Supplemental Online Materials to COVID-19: Agent-Based Simulation-Optimization to Vaccine Center Location Vaccine Allocation Problem

Xuecheng Yin [a], Sabah Bushaj [b], Yue Yuan [c] and İ. Esra Büyüktahtakın [d]

[a] Management Science and Information Systems, Oklahoma State University, United States

[b] School of Business and Economics, SUNY Plattsburgh, Plattsburgh, United States

[c] Altfest Personal Wealth Management, New York, United States

[d] Grado Department of Industrial and Systems Engineering, Virginia Tech, Blacksburg, United States

A1 Covasim-related Key Parameters

Covasim, is a stochastic agent-based simulator (Covasim (idmod.org)) developed by Kerr et al. (2021b) to perform COVID-19 analyses. The ABM involves human behaviors and daily activities to simulate the transmission process of COVID-19 under different intervention strategies, including social distancing, school closures, testing, contact tracing, quarantine, and vaccination. Covasim is shown to provide accurate projections of the number of infections and peak hospital demand under varying intervention measures and has been applied in over a dozen countries, including the US, UK, and Australia, to inform policy decisions. Specifically, Covasim is used in the research literature for spatio-temporal simulation (Gharakhanlou and Hooshangi, 2020) to derive strategies for non-pharmaceutical interventions, such as masks, testing, and contact tracing (Contreras et al., 2021; Stuart et al., 2021), and to evaluate strategies, such as reopening (Bilinski et al., 2021; Panovska-Griffiths et al., 2020; Pham et al., 2021), test-trace-quarantining (Kerr et al., 2021a), and reducing control measures (Scott et al., 2020). To our knowledge, none of the former works has used Covasim

with a mathematical programming approach to inform public policy on COVID-19.

Table A1 presents the default duration parameters, in days, used in the Covasim model and infection probability per contact. Table A2 shows the age-linked disease susceptibility, progression, and mortality probabilities. According to (Kerr et al., 2021b), the daily value of $\beta = 0.016$, currently used as the default in Covasim, was based on calibrations to data from Washington and Oregon states. This default value significantly varies in different transmission contexts. Therefore, we calibrated β to match local epidemic data in New Jersey using the nine counties shown in Figure A10. In our calibration, we use the same initial infections and population with the real data and generate the infection probability β every ten days. The β values for the first ten days were randomly generated from the set $0.15, 0.25, 0.35, 0.45, 0.55$, which is obtained from a preliminary test. Since the disease transmission spreads fast in the first 40 days and then slows down during the later periods in the real data, the value of newly generated β is greater than or equal to the previous one for every ten-day period for the first 40 days and then less than or equal to the previous 10-day period for the following periods. We calculate the weekly cumulative infections generated by the agent-based model against the real data from the planning horizon. If the difference in the mean value of the simulated weekly cumulative infections and real data is less than 100, we plot the cumulative infections generated by the agent-based model against the real data from the planning horizon. If the simulated curve fits the real outbreak curve well, we take the β values generated by the model; otherwise, we further adjust the value of β until the curve fits well. Once the β values of the nine counties are calibrated, we use the same β values for the other twelve counties with similar populations and initial infections with the counties above. For some counties for which the simulated curves did not fit the real data, we continued to adjust β values until they fit the curve of real data.

Table A1: Default disease duration parameters, in days, used in the Covasim model (Kerr et al., 2021b)

Parameter	Description	Distribution (mean, std)	Reference
τ_{inf}	Length of exposed-to-infectious	lognormal (4.5, 1.5)	Lauer et al. (2020);Du et al. (2020);Nishiura et al. (2020);Pung et al. (2020)
τ_{sym}	Length of infectious-to-symptomatic	lognormal (1.1, 0.9)	Linton et al. (2020);He et al. (2020)
τ_{sev}	Length of symptomatic-to-severe	lognormal (6.6, 4.9)	Linton et al. (2020);Wang et al. (2020)
τ_{cri}	Length of severe-to-critical	lognormal (1.5, 2.0)	Wang et al. (2020);Chen et al. (2020)
τ_{dea}	Time from critical-to-death	lognormal (10.7, 4.8)	Verity et al. (2020)
τ_{ra}	Time from infectiousness to recovery (asymptomatic)	lognormal (8.0, 2.0)	Wölfel et al. (2020)
τ_{rm}	Time from symptoms to recovery for mild	lognormal (8.0, 2.0)	Wölfel et al. (2020)
τ_{rs}	Time from severe symptoms to recovery	lognormal (18.1, 6.3)	Verity et al. (2020)
τ_{rc}	Time from critical symptoms to recovery	lognormal (18.1, 6.3)	Verity et al. (2020)
β	Transmission probability per contact	{0.15, 0.25, 0.35, 0.45, 0.55}	Determined through calibration

