An Agent-Based SEIR-D Model of COVID-19: Effects of Risk Factors and Control Measures Relevant to Farmworker Communities

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***Abstract*— While farmworkers have been deemed essential in the COVID-19 pandemic, inadequate protections have further exacerbated existing vulnerabilities to illness in many agricultural communities. In light of the numerous outbreaks reported in farmworker housing facilities, it is important to understand how the presence of relevant risk factors and the degree of control measure implementation may influence the progression of COVID-19. An agent-based model (ABM) with a susceptible-exposed-infected-recovered-deceased (SEIR-D) framework was developed using NetLogo. BehaviorSpace was used to determine the appropriate baseline transmission probability and to test the impact of the following parameters on epidemiological dynamics: barriers to healthcare, infected detection (testing), mobility (social distancing), and high-touch areas (overcrowded housing). The baseline probability of transmission was determined to be 0.11 for the current model. Barriers to healthcare were found to be moderately positively correlated with total mortality (R=0.6339) and the basic reproductive number, R_0 (R=0.6254). Infected detection was moderately negatively correlated with total mortality (R=-0.6288) and R_0 (R=-0.606). Mobility was weakly positively correlated with total mortality (R=0.3066) and R_0 (R=0.2705), although the correlation with R_0 was not statistically significant. The presence of high-touch areas was strongly positively correlated with total mortality (r=0.8725) and R_0 (r=0.8397). The values of the studied parameters appear to be associated with the resulting R_0 and mortality rate. Preliminary indications reveal the importance of future inquiry into the effects of such risk factors and control measures for farmworkers and others. In the meantime, appropriate protections should be enacted to protect the health of farmworker communities during the COVID-19 pandemic.**

Keywords—COVID-19, SARS-CoV-2, agent-based model, SIR, SEIR, SEIRD, farmworkers

I. INTRODUCTION

The novel coronavirus SARS-CoV-2 is the causative agent for human COVID-19. Similar to other respiratory coronaviruses, SARS-CoV-2 is transmitted mainly through respiratory droplets. The incubation period — the time between exposure to the virus and onset of symptoms — is thought to extend to 14 days, with a median of approximately 4-5 days (Lauer et al., 2020). According to the Centers for Disease Control and Prevention (CDC), a wide range of symptoms has been reported among those with COVID-19. Some of the most commonly reported symptoms include fever or chills, cough, shortness of breath, fatigue, muscle aches, headache, new loss of smell or taste, sore throat, congestion or runny nose, nausea or vomiting, and diarrhea. Within 5-6 days of symptoms onset, viral load — a measure of the amount of virus in the bloodstream — reaches its peak (Pan et al., 2020). Severe COVID-19 cases progress to acute respiratory distress syndrome (ARDS) around 8-9 days after symptom onset (Wang et al., 2020). ARDS is characterized by difficulty breathing and low blood oxygen levels (Zhang et al., 2020), and it can lead directly to respiratory failure. Respiratory failure is the cause of death in the majority of fatal cases (70%), with cytokine storm and sepsis leading to multi-organ damage/failure being responsible for most of the remaining cases (28%) (Zhang et al., 2020).

While many infected with SARS-CoV-2 never develop symptoms, it is interesting that among those who develop symptoms, disease progression is swift. It seems like the key to ending the pandemic is through mass immunity, ideally through a vaccine. However, vaccine development can take many years. For now, public health measures controlling community behavior are the main preventive tool to combat the spread of COVID-19. While only strict social distancing has been indicated to have a significant impact on slowing the rate of infection, such strict measures are not always feasible – or even implemented when feasible (Holt, 2020).

In the era of COVID-19, it is important to recognize that COVID-19 is not “the great equalizer,” but rather a “magnifying glass” illuminating the larger pandemic of ethnic and racial disparities in health (Williams & Cooper, 2020). This is particularly true for farmworkers, who have been deemed essential workers in the COVID-19 pandemic. Despite the critical role farmworkers play in harvesting the national food supply, farmworkers are a vulnerable group systematically exploited the agribusiness industry. As such, it is unsurprising that inadequate measures have led to numerous COVID-19 outbreaks in farmworker communities across the country (National Center for Farmworker Health, 2020). In studying the situation of farmworkers in the COVID-19 pandemic, the goal is to generate more insight into the impact of social-structural factors on health outcomes – both in the context of COVID-19 and otherwise.

In the fight against COVID-19, widespread scientific collaboration is needed now more than ever to observe, analyze, interpret, and understand the consequences of COVID-19 and develop effective solutions (Moradian et al., 2020). As such, this paper will integrate a variety of scientific disciplines including computer science, biology, and social sciences. A strong biological understanding of the virus will help explain the susceptibility of certain groups and the dynamics of viral transmission. Awareness of relevant societal factors will help explain the importance of the parameters chosen for computational study, and the results of the model simulation will hopefully generate more insight into the progression of COVID-19 and the effects of relevant risk factors and control measures for farmworker communities.

II. BIOLOGICAL MECHANISMS OF TRANSMISSION AND VIRAL PATHOGENESIS

A. Transmission

SARS-CoV-2 has been shown to have a high replication rate, particularly in the human oral pharynx and upper airway where ACE2 receptors are located (Wolfel et al., 2020). The rapid replication of the virus in the upper respiratory tract likely increases its ability to transfer from person to person. This allows for shedding of the virus with even with normal speaking. The ability of the virus to replicate and shed in completely asymptomatic individuals and in pre-symptomatic individuals further enhances the ability of the virus to transmit between individuals (Fauci et al., 2020). Environmental conditions have been shown to affect the stability of the virus in nasal mucus and sputum, with greater stability in low-temperature and low-humidity conditions (Matson et al., 2020). Because of the surface stability of SARS-CoV-2, fomite transmission may also play a role in the spread of the disease.

B. Pathology and Respiratory Implications

SARS-CoV-2 infiltrates host cells by exploiting the link with membrane-bound angiotensin-converting enzyme II (ACE2) protein. Coronavirus spike (S) glycoprotein binds to the ACE2, allowing for the virus to enter endothelial cells and macrophages in the lungs. The high infectivity of SARS-CoV-2 is partially explained by new mutations in the ACE2 receptor binding domain and an acquired furin cleavage site in the S-spike protein (Liu et al., 2020). SARS-CoV-2 uses trans-membrane serine protease 2 (TMPRSS2) to prime the S protein for binding to ACE2, significantly enhancing viral infectivity (Hoffmann et al., 2020). Given that TMPRSS2 is androgen-regulated, this process may be connected to a higher prevalence of infection and severe illness in males (Jin et al., 2020). In addition, ACE2 is located on the X chromosome, so there may be alleles that confer resistance to COVID-19. Both of these factors may help explain the lower death rate in females (1.7%) compared to males (2.8%) when other differences in risk factor profiles were adjusted (Tay et al., 2020; Epidemiology Working Group for NCIP Epidemic Response, 2020).

