# Randomized Agent-based Pandemic Intervention moDeller (RAPID)

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## Section I: Introduction

COVID-19 is a highly contagious disease with a global death toll in the millions [14]. Since its appearance in December 2019, a variety of interventions have been proposed to stem the spread of the epidemic [5],[10],[11]. As such, the need to model the effectiveness of said interventions has been vital in producing high-quality, data-driven policies from the perspective of governments and organizations.

The model is an agent-based compartmental model designed to simulate different intervention scenarios by varying the behavior of the agents and the way they interact with each other. For example, the movement of agents may be restricted or the infection rate of the virus may be reduced to simulate quarantine measures.

Specifically, agents fall into five (5) mutually exclusive compartments, namely Susceptible (**S**), Infectious Symptomatic ($\mathbf{I_s}$), Infectious Asymptomatic ($\mathbf{I_a}$), Recovered (**R**) and Vaccinated (**V**). They are then modelled as random points on a [0,1] x [0,1] plane. If a susceptible agent is within a certain radius of an infectious agent ($\mathbf{I_s}$ or $\mathbf{I_a}$), then that agent may become infected. The simulation begins with one $\mathbf{I_s}$ agent, some proportion of **V** agents $(k)$, and the rest in **S**. The spread of the virus over time is observed as the agents move around.

For this paper, the study will be focusing on the COVID-19 virus given its contemporary relevance, but it can easily be generalized to other viruses.

The problem statement for this project is as follows: *What are the effects of different intervention scenarios on the spread of an epidemic in an agent-based simulation?*

## Section II: Review of Related Literature & References

### COVID-19

According to Lotfi et al. [8], COVID-19 can spread through both direct and indirect means. That is, through human-to-human transmission or through contaminated objects. Human-to-human transmission occurs mainly via respiratory droplets when the patient coughs, sneezes, talks, or sings. These droplets typically cannot traverse more than 2 meters, but can be suspended in air for up to 3 hours. Furthermore, the reported rates of infections from a symptomatic patient ranges from one to five percent among tens of thousands of patients in China. Although infections from an asymptomatic patient have been reported, Lotfi et al. does not provide infection rates.

Regarding these asymptomatic infections, the World Health Organization [13] notes that asymptomatic individuals are generally less infectious compared to symptomatic ones, as indicated by contact tracing reports from member states, transmission studies, and systematic reviews. Several of these studies provide a lower and upper bound for the infectivity of asymptomatic versus symptomatic individuals, with results showing that between 0% to 2.2% of asymptomatic individuals infected other people compared to the 0.8% to 15.4% of symptomatic individuals.

The WHO scientific brief [13] also indicates possible figures for the split in the infectious population between symptomatic and asymptomatic cases. These figures, however, remain inconclusive due to the difficulty of studying asymptomatic cases and the limitations in studies that did. For example, one systematic review that gave an estimate of 16% of cases being asymptomatic contained studies defined asymptomatic cases as individuals that did not develop fever or respiratory symptoms instead of those that did not develop any at all. The brief does, however, cite a study conducted by Wang et al. [15] in China with appropriately defined conditions for asymptomatic cases reported that 63 out of 279 (around 23%) positive cases remained asymptomatic until discharge.

A different scientific brief by the WHO [2] discusses the period of time in which individuals with COVID-19 are able to infect others. Infection is generally confirmed through RT-PCR testing for the presence of SARS-CoV-2 viral RNA, although other factors, such as the ability of the virus to replicate, also contribute to determining whether an individual is infectious. Viral RNA has been reported in individuals 1 to 3 days before symptoms onset, while several studies found that the virus could no longer be cultured after 7 to 9 days past symptoms onset. For asymptomatic cases, the brief does not give a period of time for which they are infectious, but it does give

a recommendation of 10 days after testing positive for which to keep COVID-19 patients in isolation. This is in comparison to the recommendation of 10 days in isolation after symptoms onset and at least 3 additional days without symptoms for symptomatic patients.