Table A2: Age-linked disease susceptibility, progression, and mortality probabilities. Key: r_{sus}: relative susceptibility to infection; p_{sym}: probability of developing symptoms; p_{sev}: probability of developing severe symptoms (i.e., sufficient to justify hospitalization); p_{cri}: probability of developing into a critical case (i.e., sufficient to require ICU); p_{dea}: probability of death (i.e., infection fatality ratio). (Kerr et al., 2021b)

	0-9	10-19	20-29	30-39	40-49	50-59	60-69	70-79	80-89	90+	Overall
r_{sus}	0.34	0.67	1	1	1	1	1	1.24	1.47	1.47	1
p_{sym}	0.5	0.55	0.6	0.65	0.7	0.75	0.8	0.85	0.9	0.9	0.5-0.75
p_{sev}	0.0005	0.00165	0.0072	0.0208	0.0343	0.0765	0.1328	0.20655	0.24570	0.24570	0.1-0.2
p_{cri}	0.00003	0.00008	0.00036	0.00104	0.00216	0.00933	0.03639	0.08923	0.1742	0.1742	0.05-0.1
p_{dea}	0.00002	0.00002	0.0001	0.00032	0.00098	0.00265	0.00766	0.02439	0.08292	0.1619	0.002-0.015

A2 Details of Agent-based Simulation Model

Covasim simulates the state of each agent over several discrete time steps using a detailed compartmental model, as shown in Figure A2. At each time step, the simulation calculates the probability that a given agent on a given time step will change from one state to another, such as from susceptible to infected or from critically ill to death, using contact networks, individualistic decisions, and intervention methods. Most disease parameters, such as exposed-to-infectious, infectious-to-symptomatic, and time from infectiousness onset to recovery, are replicated using lognormal distributions. Age-linked susceptibility, progression, mortality, and contact probabilities are defined and used in contact networks. While all parameters and related probability distributions can be found in Kerr et al. (2021b), we also present Covasim-related key parameters and their values in Tables A1 and A2 in Appendix Section A1.

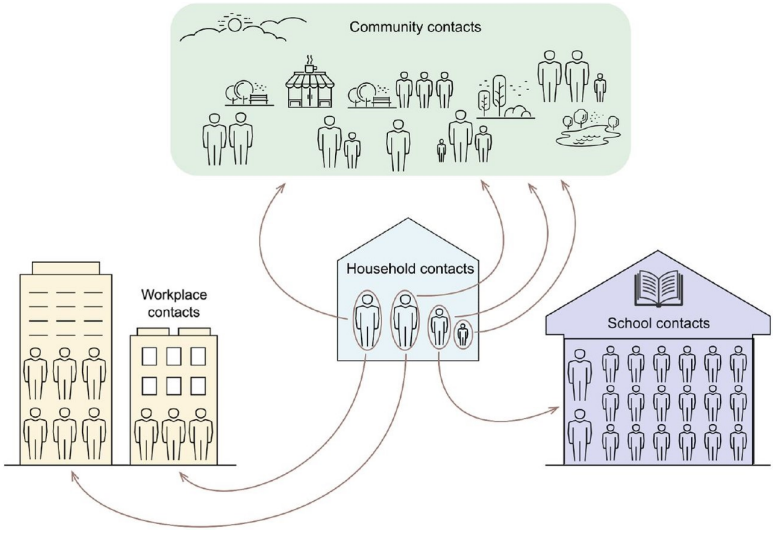

Figure A1: Contact networks for Covasim simulation Kerr et al. (2021b).

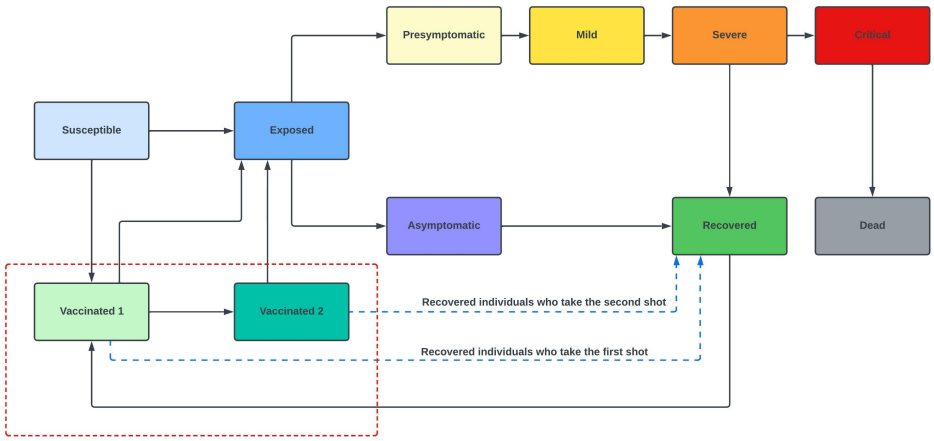

Figure A2: Compartment model that shows the progression of the disease for each agent. The red dashed box and the dashed blue lines show the compartments different than those in Kerr et al. (2021b).

