vaccine is introduced to the model, as seen in Figure 2, we must also take into the consideration the event in which someone with that vaccine becomes exposed, infected, and recovers from the disease, as well as the rates of immunity for that specific vaccine. This can be seen in Figure 4 below, for the booster variables as well. We assume once an individual has completed their settling time for the booster shot, they are fully immune and cannot become susceptible to the disease once again.



```
// Boosters
vector<proportionVector> boosters;
vector<proportionVector> boosters_exposed;
vector<proportionVector> boosters_infected;
vector<proportionVector> boosters_recovered;
vector<proportionVector> boosters_immunity_rates;
```

Figure 4: Booster State Variables

The bulk of the simulation information required to initiate the simulation is initially scraped from the default.json file mentioned above to initiate the cell data and processed by simulation_config.hpp. The variables required for different files and calculations can then be transferred from this file.



```
json.at("precision").get_to(v.prec_divider);
json.at("virulence_rates").get_to(v.virulence_rates);
json.at("incubation_rates").get_to(v.incubation_rates);
json.at("recovery_rates").get_to(v.recovery_rates);
json.at("mobility_rates").get_to(v.mobility_rates);
json.at("fatality_rates").get_to(v.fatality_rates);
json.at("Re-Susceptibility").get_to(v.reSusceptibility);
json.at("Vaccinations").get_to(v.is_vaccination);
```

Figure 5: Scraping defaults.json

To simulate the effects of the booster equations, there was a pre-added skeleton in the repository to hold data regarding the booster vaccine. There was a vector of AgeData objects created, where each index in the vector represented a vaccination type: Not Vaccinated - 0, Vaccinated with Dose 1 - 1, Vaccinated with Dose 2 - 2, and then we used Vaccinated with Booster 1 - 3. The AgeData object holds state variables for an age group, and its main purpose is to be easily referenced in the main cellular calculations. Once the data for the booster vaccine is added to default.json file, we can initialize the vector at the booster index to begin the booster calculations.

First, we have to define the vaccine equations that we were using for the first two doses, any changes that were made from the previous vaccine definitions, and then the equations we implemented for the booster shot. The original vaccine equations can be seen below. Please note, the notation for each variable is followed by subscript *i*, which represents the current cell, subscript *a*, which is the current age group, and superscript *t*, which is the current time step. Time variables include *q*, which is the current day in phase, and *Td1* or *Td2*, which is the period of a single vaccine dose.

$$V1_{i,a}^{t+1}(1) = v_{a,d1} \bullet S_{i,a}^{t} + v_{a,d1} \bullet \sum_{q\epsilon\{md_{vr} \dots T_r\}} R_{i,a}^{t}(q) \quad \mathbf{(1a)}$$

$$V1_{i,a}^{t+1}(q) = V1_{i,a}^{t}(q-1) - \quad \mathbf{(1b)}$$

$$V1_{i,a}^{t}(q-1)\left(1 - i_{a,V1}(q-1)\right) \bullet \mathbb{E}_i$$

$$\Lsh\ q\epsilon\{2 \dots T_{d1} - 1\} \cap q < mT_{d1}$$

$$V1_{i,a}^{t+1}(q) = V1_{i,a}^{t}(q-1)\left(1 - \ v_{a,d_2}(q\ - 1)\right) \quad \mathbf{(1c)}$$

$$-V1_{i,a}^{t}(q-1)\left(1 - i_{a,V1}(q-1)\right) \bullet \mathbb{E}_i$$

$$\Lsh\ if\ q\epsilon\{2 \dots T_{d1} - 1\} \cap q \geq mT_{d1}$$

$$V1_{i,a}^{t+1}(T_{d1}) = \left(V1_{i,a}^{t}(T_{d1} - 1) + RV1_{i,a}^{t}\left(T_{r,V1}\right)\right) \quad \mathbf{(1d)}$$

$$* \left(1 - v_{a,d_2}(T_{d1} - 1)\right)$$

$$-V1_{i,a}^{t}(T_{d1} - 1)\left(1 - i_{a,V1}(T_{d1} - 1)\right) \bullet \mathbb{E}_i$$

$$\Lsh\ if\ T_{r,V1} \geq T_{d1}$$

$$V1^{t}_{T(i,a)} = \sum_{q \epsilon \{1 \ldots T_{d1}\}} V1^{t}_{i,a}(q) \qquad \boldsymbol{(1e)}$$