Lastly, literature has shown that individuals who recover from COVID-19 gain immunity from the disease for a certain period of time. In a study conducted by Dan et al. [6], the immune cells and antibodies of over 200 individuals who had been exposed to and subsequently recovered from SARS-Cov-2 were analysed for immunity against the virus. From those analysed, the results indicated that the body maintains adequate levels of B cells, T cells, and antibodies to maintain immunity against the virus first least 6 months after recovery.

**Interventions on COVID-19**

There have been multiple preventative measures against COVID-19 with varying results.  Flaxman et al. [11] describes the non-pharmaceutical interventions done by european countries and assesses their effect on the virus' spread. The interventions looked at in this study include social distancing, school closure, banning of large gatherings, and large scale lockdowns. Of these measures, it was found that the effects of a lockdown are more easily identifiable, and that it reduces transmissivity between 75-87%.

Eikenberry et al. [10] conducted a study on the use of face masks and their effects on the effective transmission rate of COVID-19. It was reported that the use of face masks prevents healthy persons from contracting the virus while also preventing asymptomatic transmission from the infected. The study also included analysis on varying levels of mask use as well as the robustness of the masks. It was found that an 80% use of 20% effective masks reduces the effective transmission rate by roughly one-third and a 50% use of 50% effective masks cuts transmission rate by about half.

Polack et al. [5] reports on the safety and efficacy of the BNT162b2 mRNA Covid-19 vaccine. In clinical trials, a two-dose regimen, each dose taken 21 days apart, was found to be safe and 95% effective against COVID-19. In addition to that, the vaccine had an efficacy of 52% with a confidence interval of 95% making for more than a 99.99% probability that its efficacy is greater than 30%. Full efficacy is reached at least seven days after the second dose.

**Previous Models and Simulations**

de Lara-Tuprio et al. [12] uses the FASSSTER model, a mathematical compartmental model, to create projections of the number of infected individuals (COVID-19) in a given region depending on a choice of scenarios (i.e. levels of quarantine, levels of testing and health capacity). The model separates the population into six (6) mutually exclusive compartments; namely, Susceptible (S), Exposed (E), Infectious Asymptomatic ($I_a$), Infectious Symptomatic ($I_s$), Confirmed (C), and Recovered (R). Furthermore, the movement of individuals from one compartment to another is described by a system of differential equations. This model represents differing levels of quarantine by tweaking the rate at which Susceptible (S) individuals become Exposed (E), and it represents differing levels of health and testing capacities by tweaking the rate at which Infectious Symptomatic ($I_s$) individuals become Confirmed (C).

Silva et al. [9] proposes COVID-ABS, a SEIR (Susceptible-Exposed-Infected-Recovered) agent-based model that simulates both the epidemiologic and economic effect of COVID-19 under different scenarios. The model iterates over discrete time periods and at each iteration, it checks for contact between any pair of agents where contact is defined to occur when the distance between two agents are less than some specified threshold. To represent economic interactions, the model has five (5) types of agents; namely, People (A1), Houses (A2), Businesses (A3), Government (A4), and Healthcare (A5). Furthermore, the effect of contact between agents depends on the type of the two agents. For example, the contact is epidemiological if both agents are A1 and economical if one agent is A1 and the other is A3.

Alzu'bi et. al. [1] propose an agent-based model to extend the SIR model by increasing the amount of compartments for a more granular and realistic simulation of the COVID-19 outbreak, as well as specify an urban environment split into two neighborhoods. The paper uses a random distribution to determine agent movement and infection chances within a certain radius. This model is validated against the SIR model, and finds that limiting mobility, social interaction, and early intervention are effective in reducing the rate of infection and death.

