Risk-Informed Decision-Making Tool for Covid-19 Community Behavior and Intervention Scenario Assessment

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Abstract: The spread of the COVID-19 pandemic across the world has presented a unique problem to researchers and policymakers alike. In addition to uncertainty around the nature of the virus itself, the impact of rapidly changing policy decisions on the spread of the virus has been difficult to predict. Using an epidemiological Susceptible-Infected-Recovered-Dead (SIRD) model as a basis, this paper presents a methodology for modeling many uncertain factors impacting disease spread, ultimately to understand how a policy decision may impact the community long term. The COVID-19 Decision Support (CoviDeS) tool, utilizes an agent-based time simulation model that uses Bayesian networks to determine state changes of each individual. The model has a level of interpretability more extensive than many existing models, allowing for insights to be drawn regarding the relationships between various inputs and the transmission of the disease. Test cases are presented for different scenarios that demonstrate relative changes in transmission resulting from different policy decisions. Further, we will demonstrate the model's ability to support decisions for a smaller sub-community that is contained in a larger population center (e.g. a university within a city). Results of simulations for the city of Los Angeles are presented to demonstrate the use of the model for parametric analysis that could give insight to other real-world scenarios of interest. Though improvements can be made in the model's accuracy relative to real case data, the methods presented offer value for future use either as a predictive tool or as a decision-making tool for COVID-19 or future pandemic scenarios.

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1. INTRODUCTION

The COVID-19 pandemic has disrupted life globally, shutting down entire cities and causing the deaths of over 6.15 million people as of April 5, 2022 [1]. In the United States, with slowing vaccination rates and new highly infectious variants of the disease, COVID-19 was the leading cause of death in August 2021 [2]. To forecast and ultimately allow us to emerge from the pandemic as soon as possible, many modeling attempts have been made to predict the spread of the disease and to suggest scenarios for mitigating its worst effects.

Mimicking lockdowns and other government interventions or personal protective measures, some models make assumptions to compare different scenarios of social distancing (e.g. using different contact rates and population dynamics) [3, 4, 5, 6, 7, 8, 9, 10], while other models assume current interventions or the observed effects of intervention measures in the data will continue for some or all of the simulation time [11, 12, 13, 14, 15, 16, 17, 18, 19, 20] [21, 22, 23, 24]. Some models make no assumptions about interventions [25, 26, 27, 28, 29]. Some models go further to specifically consider the effects of mask use [8], and the effect of COVID-19 surges on the demand of critical care resources such as hospital beds [3, 8]. Some attempt to account for potential seasonal variation in transmission rate [3], while many do not. Some model results project just the number of cases or deaths [16, 26, 19, 21]. Most project both. Models vary in their scale, offering city, county, state, or national level projections.

These models use various approaches, including variations of epidemiological susceptible-exposed-infectious-recovered (SEIR) frameworks [3, 9, 11, 13, 17, 22, 24], Bayesian SEIR models [14], statistical models or machine learning [12, 15, 16, 18, 19, 20, 21, 23, 25] [29, 30], non-SEIR mechanistic models or hybrid models [4, 5, 7, 8, 26, 27], and agent based or metapopulation models

[6, 10]. In general, these models are mechanistic, statistical, or some hybrid of these approaches. Statistical models often rely on extrapolation and fitting the model to existing data. Because testing misses many real cases of the disease, statistical models fitted to confirmed COVID-19 case data are unlikely to be reliable. Statistical models fitted to hospitalization or death data may be more reliable but are still limited by inaccuracies in the data. Mechanistic models incorporate assumptions about the governing parameters for transmission of the disease such as transmission rates, or other population and disease-specific parameters. These models allow exploration of different scenarios, interventions, and possible outcomes over a longer period, but can face inaccuracies from limited knowledge of specific parameters [31].