Vaccine Dose 1 Equations [3]

The first dose equations do not change when implementing the booster, since the first dose immunity is already programmed to decrease as time goes on, which is why a second dose is needed in the first place. Each vaccine has a phase length, which means that after a certain number of days, the vaccine will have completely settled in and the individual will have the full level of immunity that could be provided by that vaccine. Equation 1a) states that the amount of vaccinated individuals on the first day of the first vaccine phase will be represented by the amount of susceptible individuals, multiplied by the vaccination rate, summed with the product of the vaccination rate and the total sum of individuals who are recovering from a COVID-19 infection and have at least passed 25 days, which is the amount set in default.json to wait for a vaccine shot if an individual was infected. Equations 1b) and 1c) represent the proportion of vaccinated individuals after the first day in the phase and before the last day in the phase. The equations are quite similar however they take into account the probability of individuals that are immunocompromised and must be vaccinated for the second shot earlier. So, if the day in phase is greater than the minimum time between doses, then a percentage of individuals can start getting the second dose earlier based on the vaccination rate, hence they would move out of the dose 1 state, and into the dose 2 state. The last term in 1b) and 1c) removes exposed individuals from the vaccinated state as well. Equation 1d) calculates the amount of vaccinated individuals on the last day of the phase, by also including those who received the first dose and were infected, and by now they are on their last day of the recovery cycle. Finally, 1e) summates all days in the V1 phase to store the total amount of vaccinated individuals with their first dose.

The second dose equations are somewhat different, since someone can only get the second shot, if they have received the first shot.

$$\begin{aligned} V2^{t+1}_{i,a}(1) = V1^{t}_{i,a}(T_{d1}) + &\sum_{q \epsilon \{mT_{d1} \ldots T_{d1} - 1\}} \left(v_{a,d_2}(q) V1^{t}_{i,a}(q)\right) \qquad \boldsymbol{(2a)} \\ &+ \sum_{q \epsilon \{md_{rv} \ldots T_{r,V1}\}} \left(v_{a,d_2}(q)\, RV1^{t}_{i,a}(q)\right) \\ &- V1^{t}_{i,a}(T_{d1}) \bullet \mathbb{E}_i \end{aligned}$$

Vaccine 2 Equations (2a) [3]

Equation 2a) describes this as all the people who are on their last day of dose 1 are moved to the first day of dose 2. This is also summated with the sum of immunocompromised people who will receive their second dose earlier as long as they have passed the minimum wait time between doses, added with the sum of individuals who have been vaccinated with dose 1 and are now recovering from the disease. This total is subtracted by those who were exposed to COVID-19 on their last day of being vaccinated with dose 1.

$$\begin{gathered} V2^{t+1}_{i,a}(q) = V2^{t}_{i,a}(q-1) - V2^{t}_{i,a}(q-1)\left(1 - i_{a,V2}(q-1)\right) \bullet \mathbb{E}_i \qquad \boldsymbol{(2b)} \\ \Lsh\; q \epsilon \{2 \ldots T_{d2} - 1\} \cap T_{r,V2} < T_{d2} \end{gathered}$$

Vaccine 2 Equations (2b) [3]

Equation 2b) simply calculated all the dose 2 vaccinations from the second day to the second last day, while subtracting the quantity of those who got exposed along the way. This is where we tweaked this equation to include those who would get their booster shot early, similar to how individuals would get their second dose early from dose 1.

