

Using Probabilistic Planning to Model the Spread of COVID-19 in Kingston, Ontario

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Abstract

Modeling and understanding the spread of disease has been a topic of much focus for epidemiological researchers in recent years, due to the effects of the COVID-19 pandemic. High levels of global attention and an abundance of recently collected data has created an environment for epidemiological models to be highly detailed and impactful. The best of these models incorporate ideas and research from a range of domains, with clarity and ease of consumption being key focuses so that they have the highest chance of impacting public policy. Probabilistic planning is leveraged to understand the spread of COVID-19 at a regional level in the city of Kingston, Ontario through an agent-based model implemented in RDDDL. This model operates with the functionality of introducing mask and vaccine mandates as sparingly as possible, as per policies created by JaxPlanner, while attempting to ensure that hospitals are operating below capacity. A variety of model configurations are experimented with, noting the performance differences in each case. The observed dynamics are well in line with the theoretical, and the intervention methods utilized proved to be highly successful at the task of mitigating hospital burden. All code is available and open source at: <https://github.com/brucechidley/RDDL-covid-sim>

1. Introduction

Understanding how a disease spreads is necessary when attempting to minimize the damage done to a population. The intricacies of exactly how a disease spreads are often quite difficult to identify, and it requires significant effort to truly capture minute details. However, this type of work is essential for knowing when and how certain intervention methods should be deployed in a population. With an epidemic moving through a population, using intervention methods as much as possible can cause the population to incur a significant economic loss, and can lead to reduced mental health for the affected citizens [1]. So, it is crucial for policymakers to be able to intervene only when necessary. It is very important that the capacity of hospitals is not exceeded, so optimal intervention implementation would be minimizing its usage while keeping hospitals operating below capacity. Due to the complex nature of epidemics, the models that describe them are oftentimes quite complicated - decreasing generalizability and risking poor adaptation to new discoveries or data. These disease models are typically constructed with the functionality of intervention techniques in order to see how spread can be slowed or stopped [2]. From this, policymakers have been able to incorporate strategies based on many such models, proving their viability in handling these kinds of highly complex scenarios [3]. However, even among the most successful and detailed of models, there are still limitations that can cause significant differences in behaviour to emerge between the model's predictions and real world outcomes. Some of the more common limitations have to do with

location and location-based data such as regional population, organization, and infrastructure. This work presents a model based in RDDDL, through JaxPlanner, that aims to minimize intervention uptime while keeping hospitals operating below capacity through the use of real geographical and regional data from the town of Kingston, Ontario as an exploration of the power of RDDDL in modeling disease dynamics and intervention. This not only serves as a baseline for future work in modeling disease spread in RDDDL, but it also examines JaxPlanner's effectiveness at solving problems of this nature.

2. Background

Understanding SIR modeling is fundamental in the field of epidemiology. The basic SIR model has many variations, and this agent-based model on the SEIRS model. The SEIRS model splits a population into four classes, which are used to track and simulate the spread of disease. All individuals in a population are in exactly *one* of these classes at a time:

1. Susceptible: Individuals who may contract the disease at any given point
2. Exposed: Individuals who have contracted the disease, but are not symptomatic and are not able to spread the disease
3. Infectious: The individuals in this class may or may not be showing symptoms, but are now able to spread the disease
4. Recovered: Here, individuals are fully recovered from the disease, meaning that they cannot spread it *and* they cannot contract it

As shown in Figure 1, an individual begins in the susceptible class, and may move through the classes linearly



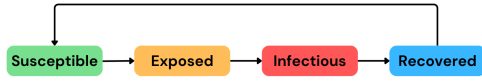


Figure 1: The classes that an individual moves through in an SEIRS model

until reaching the recovered class, where they become susceptible after a given period of time. These periods of time are not constant from person to person, and can vary due to an individual's genetics and the severity of infection amongst other factors.

We must also define the R_0 value here, which represents the average number of susceptible individuals that an infectious individual will spread disease to. The R_0 value is calculated as $R_0 = \beta/\gamma$, where β represents the number of individuals the infection is spread to per time step, and γ represents the rate of recovery.

