An Agent-Based Model of COVID-19 on the Diamond Princess Cruise Ship

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Abstract. We model the COVID-19 outbreak and shipboard quarantine with a 3-D agent-based simulation of a SEIR model which preserves the ratios of crew, passengers, and shipboard space. The stochastic model captures the movement patterns of passengers and crew members on-board the ship, as well as how this movement changed once quarantine is established. The study includes the derivation of the basic reproduction number based on contact numbers and transmission rates. We capture the number of contacts between two people when they remain within the model equivalent of a 3-foot radius for 60 minutes and the transmission probability per contact. We show that, based on the measured reproduction number, an outbreak is bound to occur in the majority of simulations even with quarantine imposed on the ship. We also show that most infection on board occurs by others of the same group (passenger or crew), with passengers causing the majority of infections.

1. Introduction.

COVID-19 was declared to be a global pandemic in March 2020, but before March there were contained outbreaks. One such outbreak became public on February 5, 2020, when the Japanese government ordered the passengers and crew on the Diamond Princess Cruise Ship to begin a two-week quarantine after a former passenger tested positive for COVID-19. This quarantine was incredibly ineffective, and the virus ran rampant on-board. On February 20th, there were 651 cases [22]. By March 1st, among 3,711 Diamond Princess passengers and crew, 712 (19.2% of those on-board) had positive test results for SARS-COV-2. [20, 23].

Cruises and other contained environments, such as jails and nursing homes, are notorious for disease outbreaks [1, 11, 21, 24]. These outbreaks have been studied to understand how to prevent such pervasive transmission. These contained outbreaks give us the opportunity to understand how different types of movement and social organization lead to different kinds of outbreaks. In contained systems, all interaction comes from within, so it is possible to understand how this movement and organization without outside influence can lead to outbreaks.

For large scale outbreaks, the most effective measures of containment are social isolation and quarantine (for mathematical examples see [7, 9] among others). Quarantine serves to separate those infected from the susceptible population while social isolation keeps susceptible and potentially asymptomatic populations separate. This is especially important for COVID-19 since asymptomatic carriers are thought to hold the same degree of transmission as symptomatic carriers [4] for pre-delta variants.

In response to the pandemic, most regional governments in the US have implemented social distancing protocols, but it is important to know the effectiveness of these protocols. Isolation and quarantine are our current best methods for flattening the curve before a treatment and/or vaccine is developed, but quarantine may not be the most effective in closed environments like cruise ships and nursing homes. Shared air systems, people in close prox-

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imity and poorly cleaned surfaces increase transmission rates [14, 30]. In addition to these uncontrollable factors, the average age of passengers plus the possibility of insufficient disease transmission protocols due to a lack of training by crew only serve to increase the number of cases [23]. In the instance of on board quarantines, passengers are entirely reliant on crew members for food and cleaning services, leading to multiple contact points, and a population that cannot fully quarantine. We can model these mathematically, and have done so with SEIR models.

SEIR models are compartmental models consisting of Susceptible-Exposed-Infected-Recovered/Removed classes, where the change in these classes is observed over time to understand outbreaks. Recently, SEIR models have been employed to mathematically model outbreaks of coronaviruses on cruise ships [5]. Other SEIR models have shown that there are high reproductive numbers on the Diamond Princess [15, 25].

While these models are well suited to understand the general shape of an outbreak, they lack in certain departments. SEIR models do not allow us to incorporate randomness, nor study individual movement. By converting the SEIR model into an agent-based model, we can understand the movement of individuals and how this movement affects the spread of COVID-19.

We model the outbreak on the Diamond Princess, along with the failed quarantine, with a 3-D agent-based simulation of an SEIR model which preserves the ratios of crew, passengers, and shipboard space. Our stochastic model captures the movement patterns of passengers and crew members on-board the ship, between the public gathering spaces, passenger cabins, and crew quarters. The model also includes the restrictions on movement for the passengers once quarantine was established. In this paper, an agent-based simulation is developed in order to evaluate how individual movement and organization lead to outbreaks on-board the cruise ship.

In our model, we utilize agents to understand the transmission dynamics between the two classes, passengers and crew. We present an agent-based model version of an SEIR system. The infection stages are susceptible (S), exposed (E), asymptomatic infectious (I_A), symptomatic infectious (I_S), and recovered with temporary or permanent immunity (R) or removed from the ship. This model is created in NetLogo3D to capture the full motion people take on cruise ships, moving between different decks. The model seeks to mimic the movement of those on board, tests potential infection rates, and determines the reproductive number $\mathcal{R}_0$ by analyzing the resulting data from 100 model runs. We also determine the effective reproductive number $\mathcal{R}_e$, which determines the reproductive rate when not everyone is susceptible and equally exposed during the ship-board quarantine. In addition to this, we determine the transmission probability per contact.

In section 2 we discuss the components of the agent-based model, including the modeled environment, agent movement, infection, and the parameters both measured and calculated. In section 3, we calculate the reproductive numbers, effective contact numbers and analyze which agents drive infection. Last, in section 4 we discuss our results and conclude the paper.

2. Model.

The agent-based model was created in NetLogo3D [28]. NetLogo is a free, open-source programmable modeling environment for simulating natural and social phenomena, used for modeling complex systems over time. In the model, there are two agent classes, passengers and crew, distinguished by color in the model. The passenger and crew members have distinct movement patterns where they move with other members of the same class, and have different quarters where they retire to at night. During the quarantine period, the movement style of each class differs. By separating the people on the Diamond Princess into two different classes, we can better understand how the function, social and movement patterns of those people can influence the spread of COVID-19. The agents have different movements (see Section 2.2), locations (see Section 2.1), and functions (see Section 2.2) on board.