Huang [3] attempts to create an agent-based simulation of a sexual activity network in order to effectively map out the spread of sexually transmitted infections such as HIV. This is done by segregating the population into separate pools of risk and activity (with some being extremely active, others being more active than normal but less risky than the extremely active pool, and most remaining relatively inactive and low-risk). The model also makes distinctions between long-term relationships with sustained contact over a long period of time and free, spontaneous agent

connections. The paper also models a dynamic change in population (with more people entering into the high activity pool over time as people are more willing to come out as homosexual over time).

Cuevas [4] uses an agent-based model to simulate the risk of transmitting COVID-19 in facilities. It does this by mapping agents as points on a two-dimensional plane, and randomly assigning rates of susceptibility to each agent. It also randomly assigns rates of mobility and contact upon initialization. The model then calculates the risk of infection for each agent by first checking for the presence of an infected agent within a determined circular neighborhood, and generates a number from 0 to 1 if there is indeed an infected agent. If it is above the rate of susceptibility of the agent, then the agent is infected. Movement behavior is split into short, local movement and long-distance displacement, which is determined by the rate of movement assigned to the agent. Local movements represent small changes in position, while long-distance movements represent large changes, such as moving from one room to another.

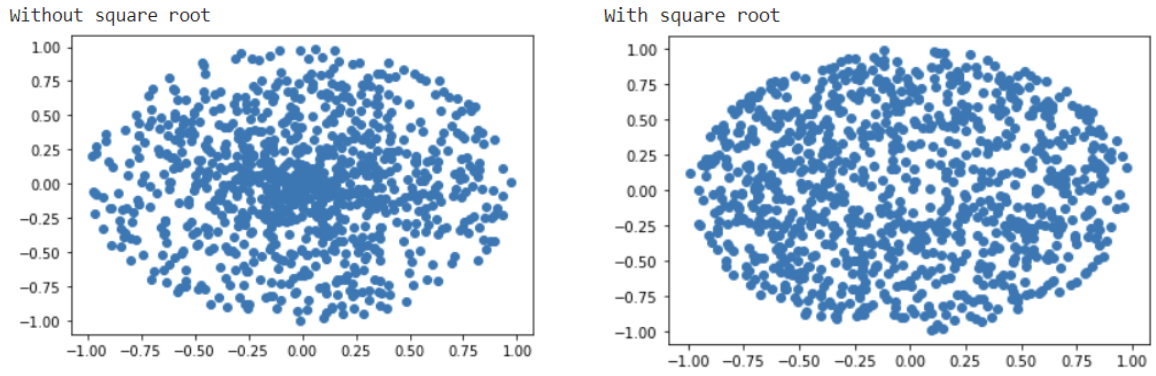
## Section III: Simulation and Modelling

### Model Description

The model intends to simulate non-homogeneous epidemic spread by representing states of infection as compartments, where transfer from one compartment to another is determined by either a probability and/or a counter determined by a Poisson distribution.

Specifically, agents fall into five (5) mutually exclusive compartments, namely Susceptible (**S**), Infectious Symptomatic ($\mathbf{I_s}$), Infectious Asymptomatic ($\mathbf{I_a}$), Recovered (**R**), and Vaccinated (**V**). Agents are then modelled as random points on a [0,1] x [0,1] plane. The simulation begins with one $\mathbf{I_s}$ agent, some proportion of **V** agents $(k)$, and the rest in **S**. The spread of the virus over time is observed as the agents move around.

Agent movement is determined by drawing a circle with a certain radius $(r_m)$ around an agent and picking a point uniformly at random within that circle. This is then the new position of the agent. This was implemented by generating a direction angle uniformly at random from $[0,\ 2\pi]$, generating a distance uniformly at random from $[0, r_m]$, and finally getting the square root of that generated distance. If the square root of the distance was not taken, then it would be more likely for points to be generated close to the center instead of uniformly distributed throughout the circle as seen in these figures:




An **S** agent has a chance to become an $\mathbf{I_a}$ agent when it comes into contact with either an $\mathbf{I_a}$ or $\mathbf{I_s}$ agent with probabilities $(\beta_a)$and $(\beta_s)$respectively. Contact is defined to occur when the distance between two agents are less than some threshold $(r_c)$.