3. Related Work

Mathematical Modeling Often serving as the basis for more complex agent-based models, mathematical models seek to explain the spread of disease from a compartmental standpoint. The states a person can be in (SEIR) relative to the disease and the rates of change of each of these states in a given population over time are modeled and can be readily tweaked to account for a variety of situations. Individuals themselves are not tracked in these models, but rather the population as a whole is estimated on each time step. Significant work was done early into the pandemic in Sweden, furthering our understanding of the disease behaviour in a population with real, up to date data [4, 5, 6]. While these models performed well for certain tasks, the simplicity and generalizations made by the models produced results that were often not in line with observed data.

Agent-Based Modeling Built from strong foundations in mathematical modeling, agent-based modeling has seen increased usage in recent years; specifically with respect to disease modeling. Early into the COVID-19 pandemic, many older agent-based models were adapted to model COVID-19's spread and resistance to intervention methods [7]. While these sorts of models were arguably the most advanced at the time, they often had limitations with regards to population behaviour and the implementation of intervention methods [2]. Building on these ideas, popular models such as OpenABM-Covid19 and Covasim emerged, which have been used by public health officials worldwide to aid in decision support, taking detailed population behaviour into account and

tracking how a variety of intervention methods affect the spread of COVID-19 [3, 8]. These are seen as state of the art COVID-19 models, and are being consistently improved upon. GSAM is another powerful model with very high scalability, allowing for billions of agents to act distinctly at the cost of specificity with regards to their environments. This type of model is good for understanding broad disease dynamics, but does not perform well when trying to understand fine details such as the effects of regional population distributions [9]. There are also models like BioWar, where nefarious agents are introduced, who act to intentionally spread disease, giving way to some interesting dynamics [10]. In addition to these, there are a plethora of other models that exist, which specialize in different tasks [11, 12, 13, 14] - many of them being open source and regularly updated.

Automated Planning Understanding the spread of disease is a long-standing exercise and problem in the field of Planning. New strategies for handling probabilistic settings are regularly emerging, opening the door for more complex and realistic models. Specifically, RDDDL is beginning to see use as a tool for developing intervention plans to hinder the spread of disease, with Harmanani modeling COVID-19 spread in enclosed spaces, grounded in real data [15]. By allowing the planner to intervene by way of masking and vaccinating, the results produced by the model were found to quite accurately reflect real world data. While this attempt was successful at describing behaviour in enclosed spaces, there has been little attempt to model such behaviour on a large scale such that the impact of disease on regional population dynamics could be analyzed in a meaningful way.

4. Methods

4.1. Modeling the environment

Space Initialization It was important that the space that the agents were to move around in represented Kingston, Ontario as closely as possible. By utilizing the OSMnx Python package [16], accurate geographical data was ingested via a simple script. This package grants access to the coordinates of all registered buildings, and the types of buildings that they are, breaking them down into the following categories:

- Residential: "House", "Apartment", "Dormitory", or "Residential", encapsulating the leftover residential buildings
- Work: "Office", "Commercial", "Industrial", "Retail", or "Warehouse"
- Commercial: "Commercial" or "Retail"
- Education: "School", "College", or "University"

It is important to note that no building can belong to more than one building type. By running a simple Python script to retrieve this building data, the information was able to be stored and ingested into the problem files that fueled the disease simulations.

Agent Initialization Agents are created with a set of attributes, and they have the ability to move between the defined locations. Each agent is assigned to an age bracket, based on the Kingston age distribution [17]. The age brackets are defined as 0, representing ages 0-9, 1, representing ages 10-19, and so on until 8, which represents the 80+ age range. These age brackets determine how agents interact with COVID-19, how they move around the space on each time step, and how they react to interventions (planner actions).

Every step in the simulation represents half a day. On the first step of each day, agents move about the problem space, interacting with other agents and potentially spreading disease. On a day's second step, they return to their homes and interact with the agents they live with. This notion of time is tracked via a simple counter that flips between 0 and 1 on each step. We also incorporate days of the week, with agent behaviour varying depending on what day of the week it is. This is tracked by a similar counter, ranging from 1 to 14 (as each day consists of two time steps).