$$\begin{aligned} &V2^{t+1}_{i,a}(q) = V2^{t}_{i,a}(q-1) - \quad \boldsymbol{(2b)} \\ &V2^{t}_{i,a}(q-1)\left(1 - i_{a,V2}(q-1)\right) \bullet \mathbb{E}_i \\ &\Lsh\; q \epsilon \{2 \ldots T_{d2} - 1\} \cap q < mT_{d2} \end{aligned}$$

$$\begin{aligned} &V2^{t+1}_{i,a}(q) = V2^{t}_{i,a}(q-1)\left(1 - v_{a,d_B}(q-1)\right) \quad \boldsymbol{(2c)} \\ &-V2^{t}_{i,a}(q-1)\left(1 - i_{a,V2}(q-1)\right) \bullet \mathbb{E}_{\boldsymbol{i}} \\ &\Lsh\; if\ q \epsilon \{2 \ldots T_{d2} - 1\} \cap q \geq mT_{d2} \end{aligned}$$

Vaccine 2 Equations (2b-2c) Tweaked [3]

These are similar to 1b) and 1c), however we take into account the booster vaccination rate as well as seen in 2c).

$$V2_{i,a}^{t+1}(T_{d2}) = V2_{i,a}^{t}(T_{d2}-1) + V2_{i,a}^{t}(T_{d2}) + RV2_{i,a}^{t}\left(T_{r,V2}\right) \quad \boldsymbol{(2d)}$$
$$-V2_{i,a}^{t}(T_{d2}-1)\left(1 - i_{a,V2}(T_{d2}-1)\right) \bullet \mathbb{E}_i$$
$$-V2_{i,a}^{t}(T_{d2})\left(1 - i_{a,V2}(T_{d2})\right) \bullet \mathbb{E}_i$$
$$\Lsh\, if\ T_{r,V2} \geq T_{d2}$$

Vaccine 2 Equations (2d) [3]

The original equation 2d) is similar to equation 1d) where we calculate the vaccinated proportion for the last day. Equation 2d) takes into account the individuals who have been vaccinated with their second dose and are on their last and second last day, summed with those who are on their last day of recovery and have received their second dose, subtracted by those who were exposed to the virus on their last or second last day.

This equation was drastically changed to allow for those who have taken the second dose to become susceptible again. Although this may not be the most efficient way to account for this, this equation allowed the simulation to keep working and allowed the booster vaccine to be implemented without error.

$$V2_{i,a}^{t+1}(T_{d2}) = RV2_{i,a}^{t}\left(T_{r,V2}\right)\left(1 - v_{a,d_B}\left(T_{r,V2}\right)\right) \quad \boldsymbol{(2d)}$$

Vaccine 2 Equations (2d) Tweaked [3]

Now, the amount of people on the last day of the phase of dose 2 is equivalent to the product of people who are on their last day of dose 2 recovery multiplied by the vaccine rated for the booster subtracted by 1. This allows the first booster equation to work smoothly since all the people who have not yet had the booster shot will be moved to the first day of the booster phase. Finally, the total number of people with their second dose is the summation of every day in the phase as shown below in equation 2e).

$$V2_{T(i,a)}^{t} = \sum_{q \epsilon \{1 \ldots T_{d2}\}} V2_{i,a}^{t}(q) \quad \boldsymbol{(2e)}$$

Vaccine 2 Equations (2e) [3]

The first booster vaccine equation 3a) is similar to 2a), where we simply sum all individuals who were on their last day of the dose 2 phase, with those who were vaccinated early with the booster, with those who are recovered enough after receiving their second dose and being infected that they can now get the booster shot, meaning they have crossed the minimum amount of days they must wait to get a vaccine after being infected.

$$VB_{i,a}^{t+1}(1) = V2_{i,a}^{t}(T_{d2}) + \sum_{q \epsilon \{mT_{d2} \ldots T_{d2}-1\}} \left(v_{a,d_B}(q) V2_{i,a}^{t}(q)\right) \quad \boldsymbol{(3a)}$$
$$+ \sum_{q \epsilon \{md_{rv} \ldots T_{r,V1}\}} \left(v_{a,d_B}(q)\, RV2_{i,a}^{t}(q)\right)$$
$$-V2_{i,a}^{t}(T_{d2}) \bullet \mathbb{E}_i$$

Vaccine 3 Equations (3a) [3]