2.1. Environment. To simplify the disparate environment of the cruise ship, we split the model environment into 3 decks - upper, middle and lower. Deck access is determined by agent type. Passenger agents can move between the upper and middle decks, which represent the leisure decks (top level) and passenger cabins (middle level). Crew agents can move between the middle and lower decks, symbolizing their work interacting with passengers and crew quarters. This model assumes that passengers primarily interact with other passengers on the leisure decks.

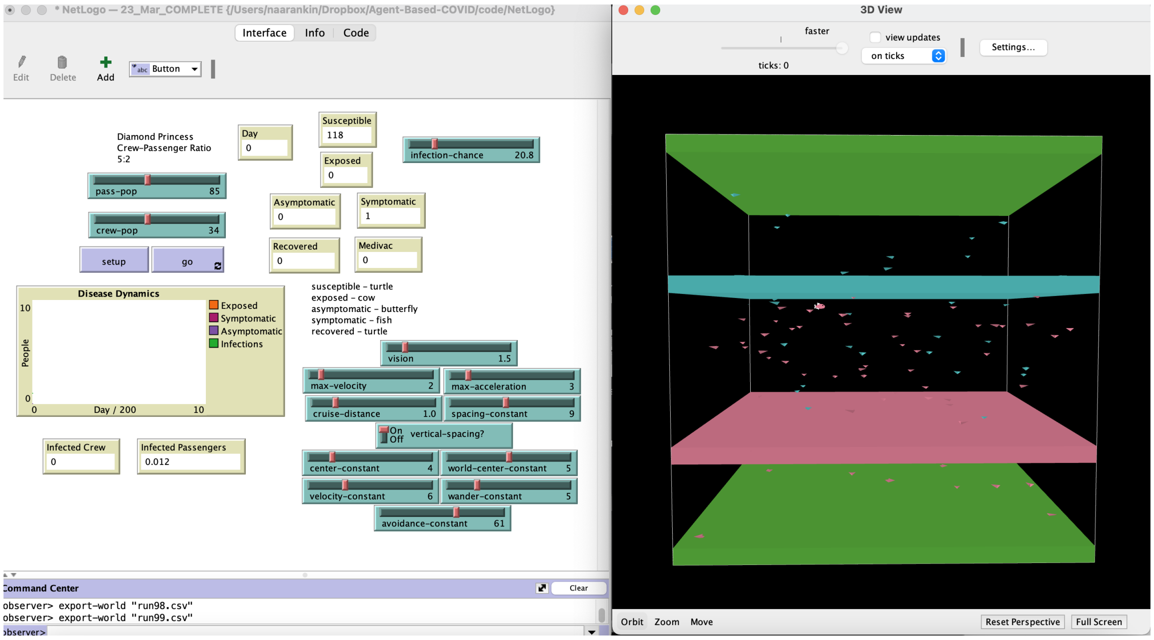
The ratio of ship size to model size was calculated. In the ship, the total volume of passenger cabins available is to 309616 cubic feet [2], calculated by the published room sizes on the Diamond Princess website. We multiplied by 7/2, to replicate the two rooming decks, with the final leisure deck being by 1.5 times the size of the rooms. This comes out to 1083656 cubic feet. The model is a $25x25x25$ cube in NetLogo3D, resulting in a total volume of 15625 cubic patches. This model size is a feature of NetLogo3D, and allows us to compute the proper scaling for size and human capacity onboard.

The Diamond Princess holds 3770 people, with a passenger-crew ratio of 5:2. When translating the ship space to model space and the volume ratio of the ship to the number of humans on board, the model space has room for 119 people, which comes out to 85 passengers and 34 crew members.

2.2. Movement. Human movement and behavior resembles the flocking of birds, with groups forming and staying together over time. This flocking behavior has been observed when studying the formation of groups [6]. Other studies have shown that interaction between individuals will tend to move in flocks when sharing information about movement through a population [17]. This movement type allows us to capture the random yet directed movement of individuals on a cruise. We have individuals flock with members of the same class, showing the movement and communication patterns of people on board.

The movement of agents was made using a vector-based 3D flocking model, based on Jon Kelin's implementation of Craig Reynolds' Boids algorithm, which is included with NetLogo3D as a tutorial [29]. The flocking model uses 12 parameters to determine how movement occurs. The *vision* is the distance that an agent can see. The *max-velocity* is the fastest an agent can go, and *max-acceleration* is the fastest an agent can accelerate. The *cruise-distance* is the minimum distance from other agents to be maintained.

The movement is determined by the sum of the following urges: *center-constant* is the urge to move towards the center of its flock. The *velocity-constant* is the urge to align its velocity with the velocity of its flockmates. The *spacing-constant* is the urge to be no closer than *cruise-distance* from other agents. The *avoidance-constant* is the urge to avoid colliding with obstacles. The *world-center-constant* is the urge to avoid the edges of the world. The *wander-*



Diamond Princess
Crew-Passenger Ratio
5:2

Day: 0
Susceptible: 118
Exposed: 0
Asymptomatic: 0
Symptomatic: 1
Recovered: 0
Medivac: 0
Infected Crew: 0
Infected Passengers: 0.012

pass-pop 85
crew-pop 34
infection-chance 20.8

susceptible – turtle
exposed – cow
asymptomatic – butterfly
symptomatic – fish
recovered – turtle

vision 1.5
max-velocity 2
max-acceleration 3
cruise-distance 1.0
spacing-constant 9
On Off vertical-spacing?
center-constant 4
world-center-constant 5
velocity-constant 6
wander-constant 5
avoidance-constant 61

```
observer> export-world "run98.csv"
observer> export-world "run99.csv"
observer>
```

Figure 2.1. *Interface of the NetLogo model on the left. This includes the flocking parameters given by the Kelin model, as well as the infection parameters and tracking values for the SEIR model. On the right, there is the 3-D model representation of the cruise ship with 3 deck levels, passengers and crew. The agent color designates passenger or crew and infection category.*

constant is the urge to move in a random way. The constant sliders control the weight of each urge in determining the behavior of each agent. The *vertical-spacing?* switch determines if agents maintain *cruise-distance* in the vertical direction [29].