As hinted at, agents are all assigned homes, picked from the extracted list of residential buildings at random. Each home contains 1-5 agents, filled per the probabilities derived from Kingston data [17]. This will be where agents go on the second time step of every day. With respect to disease interaction, if an agent enters the infectious class, they have a chance to self-isolate, and they will stay at their home for their entire infectious period. If they are hospitalized, they will not go home or to work/school until they move into the recovered state.

Agents are also assigned a place they go during the weekdays. If an agent is aged 0-19, they attend school. The school they attend is chosen such that the Euclidian distance between their home and the school is as small as possible (geographically, the closest school to their home). Some agents in the 20-29 age range will attend post-secondary school, whereas other agents in the 20-29 range and all agents 30-69 will attend work during the day (proximity not being a factor here). Agents aged 70 and above are assigned a commercial building that they visit during the day, which is chosen to be closest geographically in the same way schools are selected.

The agents in the 20-29 range who attend post-secondary institutions in Kingston are placed according to each institution's user-defined populations. Agents are sequentially assigned to each institution until their prescribed population numbers are reached. The homes of these agents are selected based on their proximity to

Parameter	Value
R_0 - Basic Reproductive Ratio	3.32 [18]
β - Average number of agents infected on each time step	$R_0\gamma$
$1/\sigma$ - Time spent in exposed class	Normal(9, 2) [19, 20]
$1/\gamma$ - Time spent in infectious class	Mild: Normal(16, 4) [21] Severe: Normal(36.2, 8) [22] Critical: Normal(36.2, 8) [22]
$1/\omega$ - Time spent in recovered class	Varied
Probability of mild, severe, or critical case	Age Dependent [22, 7]
Probability of self-isolation	Varied
Probability of masking	0.7 [23]
Probability of vaccinating	Age Dependent [24]

Table 1

Parameters comprising the main disease dynamics.

their given school, placing them in the closest residential buildings possible such that they are not above capacity. By this algorithm, dormitories will be filled up first, followed by other accommodations. The location these agents visit during the day is set to be a random building belonging to the institution they are attending.

Finally, each agent is given a place they go during the weekends. If the agent is aged 0-9, they will remain at home. Otherwise, the agent will go to two of the geographically closest commercial buildings throughout the weekend.

Transit between locations will not be accounted for in this model, with agents instantly moving from location to location.

Disease Mechanics Agents in this model flow through the SEIRS chain whenever they are exposed to COVID-19. The most involved dynamics here surround the movement of agents from the susceptible class to the exposed class. At each location, agents have a probabilistic chance of contracting disease from any given agent who is at the same location and in the infectious state. We define the chance of the chance of *one* infectious agent passing COVID-19 to *one* susceptible agent to be equal to

$$\frac{(R_0 / (\text{time spent in infectious class}))}{(\text{number of susceptible agents at the location})}$$

where R_0 is defined per the value in Table 1. This will result in each infectious agent spreading COVID-19 to a total number of agents equal to R_0 on average. So, on

each time step, a susceptible agent at a location contracts the disease equal to the above probability, calculated and checked for all infectious agents at their location. Once an agent is out of the susceptible class, they move through the other classes linearly, remaining in each class for the lengths of time outlined in Table 1.

As previously mentioned, agents have a chance of self-isolating, but they are also hospitalized depending on the severity of their infection. If the case is mild, they are not hospitalized, and either self-isolate or continue to go about their routine. If the case is severe or critical, then the agent is hospitalized in a regular or ICU hospital bed respectively. In both hospitalization cases, they are effectively removed from the simulation, and cannot infect any other agents.

Agents can also be masked or vaccinated, based on actions taken by the planner. The effectiveness of masks and vaccines against COVID-19 is something that is constantly being studied and debated, and as such, there is no one single correct number reflecting this. So, we decided to approximate these values based on data describing the generally observed phenomena. We let an agent being masked multiply the chance of transmission by 0.8 [25] in both directions (multiplying by 0.8 if the susceptible agent is wearing a mask, and also multiplying by 0.8 if the infectious agent is wearing a mask), and we let an agent being vaccinated multiply the chance of transmission by 0.4 [26] in the receiving direction (multiplies by 0.4 if the susceptible agent is vaccinated, but does not affect the rate at which the infectious spreads disease).