As shown in Figure A2, in the Covasim simulation, each individual has the following health statuses: the *Susceptible* compartment represents people who can potentially be infected. The *Exposed* compartment represents the group of people who are exposed to the virus. The *Asymptomatic* compartment denotes the infected people who never develop symptoms, while the *Presymptomatic* compartment represents infected people who are not yet displaying symptoms of an illness or disease. The *Mild* compartment indicates infected people who have minor symptoms. The *Severe* compartment represents infected people with severe symptoms. The *Critical* compartment represents people who have even more severe symptoms and need to be treated in the intensive care unit (ICU). The *Recovered* compartment shows the recovered people, and the *Dead* compartment represents people who are dead from critical symptoms.

Susceptible individuals can contact the infections and be exposed to the virus. On the one hand, a proportion of exposed individuals show no symptoms and thus become asymptomatic. The asymptomatic infections recover from the disease automatically. On the other hand, part of the exposed individuals develops symptoms. The symptoms can vary from mild to severe and then to critical. The majority of people with every degree of symptoms recover. However, some individuals with critical symptoms may die due to their weak immunity or the delayed treatment process.

A3 Linearization

Constraints (1n) and (1m) are non-linear. To write an equivalent linear presentation of the inequality (1n), we define a new variable $U^i_{j,r,l}$ and a parameter $o^{i,UB}_{j,r}$, where $U^i_{j,r,l} = y_{r,l} o^{i,1}_{j,r}$ and $o^{i,UB}_{j,r}$ is the upper bound of parameter $o^{i,1}_{j,r}$. Thus, constraint (1n) can be linearized by the following equations:

$$U^i_{j,r,l} \leq o^{i,UB}_{j,r} y_{r,l} \qquad j \in J, \quad r,l \in \hat{R}, i \in \{3\}, \tag{A1}$$

$$U^i_{j,r,l} \leq o^{i,1}_{j,r} \qquad j \in J, \quad r,l \in \hat{R}, i \in \{3\}, \tag{A2}$$

$$U^i_{j,r,l} \geq o^{i,1}_{j,r} - o^{i,UB}_{j,r}(1 - y_{r,l}) \qquad j \in J, \quad r,l \in \hat{R}, i \in \{3\}, \tag{A3}$$

$$0 \leq U^i_{j,r,l} \leq o^{i,UB}_{j,r} \qquad j \in J, \quad r,l \in \hat{R}, i \in \{3\}. \tag{A4}$$

Constraint (1m) can be linearized by using a similar method, converting the full non-linear optimization model (1a)–(1z) into an MIP.

A4 Simulation-Optimization Algorithm

Algorithm 1 represents the step-by-step implementation of the optimization and simulation loops interactively. We implement our model to the COVID-19 case in the New Jersey state in the United States; each stage in the model represents a one-day period. In total, we consider a 90-day planning horizon, which is equal to three months. For this specific implementation, in Algorithm 1, we set $\overline{lp} = 3$, $\hat{J} = 30$, and $\overline{lp} * \hat{J} = 90$, and thus we run the simulation optimization in three steps. In the first step, the number of initial susceptible individuals and infections from JHU (2020) is imported into the optimization model to generate the vaccination center locations and vaccine allocations for the first 30-days period. Then the results are input into the simulation model to simulate the number of susceptible individuals and infections for the first 30-days period. In the second step, the simulation results of the first 30-days are input into the optimization model, and the optimization model generates the optimal vaccine allocation decisions for the second 30-days period. The optimization model's vaccine allocation results for the second 30-days are combined with the first 30-days together and then imported into the simulation model to estimate the total number of susceptible individuals and infections for the first 60-days. In the last step, we repeat the second step and combine the 90-day vaccine allocation results. Thus, we solve the model for

a total 90-day time period. For step 2 and step 3, the vaccination center allocation variable x_r^i is fixed to be the same as the solution of step 1. This indicates that the model generates the vaccine allocation decisions under the same x_r^i values in each loop of the simulation-optimization process. In addition, a simulation replication experiment is performed to study the influence of randomness on the agent-based simulation in Appendix Section A5. We run 10 replications for the simulations and use the mean value as the input in the optimization model. We compare the results of replications with our previous results in Figures A3-A5, and the trajectories are found visually close to each other. Since replications require extensive computational effort without much benefit in the output, we use a single simulation for all the results in the main manuscript.