Development for the COVID-19 Decision Support (CoviDeS) model presented here and its accompanying online tool began in April 2020 and continued throughout June 2021. As the situation with COVID-19 is rapidly changing and more information regarding the transmission of the disease becomes known, the input parameters of the model have changed to more accurately model disease dynamics under different scenarios of intervention. With new information about the virus since the last updates to the model in June 2021, it is expected that the model in its present state will not reflect current COVID dynamics and the accuracy will continue to decrease over time. Despite this, it is believed by the authors that this model still provides unique insight into the relative effect of varying population and disease parameters on the spread of COVID-19 in a community, even in the absence of extensive data. The flexibility of this model allows the user to perform sensitivity analysis for a particular set of parameters which allows the results of the model to be interpreted more easily than many of the existing models, such that insights can be drawn regarding the relationships between various inputs and the transmission of the disease. For example, one might question if schools should reopen with the emergence of new variants of a disease, how media coverage might influence spread, how testing should be conducted in the population, or why masks might be mandated even after vaccines have been administered to a growing part of the population. This paper details an approach for modelling a complex, dynamic problem such as COVID-19 that allows modelers to answer these and other difficult questions. Results of simulations for the city of Los Angeles are presented to demonstrate the use of the model for parametric analysis that could give insight to real world scenarios of interest.