4.2. Planner Actions and Goal

Mask Intervention One set of actions the planner can take has to do with mask implementation. The two actions in this category are to enforce a mask mandate among all agents, or to only enforce it among post-secondary students. When either of these actions are taken, the affected agents apply a mask at a rate of 0.7 [23]. When a mask action is taken, it must be active for a minimum of 14 time steps, at which point the planner can re-apply the mandate, or remove the it. This forces the mask intervention methods to be applied on a "per week" basis, more closely mimicking real intervention when compared to the possibility of switching it on and off on any time step.

Vaccine Intervention The other set of actions the planner can take revolves around vaccine mandates. Similar to the mask intervention implementation, a vaccine mandate can be implemented for all agents, or only for post-secondary students. When the planner takes one of these actions, agents become vaccinated at a given rate based on their age bracket [24]. Once an agent is vaccinated, they remain so for the entire duration of the

simulation. In reality, vaccination effectiveness wanes over time, but since our experiments examine a relatively short period of time, this is not something that is considered.

Planner Goal The goal of the planner is to maximize a reward function, defined by the following equation:

$$\text{Reward} = (\text{Students Masked} * \text{Student Mask Penalty}) + (\text{Others Masked} * \text{General Mask Penalty}) + (\text{Students Vaccinated} * \text{Student Vaccination Penalty}) + (\text{Others Vaccinated} * \text{General Vaccination Penalty}) + (\text{Hospital Beds Exceeded} * \text{Regular Bed Penalty}) + (\text{ICU Beds Exceeded} * \text{ICU Bed Penalty})$$

Each penalty is a negative value, meaning that this equation has a maximum 0, which the planner will try to be as close as possible to. On each time step, the number of agents who are masked or vaccinated is multiplied by the respective penalty value, with post-secondary student penalties being lower than general population penalties. In the problem file, a number of regular and ICU hospital beds that mark the "hospital capacity" are defined. If either of these capacities are exceeded, then a penalty is incurred per bed over the limit on every time step this holds. The penalty values were defined in a way to elicit realistic behaviour from the planner. They can be modified based on what is deemed to be important.

5. Evaluation

Base Model A base model was first established, where planner actions have no effect, and agents do not self-isolate or become hospitalized. Stochasticity was removed where reasonable, having time spent in the exposed class equal to 9, time in the infectious class equal to 16, and time in the recovered class equal to 14. One problem file was created, which was used to run 1000 randomly seeded trials, and ranges for the number of agents in each SEIR class at a given time were identified. Figure 2 shows the dynamics of each class of this model with 105 (initially with 93 susceptible and 12 infectious) agents over 300 time steps with a black line superimposed representing theoretical agent numbers created through solving a system of ordinary differential equations (ODEs) over time. This system of ODEs was initialized with the same parameters as with the base model in RDDDL. It is important to note that this ODE model assumes that the population in question is evenly distributed in the space, and it does not operate on the agent level. Therefore, it is a rather crude estimate, but can be used as a starting point to compare the quality of an agent-based model. While the theoretical values are within the maximum and minimum observed values from the agent-based model at each time step, they seem to reach equilibrium values that do not exactly line up with the output of the agent-based simulations - this is