After viral entry into host cells, the downregulation of membrane ACE2 results in increased levels of angiotensin II in lung tissues and increased stimulation of the Type 1 Angiotensin II Receptor (ATR1), which controls angiotensin II-induced blood vessel permeability and mediates severe acute lung injury. This mechanism may explain why SARS-CoV-2 primarily causes pneumonia with vascular injury (Lega et al., 2020). This attack of SARS-CoV-2 on the lungs is likely even more damaging among those with pre-existing chronic respiratory conditions.

Individuals with Chronic Obstructive Pulmonary Disease (COPD), including chronic bronchitis, have been shown to have an increased risk of severe illness from COVID-19 (CDC, 2020). Increased expression of ACE2 and TMPRSS2 has been demonstrated in the bronchial tissue of COPD patients (Higham & Singh, 2020; Sharif-Askari et al., 2020). High expression of ACE2 in bronchial epithelial cells has been shown to increase the expression of genes involved in viral replication, potentially enhancing the ability of SARS-CoV-2 to enter host cells (Li et al., 2020). As a result, upregulated ACE2 may enhance pathogenesis of COVID-19 in COPD patients. Given the role of TMPRSS2 in priming the SARS-CoV-2 S protein for binding to ACE2, upregulated TMPRSS2 may have a similar function.

Individuals with asthma may also have an increased risk of severe illness. It has been demonstrated that IL-13, a cytokine associated with type 2 inflammation, increases *TMPRSS2* expression in bronchial epithelial cells from patients with asthma and allergic rhinitis (Kimura et al., 2020). The increased expression of TMPRSS2 could increase the susceptibility of patients with asthma and allergic rhinitis to COVID-19.

C. Immunology and Multi-Organ Implications

SARS-CoV-2 infection and its destruction of lung cells trigger a local immune response, recruiting macrophages and monocytes that release cytokines and instruct adaptive B and T cell immune responses (Tay et al., 2020). A dysfunctional immune response in some patients triggers a cytokine storm that mediates widespread lung inflammation which, unrestrained, can itself cause damage in the lung by excessive secretion of proteases — enzymes which break down proteins and peptides — on top of the direct damage caused by the virus itself (Tay et al., 2020). Direct virus damage and dysfunctional host immune response lead to diffuse alveolar damage that limits gas exchange efficiency in the lungs. This causes difficulty breathing, low blood oxygen levels, and makes the patient more vulnerable to secondary infections (Xu et al., 2020).

The increase of neutrophils and depletion of lymphocytes in circulating blood is characteristic of persistent immune activation and typically associated with the worsening of the disease. The increase of neutrophils is associated with tissue damage and cytokine storm, which may worsen the shortage of virus-specific lymphocytes (Lega et al., 2020). In addition, the lymphocytes from patients with severe disease often present an exhausted phenotype, indicating functional impairment (Zheng et al., 2020). Cytokine-associated signaling pathways enabled through cytokine storm may promote the activation of lymphocyte apoptosis in sepsis and subsequently enable multi-organ damage (Luan et al., 2015).

The likelihood of developing a dysfunctional immune response increases with age and is higher for those with some underlying medical conditions such as diabetes and obesity. Given that diabetes mellitus is a low-grade chronic inflammatory state, COVID-19 patients with diabetes are at a higher risk of developing an excessive uncontrolled inflammatory response (Sandooja et al., 2020). Even short-term hyperglycemia observed in diabetes can briefly suppress the innate immune response, potentially having implications for critically ill patients (Jafar, Edriss, & Nugent, 2016). Dysfunctional hypertrophic adipocytes in obesity produce an excessive amount of cytokines that lead to increased recruitment of macrophages, in turn enabling these cells to produce high amounts of proinflammatory molecules such as IL-1β, IL-6, IL-8, TNFα, and monocyte chemoattractant protein-1 (MCP-1)

(Guilherme et al., 2008; Maurizi et al., 2018; Lumeng et al., 2007). This can lead to a state of chronic inflammation that impairs innate immunity, creating a conducive environment for the development of a macrophage activation syndrome (MAS)-mediated hyperinflammatory response in severe COVID-19 cases (Giamarellos-Bourboulis et al., 2020).

III. THE CASE OF FARMWORKER COMMUNITIES

A. *Farmworkers and Power Dynamics*

Farmworkers are considered to be a vulnerable population, consisting of a diverse group of individuals who, due to socioeconomic inequities, are inevitably at a greater risk of poor physical, psychological, and social health. In the context of farmworker communities, health disparities are inherently avoidable, resulting from unjust power dynamics that deprive individuals of basic human rights: the right to work in just and favorable conditions, the right to social protection and an adequate standard of living, the right to the highest attainable standards of physical and mental well-being, and the right to equal protection against discrimination, among others (United Nations). The vulnerability of farmworker communities is rooted in a history of exploitation by the agribusiness industry, enabled by minimal legal protections for farmworkers under United States law, and further exacerbated by systemic social injustices such as xenophobic and racial discrimination. Still relevant today, Cesar Chávez argued this point in a letter to the alliance of California grape growers in 1969:

> The color of our skins, the languages of our cultural and native origins, the lack of formal education, the exclusion from the democratic process, the numbers of our slain in recent wars—all these burdens generation after generation have sought to demoralize us, to break our human spirit. But God knows we are not beasts of burden, we are not agricultural implements or rented slaves, we are men. And mark this well . . . we are men locked in a death struggle against man's inhumanity to man in the industry that you represent. . . . We hate the agribusiness system that seeks to keep us enslaved and we shall overcome and change it . . . by a determined nonviolent struggle carried on by those masses of farmworkers who intend to be free and human. (Chavez, 1969).

The vulnerability of farmworkers contributes to barriers to effective healthcare. Poorer living conditions can have implications for physical health, leading to health disparities among farmworker communities. Such health disparities could have implications for the progression of disease among those infected with COVID-19.

B. *Biological Connections and Health Disparities*

As previously mentioned, sex, age, and underlying medical conditions have all been indicated to play a role in the development of severe disease and death from COVID-19. Age-related concerns may not be as much of an issue given that farmworkers are relatively young: farmworkers have an average age of 38, and only about 14% of workers are over the age 55 according to the National Agricultural Workers Survey (Hernandez & Gabbard, 2018). However, given that males were determined to comprise approximately 68% of the hired crop labor force, the higher death rate among males may be important to note for farmworker communities (Hernandez & Gabbard, 2018). Still, it is perhaps most important to explore the relevant underlying medical conditions to understand how health disparities may impact the situation of COVID-19 among farmworkers.

Due to the variety of respiratory hazards in farming ranging from chemical pesticides to organic dust, farmworkers are known to have high morbidity and mortality from certain respiratory illnesses (Linaker & Smedley, 2002). Specifically, crop and livestock farmworkers have been found to have significantly elevated mortality for a number of respiratory conditions including asthma, bronchitis, tuberculosis, pneumonia, and influenza (CDC, 2007). A potentially disproportionate prevalence of type 2 diabetes among farmworkers, a known risk factor for severe illness from COVID-19, is also important to note. Nearly 83% of all farmworkers are Hispanic, and Hispanics have a 66% greater risk of developing type 2 diabetes compared to non-Hispanic whites (Hernandez & Gabbard, 2018; Fortmann et al., 2019). This is due to poor socioeconomic conditions, which lead to significantly higher rates of reported food insecurity – where access to nutritious foods is limited – among migrant and seasonal farmworkers compared to the general population (Kiehne & Mendoza, 2015).