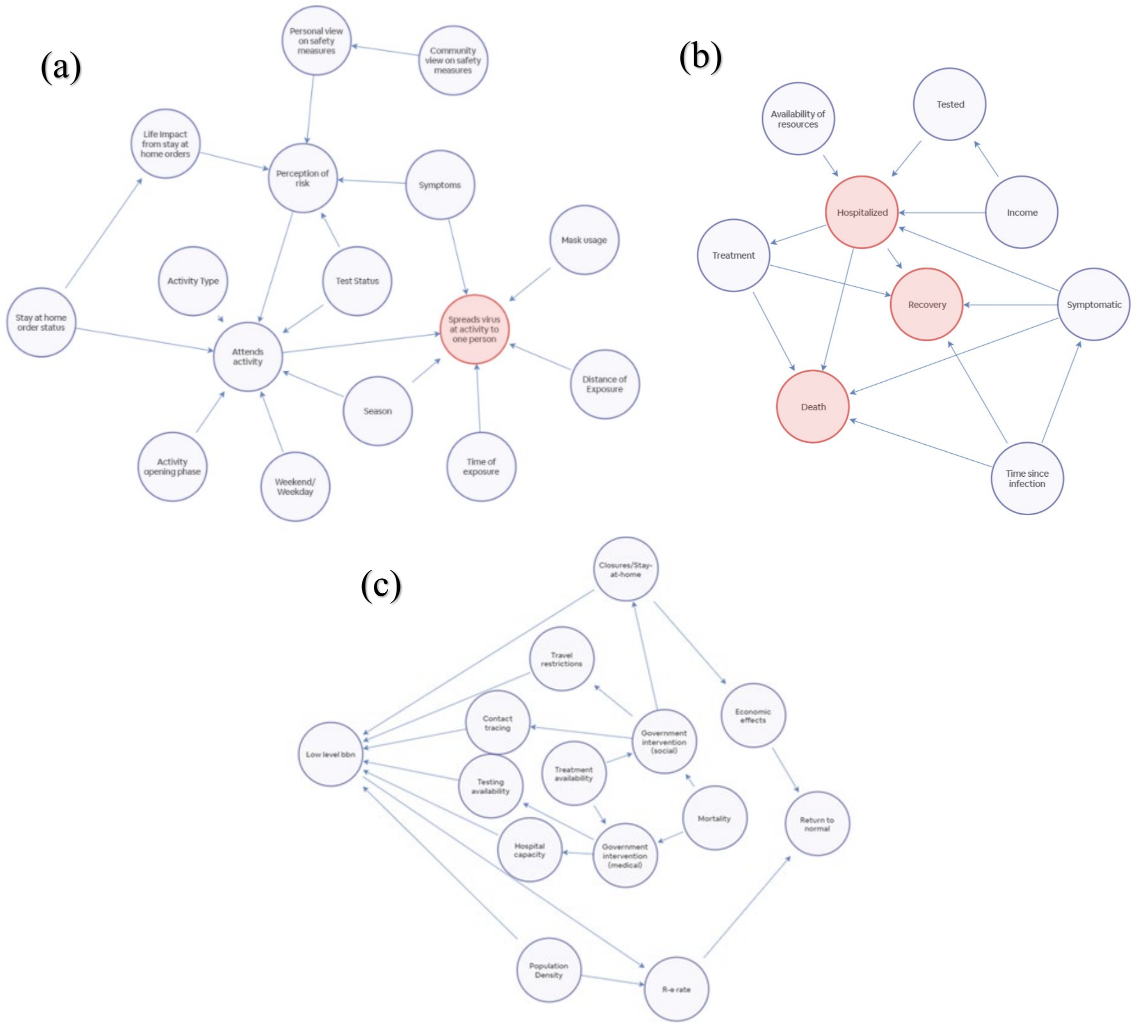
2. MODEL LOGIC

The CoviDeS model is designed to work on a city/county-wide scale, following a fixed population that can travel within the bounds of the defined region. It is a mechanistic Susceptible-Infected-Recovered-Dead (SIRD) epidemiological agent-based model, with the exposure state of the classic SEIR models removed and the addition of a state for death. While exposure still occurs in this SIRD model, the exposure state of individuals is not stored and reported in the model. The state of each individual in the population is tracked over the course of the simulation as well as the available resources, such as testing, hospital beds, and ventilators. State changes from susceptible to infected to recovered or dead depend on many factors like the epidemiology of the disease, individual behavior such as mask use, and indirectly on factors like income demographics, population density, government intervention, and the available resources (see Figure 1). The customizability of the model allows the user to not only analyze a wide variety of COVID-19 scenarios for communities of various types and sizes, but also modify model parameters governing the behavior of individuals in the community. The ability to modify these parameters also allows the users to perform sensitivity analysis for each parameter.

2.1. Dynamic Bayesian Belief Networks

The influence of these parameters on the spread of the disease are governed by Dynamic Bayesian Belief Networks (DBNs) as shown in Figure 1. Bayesian networks are probabilistic models that can represent conditional dependencies between many random variables. In the CoviDeS model, the behavior of individuals and the conditions of their community influence the likelihood of an infected individual participating in activities outside their home. The DBN conditionally links input parameters, creates probabilistic relationships between them, determines the likelihood of switching between SIRD states. At the end of each time step, it computes and records the expected number of total infections, deaths, hospitalizations, and recoveries at each time step in the community. This method allows the use of both expert knowledge and data with distributions and uncertainty bounds to project spread of the virus and health outcomes for a community.

Figure 1: Dynamic Bayesian Belief Networks for (a) factors that influence the spread of the virus (b) factors that influence hospitalization, recovery, and death, and (c) factors that influence resource changes



The DBN in Figure 1b represents the dependencies and probabilities of individuals entering the recovered (R), deceased (D), or hospitalized (H) states from the sick (S) state. Hospitalization depends on the probabilities of having symptoms, test status, income, etc. Death and recovery rates utilize conditional probabilities linking ventilator status, infection status, etc. The recovery rates used also follow a stepwise Poisson distribution based on the average recovery rate of individuals with a range of symptoms and treatment quality.

$$Recovery\ Rate = \frac{1-e^{-t/t_r}}{t_r} \tag{1}$$

Where t is the number of days since infection, and t_r is the average recovery time. An exponential function based on the averages from [32] for severe, mild, and asymptomatic infections.

A DBN that represents the effect of prevalence of COVID-19 on resource availability is shown in Figure 1c. If the prevalence is increasing, travel restrictions and hospital resources will be impacted in this DBN, with the possibility of more interventions in place and more resources allocated to hospitals.

2.2. Interactions

Once a start date for simulation has been chosen and the number of confirmed cases on that day is input to the model, the model makes an estimate of the true number of infections based on the number of initial confirmed cases. The estimate can be made using a multiplier [33], then the potential infection dates of all the initial cases are used to locate the first potential case. To better capture social circles within a large community, each individual "A" is placed in a "work group" and a "home". Assumptions for these interactions are listed in Table 1.

Table 1: Interaction Assumptions

Activity	Frequency of Attendance	Types of Encounters	Likely Number of Encounters	Influence of Local Policies
Home	~7 days/week	Home group	Based on group size	Minimal
Work/School	5-6 days/week	Work group	Based on group size	Depends on work group
Daily shopping	1-4 days/week	Random	Up to 20 (40 on holidays)	Reduced
Restaurant/ casual outings	0-4 days/week	Random	Up to 25 (35 on holidays)	Closure and gradual reopening
Parties	0-5 days/month	Random	Up to 45 (100 on holidays)	Reduced
Large events	0-10 days/year	Random	Up to 700	Closure and gradual reopening

The likelihood of one of these interactions leading to the virus spreading to "B" is a conditional probability distribution that is dependent on the virus transmission rate, the individual A's symptoms, the length of interaction and distance between A and B during the interaction, and whether individuals A and/or B are wearing masks during the interaction. Note that the likelihood of individual A participating in optional activities depends on their individual perception which may vary over time based on A's political views, symptoms, awareness of community spread, and fatigue with local policies. These interdependencies are illustrated in Figure 1a.