Since there is no second booster, we do not worry about subtracting potential individuals who will receive the next shot earlier due to being immunocompromised. However, if we were ever to add to this simulation, that will always be a possibility. Right now, we simply calculate the amount of people per day in the booster phase in 3b), starting from the second day to the second last day as in the original 2b) equation. We will subtract those individuals who were exposed to the virus on the previous day.

$$VB_{i,a}^{t+1}(q) = VB_{i,a}^{t}(q-1) \quad \boldsymbol{(3b)}$$
$$-VB_{i,a}^{t}(q-1)\left(1 - i_{a,VB}(q-1)\right) \bullet \mathbb{E}_i$$
$$\Lsh\, q \epsilon \{2 \ldots T_{dB}-1\} \cap T_{r,VB} < T_{dB}$$

Vaccine 3 Equations (3b) [3]

Equation 3c) takes into account those individuals who have reached the last day for the booster phase, and can no longer become susceptible. This is similar to the original 2d) equation that summates individuals from the last and second last day of the phase, and subtracts those who may have been exposed on those days as well.

$$VB^{t+1}_{i,a}(T_{dB}) = VB^{t}_{i,a}(T_{dB}-1) + VB^{t}_{i,a}(T_{dB}) \quad \textbf{(3c)}$$
$$+RVB^{t}_{i,a}(T_{r,VB}) - VB^{t}_{i,a}(T_{dB}-1)\left(1 - i_{a,VB}(T_{dB}-1)\right) \bullet \mathbb{E}_i$$
$$-VB^{t}_{i,a}(T_{dB})\left(1 - i_{a,VB}(T_{dB})\right) \bullet \mathbb{E}_i$$

Vaccine 3 Equations (3c) [3]

Finally, as like all vaccine equations, the last equation, 3d, provides the summation for all days in the phase for the booster shot.

$$VB^{t}_{T(i,a)} = \sum_{q\epsilon\{1\ldots T_{dB}\}} VB^{t}_{i,a}(q) \quad \boldsymbol{(d)}$$

Vaccine 3 Equations (3d) [3]

Now, the flow changes from SEVIRDS to SEVBIRDS, where an additional B for the booster vaccine is added after the original two vaccines. Once again, individuals can get the virus after their second shot of the vaccine, and go through the entire susceptible to recovered phase again. However, once they have received their booster shot, they are considered fully immune and cannot become susceptible.

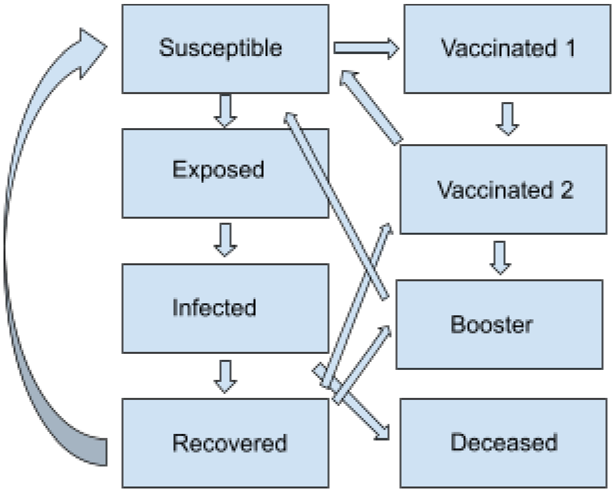


Figure 6: SEVBIRDS Flow Chart

The equations for the other state variables such as S, E, I, R, D have not changed since the last repository, and hence can be reused to apply to the booster equation as well. There are however certain constants used in these equations that are helpful to understand.

$$\lambda_a(q) = Virulence\ rate$$

$$\gamma_a(q) = Recovery\ rate$$

$$\digamma_a(q) = Fatality\ rate$$

$$\mu_a(q) = Mobility\ rate$$

All these constants are functions of the current day in the phase, as well as pertaining to a certain age group. The virulence rate represents the ability of the virus to multiply, while recovery rate is the probability of those who are infected with the virus to recover. The fatality rate is the rate at which an infected individual becomes deceased, and the mobility rate is how much the population tends to move around, spreading the disease further. Once again, these rates are set in the defaults.json file before the simulation begins.