It is critical to recognize that the health disparities among farmworkers are not rooted in genetic differences, but rather social-structural conditions. However, such conditions lead to very real biological consequences that can put individuals at a higher risk of developing severe disease and dying from COVID-19. Exposure to respiratory hazards and inadequate protections against such hazards drive disparities in respiratory health. Many farmworker communities are located in rural areas considered food deserts, where access to nutritious foods is limited. Lower income from systematic exploitation by the agribusiness industry, physical isolation in employer housing, and inadequate transportation make it such that many farmworkers cannot afford nutritious foods even when available. Importantly, the risk for type 2 diabetes is twice as high for those with food insecurity (Hill et al., 2013). In light of this, it is critical to examine the social-structural factors affecting farmworker communities in order to better understand how farmworkers are affected by the COVID-19 pandemic.

C. *Key Social-Structural Factors*

Given the respiratory droplet route of transmission, close contact is a major risk factor for exposure to SARS-CoV-2 and contraction of the disease. However, avoiding close contact may be especially difficult in farmworker communities given the nature of agricultural work. This is especially true for those who rely on shared housing and transportation. The National Agricultural Workers Survey found that an estimated 16% of workers live in employer-provided housing, and 33% of farmworkers reported living in "crowded" dwellings with greater than one person per room. Of those commuting to work, 33% of workers did not provide their own transportation — 13% rode with others, 15% rode with a "raitero" (a person who charges a fee for providing a ride to work), and roughly 6% rode on a labor bus, truck, or van. Shared transportation, like shared housing, may also increase the risk of exposure to COVID-19.

Additionally, major associations of crop producers have issued relatively weak guidance for controlling the spread of COVID-19. For example, Western Growers, the leading association of fruit and vegetable producers in California and Arizona, stated that personnel with potential exposure to SARS-CoV-2 may continue to work as long as the contact remains asymptomatic (Western Growers, 2020). For workers living in employer-provided housing, Western Growers recommended that workers testing positive for COVID-19 be placed in an isolated dwelling to the extent feasible, but this neither guarantees compliance nor the effectiveness of such measures. For those in employer-provided housing, proper sanitation is often a challenge, and social distancing is difficult to properly implement.

In addition to overcrowding, insufficient sanitation, and inadequate implementation of control measures, sufficient testing of workers is another challenge. No comprehensive, systematic testing is currently being conducted for farmworkers, making it difficult to track contacts (National Center for Farmworker Health, 2020). Due to the fact that farmworkers are often socially vulnerable, many farmworkers also fear testing for COVID-19 because a positive test may result in a permanent job loss.

It is also important to recognize certain barriers to healthcare commonly faced by farmworkers, as well as concerns regarding healthcare quality. Agricultural communities tend to be located in more rural areas, where residents on average must travel about twice as far to the nearest hospital (Lam, Broderick, & Toor, 2018). For those without their own means of transportation, seeking proper care may be delayed until a person has become critically ill. Delaying treatment could have significant effects on the health outcomes of such individuals. In addition, only 47% of farmworkers reported having health insurance according to the National Agricultural Workers Survey. Many farmworkers are also undocumented, with only 51% of all farmworkers having work authorization. Lack of health insurance and fear of legal challenges, combined with little to no paid sick leave, heavily disincentivizes farmworkers from seeking care. Even among those who do seek care, issues of healthcare quality emerge. For 77% of farmworkers, Spanish was reported to be the language in which they were most comfortable conversing. As such, the insufficient availability of interpreters in healthcare settings may pose a challenge to effective treatment. This is especially true for rural settings where resources are more limited.

Ultimately, it was determined that the risk factors of healthcare barriers and overcrowded housing, along with the control measures of testing and social distancing, were relevant measures to study the progression of COVID-19 in farmworker communities.

IV. METHODOLOGY

For a more detailed explanation of the methodology, see the appendix.

A. Equation-Based Models: SIR, SEIR, and SEIR-D

Typical epidemiological models take the form of Susceptible-Infected-Recovered (SIR), based on the Kermack and McKenrick model of differential equations. In the SIR model, The population is divided into three distinct compartments: susceptible (S) healthy individuals who are vulnerable to infection, infected (I) individuals who have the disease and can transmit it, and recovered (R) individuals who previously had the disease and are now assumed to be completely immune or otherwise removed from further spreading the disease (such as individuals who died from the disease).

A common extension of the SIR model is the SEIR model, which includes exposed (E) individuals who have been exposed to the disease-causing agent but are not yet infectious because the latent period of the virus has not concluded. The SEIR-D model explicitly separates deceased (D) individuals from recovered individuals to make it easier to study disease-related mortality. In addition to these, a multitude of other extensions and modifications to the traditional SIR model have been employed to more accurately model certain circumstances.

The basic reproductive number (R_0) is a fundamental calculation for SIR-type models, representing the average number of secondary infections produced by a single infectious person in a population where everyone is susceptible. R_0 is used to measure the potential of transmission of a communicable disease (Delamater et al., 2019). Equation (1) shows a typical calculation of R_0, where τ is the probability of transmission given contact between a susceptible and infected individual, $\bar{c}$ is the average rate of contact, and d is the duration of infectiousness (Jones, 2007). A value of R_0 greater than 1 indicates that an epidemic may occur, and a value of R_0 less than 1 indicates that the disease will decline and eventually die out.