These parameters are described in Table 2.1, and determine the direction and velocity that an agent moves in. The model interface is shown above, including the values for each of the twelve parameters, defined below.

The agents flock with other agents of their same type, following the assumption that passengers tend to interact with other passengers, and the same for crew members. The model is split into two functions, day and night. In the day, agents are free to flock over their two open decks. At night, the agents return to the level of their quarters. Once the agents are at that level, they follow a random walk to the first open cabin. Maintaining the same cabin each night is not considered significant since the model only has single occupancy cabins. Each 12-hour cycle consists of 100 ticks, making a full day 200 ticks. The model is run for 30 days, the length of time of the Diamond Princess cruise in quarantine [19].

The movement is also based on the ship timeline. For the first ten days of the trip, when there is free movement around the ship, passengers and crew follow this daytime flocking, nighttime random walk procedure, only quarantining, i.e. remaining in their cabin, if they are symptomatic. For the final 20 days of the model, the passengers are quarantined in their rooms 24/7, while the crew members flock between decks and only quarantine if they are symptomatic. After 15 days, crew members and passengers receive personal protection equip-

Table 2.1
Agent infection timeline.

Movement Parameter	Description
vision	distance an agent can see and from which create a flock
max-velocity	fastest an agent can move
max-acceleration	fastest an agent can accelerate
cruise-distance	minimum distance to maintain from other agents
center-constant	urge to move to the center of the flock
velocity-constant	urge to align agent velocity with that of the flock
cruise-distance	distance to keep agent from flockmates
spacing-constant	urge to remain within *cruise-distance* from others
avoidance-constant	urge to avoid colliding with deck barriers
world-center-constant	urge to avoid the edges of the world
wander-constant	urge to move in a random way
vertical-spacing?	if agents seek to distance from flock in the vertical space

ment (PPE), which reduces the transmission rate by 65% [10].

2.3. Infection. In this model, we convert the traditional SEIR (Susceptible-Exposed-Infected-Recovered/Removed with separation of symptomatic and asymptomatic infectious classes) compartmental model into an agent-based model with infection. Each agent starts out with a status as a susceptible, with one passenger being symptomatic. When agents move about the ship, they also infect other agents. If an agent is within a 0.259 patch radius (a 3-foot sphere in model space) for more than 4 ticks (1 hour in model time) of a symptomatic or asymptomatic agent, they have a 20.8% chance of being infected. The radius was chosen to match the CDC recommended 3-foot radius and the hour-long contact was chosen for the length of time for close contacts [3]. The .208 infection rate was calculated in a previous model based on early reports of South Korean infections before June 2020 [5]. In NetLogo, a random floating-point number between 0 and 100.0 from a normal distribution is chosen whenever an agent is in range for the specified time. If that selected number is below 20.8, the agent will be infected.

Table 2.2
Agent infection timeline.

Day of Infection	**Ticks**	**Stage of Infection**
0-3	0-600	Exposed
4-5	601-1000	Asymptomatic/Symptomatic
6-10	1001-1800	Asymptomatic/Symptomatic
10-	1800-	Recovered

After infection, there is a 3 day exposure period. During this time, the agent is infected but not yet infectious. After these 3 days, the agent will be infectious and either asymptomatic or symptomatic. From day 4-5, the agent can move from asymptomatic to symptomatic. After this, from day 6-10, an agent will remain in their asymptomatic or symptomatic state. After day 10, an agent will enter the recovered class or reach a state of severe illness. If an agent has severe illness, they are removed from the model, indicating that they were evacuated from the ship. This process can be viewed in the infection flowchart can be shown in Figure 2.2.