As individual A participates in daily routines, they may also encounter people during transit, depending on their method of transportation and population density (ρ_{pop}). The work of Hu et. al. [34] helped with determining the multiplier used for calculating the contact rate. In the CoviDeS model, the number of people encountered in open public space follows an exponential distribution:

$$N_{travel} = 14.54 * \left(1 - \exp\left(-\frac{1 * \rho_{pop}}{5863}\right)\right) \quad (2)$$

$$N_{events} = rand(0, X) \quad (3)$$

Where X is the max number of people expected to be met at a given location which depends on the event type and state of lockdown as a stepwise function

The probability that B gets infected by A is given by:

$$P(B_I) = p(A\ attends\ event) * p(A\ interacts\ with\ B) * p(exposure) * p(infection\ given\ exposure) \quad (4)$$

2.3. Testing and Vaccines

If tests and/or vaccines are available, there is a chance an individual will be tested or vaccinated on a specified date. This likelihood ultimately depends most on the availability, but preference is given to certain groups such as those with COVID-19 symptoms, those who are hospitalized, and those who have the Essential Worker group property. Individuals who are sick and exhibit severe symptoms are rarely tested in this model to reflect the suggestion that those with severe COVID-19 symptoms stay home, avoiding testing sites. Once testing resources have become sufficient to allow people to get tested multiple times, any individual may become tested again after a first test. If they tested positive previously, they are more likely to re-test to obtain a negative test. A test can return a false positive or negative. The rate of a false result can be altered in the inputs at the user's discretion.

Any individual who tests positive for the first time or tests positive after their previous test was negative will be added to the total confirmed cases list. Since testing relies on a positive result, false positives will also be added to this confirmed case list. Three different vaccine supplies are present in the model. By default, the model uses properties of the Moderna, Pfizer, and Johnson and Johnson vaccines to represent the vaccines available in the US, but the properties may be altered in the inputs by the user. A person seeking to be vaccinated may receive any of the three vaccines and will receive a second dose after one month for those vaccines which require two doses. The effectiveness of the vaccine depends on the amount of time since vaccinated, with no effectiveness for 14 days, 60% nominal effectiveness at 14-21 days, reaching a peak in effectiveness 21 days after the complete dose, and slowly decreasing afterwards [35].

If the individual has been vaccinated with the full dosage for greater than 21 days, the effectiveness of their vaccine is determined by the following equation, which follows a sigmoid function:

$$E_t = \frac{1}{(1 + \exp(\lambda * (t - 365))} \tag{5}$$

Where E_t is the effectiveness on the current day (t), and λ is determined by:

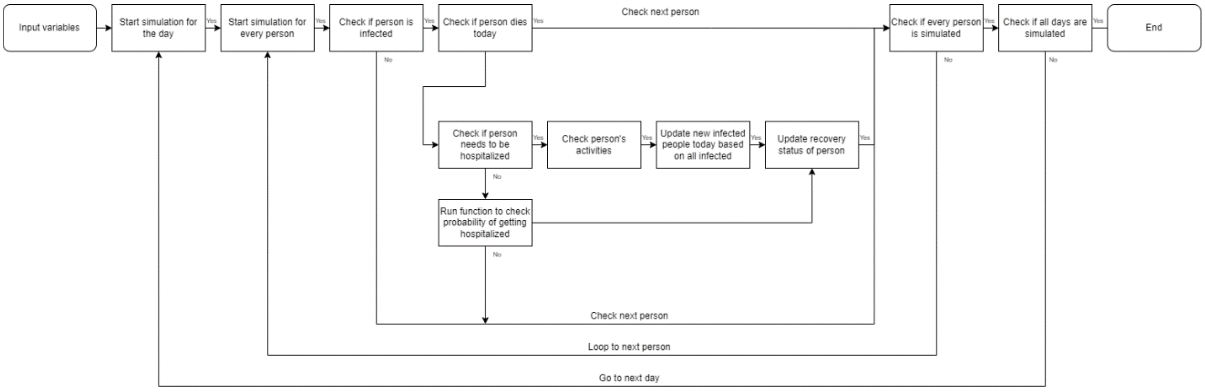
$$\lambda = -\frac{1}{365} * \log\left(\frac{1}{E_{nom}} - 1\right) \tag{6}$$

Where E_{nom} is the nominal effectiveness of the vaccine as reported by the manufacturer.