$$R_0 = \tau \cdot \bar{c} \cdot d \tag{1}$$

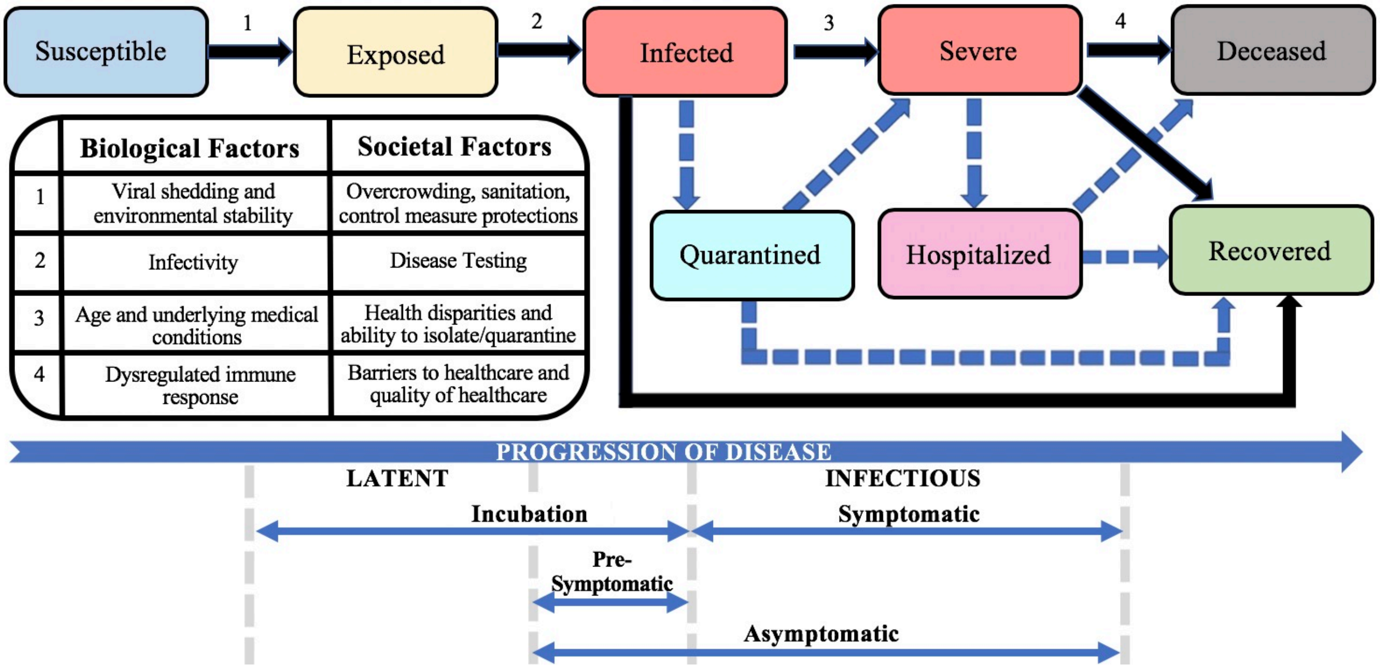
While compartmental models have proven to be quite useful in epidemiology, there are certain limitations. These models cannot account for variability in the population structure: all members of the community are assumed to be equally susceptible to disease. Notably, these models also cannot account for the individual behaviors and interactions of those in a population (Bonabeau, 2002). This is particularly important for calculating R_0 in that the contact rate $\bar{c}$ may be difficult to accurately model without accounting for individual interactions.

B. Agent-Based Modeling

Agent-based models (ABMs) include a population of agents, an environment, and a set of rules guiding the behavior of the agents. ABMs are useful for "what-if" analyses, allowing epidemiological researchers to assess the behavior of a system under various conditions and evaluate which control measures to adopt to effectively combat the spread of disease (Perez & Dragicevic, 2009). As a result, an agent-based model using an SEIR-D framework was developed to more accurately model the progression of COVID-19 (Fig. 1). While the probability of transmission was a parameter included in the model, the contact rate was able to be more accurately modeled by virtue of the ABM simulation.

C. NetLogo Model and Simulation

The agent-based model was developed using NetLogo, an open-source, multi-agent programmable modeling environment (Wilensky, 1999). The model is based on the epiDEM Basic and Covid-19 and Health System Capacity models (Yang &



	Biological Factors	Societal Factors
1	Viral shedding and environmental stability	Overcrowding, sanitation, control measure protections
2	Infectivity	Disease Testing
3	Age and underlying medical conditions	Health disparities and ability to isolate/quarantine
4	Dysregulated immune response	Barriers to healthcare and quality of healthcare

Fig. 1. Progression of Disease and Relevant Biological and Societal Factors. The agent-based model follows a Susceptible-Exposed-Infected-Recovered-Deceased framework. The black arrows represent the definitive progression of disease within the simulation. The blue dashed arrows represent options within the simulation to isolate infected humans in quarantine and to hospitalize humans with severe disease. The table of biological and societal factors lists relevant factors at each step of disease progression as follows: (1) A susceptible human in contact with an infected human or on a high-touch area has a probability of exposure. (2) After the latent period has concluded, an exposed human is infected. (3) If the human becomes symptomatic, the human has a probability of developing severe disease. (4) Asymptomatic humans and symptomatic humans without severe disease will always recover from infection. Humans with severe disease have a probability of dying or recovering.

Wilensky, 2011; Medeiros-Sousa, 2020). While the model can be used to generally simulate the epidemic dynamics of an infectious disease in a closed population, the simulation was specifically designed for COVID-19. The interface can be seen in the appendix (Fig. A).

The individual agents, humans, wander around the world in random motion, though the distance moved by the agents (mobility) is controlled by the user. Unless otherwise directed, humans move within the interaction zone (Fig. 2). A susceptible human who is any of the eight surrounding neighbors of an infected person or is in the same location as an infected human will have a chance of exposure determined by the following parameters set by the user: the transmission probability, the days to control measure implementation, the proportion of humans following measures, and the level of protection conferred by following such measures. If enabled, a susceptible human on a designated high-touch area has a chance of exposure based on whether disinfection is enabled and whether the human is following control measures (Appendix, Table A).

Humans exposed by a given probability become infectious after the latent period, which was set to an average of three days. Once a human is infectious, the human can infect other susceptible humans. If isolation is enabled, a percentage of infected humans determined by the user will be moved to quarantine (Fig. 2). A percentage of infected humans set by the user will also become symptomatic, considering that first symptoms may appear two days after the latent period has concluded. Symptomatic humans have a given probability of developing severe illness based on whether they pertain to the risk group, where the proportion of humans in the population in the risk group was initially set by the user (Appendix, Table A).

Humans with severe disease can be moved to the hospital if the number of humans in the hospital region is less than the hospital capacity, which is set by the user (Fig. 2). In the case that barriers to healthcare are not equal to 0 (no barriers), the complement of the value of barriers to healthcare is effectively a multiplicative factor that reduces the number of humans that are moved to the hospital.

Among infected humans, asymptomatic humans and symptomatic humans without severe disease will always recover after the recovery time, which is set by the user. Among humans with severe disease, the time to recovery is twice as long for humans who are not hospitalized and 1.5 times as long for humans who are hospitalized. The logic behind this was that humans with access to care could recover faster; however, these values could be modified for future use if needed. After the recovery time has passed, humans with severe disease have a given probability of recovery or death based on whether the human was hospitalized and whether the human belongs to the risk group (Appendix, Table A). Humans who have recovered are assumed to be immune.