We compare the results of simulation-optimization with the optimization model without simulation in Appendix Section A6. In this section, Figures A6-A8 show that the optimization model projects a similar prediction with simulation-optimization at the beginning, but the number of infections significantly increases later in the time horizon. Therefore, the prediction of simulation-optimization is robust compared to the optimization model without the agent-based simulation.

A5 Comparison with simulation replications

To address the randomness of the simulation model output, we perform multiple replications of the simulations and use the mean value of output as the input for the optimization model. We run 10 replications for the simulations and compare the results of cumulative infections of replications with previous estimations and the original data (Figures A3-A5). According to the results, the trajectories of replications are visually close to the previous estimation obtained with a single replication and the original outbreak data. While there are slight differences in the replicated and non-replicated simulations, we do not expect the replications to change the overall results and insights presented in the paper. Also, each replication takes a long run time of two hours on average. Thus, for computational efficiency, we use a single replication to get the simulation results.

Algorithm 1 OPT-ABM Simulation-Optimization Algorithm

Initial Setup: Define the initial simulation-optimization loop index as lp and the total number of loops, $\overline{lp}$. Set the number of optimization periods in each loop, $\hat{J}$, and the planning horizon as $\overline{lp} * \hat{J}$.

Set the initial loop, $lp = 1$;

OPT (Optimization) Routine

Optimization Input: The initial number of susceptible S_{jr} and initial infections I_{jr} for $j = (lp-1) * \hat{J}$ (if $lp \geq 2$ from simulation, else from database); the population data of region $r \in \{0, \dots \hat{R}\}$, vaccination capacity and supply, and available budget; **If** $lp = 1$, **then** input the total number of vaccination centers; **Else** fix vaccine center locations. **Solve** the optimization model (1a)–(1z) for period $j = \{(lp-1) * \hat{J}, \dots, lp * \hat{J}\}$. **Optimization Output:** The number of each type $i \in \{1, 2, 3\}$ vaccine allocated to each region $r \in \{0, \dots \hat{R}\}$ in each period $j = \{(lp-1) * \hat{J}, \dots, lp * \hat{J}\}$, ζ_{ij}^r, vaccination center service decision y_{rl} for $r, l \in \{0, \dots \hat{R}\}$, and **If** $lp = 1$, **then** vaccination center location decisions x_r^i for $r \in \{0, \dots \hat{R}\}$; **Else** use x_r^i from loop $lp = 1$. Store ζ_{ij}^r, x_r^i, and y_{rl}.

ABM (Simulation) Routine

Simulation Input: The initial number of susceptible individuals S_{0r} and initial infections I_{0r}. Input ζ_{ij}^r for $i \in \{1, 2, 3\}$ for $j = \{0, \dots, lp * \hat{J}\}$ from optimization. Set $j = 0$.

While $j \leq lp * \hat{J}$ **do**

Simulate the number of susceptible, infected, asymptomatic, presymptomatic, mild, severe, critical, recovered, dead, and vaccinated individuals in day j.

Store I_j. $j++$.

End while

Simulation Output: Calculate the output number of infected individuals I_j and susceptible individuals S_j at period $j = lp * \hat{J}$.

$lp++$;

While $lp \leq \overline{lp}$ **do**

Run OPT for $j = \{(lp-1) * \hat{J}, \dots, lp * \hat{J}\}$;
Run ABM for $j = \{0, \dots, lp * \hat{J}\}$;
$lp++$;

End while

Final output: Return x_r^i, y_{rl}, I_j, ζ_{ij}^r for region $r, l \in \{0, \dots \hat{R}\}$, vaccine type $i \in \{1, 2, 3\}$, and period $j = \{0, \dots, \overline{lp} * \hat{J}\}$.