3.1 Configurations

This section explains the basic configurations that are set to complete the simulation in defaults.json. Firstly, as aforementioned, each vaccinated individual must complete a given amount of phase days specific to the vaccine. Once that phase is complete, they are eligible to get the second vaccine if they have completed the minimum time between doses, known as Td1 or Td2. Moreover, if the person became infected after receiving one of these doses, they must wait a certain amount of time after recovery to get the next dose (if applicable). These values were set below. The amount of days for each variable is the same for each vaccine.

```
"min_interval_between_doses": 14,
"min_interval_between_recovery_and_vaccine": 25
```

The length of the booster phase was as long as the phase of the second dose (14 days), and shorter than the phase of the first dose (31 days). In essence, the quickest path someone could take to become fully vaccinated, assuming they never get infected, is Phase_V1 + 14 + Phase_V2 + 14 + Phase_B = 87 days.

The vaccination rates, recovery rates, and incubation rates for the booster were set to the same as the second dose, however the immunity attained after getting the booster was set to 86% in the first week, which then increases to 87% in the second week. Obviously this was set higher than the immunity rates for the second dose, since the booster is meant to provide more protection. The other rates and constants can be accessed in defaults.json.

4 Simulation Results and Comparisons/Discussion

In the original model, the amount of people who are in phase for the first dose of the vaccine gradually increases and then begins to drop, as the second dose is introduced. The proportion of the population that only has the first dose gradually goes down to zero, as the amount of people with the second dose increases. Eventually, there are certain individuals that are in phase for the second dose who become exposed and are no longer considered part of the second dose phase. The amount of people in the second dose eventually flat lines as there is no other vaccine for people to move on to. The amount of susceptible individuals will also eventually fall to 0 as a result of full immunity being established after the second vaccine.This can be seen in the graph below.

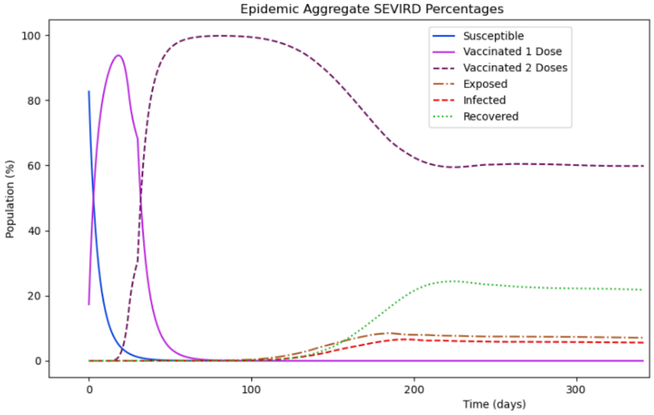


Figure 7: SEVIRDS Monitoring over 300+ Days

Moreover, since there is constant immunity after the second dose, the amount of individuals that are exposed, infected, and as a result that recover from the virus will gradually decrease as well over time, even though there is an initial spike in cases. This can be realized in Figure 8.

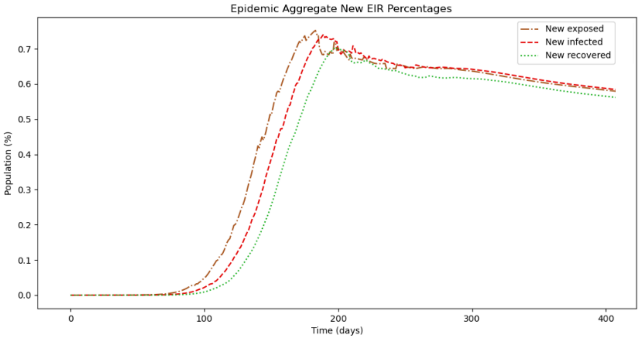


Figure 8: EIR Rise and Decline over 400 Days

After the booster vaccines are implemented, we can track the amount of individuals that are currently in each vaccine's respective phase. As seen in Figure 7, the first spike in vaccinations begins with the first dose, and upon declining the spike continues to occur for the second dose. The interesting moment here occurs when there is a constant decline, followed by waves of people in vaccination phases, in vaccinations for both dose 1 and dose 2, since even after receiving the second dose and completing the full phase, an individual can still become infected. Eventually, the amount of vaccinations for both doses flat lines, which is when the booster vaccines begin to rapidly incline. The amount of booster vaccines will always increase, since there is no susceptibility after completing the booster phase. The vaccination rates can be understood in Figure 9.