D. *Verification/Validation*

Preliminary runs in NetLogo were conducted before developing the desired experiments. Firstly, the monitors reporting the number of susceptible, exposed, infected, recovered, and deceased humans were observed to ensure that the values were reasonable. The sum of the numbers reported by these monitors was checked to make sure it equaled the size of the initial population. A general trend of increasing R_0 and mortality was observed with increasing transmission probability as expected. When there were complete barriers to

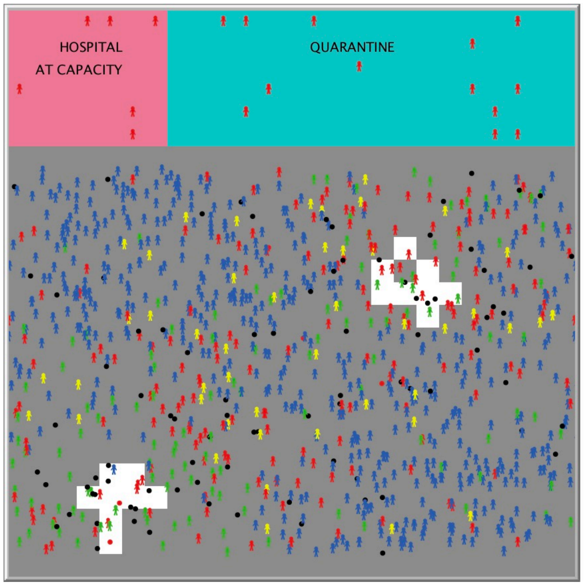


Fig. 2. The NetLogo World. The colors and shapes of the agents represent the health status of the humans (blue = susceptible, yellow = exposed, red = infected, green = recovered, and black dot = deceased). The world is divided into three environments: the interaction zone at the bottom, the hospital at the upper left, and quarantine at the upper right. The white patches within the interaction zone represent high-touch areas. When the number of humans in the hospital region equals the hospital capacity set by the user, the label "AT CAPACITY" appears.

healthcare, no humans were seen to enter the hospital area of the world. When humans were allowed to enter the hospital, the number of humans in the hospital area was observed to equal the value set by the hospital capacity when the "AT CAPACITY" label appeared. When the proportion of humans following measures was set to 1 and mobility was set to 0, no humans were observed to move even after the days to control measures passed. When the proportion of humans following measures was set to 0 and mobility was set to 0, all humans were still moving freely after the number of days to control measures passed. When the option to isolate infected humans was enabled but the infected detection was set to 0%, no humans entered the quarantine area of the world. The preliminary runs in NetLogo indicated that the model runs as specified and that the data output is reasonable based on the adjusted parameters. As such, it was determined that the model could be used to implement experiments on selected parameters.

E. Baseline Establishment and Implementation

BehaviorSpace was used to find a baseline value for transmission probability to be used in combination with other established baseline values (Appendix, Table B). After preliminary runs in NetLogo, an approximate range of 0.1 to 0.15 was found to result in the desired range of values for R_0 and the various mortality rates. A sweep for transmission probability using these values was performed in BehaviorSpace. In addition to R_0 and the mortality rates, the number of susceptible, infected, and recovered humans were recorded. SIR graphs were generated for each transmission rate to visualize the progression of the disease (Appendix, Fig. B - Fig. G). Based on the appearance of the graph, a mean final R_0 of 1.325, and a total mortality rate of 4.96% (which is within the range of current COVID-19 estimates), a transmission probability of 0.11 was selected to be the baseline value. Using the baseline values, sweeps were performed in BehaviorSpace for the following parameters: barriers to healthcare, infected detection (to mimic testing), mobility (to mimic social distancing), and high-touch areas (to mimic overcrowded housing), as these were determined to be particularly relevant parameters to farmworker communities.

V. RESULTS

The following measurements were recorded from the BehaviorSpace experiments (Table 1): R_0, total mortality (percentage of deaths out of the initial population), infected mortality (percentage of deaths out of cumulative infections), and symptomatic mortality (percentage of deaths out of cumulative symptomatic cases). The Pearson Correlation Coefficient was calculated for barriers to healthcare, infected detection, and mobility because these were continuous variables. Point-Biserial Correlation was used for high-touch areas given that the true/false nature of the variable made it dichotomous. Statistical significance was calculated for the values as well (Table 1). Barriers to healthcare were found to be moderately positively correlated with total mortality (R=0.6339) and R_0 (R=0.6254). Infected detection was moderately negatively correlated with total mortality (R=-0.6288) and R_0 (R=-0.606). Mobility was weakly positively correlated with total mortality (R=0.3066) and R_0 (R=0.2705), although the correlation with R_0 was not statistically significant.

TABLE I. EXPERIMENTAL RESULTS OF SWEEPS ON PARAMETER VALUES

Mean Value	**Barriers to Healthcare (0=no barriers to 1=complete barriers)** [a]	**Mobility (0=stationary to 1=unrestricted)** [b]	**Infected Detection (1, 5, 10, 20%)** [c]	**High-Touch Areas (True/False)** [d]
Total Mortality	**~5-25%** R=0.6339	**~1-6%** R=0.3066	**~0.5-19%** R=-0.6288	**~5-23%** r=0.8725
Infected Mortality	**~14-26%** R=0.6376	**~9-14%** R=0.2959	**~11-21%** R=-0.5505	**~14-24%** r=0.7923
Symptomatic Mortality	**~23-43%** R=0.6518	**~15-23%** R=0.2906	**~16-34%** R=-0.5898	**~23-40%** r=0.8019
R0	**~1.33-4.10** R=0.6254	**~0.88-1.42** R=0.2705*	**~0.74-5.28** R=-0.606	**~1.33-4.26** r=0.8397

[a] All values for barriers to healthcare were statistically significant at $p<0.01$. [b] The values for the correlation between mobility and the mortality measures were statistically significant at $p<0.05$. *The correlation between mobility and R0 was not statistically significant at $p<0.05$. [c] All values for infected detection were statistically significant at $p<0.01$. [d] All values for high-touch areas were statistically significant at $p<0.01$.

The presence of high-touch areas was strongly positively correlated with total mortality (r=0.8725) and R_0 (r=0.8397).

VI. DISCUSSION

The potential implications for the results of the experiments are numerous, but any interpretation must be mindful of the possibility that the pre-selected parameter values may have influenced the results. That said, it is interesting to note how mobility seemed to have a weaker correlation with mortality and R_0. This may be due to the fact that mobility was controlled by two different parameters: the number of days to control measures and the proportion of humans following measures. In the sweep, the days to control measures were set to 14 and the proportion following measures was set to 0.5. In other words, the humans in the simulation moved unrestricted until 14 days (ticks) had passed, at which point only half of the humans changed their movement behavior to reflect the value of mobility. When movement was restricted but still allowed for humans following the control measures (mobility = 0.5), an insignificant difference was observed in the resulting measures. When humans following control measures were instructed to remain stationary (mobility = 0), there did appear to be a noticeable difference in the resulting measures. This falls in line with previous studies, which have found that only strict social distancing has been indicated to have a significant impact on slowing the rate of infection (Holt, 2020). For farmworker communities, the inability to adequately social distance due to the nature of farm work may prove to be important in the spread of COVID-19.

With respect to high-touch areas, the strong correlation between high-touch areas and R_0/mortality makes sense given that humans have an increased probability of exposure to the virus in overcrowded areas. When opportunities to social distance are limited, individuals are more likely to come in close enough contact with infected individuals who may transmit the virus through respiratory droplets. With more infections, there is subsequently a greater probability of deaths in the population. For farmworkers, housing provided by employers also often lacks proper sanitation and clean water, which could further increase the spread of the virus in close quarters and lead to more deaths (Scherzer et al., 2010).