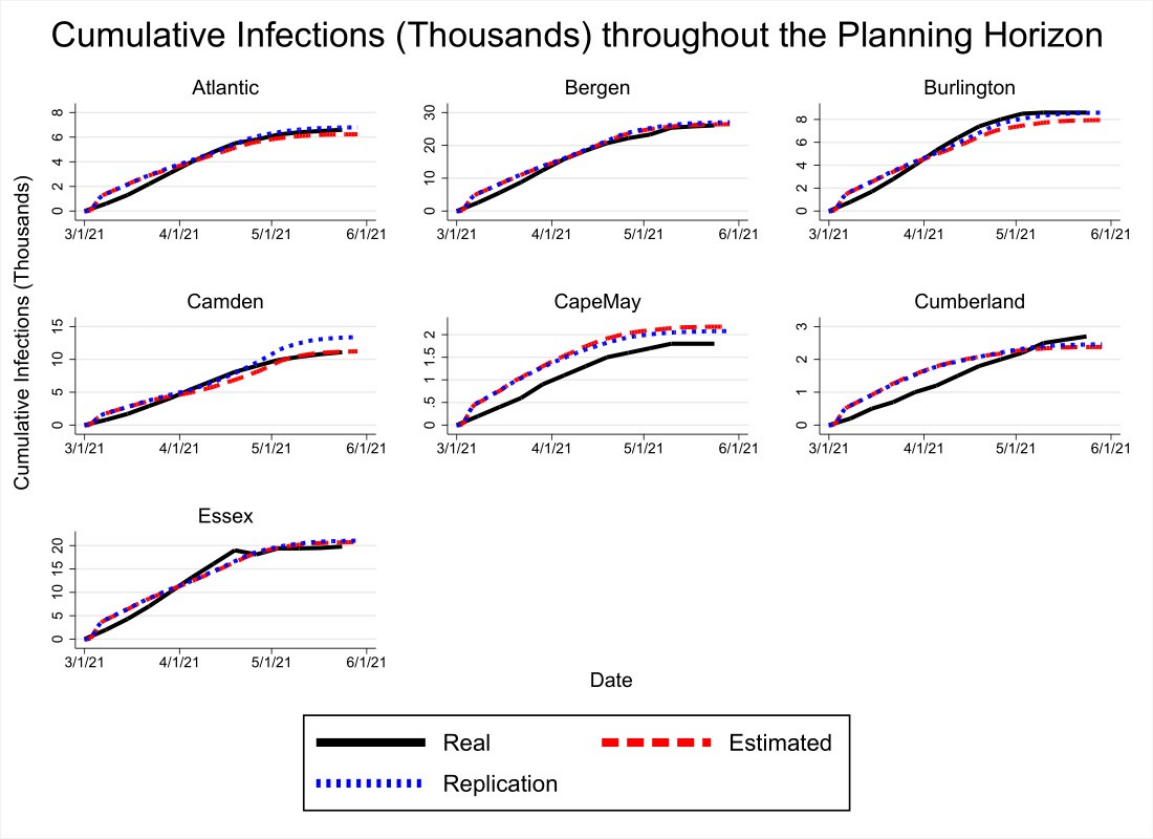

Figure A3: Cumulative infections (thousands) throughout the planning horizon for New Jersey counties - 1.