If the individual has received one dose out of a two-dose vaccine, E_{nom} becomes E_{pn}, which is the nominal effectiveness of having one of the two doses of the vaccine. A person who is vaccinated is less likely to contract the virus after encountering it in the model.

An overview of the model logic is shown in Figure 2.

Figure 2: Model Logic



3. TEST CASES

3.1. Subcommunity/Campus Model

The model features a module designed to focus on how the virus might spread within a smaller sub-community while it spreads within the general population. The general size of the population that participates in these activities should be known beforehand and should be significantly smaller than the surrounding community population. The individuals in this sub-community participate in a set of pre-defined activities that occur on a regular basis. The features described here are meant for use with a university campus, but activities and environment settings can be modified to describe different communities and activities, such as work or recreation.

At the beginning of each day in the model, a subset of the population will attempt to enter the campus as members of one of several campus-specific groups. For universities, these groups are faculty, staff, undergraduate students (living on campus), undergraduate students (living off campus), graduate students, and visitors. The number of people that will attempt to enter as members of each group depends on the number of people that are normally needed to perform campus activities and the percentage of those activities that are currently being performed on campus (based on opening plans). Based on an individual's state (e.g. hospitalized or dead) at the time of entry, some may be unable to enter campus. Additionally, if the school prohibits those who are known to be infected from entering, people who have tested positive will be barred from entry as well.

All individuals on campus may participate in activities with a varying likelihood depending on the group they belong to. The activities defined for universities include classes, laboratory work, office work, shopping and dining, work at shopping and dining centers, commuting to and from campus, and time spent in dorms. If an infected person enters campus, they may spread the virus while participating in these activities, creating new infections. The average number of people encountered is taken as a sum of the number of people encountered during the activity itself, which is calculated exponentially as

$$N_{Activity} = 2 * \left(1 - \exp\left(-\frac{activity.duration}{2}\right)\right) \tag{7}$$

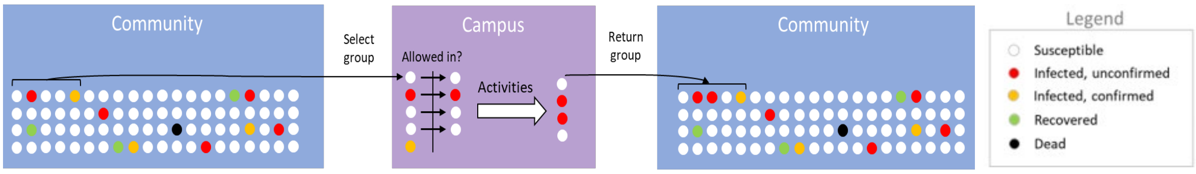
And the number of people encountered while walking around campus is calculated as

$$N_{Walk} = X * \left(1 - \exp\left(-\frac{Population\ density}{120}\right)\right) \tag{8}$$

Where X is an average number of people expected to be encountered by that individual while walking around campus in a day.

Using the average, the actual number of people contacted is calculated using an inverse lognormal function rounded to the nearest number. The infections arising from these encounters are governed by the DBN for spreading the virus as previously described and are stored separately for each activity to track which activities are creating the most risk. After all activities are completed, the individuals are returned to the larger population, where the model runs as described previously. The process of entry into a campus, participation in activities, and return to the community is outlined in Figure 2.