With respect to testing, the significant correlation with R_0 and mortality can be explained by the ability to effectively remove infected individuals from spaces where they would otherwise interact with susceptible people. If infected individuals are not identified and isolated, they can transmit the virus to others, some of whom may have underlying medical conditions that would increase their probability of severe illness and death. For farmworkers, the lack of systematic testing by employers and the lack of paid sick leave may inhibit adequate testing.

With respect to barriers to healthcare, the restricted ability of humans with severe illness to go to the hospital in real life would increase the probability of death among those humans. As such, the significant positive correlation between barriers to healthcare and mortality makes sense. If treatment is sought only when a person is in critical condition, the biological progression of the disease may have already passed a certain threshold whereby treatment at that stage is less effective than it would have been if treatment began earlier. In addition, if individuals are not isolated, they could still be transmitting the virus to others in the population. For farmworkers, barriers to healthcare can be tremendous, ranging from lack of transportation to the inability to afford the cost of treatment.

VII. CONCLUSION

It is important to note that this model is a simplification of the situation of COVID-19, involving assumptions such as immunity among recovered humans. Care must be taken when attempting to apply the statistical findings of the simulation outside of the context of the model, particularly the data on R_0 because R_0 is an often misinterpreted and misrepresented measure (Delameter et al., 2019). Despite the limitations of the study, it can be seen that the challenges faced by farmworkers could potentially put farmworker communities at higher risk in the COVID-19 pandemic. As essential workers, farmworkers are already at a higher risk of exposure to the virus compared to those who are able to work from home. Further, given the vulnerability of farmworker communities and lack of adequate protections, farmworkers may especially at risk. Future studies may consider employing GIS to model the conditions of a particular farmworker community, as well as testing how the relative proportion of individuals with certain underlying medical conditions impacts the overall mortality.

Until then, it is imperative that protections and appropriate control measures be implemented to protect the safety of farmworkers in the COVID-19 pandemic. Further, it is vital that measures are taken to improve the living conditions of farmworkers beyond the context of COVID-19 given their unjust treatment by the agribusiness industry. While the efforts of farmworkers as essential workers should not go unnoticed, their humanity must also be recognized beyond their contribution to the national food supply. Hopefully, the larger pandemic of health disparities revealed by the COVID-19 pandemic can drive further efforts to improve the conditions of farmworker communities across the country.

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IX. APPENDIX: OVERVIEW, DESIGN CONCEPTS, DETAILS (ODD) PROTOCOL

A. *Model Description*

The computer software NetLogo is used to implement a data-driven ABM for human infectious diseases spread by respiratory droplets, such as COVID-19. The following sections provide a more detailed description of the model according to the ODD format, which is the standard for ABMs.

B. *Purpose*

The purpose of the model is to create an ABM of an infectious disease spread in a closed population. While this model focuses on SARS-CoV-2, the virus that causes COVID-19, it can be applied to other infections spread through respiratory droplets. The model parameters have particular relevance to farmworker communities, but this model may also be used to better understand the epidemiology of COVID-19 in general and in other populations with health disparities. The model interface can be seen in Fig. A.

C. *Entities, State Variables, and Scales*

- **Agents/Individuals:** The model has one type of agent. The agents represent humans being modeled. The state variables for each agent include susceptible, infected, recovered, deceased, protected (following measures), and risk group status. Susceptible humans are those who are vulnerable to infection. Infected humans are those who have the disease and can transmit it to other humans. Recovered humans are those who previously had the disease and are now considered immune. Deceased humans are those who died from the disease. Humans who are considered protected are those following control measures. Humans belonging to the risk group have a higher risk of severe disease and mortality.
- **Spatial Units:** Each grid cell or patch in NetLogo represents approximately 450 square feet of land.
- **Environment:** The model environment is divided into three environments: Interaction-zone (gray area), Hospital (pink area) and Quarantine (cyan area). There is an option to include high-touch areas (white) within the interaction-zone. Time is an environmental variable within the model. Each time step in the model represents 24 hours (1 day).

D. *Process Overview and Scheduling*

The model proceeds in discrete time steps that represent days. The model runs until no agents are exposed or infected (i.e. all agents are either susceptible, recovered, or deceased). Each time step following submodels are run: move-humans, touch-surface, become-infectious, infect-others, develop-symptoms, check-for-hospital, go-to-hospital, recover-or-die, and calculate-r0. Submodels are described in the "Submodels" section.

E. *Design Concepts Process Overview and Scheduling*

- **Basic Principles:** The infection part of the model is based on an SEIR-D (susceptible, exposed, infected, recovered, and deceased), a widely used model in infectious disease modelling. When a susceptible agent comes into contact with an infected agent, there is a probability that the susceptible agent will become exposed to the disease. The value for the basic reproductive number (R_0), the expected number of individuals infected by one infectious individual in a completely susceptible population, is calculated. The model takes a simplistic approach to agent movement, with random motion that can be controlled by adjusting mobility. Unless designated to enter quarantine or the hospital, agents will move within the interaction zone.
- **Emergence:** The emerging result from the model is the progress of infection. Based on the types of agents that are initially infectious and other agents who come in contact with these agents, patterns can emerge for how an outbreak will spread. For example, if a human is protecting itself from exposure by following control measures, the probability of a human becoming infected will be lower, leading to a smaller outbreak. Designation of infected humans to quarantine when sick can also impact how the outbreak occurs.
- **Adaptation:** The current version of the model does not involve adaptation. Agents reproduce observed behaviors based on a set of rules given to them. For example, if an agent becomes sick, entry into quarantine or the hospital will depend on selected parameters. Agents do not adapt their behavior by deciding to quarantine or go to the hospital.
- **Sensing:** As they move through the environment, infected agents will sense if other agents close to them are susceptible.
- **Interaction:** The model assumes direct interaction or close proximity between agents. If a susceptible agent is in any of the eight surrounding neighbors of the infected agent or if the two agents occupy the same space (on the same NetLogo patch), it is assumed that they have had some type of interaction which may lead to the infection of the susceptible agent.
- **Stochasticity:** Stochasticity is seen in the spread of the infectious disease through the population. When an infectious agent comes into contact with a susceptible agent, there is a probability that determines whether the susceptible agent will become exposed. Once exposed, the length of time the agent will remain exposed before becoming infected is determined by Poisson probability distribution. Similarly, the length of time an agent stays infectious is determined by Poisson probability distribution.
- **Observation:** For every run of the model, data is collected on the number of agents who are susceptible, exposed, infected, recovered, and deceased at each time step. The output is collected at every time step to see how the infection changes over