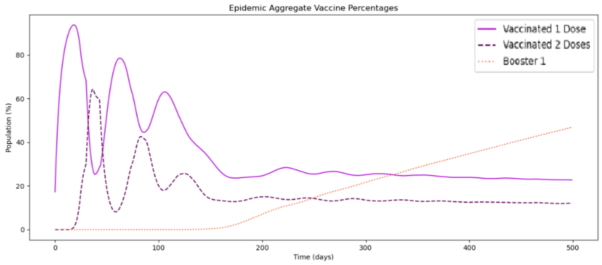


Figure 9: Vaccination Rates for each Vaccine

Similarly, when we analyze the SEVBIRDS graph with the values of the state variables, we can see how the amount of susceptible cases gradually declines instead of suddenly as in the SEVIRDS case. This makes more sense since there will always be susceptible individuals despite the second vaccine dose, and it allows for the susceptible cases to decrease in waves gradually instead of rapidly one time. Also, as we can see in Figure 10, all other variables will gradually flat line except for the amount of individuals that have received the booster shot.

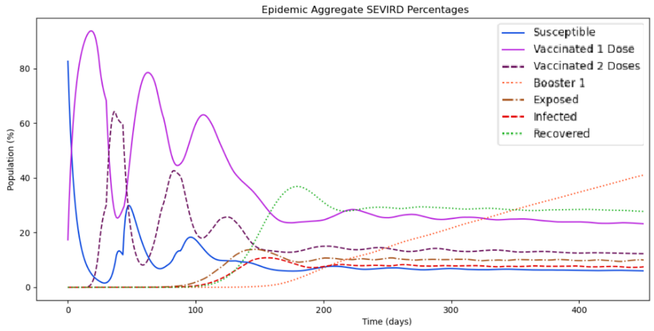


Figure 10: SEVBIRDS Monitoring over 400+ Days

Furthermore, the amount of new exposed, infected and recovered individuals decreases over time similar to the last simulation. However for this simulation, the behaviour for the three variables is more spiky and declines in waves. After the initial decline, a slight rise in cases can be seen before they start to decline once again. This once again can be explained by the larger number of individuals becoming susceptible in this simulation. This can be referred to in Figure 11.

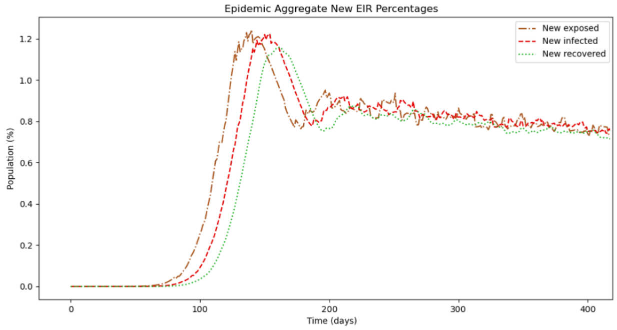
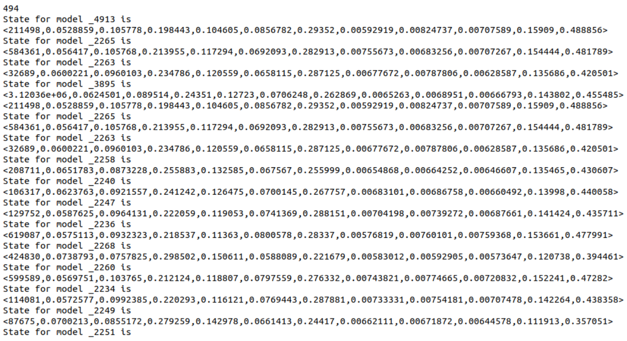