Figure 2: Schematic for process of entry and exit from subcommunity

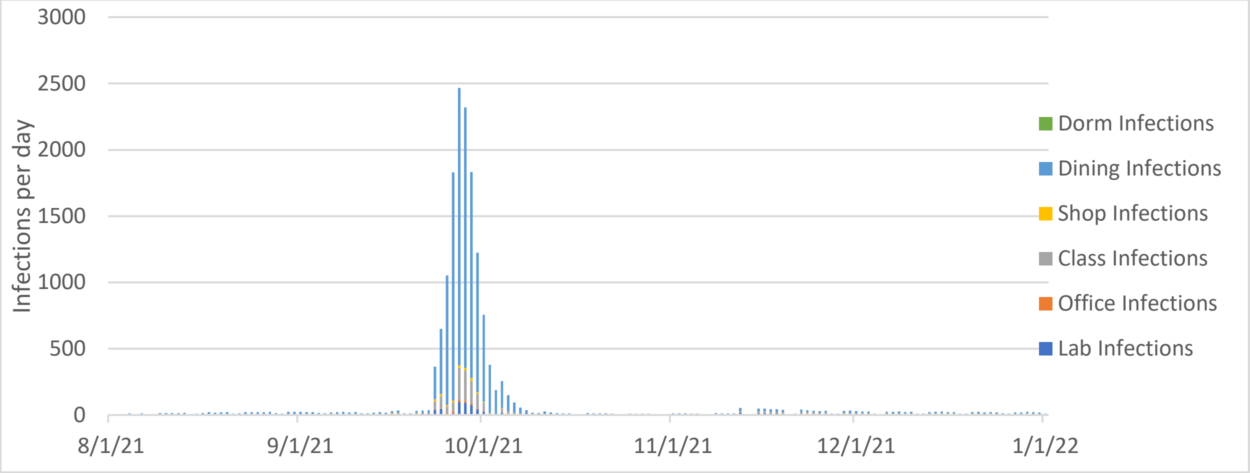


A sample case was run for a population of ten million and a single campus that may see a maximum of 100,000 people coming in on a given day, including visitors. The results of this test are shown in Figure 3. Figure 3a represents the case with the campus present, and 3b represents the case of campus closure. After the campus' opening at the end of September 2021, a significant uptick can be seen in the number of cases in the larger community as the infection is able to spread among the regular visitors. The number of cases slowly declines after that initial uptick, since most campus activities confine individuals to interactions with the same group of people each day, limiting the spread to those people being interacted with. After the initial wave of infections, there is not enough interaction on campus between sick individuals and susceptible individuals to maintain the rise. This effect is also seen in Figure 4, which shows the new infections each day from campus activities only. There is an initially high number upon opening, but it quickly reduces to almost none.

Figure 3: Test case of Covid 19 cases in a community of ten million
a) campus of approximately 100,000 people opening, and b) campus closure

Note that the Monte Carlo sampling of the model uncertainty has resulted in an initially higher number of cases in 3b.

Figure 4: New Covid 19 infections resulting from daily activities on a campus.

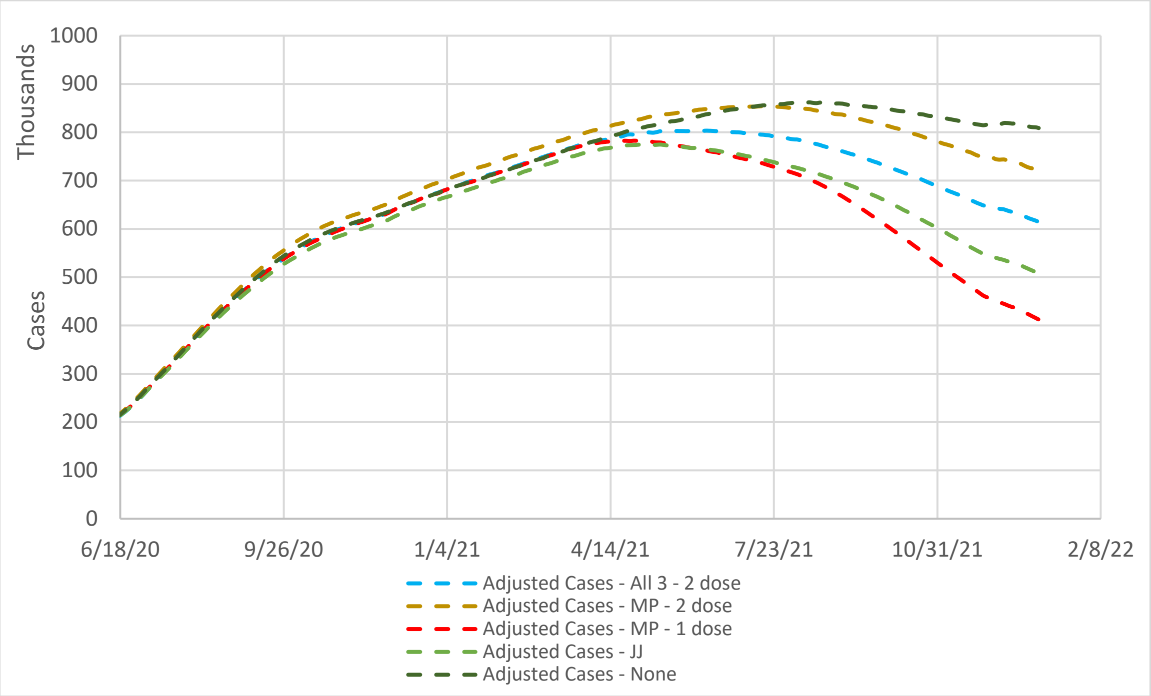


The feature for adding a campus to the model can be modified to describe other small communities within the population at large, including nursing homes or hotels. Since this feature uses customizable activities to describe how individuals in pre-defined roles may interact with one another repeatedly over many days, the user would only need to change the parameters defining the likelihood of individual activities/ roles to describe a different sub community.