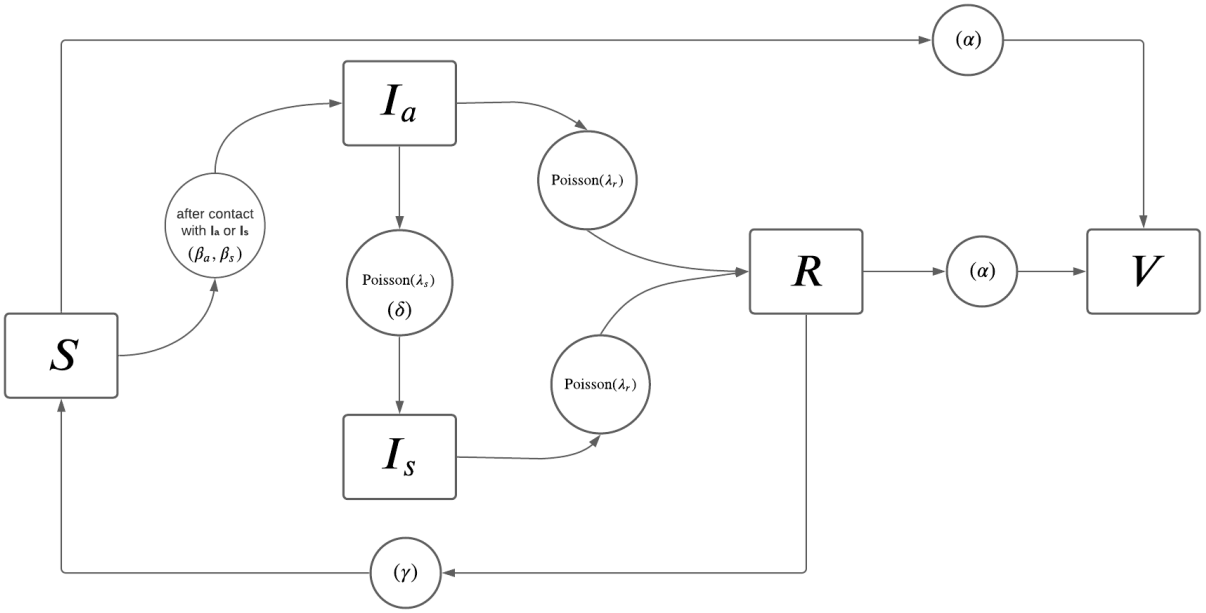
An $\mathbf{I_a}$ agent has a chance to become an $\mathbf{I_s}$ agent with probability $(\delta)$. In the case that it falls within the probability threshold to become symptomatic, a Poisson

distribution with mean $(\lambda_s)$ is used to determine how many days will pass until it transitions into an $\mathbf{I_s}$ agent. After this period of time, it transitions.

An $\mathbf{I_a}$ agent becomes an **R** agent after some period of time determined by generating a recovery counter through a Poisson distribution with mean $(\lambda_r)$. If this agent transitions into an $\mathbf{I_s}$ agent, its recovery counter is refreshed with the same Poisson distribution.

Lastly, **S** and **R** agents become **V** agents with probability$(\alpha)$, and **R** agents return to being **S** agents with probability $(\gamma)$.

These are summarized in the following diagram:




**Limiting Assumptions**

The model has several governing assumptions that must be actively recognized in order to have a correct picture of its validity and fidelity.

The model assumes that the compartments are exhaustive and mutually exclusive, which may be an oversimplification of the real world states of infection. For example, it is plausible that some people after recovering may return to being infectious despite no longer being infected themselves.

The population of the model is assumed to be constant the whole time. A different implementation may have some percent of agents die after becoming symptomatic. It could also be the case that new agents could be introduced through birth.

The model assumes that agents in **R** have immunity while it may be the case that there is no immunity after recovery.