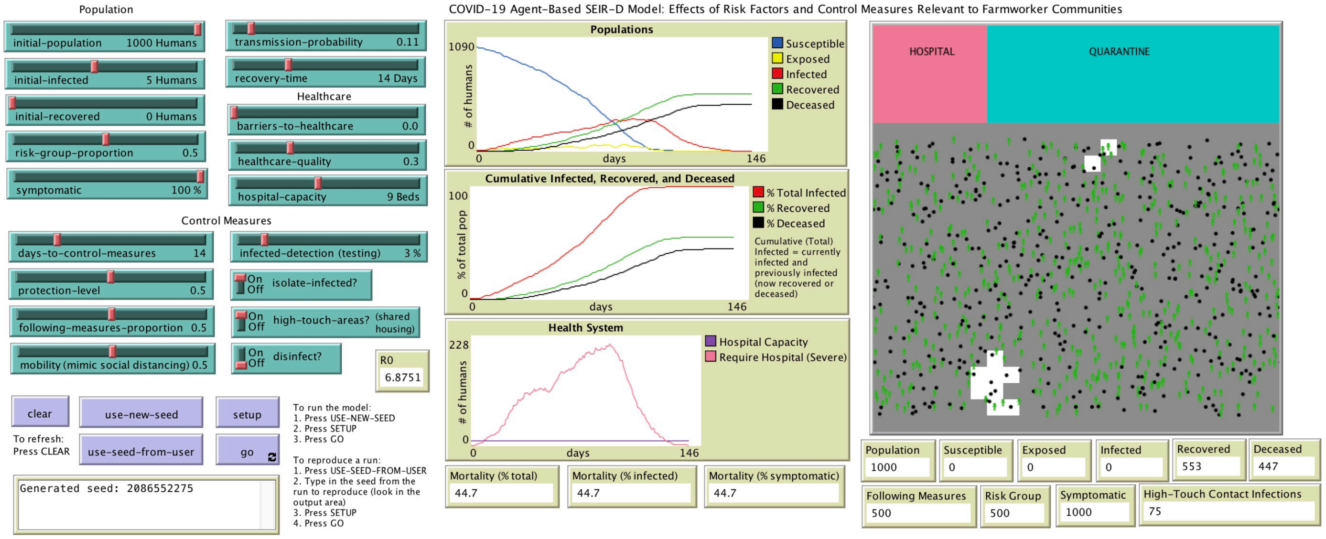
time. Data is collected on the cumulative number of symptomatic infections, the number of humans following control measures, the number of humans belonging to the risk group, and the number of high-touch contact infections. Data on R0, total mortality (% of initial population), infected mortality (% of cumulative infections), and symptomatic mortality (% of cumulative symptomatic infections) is also collected. The symptomatic data are only collected the time step that an agent becomes infected.

F. *Initialization*

The world was setup by designating a large interaction zone in the lower portion of the world, a hospital in the upper left portion of the world, and a designated quarantine region in the upper right portion of the world (Fig. A). If high-touch-areas are included, these white patches can be considered shared housing. Agents are added to the world based on the initial size of the population. Agents are randomly distributed throughout the interaction zone. A given number of agents are assigned to susceptible, infected, or recovered status based on selected parameters. Agents are also assigned to become symptomatic, follow control measures (where the agent's chance of exposure is decreased) and to pertain to the risk group (where the agent's chance of severe disease and death is increased) based on the respective proportions designated for each parameter.

G. *Submodels*

- **Move-humans:** In the model, agents move randomly. The distance traveled by the agents is determined by the mobility parameter.
- **Touch-surface:** When an agent is on a patch that is designated as a high-touch-area, the individual has an increased probability of exposure depending on the choice to disinfect.
- **Become-infectious:** An agent who has been exposed the virus will become infectious after the latency period.
- **Infect-others:** When an infected agent comes into contact with a susceptible agent, the infected agent will determine if they will infect the susceptible agent based on the transmission rate and whether the susceptible agent is protected from exposure by following control measures. If the infected agent infects the susceptible agent, the susceptible agent will change their health status from susceptible to exposed.
- **Develop-symptoms:** A given proportion of infected agents will become symptomatic two days after the end of the virus latent period. Asymptomatic agents will recover after the recovery time.
- **Check-for-hospital:** The simulation will check if infected-symptomatic people need a hospital. For the agents of the risk group, a 20% chance of needing a hospital was considered. For agents who are not of risk group, a 5% chance of needing a hospital was considered.
- **Go-to-hospital:** Based on whether the hospital is crowded and barriers to healthcare, an agent with severe disease may be hospitalized.
- **Recover-or-die:** An agent will use a Poisson probability distribution to determine the number of time steps it will stay infected before it recovers. Similarly, based on severity of the disease, hospitalization, and risk group status, an agent will use a Poisson probability distribution (taking into account healthcare quality as relevant) to determine the chance of recovery. Once an agent has recovered they cannot become infected again.
- **Calculate-r0**:; The basic reproductive number (R_0) is calculated based on the Kermack McKendrick mathematical derivation that R_0 = beta*S(0)/ gamma = N*ln(S(0) / S(t)) / (N - S(t)), where N is the total population, S(0) is the initial number of susceptibles, and S(t) is the total number of susceptibles at time t. At the end of the simulation, the R_0 reflects the estimate of the basic reproduction number, the number of secondary infections generated by an infected human throughout their infectious period



initial-population 1000 Humans
initial-infected 5 Humans
initial-recovered 0 Humans
risk-group-proportion 0.5
symptomatic 100 %
transmission-probability 0.11
recovery-time 14 Days
barriers-to-healthcare 0.0
healthcare-quality 0.3
hospital-capacity 9 Beds
days-to-control-measures 14
protection-level 0.5
following-measures-proportion 0.5
mobility (mimic social distancing) 0.5
infected-detection (testing) 3 %
On Off isolate-infected?
On Off high-touch-areas? (shared housing)
On Off disinfect?
R0 6.8751

To refresh:
Press CLEAR

To run the model:
1. Press USE-NEW-SEED
2. Press SETUP
3. Press GO

To reproduce a run:
1. Press USE-SEED-FROM-USER
2. Type in the seed from the run to reproduce (look in the output area)
3. Press SETUP
4. Press GO

```
Generated seed: 2086552275
```

Mortality (% total) 44.7
Mortality (% infected) 44.7
Mortality (% symptomatic) 44.7
Population 1000
Susceptible 0
Exposed 0
Infected 0
Recovered 553
Deceased 447
Following Measures 500
Risk Group 500
Symptomatic 1000
High-Touch Contact Infections 75

Fig A. NetLogo Interface. Parameters that the user can adjust are on the top left. The setup buttons are on the bottom left, with options to run the model with a new-seed or reproduce a run with a seed input from the user. The middle portion of the interface contains graphs. The right portion of the interface contains the world. The majority of the monitors are located at the bottom of the interface.

FIG. B-G TRANSMISSION PROBABILITY SWEEP SIR GRAPHS

NOTE: The blue curve represents the number of susceptible humans in the population over time, the red curve represents the number of infected humans in the population over time, and the blue curve represents the number of recovered humans in the population over time.