Figure 11: New EIR Rise and Decline over 400 Days

4.1 Simulation Final Results

The simulation output is given for each day in a log file, which is later parsed for the GIS Viewer. Each output has an associated cell id as mentioned before, that tracks the PHU in Ontario. In the results, the summation of each given state must equal to 1, meaning 100%, and each state is represented as a percentage of the total. In short, the sum of all the variables in SEVBIRDS can not exceed 100%, or else this will cause an error in the simulation (S+E+V+B+I+R+D = 1). An example state output log file for a given day can be seen in the figure below.



```
494
State for model _4913 is
<211498,0.0528859,0.105778,0.198443,0.104605,0.0856782,0.29352,0.00592919,0.00824737,0.00707589,0.15909,0.488856>
State for model _2265 is
<584361,0.056417,0.105768,0.213955,0.117294,0.0692093,0.282913,0.00755673,0.00683256,0.00707267,0.154444,0.481789>
State for model _2263 is
<32689,0.0600221,0.0960103,0.234786,0.120559,0.0658115,0.287125,0.00677672,0.00787806,0.00628587,0.135686,0.420501>
State for model _3895 is
<3.12036e+06,0.0624501,0.089514,0.24351,0.12723,0.0706248,0.262869,0.0065263,0.0068951,0.00666793,0.143802,0.455485>
<211498,0.0528859,0.105778,0.198443,0.104605,0.0856782,0.29352,0.00592919,0.00824737,0.00707589,0.15909,0.488856>
State for model _2265 is
<584361,0.056417,0.105768,0.213955,0.117294,0.0692093,0.282913,0.00755673,0.00683256,0.00707267,0.154444,0.481789>
State for model _2263 is
<32689,0.0600221,0.0960103,0.234786,0.120559,0.0658115,0.287125,0.00677672,0.00787806,0.00628587,0.135686,0.420501>
State for model _2258 is
<208711,0.0651783,0.0873228,0.255883,0.132585,0.067567,0.255999,0.00654868,0.00664252,0.00646607,0.135465,0.430607>
State for model _2240 is
<106317,0.0623763,0.0921557,0.241242,0.126475,0.0700145,0.267757,0.00683101,0.00686758,0.00660492,0.13998,0.440058>
State for model _2247 is
<129752,0.0587625,0.0964131,0.222059,0.119053,0.0741369,0.288151,0.00704198,0.00739272,0.00687661,0.141424,0.435711>
State for model _2236 is
<619087,0.0575113,0.0932323,0.218537,0.11363,0.0800578,0.28337,0.00576819,0.00760101,0.00759368,0.153661,0.477991>
State for model _2268 is
<424830,0.0738793,0.0757825,0.298502,0.150611,0.0588089,0.221679,0.00583012,0.00592905,0.00573647,0.120738,0.394461>
State for model _2260 is
<599589,0.0569751,0.103765,0.212124,0.118807,0.0797559,0.276332,0.00743821,0.00774665,0.00720832,0.152241,0.47282>
State for model _2234 is
<114081,0.0572577,0.0992385,0.220293,0.116121,0.0769443,0.287881,0.00733331,0.00754181,0.00707478,0.142264,0.438358>
State for model _2249 is
<87675,0.0700213,0.0855172,0.279259,0.142978,0.0661413,0.24417,0.00662111,0.00671872,0.00644578,0.111913,0.357051>
State for model _2251 is
```

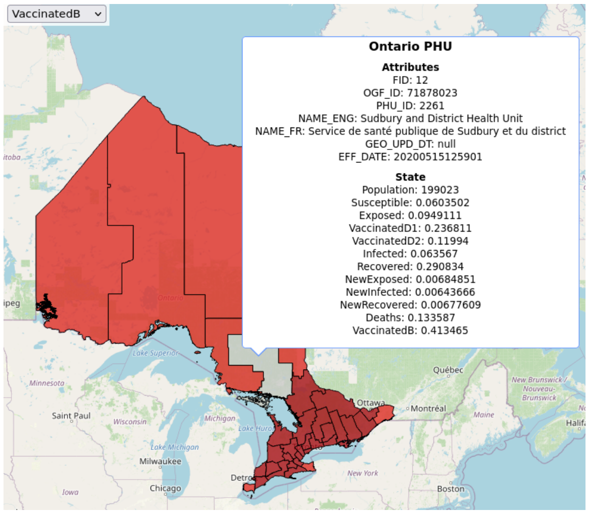
Figure 12: State Output for Day 494 in Simulation

In our simulation, on day 499, the value of each state variable as a percentage can be seen in the table below.