The model also assumes that the movement of agents is determined by a random walk in a certain radius, when it may very well have more complex underlying rules. It may be the case that some agents are predisposed to move farther than others on average, it may also be the case that agents follow more consistent patterns of movement.

It is assumed the effectiveness of vaccination ignores if an agent has contracted the virus. It may be the case that previously being infected has an effect on the effectiveness of vaccination. Furthermore, the supply of vaccines is assumed to be sufficient for the population.

The model assumes that no one is perpetually infected, and that all infected agents eventually recover after a certain period of time.

The model also assumes single patient ground zero, a single infected patient at the start of the simulation, when there may be several vectors of infection simultaneously entering the area (such as perhaps a group of infected tourists entering the city).

**Computational Procedure**

The program has two main methods used iteratively to run through the simulation.

The first is *observe*, which retrieves the position of each agent and the compartment they belong to then displays it on a [0,1] x [0,1] grid.

The second is *update*, which updates all compartments according to the behavioral rules outlined in the section above. This is done in the following order, as governed by the behavior described in Model Description:

1. $\mathbf{I_a}$ and $\mathbf{I_s}$ transition into **R** agents.
2. **R** agents transition into **S** agents.
3. $\mathbf{I_a}$ agents transition into $\mathbf{I_s}$ agents.
4. **S** agents transition into $\mathbf{I_a}$ agents from contact with $\mathbf{I_s}$ agents.
5. **S** agents transition into $\mathbf{I_a}$ agents from contact with $\mathbf{I_a}$ agents.
6. **S** and **R** transition into **V** agents
7. All agents move.

**Simulated Conditions**

As stated in the introduction, the objective of this study is to test the influence of various simulated conditions on an agent-based model for epidemic spread. These

scenarios are represented by changing parameters in order to represent changes in real world values.

Control

The control scenario is simulated using the following default values:
$n = 200$, $r_m = 0.3$, $r_c = 0.02$, $\beta_s = 1$, $\beta_a = 0.125$, $\delta = 0.77$, $\lambda_s = 2$, $\lambda_r = 8$, $\gamma = \frac{1}{180}$, $k = 0$, $\alpha = 0$ where $n$ is the number of agents in the simulation and the other parameters are as defined in the Model Description.

The parameters $n$, $r_m$, and $r_c$ were derived by assuming that the scale of the [0,1] x [0,1] grid is 100:1 meters. Thus, the size of the grid would be 10000m$^2$. Since the population density of NCR is about 21000 per km$^2$ [7], there would be about 200 people in 10000m$^2$. Thus, $n = 200$. Furthermore, $r_c = 0.02$for a contact radius of 2 meters and $r_m = 0.3$for a movement radius of 300 meters.

For the control scenario, $\beta_s$is assumed to be 1, given that coming into close contact with another symptomatic person over the duration of a day has a very high probability of transmitting the disease. The mean of the value of 0.125 for $\beta_a$was derived from the figures given by the WHO scientific brief [11] as indicated in the related literature. From the brief, between 0% to 2.2% of asymptomatic individuals infected other people, compared to the 0.8% to 15.4% for symptomatic individuals. The mean of 0 and 2.2 is 1.1, while the mean of 0.8 and 15.4 is 8.1, giving a ratio of roughly 1:8, or 0.125.

The parameters $\lambda_s$, $\lambda_r$ and $\gamma$ were similarly given values according to the related literature. The value of 2 for $\lambda_s$ is the mean duration before symptoms onset (1 to 3 days), while the value of 8 for $\lambda_r$is the mean duration of infectivity past symptoms onset (7 to 9 days) [2]. Lastly, the value of $\frac{1}{180}$ for $\gamma$(the rate at which **R** agents transition into **S** agents) approximates the duration of immunity from the virus after recovery (6 months or 180 days) [6].