3.2. Sensitivity Analysis of Vaccines in Los Angeles County

The model can provide insight to the potential outcomes of various scenarios of vaccine dissemination. In the early stages of vaccine rollout in the US, the major limitation was vaccine supply. In the later stages, the limitation has often been vaccine hesitancy. These vaccine parameters are incorporated into the model as described in the model logic section. With the available 2-dose vaccines, Moderna and Pfizer, the first dose averages around 52% effective and a second dose is optimally given at 4 weeks after the initial dose to provide the maximal protection against the disease (approximately 95%) [36]. The Johnson & Johnson vaccine, a one-dose vaccine, provides lower protection at approximately 66-85% effectiveness. This test case for Los Angeles attempts to answer questions of the relative effect of different vaccine dissemination strategies. For example: When vaccine supply is the limiting factor, what would be the effect on transmission of the disease if two doses (Moderna or Pfizer) are given on schedule as opposed to one dose of Johnson & Johnson, which has a slightly lower effectiveness, given to a larger part of the population? What would be the effect of a one-dose strategy using all 3 vaccine types, potentially reaching more of the population but with a lower effectiveness? Figure 6 presents graphical representations of the results of our model when run for the city of Los Angeles. Note that modeling error was corrected by adjusting the mean of the model results toward the real case counts as of 2/16/2021.

Figure 6: Projections for number of cases under different vaccine distribution scenarios



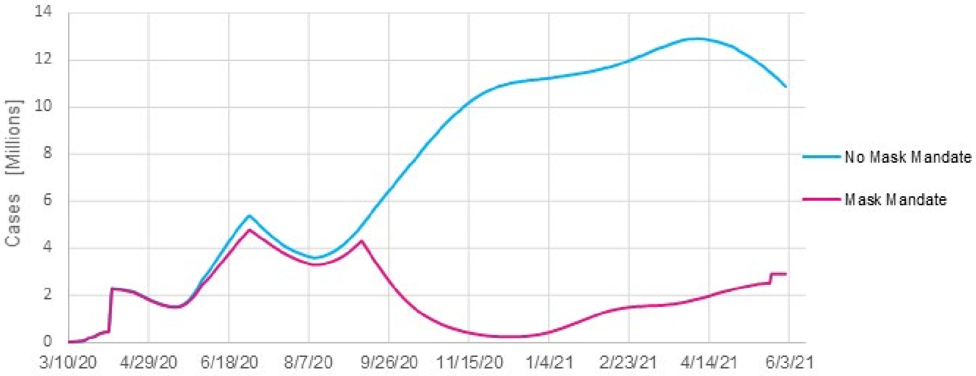
For visual clarity, we have omitted the uncertainty bounds for the cases presented. Our results indicate that giving one dose of the Pfizer and Moderna vaccines to a larger population in a shorter time would result in lower transmission of the disease as compared to giving the full course of vaccines to a smaller number of people, or other combined scenarios. For example, looking at the date October 31, 2021, a single dose scenario of Pfizer/Moderna results in an average projected active case count between 300,000 and 800,000 (at the 5th and 95th percentiles), with an average of approximately 525,000 cases. For the same date, a Johnson and Johnson only scenario results in a slightly higher case count, between 400,000 and 820,000 cases, with approximately 600,000 cases on average. The scenario in which individuals receive two doses of a Pfizer/Moderna vaccine on time results in as low as 500,000 cases or as high as 1,070,000 cases, with approximately 775,000 cases on average. A combined scenario of the three vaccines used on time yields case counts averaging around 700,000, with uncertainty between about 450,000 and 950,000 cases.