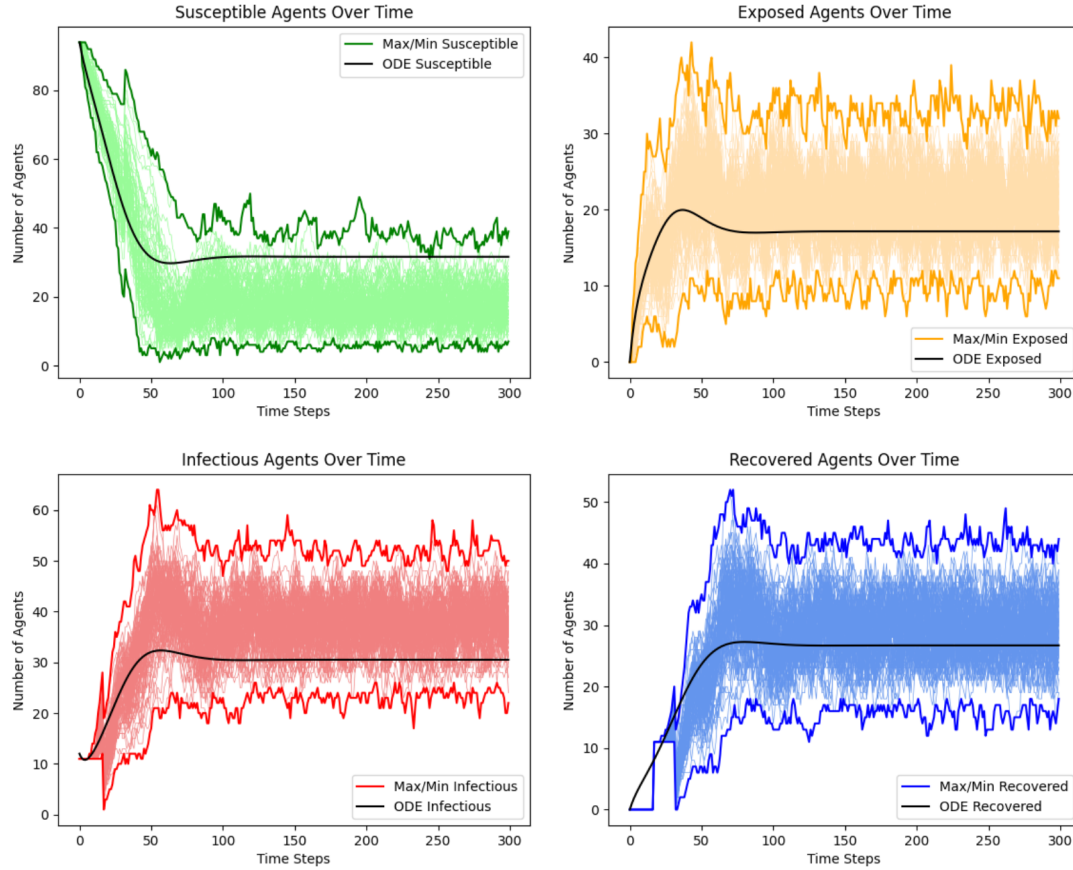


Figure 2: Each graph shows agent numbers observed in a specific class at each time step over 1000 trials - each trial initialized with 93 susceptible and 12 infectious agents. The maximum and minimum values observed at each time step are shown in a dark colour along with a random sample of 100 trials in a lighter colour. Each graph has a black line corresponding to the agent numbers at each time step predicted by solving the system of differential equations sharing the same initial configuration. The initial jump in agents on the bottom two graphs has to do with the 12 infectious agents having the same infectious period, causing them to move out of the class at the same time.

likely due to the agent-based model being built on the specific geography of Kingston, leading to unique simulation behaviours. For example, higher concentration areas (such as post-secondary institutions) will cause disease to spread faster and more effectively, leading to a larger population becoming infected compared to a population that is evenly distributed about some space. These two models being similar in behaviour indicates that the RDDI model accurately simulates disease dynamics, with the four SEIR classes generally oscillating towards a reasonable equilibrium.

Generating Results A series of simulations were run, and data was extracted from the outcomes. Each simulation operated in a world with around 100 agents (varies

slightly depending on random initialization of agents in each problem file) and was run for 100 time steps. Due to this scale, the regular hospital bed capacity was set to be 2, and the ICU bed capacity was set to be 1. With this configuration, dynamics were observed that are consistent with the theory backing up the creation of the model, and we were able to draw meaningful conclusions from the actions taken by JaxPlanner.

To understand the model's performance in depth, a number of configurations were compared with each other. With actual COVID-19 dynamics, time spent in the recovered class can be several months [27]. However, seeing as how our model only runs for 100 time steps, this value was varied between 2, 14, and 28 time steps. Another parameter that was varied was the rate of self-isolation.