Increased Vaccination Capacity

Vaccination capacity refers to the amount of vaccines that are deployed in a particular area. This is reflected in the model in two ways: (1) an increase in the proportion of **V** agents at the beginning of the simulation$(k)$ and (2) an increase in the probability at which **S** and **R** agents transition into **V** agents$(\alpha)$.

Lockdown

Lockdown refers to the protocol wherein individuals stay at home and limit their tendencies to go outside or travel. However, it is unavoidable that they would still need to go out for particular needs such as to go to their jobs or buy supplies.This is reflected in the model as a decrease in the radius ($r_m$) of the circle in which an agent is able to move.

Social Distancing

Social distancing refers to the practice of keeping a distance between others as to prevent the spread of the virus. This is reflected in the model as a decrease in the contact radius ($r_c$) for $\mathbf{I_a}$ and $\mathbf{I_s}$ agents.

Facemask Use

Facemask use refers to the scenario in which people put on face coverings in order to reduce transmission from person to person. This is reflected in the model as a decrease in the infection rates ($\beta_a$)and ($\beta_s$).

The following combinations of the above conditions will also be simulated:

Facemask Use and Social Distancing

A decrease in the contact radius ($r_c$) for $\mathbf{I_a}$ and $\mathbf{I_s}$ agents as well as a decrease in the infection rates ($\beta_a$)and ($\beta_s$).

Facemask Use and Social Distancing and Lockdown

A decrease in the contact radius ($r_c$) for $\mathbf{I_a}$ and $\mathbf{I_s}$ agents, a decrease in the infection rates ($\beta_a$)and ($\beta_s$), and a decrease in the radius ($r_m$) of the circle in which an agent is able to move.

**Result Analysis Methods**

For each scenario, tests were iteratively run to determine (1) the scenario's likelihood of turning into an outbreak and (2) average peak infected population during outbreaks.

These results were retrieved by running each scenario a hundred times for a year (365 days) each, and collecting data from each run. An outbreak is determined to have occurred if the peak population of infected agents ($\mathbf{I_a}$ and $\mathbf{I_s}$ ) goes over 2% of the population at any point.

The results were obtained according to the following rules:

1. **The percent of total tests where an outbreak occurs** is retrieved by counting the proportion of all simulations where an outbreak occurred.
2. **The average peak infected population** was retrieved by summing the peak number of infected agents ($\mathbf{I_a}$ and $\mathbf{I_s}$) for each scenario where an outbreak occurred, and dividing it by the number of scenarios where an outbreak occurred.

## Section IV: Results and Discussion

### Results

| **Scenario (Control)** | **Percent of Total Tests where Outbreak Occurs** | **Average Peak Infected Population (n = 200)** |
|---|---|---|
| Control #1 | 69% | 46.16 |
| Control #2 | 64% | 42.39 |
| Control #3 | 68% | 40.74 |
| Control #4 | 58% | 42.34 |
| Control #5 | 58% | 43.33 |

The control scenario remains reasonably consistent with 58-69% of all simulations turning into outbreaks. The peak infected population for a population of 200 ranges from 40-46.

| **Scenario (Increased Vaccination)** | **Percent of Total Tests where Outbreak Occurs** | **Average Peak Infected Population (n = 200)** |
|---|---|---|
| Increased Vaccination Capacity $(k = 0.5)$ | 19% | 8.84 |
| Increased Vaccination Capacity $(k = 0.25)$ | 43% | 18.98 |
| Increased Vaccination Capacity $(k = 0.1)$ | 55% | 33.95 |
| Increased Vaccination | 61% | 18.52 |

| | | |
|---|---|---|
| Capacity $(\alpha = 0.01)$ | | |
| Increased Vaccination Capacity $(\alpha = 0.02)$ | 57% | 13.14 |
| Increased Vaccination Capacity $(\alpha = 0.05)$ | 34% | 7.44 |
| Increased Vaccination Capacity $(\alpha = 0.1)$ | 23% | 5.91 |

In the scenarios where a portion of the population is vaccinated at the beginning of the simulation, a trend can be seen where larger vaccinated populations result in fewer outbreaks as well as a lower average peak infected population. When half of the population is already vaccinated, outbreaks occurred 19% of the time with an average peak of about 9 infected individuals. On the other hand, when only a tenth of the population is vaccinated, outbreaks occurred 55% of the time with an average peak of 34 infected individuals.