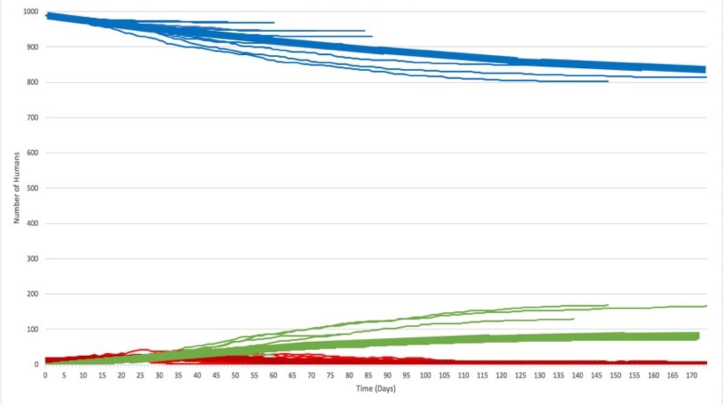


Fig. B. Transmission Probability = 0.1

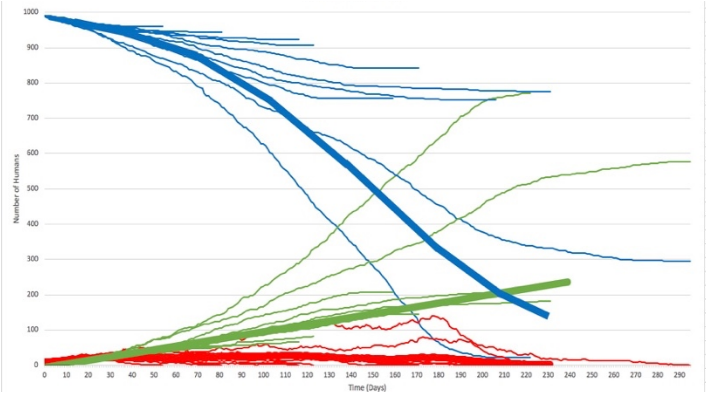


Fig. C. Transmission Probability = 0.11

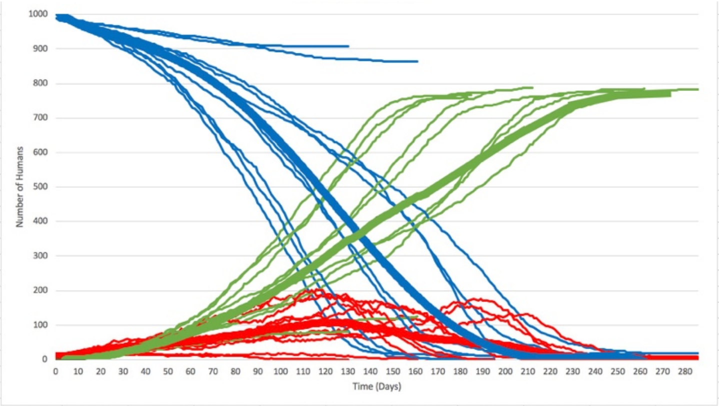


Fig. D. Transmission Probability = 0.12

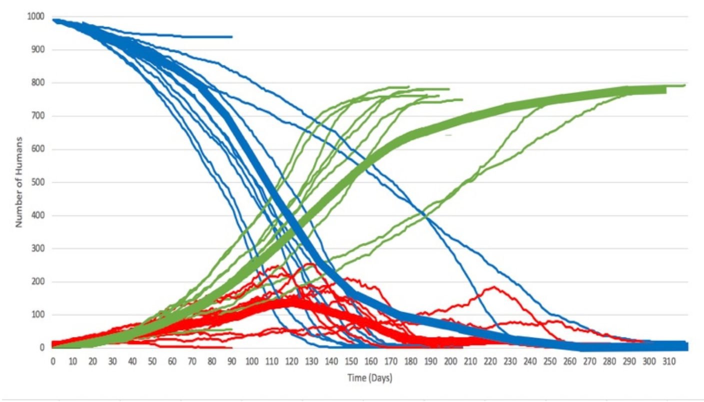


Fig. E. Transmission Probability = 0.13

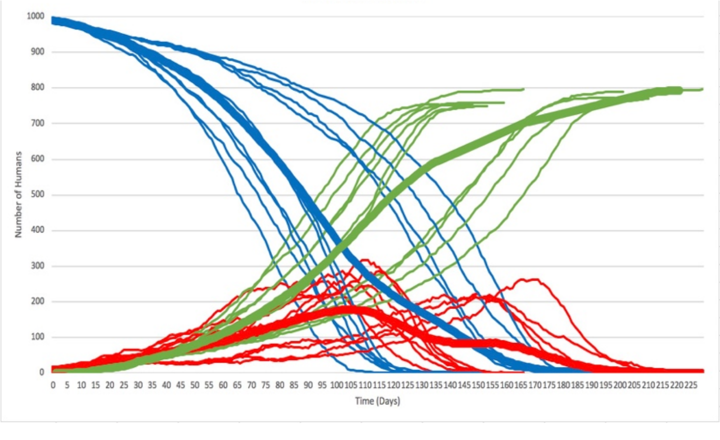


Fig. F. Transmission Probability = 0.14

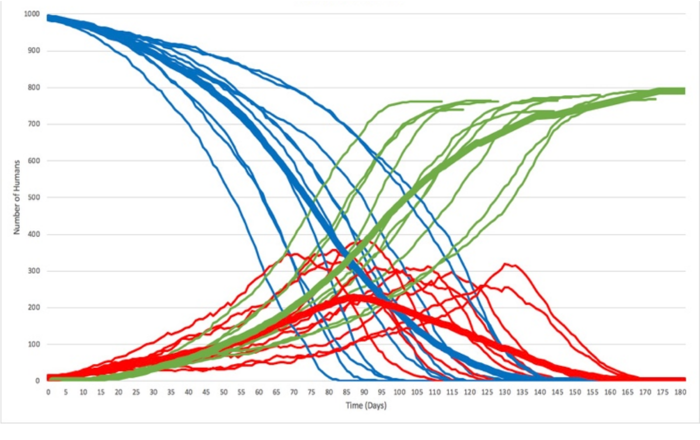


Fig. G. Transmission Probability = 0.15

TABLE A. PROBABILITIES SET WITHIN MODEL CODE

Probabilities	**Condition 1**	**Condition 2**	**Value in Model Code**
Exposure from high-contact area	disinfect? **true**	protect? **true**	1%
		protect? **false**	5%
	disinfect? **false**	protect? **true**	5%
		protect? **false**	20%
Need for hospital	risk-population? **true**	N/A	20%
	risk-population? **false**		5%
Average survival for severe disease	hospitalized? **true**	risk-population? **true**	93%[a]
		risk-population? **false**	99%[a]
	hospitalized? **false**	risk-population? **true**	20%
		risk-population? **false**	60%

[a] Assuming full healthcare quality *(healthcare quality = 1).*

TABLE B. BASELINE VALUES USED FOR PARAMETER SWEEPS

Parameter	**Baseline Values**
random-seed	-500, -400, -300, -200, -100, 100, 200, 300, 400, 500
initial-population	1000
initial-infected	10
initial-recovered	0
risk-group-proportion	0.5
symptomatic	60%
transmission-probability	0.11
recovery-time	14 days
barriers-to-healthcare	0
healthcare-quality	1
hospital-capacity	2 beds
days-to-control-measures	14 days
protection-level	0.5
following-measures-proportion	0.5
mobility	1
infected-detection	5
isolate-infected?	true
high-touch-areas?	false
disinfect?	false