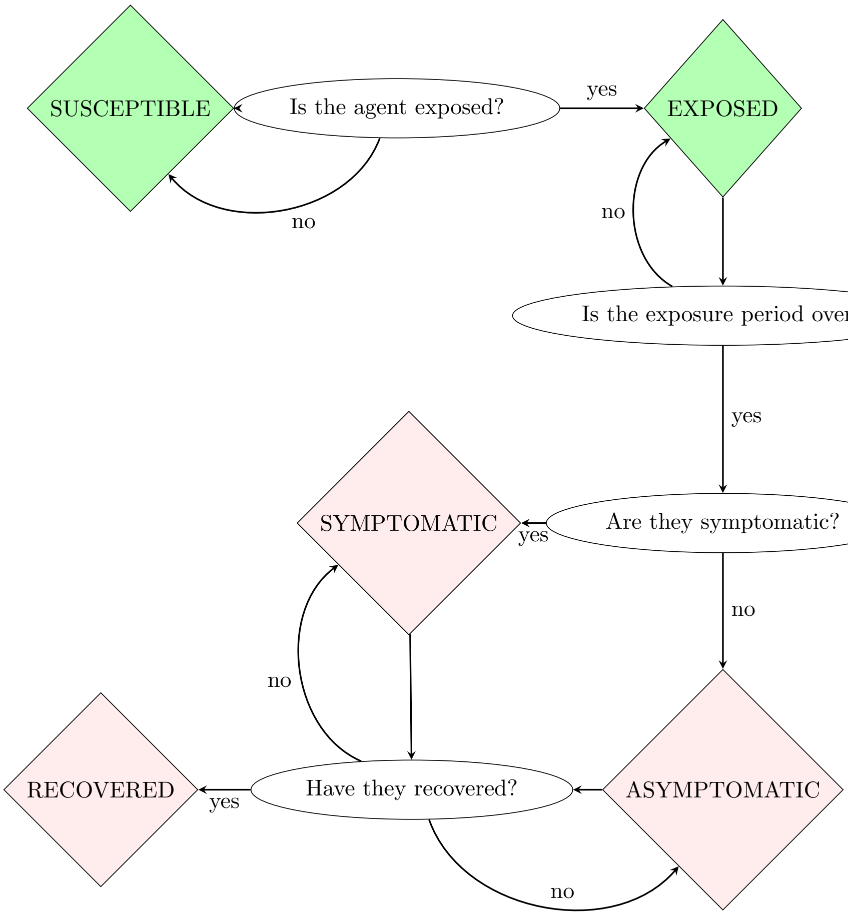


Figure 2.2. *Infection flowchart for a gents. A pink state indicates that the passenger is quarantining, green is roaming their decks. For crew members, they only quarantine when symptomatic.*

2.4. Parameters. Within the model, we use parameters to determine how infection occurs. The base parameter values can be found in Table 2.3. In NetLogo all parameters are assigned a probability multiplied by the base value. This means each of the parameters is varies stochastically in the simulation The parameter β is the transmission probability and was calculated using initial outbreak data from South Korea and New York City. The parameter λ is the rate at which exposed individuals become infectious, regardless of whether the agent becomes symptomatic or asymptomatic. The parameter σ is the percentage of these asymptomatic cases when exposed agents become infectious. The exposed agents become symptomatic infectious with a percentage of $100\% - \sigma$. The parameter α is the rate of an asymptomatic case developing symptoms. The recovery rate from symptomatic or asymptomatic infection is ρ and μ is the rate of removal for severe illness, where the agent is removed from the ship. Since the model runs for only 30 days, we can assume zero birth and natural death for such a brief time period.

Table 2.3

Agent infection parameter base values. Each variable is chosen as a random float from a normal distribution for each agent.

Notation	Description	Value	Reference
β	Transmission probability	0.208	[5]
λ	Rate of Entering Infectious Period	1/3 days^{-1}	[16]
α	Rate of Developing Symptoms	0.67 days^{-1}	[16, 27]
σ	Percent of Asymptomatic Cases	30%	[8]
ρ	Recovery Rate	1/10 days^{-1}	[5]
μ	Rate of Severe Illness Removal	1/10 days^{-1}	[22]

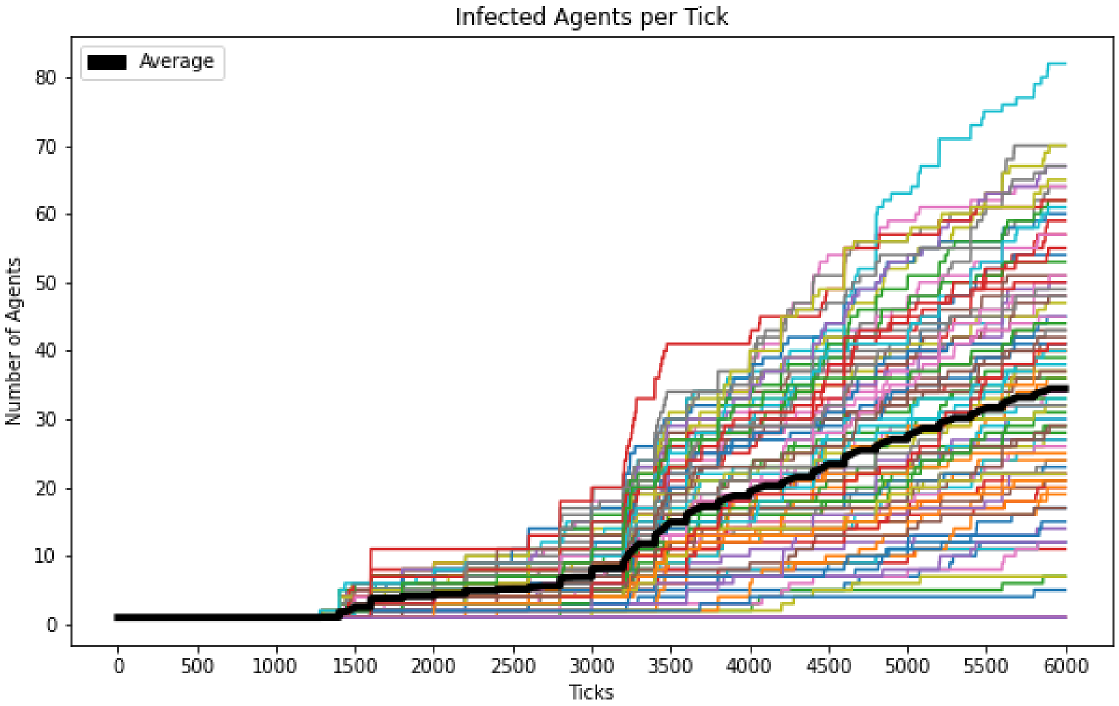


Figure 3.1. *Number of infected agents at each time point over 100 simulation runs. The black line is the average number of infected agents over all runs.*

3. Results. A population model described by a system of differential equations is a deterministic model, meaning that each time the model is run the same result is achieved. Agent-based models are nondeterministic models, meaning the final outcome is dependent on each moment in the model, and we will not obtain the same result with every run. We ran the simulation 100 times and plot the number of total infections in Figure 3.1.