For the scenarios where vaccination occurs gradually throughout the simulation, it can be observed that simulations with higher vaccination probabilities have less outbreak occurrences; going from 61% of simulations for $\alpha = 0.01$down to 23% of simulations for $\alpha = 0.1$.

| **Scenario (Lockdown)** | **Percent of Total Tests where Outbreak Occurs** | **Average Peak Infected Population (n = 200)** |
|---|---|---|
| Lockdown $(r_m = 1)$ | 67% | 44.27 |
| Lockdown $(r_m = 0.2)$ | 55% | 42.07 |
| Lockdown $(r_m = 0.1)$ | 66% | 45.02 |
| Lockdown $(r_m = 0.05)$ | 65% | 44.18 |
| Lockdown $(r_m = 0.01)$ | 62% | 33.32 |
| Lockdown $(r_m = 0.007)$ | 59% | 24.81 |
| Lockdown $(r_m = 0.005)$ | 47% | 19.11 |

| | | |
|---|---|---|
| Lockdown ($r_m = 0.001$) | 20% | 6.15 |
| Lockdown ($r_m = 0$) | 0% | 0.00 |

In the scenarios where a lockdown is simulated, the percent of tests where outbreaks occurred remained relatively the same unless $r_m$ assumed smaller values. Outbreak occurrance percentages of above 50% were observed for simulations where $r_m \geq 0.007$ while $r_m = 0.005$ was close to this at 47%. However, when $r_m = 0.001$ only 20% of tests resulted in an outbreak and interestingly, the simulations for $r_m = 0$ never resulted in an outbreak.

| **Scenario (Social Distancing)** | **Percent of Total Tests where Outbreak Occurs** | **Average Peak Infected Population (n = 200)** |
|---|---|---|
| Social Distancing ($r_c = 0.015$) | 26% | 10.58 |
| Social Distancing ($r_c = 0.01$) | 2% | 5.00 |

The social distancing scenarios resulted in outbreak occurrence percentages of 26% and 2% for $r_c = 0.015$ and $r_c = 0.01$ respectively. It is observed that a lower contact radius results in less outbreak occurrences. It should be noted that the change between the set of simulations is half a meter.

| **Scenario (Face Masks)** | **Percent of Total Tests where Outbreak Occurs** | **Average Peak Infected Population (n = 200)** |
|---|---|---|
| Face Masks ($\beta_s = \frac{2}{3}$) | 39% | 15.67 |
| Face Masks ($\beta_s = 0.5$) | 19% | 7.74 |

The face masks scenarios resulted in outbreak occurrence percentages of 39% and 19% for $\beta_s = \frac{2}{3}$ and $\beta_s = 0.5$ respectively. The values selected for $\beta_s$ is based on findings from the study conducted by Eikenberry et al. [10] were combinations of mask usage and effectivity decrease transmission between individuals.

| **Scenario (Combinations)** | **Percent of Total Tests where Outbreak Occurs** | **Average Peak Infected Population (n = 200)** |
|---|---|---|
| Social Distancing and Face Masks ($r_c = 0.015,\ \beta_s = \frac{2}{3}$) | 10% | 5.80 |
| Lockdown, Social Distancing, and Face Masks ($r_m = 0.1,\ r_c = 0.015,\ \beta_s = \frac{2}{3}$ | 7% | 5.71 |

In the combined intervention scenario of social distancing and face masks, outbreaks occurred 10% of the time at $r_c = 0.015$and $\beta_s = \frac{2}{3}$ . In the scenario with combined lockdown, social distancing, and face masks, outbreaks occurred 7% of the time at $r_m = 0.1$, $r_c = 0.015$, and $\beta_s = \frac{2}{3}$.