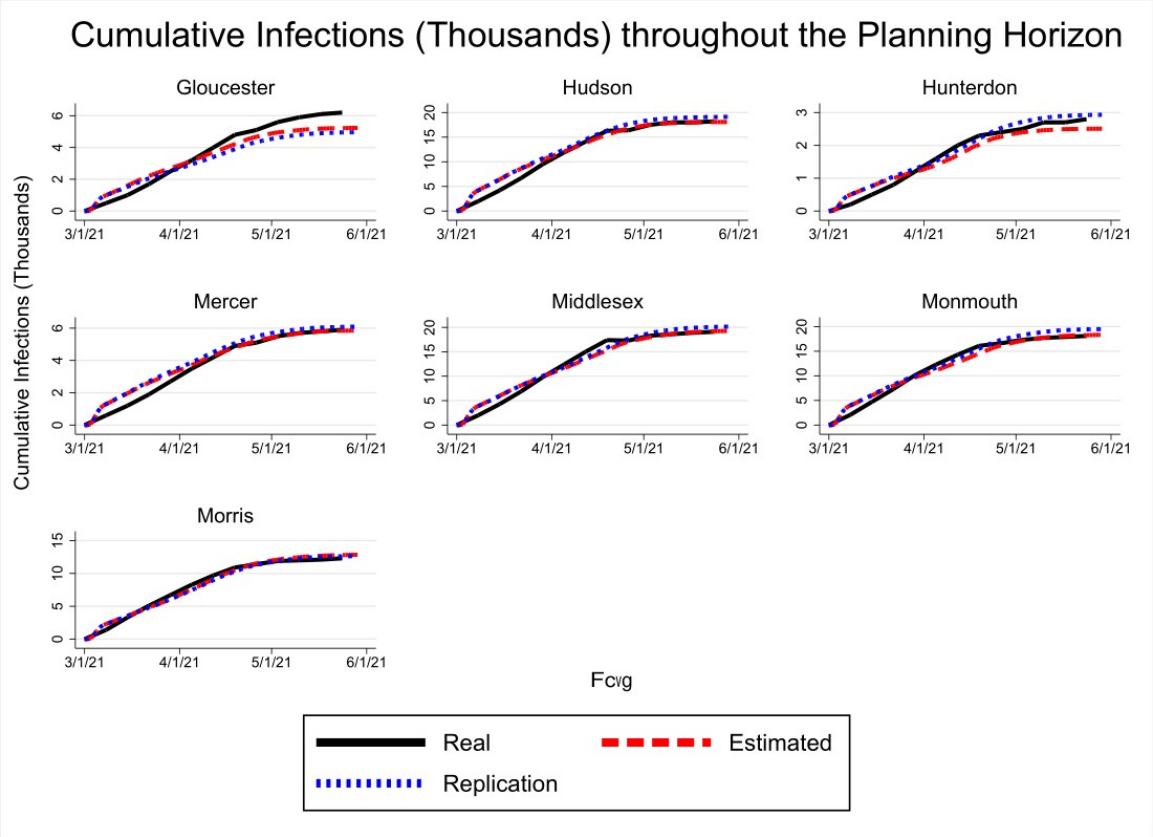

Figure A4: Cumulative infections (thousands) throughout the planning horizon for New Jersey counties - 2.

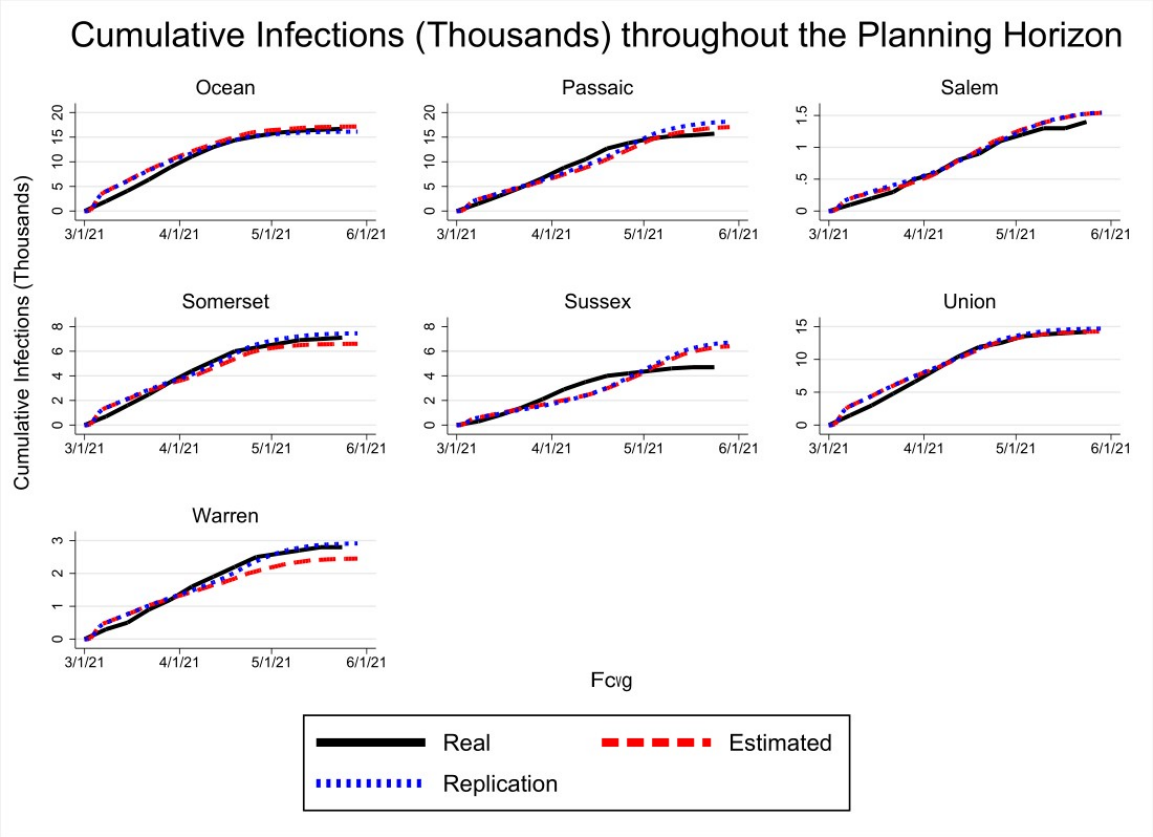

Figure A5: Cumulative infections (thousands) throughout the planning horizon for New Jersey counties - 3.

A6 Comparison of optimization with simulation-optimization

In this section, we compare the output of the optimization model with the results of the simulation-optimization model. In Figures A6-A8, "OR" indicates that we use the optimization model without any simulation to predict infections for the whole planning horizon, while "Estimated" refers to the predictions of the simulation-optimization model presented in this paper. Since the cumulative number of infections predicted by the optimization model is much more than simulation-optimization, we only present the first month's results. Overall, the simulation-optimization model provides better predictions on infections than the optimization model, as shown in Figures A6-A8.