Variable	Percentage
Susceptible	5.9%
Exposed	9.4%
Vaccinated Dose 1	22.7%
Vaccinated Dose 1	12.1%
Infected	7.3%
Recovered	27.5%
Deceased	14.9%
Booster Received	46.9%

Table 1: State Variables on Last Day of Simulation

As mentioned before, some conclusions that can be drawn from these results is that susceptibility will never drop down to 0, rather it will always be some small percentage. Moreover, by the end of the simulation, around 15% of the population has passed away. However, as we can see, the current infections are fairly low, which means cases will only continue to drop as time goes on. The GIS simulation on day 499 with color coding based on darker tones for higher vaccinated areas with the booster shot, can be seen below. The image also shows other state variables and their associated values. The highly populated PHUs near the southern part of the province have a higher percentage of booster vaccinated individuals. This is mostly because the virus originally began in one or a few of those cells, later spreading to the north. Hence, vaccinations started earlier as well in the southern PHUs.


VaccinatedB

Ontario PHU

Attributes
FID: 12
OGF_ID: 71878023
PHU_ID: 2261
NAME_ENG: Sudbury and District Health Unit
NAME_FR: Service de santé publique de Sudbury et du district
GEO_UPD_DT: null
EFF_DATE: 20200515125901

State
Population: 199023
Susceptible: 0.0603502
Exposed: 0.0949111
VaccinatedD1: 0.236811
VaccinatedD2: 0.11994
Infected: 0.063567
Recovered: 0.290834
NewExposed: 0.00684851
NewInfected: 0.00643666
NewRecovered: 0.00677609
Deaths: 0.133587
VaccinatedB: 0.413465

Figure 13: GIS Simulation for Ontario Boosters

5 Future Work

For future work on the current repository, we would like to better understand the effects of the relationship between the second vaccine dose and the booster shot (improve equation 2d). Moreover, there may be additional booster vaccines in the future, so there should be a continuous way to allow for future vaccines to be added in the simulation without drastic changes in the code structure.

Furthermore, the simulation can be expanded to include more provinces and even all of Canada, however this will require population and age data on a large scale, and will require multi-level cellular complexity, with Canada itself being a top model.

6 Conclusion

The project was to add the effects of an additional booster vaccine to an existing SEVIRDS model that simulates the effects of COVID-19 in the province of Ontario. The project was based on the SIRD model that was presented by Zhong et al. in [2], in which the population follows the spread of a disease through different states, with an individual either recovering from the disease or passing away.

The project entailed using Cell-DEVS in Cadmium to provide agent based simulations over PHUs in Ontario, that were treated as singular cells, referred to as geographical cells. The PHU and other initialization data was preloaded from .json files to be used by the simulation at compilation.

Once the simulation was complete, we compared the results from the previous simulation with those that were generated taking the booster shot into account and presented our conclusions and findings.

Acknowledgements

We would like to thank Professor Ruiz Martin for teaching the SYSC5104 course, as well as guiding us through the SEVIRDS modelling outline, allowing us to produce this final SEVBIRDS simulation model.

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[1]"Geography-Based-SEIRDS-Vaccine-Booster," *GitHub*. [Online]. Available: https://github.com/SimulationEverywhere-Models/Geography-Based-SEIRDS-Vaccine-Booster. [Accessed: 10-Dec-2021].

[2] Zhong, S., Q. Huang, D. Song. 2009. "Simulation of the Spread of Infectious Diseases in a Geographical Environment". Science in China Series D: Earth Sciences 52(4):550-561.

[3] C. R. Martin, "SEVIRDSVaccinations.doc." Ottawa.