Comparing the mean values, our results indicate that giving a single dose of either Pfizer, Moderna, or Johnson and Johnson vaccines to a larger percentage of the population would be more effective at lowering the case count over time than fulfilling the full courses of the two-dose Pfizer or Moderna vaccines. This suggests that disseminating a slightly less effective vaccine that can reach a larger percentage of the population quickly could have better public health outcomes in the long term. This is likely only valid in the early stages of vaccine rollout when supply was the main limitation. When vaccine hesitancy takes precedence, it may be more effective to give the 2-dose vaccines on time. Further work would need to be done to model the effect of virus variants of the effectiveness of these vaccines over time.

3.3. Mask Mandate

We also attempt to model the effects of universal mask use with the CoviDeS model. Based on data regarding the effectiveness of masks in preventing droplet spread [37], we compare the status quo to a hypothetical situation where there is a country-wide mask mandate. While the current version of the model may not perfectly reproduce the numbers of confirmed cases in the real data, it does replicate the general trends (first and second waves) and projects the impact of policy (e.g. stay-at-home orders, masks) on the spread of disease. In the hypothetical case of a 100% mask mandate starting in mid-September and no new stay-at-home orders, the model projects a significant improvement in active cases (the number of active/ongoing COVID-19 cases on any given day) when comparing to the status quo. The number of active cases in the mask mandate scenario are lower by ~10 million in the first half of 2021. In January 2021, the active cases begin to rise again even as the mask mandate continues because, as time passes and no new quarantine/stay-at-home orders are implemented, individuals begin to go out more (as captured by the quarantine fatigue aspect of our model), reducing the effectiveness of the mask mandate. Further, people may become infected in places where mask mandates cannot extend, such as in private homes.

Figure 7: Projections for number of cases under different mask policy scenarios



These results support the claims of medical experts and observations in places like Arizona and Japan, for example, where mask mandates were put into place and cases/deaths fell significantly. In Arizona, COVID-19 cases spiked 151% after a statewide stay-at-home order expired and dropped 75% following local mask mandates [38]. Japan had no mandatory lockdowns, but with their mask observance, experienced only 7 deaths per million, while the US experienced 385 deaths per million in 2020 [39]. These data and our simulations indicate that 100% mask use would result in precipitous decreases in cases across the US. While it could be a simple and effective solution, the reliance on a mask mandate in the absence of other mitigation measures (e.g. banning gatherings, business/recreational closures, or potentially stay-at-home orders) would likely not be the best policy, as the enforcement of this individual behavior at each moment would prove highly difficult.

4. MODEL FLEXIBILITY

The CoviDeS model as described gives the user flexibility to understand the mechanisms of transmission with minimal changes to the main code. The benefits of this model flexibility were exemplified in our early attempts at modeling the use of vaccines. Due to a lack of vaccine data early in the pandemic, a simplistic vaccine model was created which had the capability to simulate a vaccine with a permanent effectiveness of 95%. As vaccines began to roll out in the US, our understanding of the effects of vaccines also changed. Because of the parameterized nature of the model, we were able to integrate new data to modify the vaccine efficacy such that it accounted for diminished protection over time, include new parameters that would reflect the effects of multiple vaccines, and include behavioral dynamics such as vaccine hesitancy. Together, these parameter changes can give users a better understanding of how specific changes to vaccine rollout could impact the transmission and severity of the virus in a population.

As another example, one might want to include the specific dynamics of transmission that are caused by different variants of the virus. The flexibility of the CoviDeS model could allow a user to model, for example, the Delta and Omicron variants simultaneously with simple changes to the parameters in the *main* function and the *interactions* function. Specifically, this could be accomplished by overlapping the populations of Delta and Omicron infected individuals, who would then have different rates of transmission and different likelihoods of hospitalization and survival rates. The *interactions* function would be run once for each variant (assuming people cannot be infected with both variants at once), and the individuals would enter one of two states (e.g. infected1/infected2, hosp1/hosp2, death1/death2). These examples and those explained throughout this paper demonstrate the flexibility and interpretability of this model. This interpretability allows one to forecast the likely effects of many different policy decisions, and could inform more rational decision-making in the public sphere.

4. CONCLUSION

The CoviDeS model and its extensive parametrization allows for novel insights to be drawn about the transmission of the COVID-19 virus. As compared to other models that use data-driven approaches, this model can more clearly show the effects of specific policy decisions and function in the absence of large data sets, as was the case in the early stages of the pandemic. It can incorporate unique epidemiological features of the virus and details about how we as individuals and communities might respond to various scenarios. With relatively small adjustments to the model, it could provide useful assistance to decision makers as the current COVID-19 pandemic continues or could be used to better prepare and respond to future epidemic and pandemic events.

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