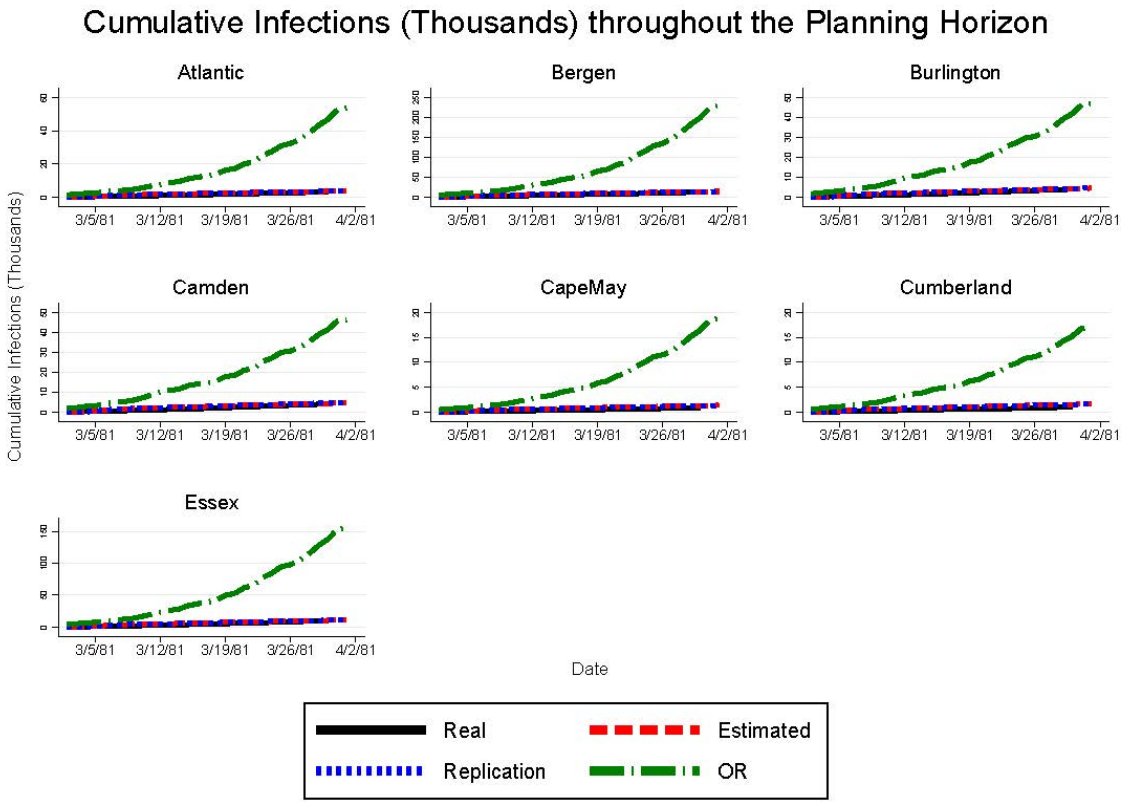

Figure A6: Cumulative infections (thousands) throughout the planning horizon for New Jersey counties - 1.