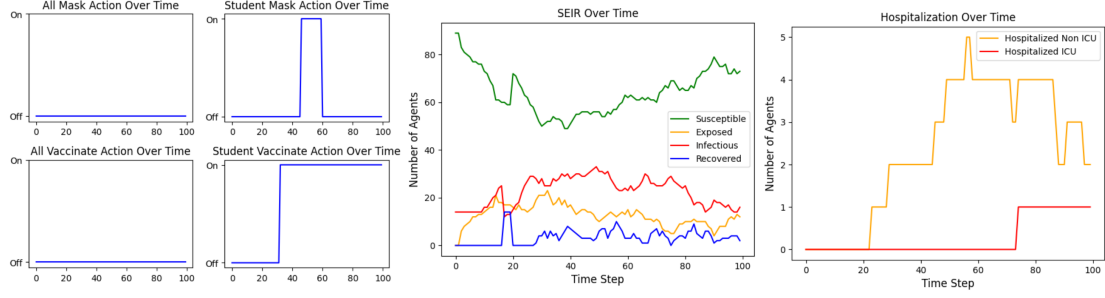


Figure 3: Outcome for a typical simulation, with planner action on the left, an SEIR graph in the middle, and hospitalizations on the right.

The rate of self-isolation is a parameter that is particularly difficult to estimate due to a lack of reliable data, and it is often the case that individuals may continue their day-to-day activities unaware that they are infected at all. For this reason, we vary the values of this parameter between 0, 0.3, 0.5, and 0.7. With respect to the actions that JaxPlanner can take, we looked at cases where the planner did *not* have masking/vaccinating capabilities in addition to the cases where it did, to see how much of an impact it actually had on the reward calculation. Simulations were run for every possible parameter configuration from the options listed above (i.e. the cross product of all parameter combinations).

For every configuration, simulations were run several times over and their results were aggregated. First, only the time spent in the recovered class was varied, with the model having no self-isolation or intervention. For each of these three configurations, 20 problem files were generated that the simulations drew from. 20 simulations were run per problem file, with the simulation seeds being tracked along with the relevant data produced. The other configurations were then incorporated, where self-isolation rates and planner actions vary, with simulations drawing upon the previously generated problem files with respect to time spent in the recovered class. Using the saved seeds, simulations for these configurations were run 20 times on each of their respective 20 problem files.

Figure 3 is an example of how a typical simulation played out. Note that the planner elected to vaccinate students around time step 30, coinciding with increasing cases and agents becoming hospitalized. As soon as this action was taken, the active cases began to diminish, showcasing the effectiveness of agent vaccination in this model. Around time step 40, the planner masked students, lining up with a spike in hospitalizations. Note that like most behaviours in this model, hospitalization is stochastic. So, even though the planner may have performed the optimal actions at a given time, the number of regular hospitalizations reached 5, which is 250% of the specified

capacity of 2. On a larger scale, this stochasticity would not have such a pronounced effect.

Configuration		% Improvement
Rate of Self-Isolation: 0	No intervention	Base
	Intervention	29.4
Rate of Self-Isolation: 0.3	No intervention	21.7
	Intervention	41.6
Rate of Self-Isolation: 0.5	No intervention	49.2
	Intervention	57.1
Rate of Self-Isolation: 0.7	No intervention	66.8
	Intervention	68.3

Table 2

The percent improvement for each configuration over the base model.

Evaluating JaxPlanner Performance Once all simulations have been run, the resulting data can be compared for each configuration. Focusing on the total reward gives an idea of how well each configuration performed relative to each other. To visualize the rewards for all configurations, Figure 4 shows a series of box plot graphs - one for each recovery rate that was chosen. Each configuration's box plot is built using the average total reward for each of the 20 problem files, for which 20 simulations were run. We can visually deduce from this that self-isolation and intervention improved the model performance, with a combination of both generally leading to the best total reward. Table 2 summarizes this in a different way, showing the average percent improvement of different configurations when compared to the base model with no intervention or self-isolation. This implies that the goal of the model was reached. By implementing intervention methods, the planner was able to reduce the severity at which hospitals operated above capacity, all while activating these interventions as little as possible. The improvement of the reward function for all configurations when compared to the base model is evidence of this.