We can see the best-case scenario, where the outbreak dies out completely, as well as the worst-case scenario at the top where nearly two-thirds of the agents in the system are infected. In the best-case scenario, as well as the simulations with less drastic outbreak sizes, the infected agents recover before the quarantine occurs. This illustrates that catching infections as early as possible is crucial in stopping a serious outbreak from occurring.

3.1. Calculating Reproductive Number. $\mathcal{R}_0$ is the basic reproductive number and shows the number of new cases that can be generated by each infected individual. If this number is greater than 1, an outbreak is expected to grow.

In this paper, we calculate the $\mathcal{R}_0$ using the methodology from Vynnycky and White [26]. In this, the $\mathcal{R}_0$ is related to the growth rate, Λ, of an epidemic. In February 2020, at the time of the ill-fated Diamond Princess cruise, none of the crew members or passengers had immunity to COVID-19. In following equation, it can be assumed that the exposed period and infectious period follow an exponential distribution, where D is average duration of the exposed period, and D' is the average duration of the infectious period.

$$\mathcal{R}_0 = (1 + \Lambda D)(1 + \Lambda D') \tag{3.1}$$

We can see how this formula and appropriate values for D and D' are derived by following the SEIR example from Ma [18]. For simplification, we combine the symptomatic and asymptomatic cases as well as the crew and passenger categories. We use this simplification since we are calculating D and D' from Figure 3.1 where these category separations are collapsed into just a single infected class.

$$\begin{aligned} \frac{dS}{dt} &= -\beta c S I \\ \frac{dE}{dt} &= \beta c S I - \lambda E \\ \frac{dI}{dt} &= \lambda E - (\rho + \mu) I \\ \frac{dR}{dt} &= \rho I, \end{aligned} \tag{3.2}$$

where β is the transmission probability, c is the contact rate, λ is the rate of becoming infectious after being exposed, ρ is the recovery rate, and μ is the rate of removal from the ship due to severe illness.

We assume that the mean exposure period and infectious period is exponential. The Jacobian evaluated at the disease free equilibrium is

$$J = \begin{pmatrix} -\lambda & \beta c \\ \lambda & -(\mu + \rho) \end{pmatrix}, \tag{3.3}$$

with eigenvalues $\Lambda_{\pm}$

$$\Lambda_{\pm} = \frac{-(\lambda + \mu + \rho) \pm \sqrt{(\lambda - \mu - \rho)^2 + 4\lambda\beta c}}{2}. \tag{3.4}$$

Using the Next Generation method [12] we divide the Jacobian into a matrix with the first infections, F, and another matrix containing all other transitions, V, with $J = F - V$, where

$$F = \begin{pmatrix} 0 & \beta c \\ 0 & 0 \end{pmatrix} \quad \text{and} \quad V = \begin{pmatrix} \lambda & 0 \\ -\lambda & \mu + \rho \end{pmatrix} \tag{3.5}$$

The maximum eigenvalue of $F \cdot V^{-1}$ is the basic reproduction number $\mathcal{R}_0 = \frac{\beta c}{\mu + \rho}$. Next, following Ma [18], we rewrite the basic reproduction number in terms of $\Lambda_+ = \Lambda$

$$\begin{aligned} \mathcal{R}_0 &= \frac{(\lambda + \Lambda)(\mu + \rho + \Lambda)}{\lambda(\mu + \rho)} \\ &= (1 + \Lambda/\lambda)(1 + \Lambda/(\mu + \rho)) = (1 + \Lambda D)(1 + \Lambda D'), \end{aligned} \tag{3.6}$$

with $D = 1/\lambda$ and $D' = 1/(\mu + \rho)$.

Following Vynnycky and White [26], we obtain the growth rate, Λ, graphically. We know that in theory, the number of infectious individuals increases at a constant rate in the initial stages of an epidemic. This can be described as

$$I(t) \approx I(0)e^{\Lambda t} \tag{3.7}$$

where I(0) is the number of infectious individuals at time 0. When we take the natural log of both sides, we obtain the following:

$$\ln(I(t)) = \ln(I(0)) + \Lambda t \tag{3.8}$$

When we plot this line against time, we obtain a straight line with a slope equal to Λ [26]. For our system, we split the plot of the natural log of I(t) into two parts. For Λ_1, the growth rate is calculated from day 2-15 (from the start of a day of interaction until the length of the average exposure period + the day of quarantine). Λ_2 is calculated from day 15 to day 30, when everyone was removed from the ship. These two lines can be seen in Figure 3.2. We obtain these lines using the numpy polyfit function in Python, which fits a polynomial of degree one (linear regression) by minimizing the squared error (least squares).

We must then multiply the Λ value by 200, since each day is made up of 200 ticks of model time. We use the specified exposure time D of 3 days for $1/\lambda$, and infectious time D' of 20 for $1/(\mu + \rho)$.