**Discussion**

Potential Pandemics

One surprising result is that unlike the SIR model, an outbreak is not guaranteed by the presence of a patient zero. There are many runs where after having introduced a patient zero, the virus fails to spread as agents remain sufficiently distant or transmission does not occur because agents recover before spreading the virus.

This may be a consequence of the way the model non-homogenously simulates movement and represents transmission as dependent on distance. This introduces substantially more variability to how an outbreak spreads— it is possible that the infection spreads more rapidly than normal due to abnormal clumping. As a consequence, the model is much more chaotic and dependent on initial states.

Interpretations and Insights

Increasing vaccination capacity is generally shown to ameliorate the effects of the pandemic, decreasing the amount of outbreaks and peak infections. Interestingly enough, even minor changes in alpha, while not significantly affecting the amount of overall outbreaks compared to the control scenario, can substantially decrease the

average peak infection. This may be because gradual vaccinations may have a ‘smoothing’ effect on the outbreak over time, decreasing the pool of susceptible agents while only minorly affecting initial circumstances.

Lockdowns have an interesting property where changes to movement rate have an insignificant effect on data until the rate of movement becomes extremely close to zero. This may be because decreasing interaction with other agents may still increase clumping up until a certain point, and compensate for the dip in mixing.

Social distancing is shown to have a very large effect on average peak infection and proportion of outbreaks, even with small, incremental changes. This may be because decreasing the contact radius substantially decreases the amount of opportunities for disease transmission, and as such has meaningful effects on model behavior. This may also compound with the chaotic nature of the model, where even minor changes in initial stages can have large diverging effects on the end result.

Face masks, as expected, substantially decrease the proportion of outbreaks and the average peak infection.

Interestingly enough, while the combination scenarios decreased the proportion of outbreaks and the average peak infection, the proportion of outbreaks in the combined scenarios were approximately equal to the product of the proportion of outbreaks of each constituent scenario. This may be because the interventions are themselves independent of each other, and as such affect the percent of outbreaks independently.

## Section V: Conclusion and Recommendations

### Conclusion

The problem statement of this paper was: What are the effects of different intervention scenarios on the spread of an epidemic in an agent-based simulation?

This was tested by implementing an agent-based model that mapped agents onto a [0,1] x [0,1] grid. Agents were then segregated into different compartments with behavioral rules for disease transmission, movement, and recovery.

Several different scenarios were then tested out by adjusting the parameters in accordance with real world statistics. The results show that each intervention has a positive effect on outbreak chance and peak average infection population, with minor changes in lockdown as the sole exception.

### Recommendations

The authors of this paper recommend a variety of potential improvements to the model to make results more closely aligned with the complexity of real world interpretations.

The first potential improvement is to increase the complexity of agent behavior and interaction. Agents may be categorized into more compartments, such as Exposed, Confirmed, Quarantined, or Deceased. Agents may have a variety of movement rules (allowing the model to simulate both superspreaders and hypochondriacs) as

well as change behavior based on compartment (for example, staying in and moving less upon displaying symptoms). A more complex environment may also be modelled, allowing for regions where infection radiuses are higher (high-contact environments) or regions regularly visited by agents (schools, supermarkets, offices) to simulate the routines embedded in real-world outbreaks.

The second potential improvement is to introduce novel strains, and explore the potential ramifications of several viral strains interacting in the same environment. This may provide meaningful insights on the nature of how multiple strains spread and interact, as well as the most effective interventions given varying vaccine effectiveness.

The third potential improvement is to increase the methodological rigor of the study. This would manifest in the form of more trials for each scenario, trials that simulate for longer (to describe long-run effects of a particular intervention), and gathering default parameters from a wider range of studies and datasets. It would also be fruitful to mix different scenarios with more trials and variation in permutations to see how different interventions interact.

## Section VI. References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