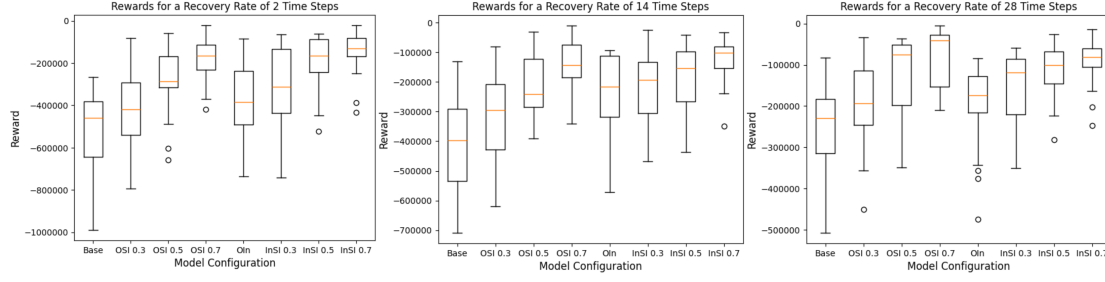


Figure 4: Each graph shows box plots for each configuration based on the total reward for a whole simulation (a number smaller in magnitude is better). Each configuration was run on 20 times on 20 problem files (identical problem files and simulation seeds per graph), and the average total rewards for each problem file are the values that comprise each box plot. The following configurations are in each graph: no intervention and a self-isolation rate of 0 (Base), no intervention and a self-isolation rate of 0.3 (OSI 0.3), no intervention and a self-isolation rate of 0.5 (OSI 0.5), no intervention and a self-isolation rate of 0.7 (OSI 0.7), intervention and a self-isolation rate of 0 (OIn), intervention and a self-isolation rate of 0.3 (InSI 0.3), intervention and a self-isolation rate of 0.5 (InSI 0.5), and intervention and a self-isolation rate of 0.7 (InSI 0.7).

6. Discussion

Limitations The most stand-out limitation for this research was the operating capacity of JaxPlanner. When JaxPlanner is searching for a plan, there is a maximum memory allotment that cannot be exceeded. This is acceptable for most small-scale models, but with a model as complex as this one, the memory limit was quickly reached. It is for this reason that the simulations were run with around 100 agents - significantly lower than the population of Kingston, which is around 100 000. This number was this was the most that JaxPlanner would allow for given 100 time steps (50 days). Despite this, meaningful results were obtained, with dynamics mimicking that which is found in the real world.

Another limitation was the lack of high quality data that was available. Much of the data with respect to disease dynamics is being actively researched, with results varying quite significantly between publications. Rough estimates were obtained, but these are often based on studies that operate all around the world - far from Kingston, Ontario.

There were also assumptions made with regards to the disease dynamics themselves. In reality, people have a chance of dying due to COVID-19 complications. A more realistic model would incorporate births and deaths, and may even see individuals in the population moving through age brackets. The rate of transmission is also different in reality, being affected by age and the type of infection (symptomatic or asymptomatic), amongst other factors.

Future Work Future work may add more complex disease mechanics to this model, noting the subtle differences that would emerge. Fine-tuning on this existing

model could also be attempted, utilizing optimization techniques to improve the performance and scale allowable via JaxPlanner. Other planners may also be tested to see how performance and results may differ. Another topic to explore could be the verification of existing data and identifying which parameters affect the outcome of simulations the most via modern sensitivity analysis techniques in conjunction with different planners.

7. Conclusion

This paper describes an agent-based COVID-19 model implemented in RDDDL based on the geography of Kingston, Ontario, incorporating complex disease mechanics. Through the use of JaxPlanner, intervention methods were added in the form of masking and vaccination actions, which were successfully executed to ensure that hospitals were operating at or below capacity as often as possible, while minimizing the time that these intervention methods were active. This both a demonstration of the power of JaxPlanner in complex multi-agent domains, and of the versatility of RDDDL in large-scale simulations.

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