We then calculate the basic reproduction number $\mathcal{R}_0$ for each Λ. For day 2-15, with a $\Lambda_1 = .000487$, the following is obtained:

$$\mathcal{R}_0 = (1 + .000487 * 200 * 6)(1 + .000487 * 200 * 20) = 4.6727 \tag{3.9}$$

Quarantine is imposed on Day 10, but we can see looking at Figure 3.2 that there is a delay before the effect of quarantine appears on the reproduction number. At this point, since a

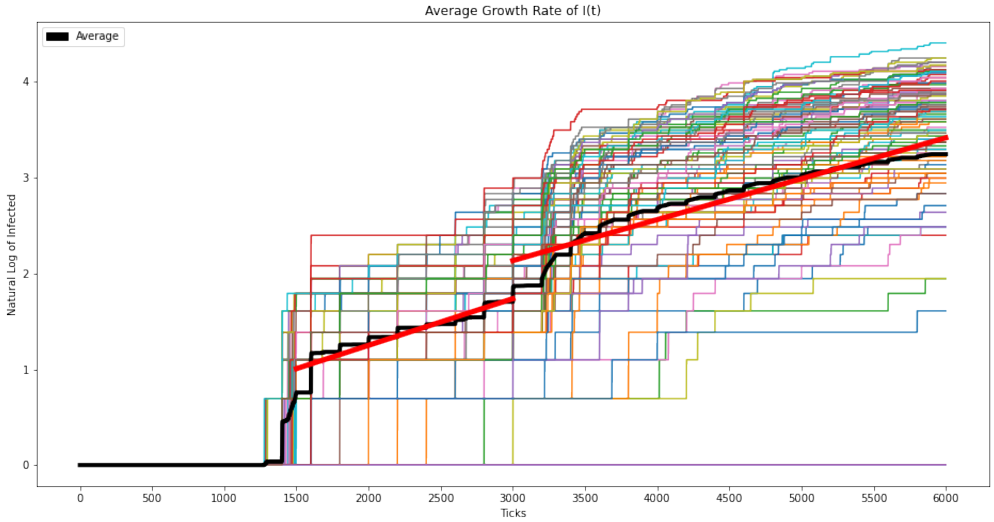


Figure 3.2. *Average Growth Rate of Infected. The slope of the line, λ, gives us the growth rate of the epidemic. $\lambda_1 = 0.000487$ and is the growth rate from Day 2-15. $\lambda_2 = 0.000427$ and is the growth rate from Day 15-30. 200 ticks is equivalent to one 24 hour cycle in model time.*

change has been imposed to attempt to control the spread of the disease, this is now called the effective reproduction number, signified by $\mathcal{R}_e$. For days 15-30, with a $\Lambda_2.000427$, the following reproductive number is obtained:

$$\mathcal{R}_e = (1 + .000427 * 200 * 6)(1 + .000427 * 200 * 20) = 4.0994 \tag{3.10}$$

Each of these reproductive numbers are greater than 1, implying that both at the beginning of and near the end of quarantine, the outbreak will grow. The slightly lower $\mathcal{R}_e$ implies that quarantine works to decrease transmission, but not enough to fully stop an outbreak.

3.2. Average Daily Contact Numbers. In order to estimate the number of contacts each agent has, we collected the average number of daily contacts per agent per day over twenty model runs. The mean of these averages was 39.57 contacts, as seen in the histogram in Figure 3.3.

3.3. Transmission Probability per Contact. Agent-based models allow us to understand how the actions of individuals determine the outcome of the system. We ran the model 20 times to collect the average number of contacts each individual comes across, resulting in 39.544 contacts per day. This number shows us the general interactions that agents have. However, when studying infection dynamics, we specifically want to understand how infected individuals interact with others. The probability of transmission shows us the number of hidden infected contacts each susceptible individual comes across. With this calculated $\mathcal{R}_0$

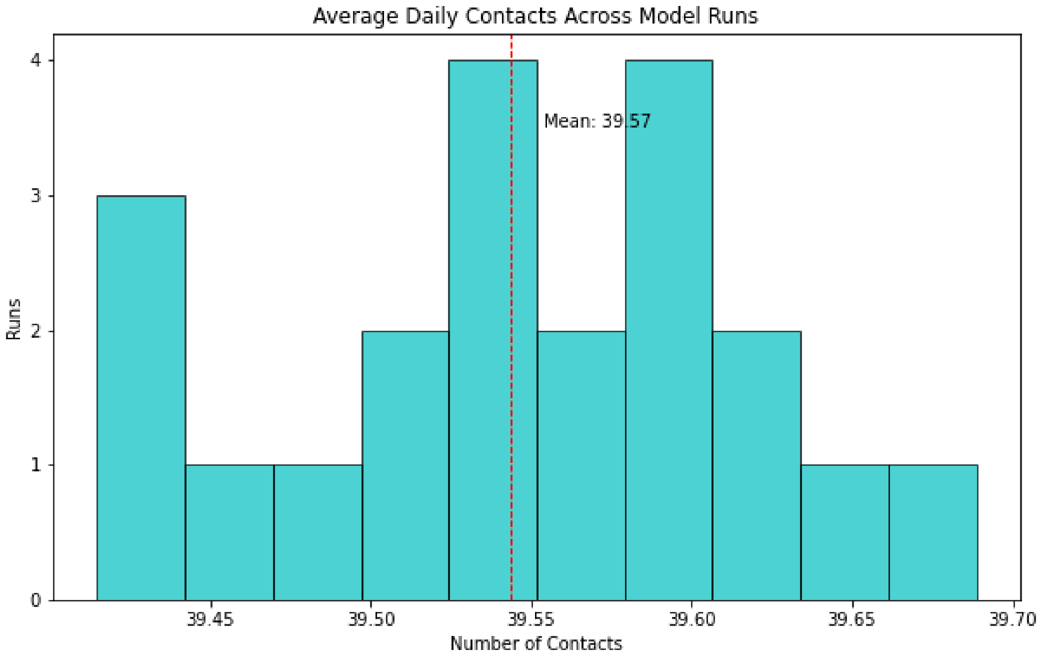


Figure 3.3. *The histogram of average daily contacts per agent over 20 model runs. The overall mean is 39.57 contacts per day.*

and $\mathcal{R}_e$, we can calculate the effective contact number in the method described by Hunter et. al [13]. The transmission probability per contact p can be found with

$$p = \frac{\mathcal{R}_0}{cD'} \tag{3.11}$$

where c is the contact rate and D' is the duration of the infectious period.

For the first 15 days of the cruise, we find the transmission probability per contact with $\mathcal{R}_0$

$$p = \frac{4.6727}{(39.544)(20)} = 0.590\%, \tag{3.12}$$

with an effective transmission rate of pc =23.3% per day.

For the second half of the cruise, the number of contacts has been reduced with quarantine imposed. Shipboard quarantine does not equal complete isolation as only symptomatic crew and all passengers are confined to quarters. Asymptomatic crew members are still servicing passenger cabins and infected passengers still interact with service crew. We can find the reduced daily transmission rate, pc, with $\mathcal{R}_e$ by

$$pc = \frac{4.0994}{20} = 20.5\%. \tag{3.13}$$

This decreased transmission rate demonstrates that the quarantine does slightly diminish transmission, but not a significant enough amount to stop an outbreak from occurring.

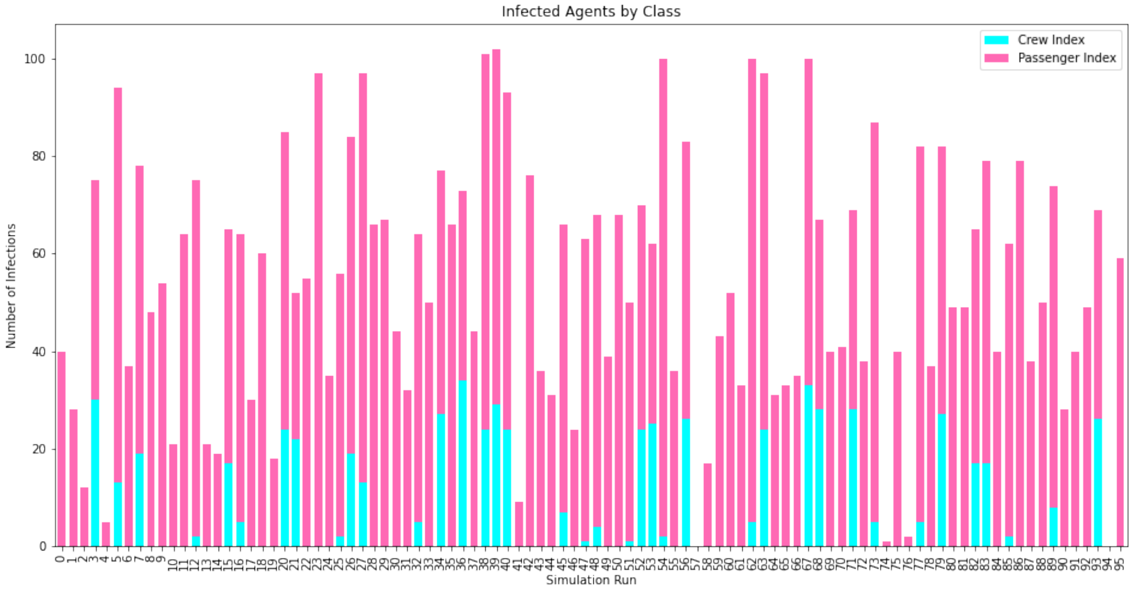
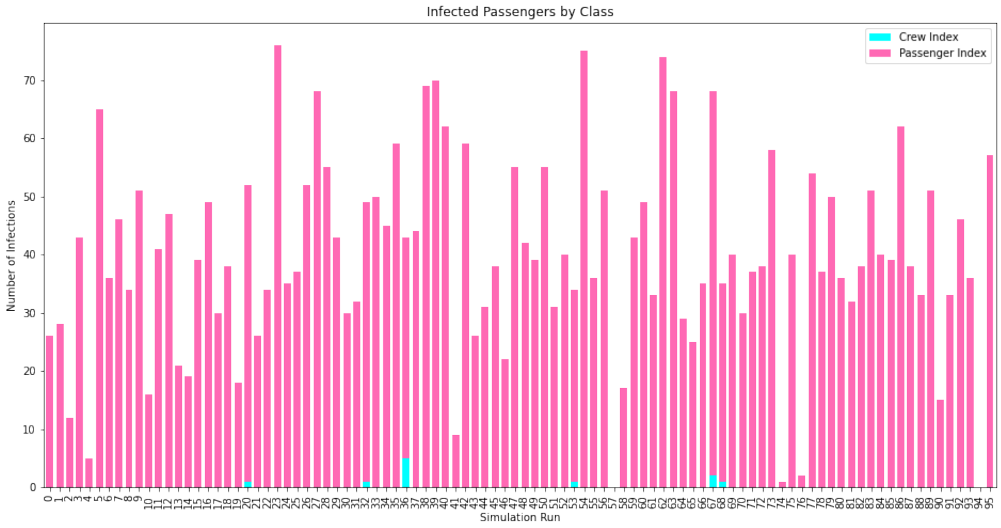


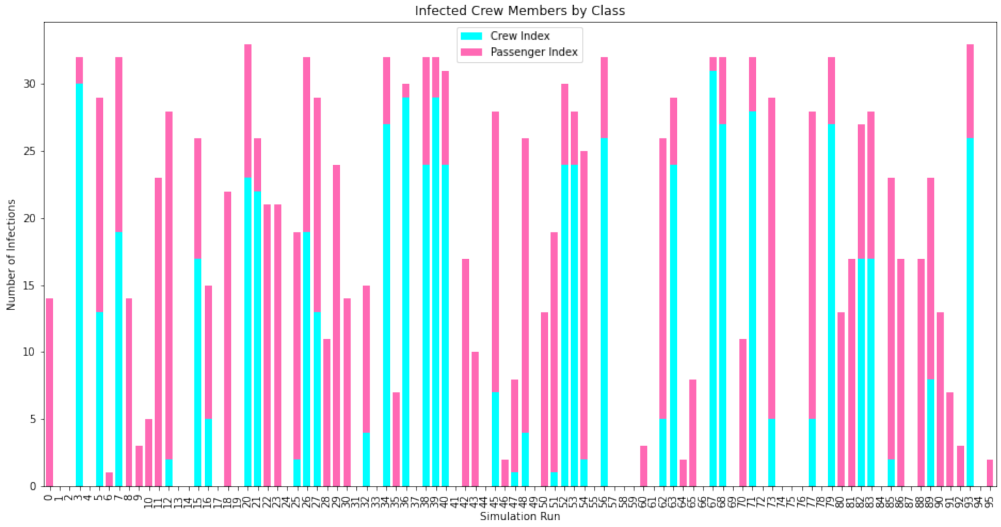
Figure 3.4. *Index case class type for each infected agent by model run. The pink portion of the bar shows the number of exposed, infected, or recovered agents infected by a passenger, while the cyan portion shows that the number of agent infected by a crew member. The y-axis gives the total number of infections for each run. The x-axis designates the run number.*

3.4. Index Case Analysis. With the agent-based model we can capture the characteristics of individuals and infection. At the end of each of the 100 simulation runs, we examine the traits of the agents that are in the exposed, asymptomatic, symptomatic, and recovered class. In Figure 3.4, we can track which class type, *i.e.* passengers or crew members, infected each agent. This individual that infects the other is the index case. The cyan portion of the bar indicates the number of the infections that were spread by infected crew members. The pink portion of the bar indicates the number of the infections that were spread by infected crew members. The pink and cyan portions together give the total number of infections from that simulation run. Figure 3.4, indicates that the majority of cases are caused by passengers infecting others. However, the most drastic outbreaks all have a sizable number of cases caused by crew member infections. On the ship, the crew to passenger ratio is 5:3, indicating that the higher number of infected passengers is a function of that ratio. We thus analyze the index cases for each class type, to see what drives infection regardless of the size of the group.

We can then analyze the index case characteristics by class. In Figure 3.5.a we see that the majority of passenger infection is driven by other passengers. In Figure 3.5.b we see that the majority of crew infection is driven by other crew members. However, in all scenarios at least one crew member was infected by a passenger. The outbreak originates in the passenger class, so crew members must always be infected by passengers initially. However, once that transmission has occurred, the majority of infection occurs within the class.



(a) Passenger Infections



(b) Crew Member Infections

Figure 3.5. *Index case class type for each infected agent by simulation run. Figure (a) shows who is infecting the passengers and figure (b) shows who is infecting the crew members. The pink portion of the bar shows the number of exposed, infected, or recovered agents infected by a passenger, while the cyan portion shows that the number of agent infected by a crew member.*

4. Conclusion.

This model provides us a way to examine outcomes of individuals on-board cruise ships when COVID-19 outbreaks occur. With this agent-based model, we can create a system that models the real world with daytime passenger and crew movement about the ship with nightly returns to sleeping quarters. Unlike a SEIR model, the model is not deterministic. The stochastic effects are illustrated by the different results in contact numbers, infections, and index cases for each simulation run. However, over the course of 100 simulation runs, we can to derive a mean reproduction number, effective reproductive number, a mean contact number, and a transmission probability per contact, and to determine how the infections are spread by index case studies. As shown with our calculated reproduction number of 4.6727 and effective reproductive number of 4.0994 and by the simulation results by each run, an outbreak will occur the majority of the time.

We can also compare the results of our model to the outcomes of the real Diamond Princess. In the real ship, 19.2% of the ship ends up being infected before the quarantine ends. Previous SEIR models show 21% of those on-board being infected [5]. In this agent-based simulation, we find that 29% of the ship inhabitants become infected.

Additional model work may capture complete contact tracing including time of infection and infection spread by individual, but current analysis shows that agents of the same class are the main drivers of infection among other agents. Infected passengers end up infecting the highest number of people, because of the size of that class. Further studies should include the analysis of who is driving infection at each time step of the model, to understand who the primary infectors are before and after quarantine.

Future work could also involve using different motion patterns, such as random walks to see how that changes the dynamics and to analyze a more abstract version of human movement. However, the movement would still need to capture the passengers grouping together for meals and activities, so a purely random walk would not suffice. This model also examines a phenomenon from early on in the course of the pandemic. Recreating current cruise ships with the transmission rates of the new COVID-19 variants could provide insight as to how future outbreaks may occur.

Additional work could be done by comparing the reproductive numbers derived by the ODE model, which we use to derive the agent-based model $\mathcal{R}_0$. This could allow us what differences arise from the inclusion of the spatial element in the agent-based model.

It is clear that a quarantine on-board cruise ships is not effective for SARS-COV-2. Even with a starting point of just one person, the virus will spread rapidly. The movement of individuals and groups will cause an outbreak to occur. It is crucial for us to reevaluate our travel methods and movement patterns, especially on a global scale, in order to bring about an end to to this pandemic.

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6. Supplemental Information.

The code used to create this model and subsequent analyses can be found at: https://github.com/nahomiiiie/ABM_DiamondPrincess/settings

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