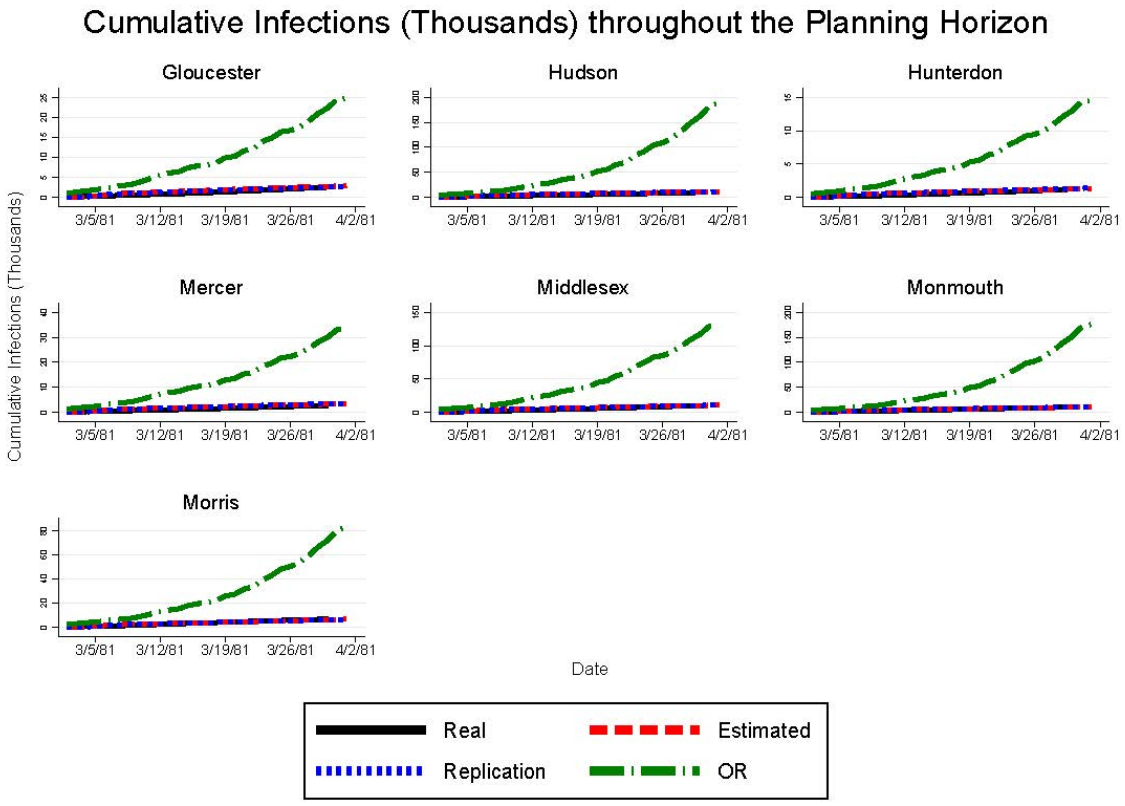

Figure A7: Cumulative infections (thousands) throughout the planning horizon for New Jersey counties - 2.

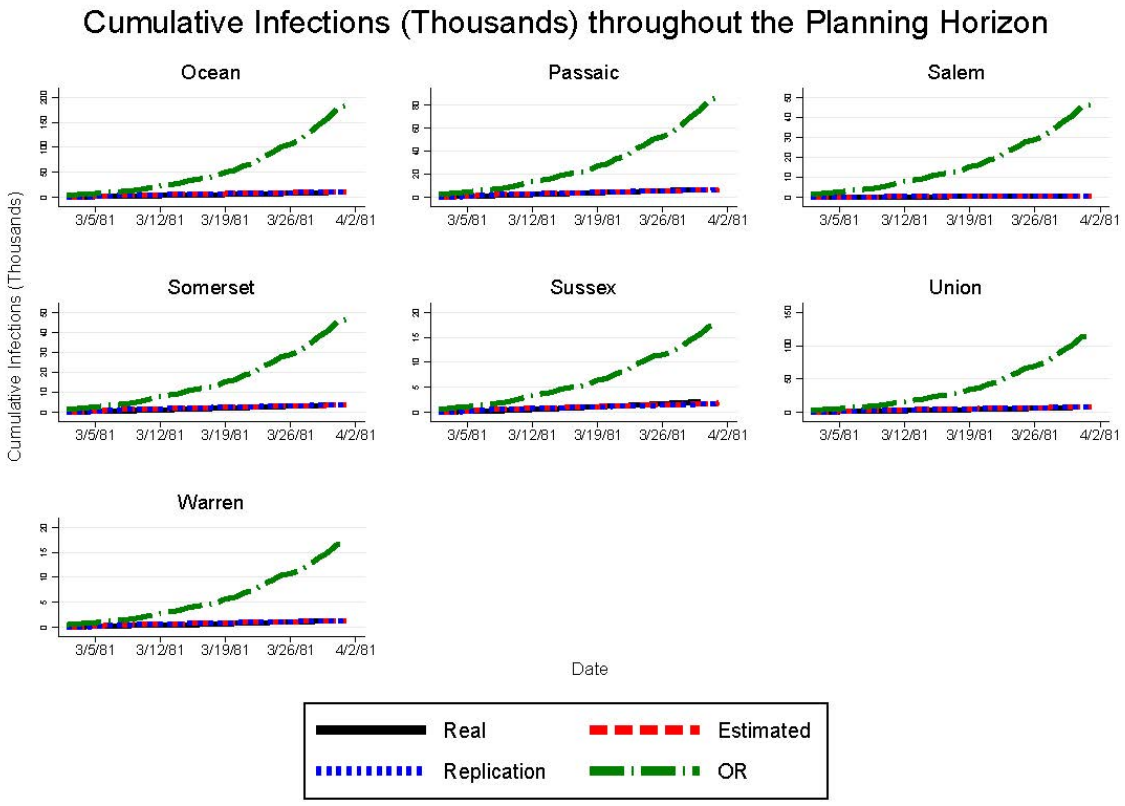

Figure A8: Cumulative infections (thousands) throughout the planning horizon for New Jersey counties - 3.

A7 Case Study Data

This section presents the data used to formulate and test the model. The data includes the population for each county in New Jersey State, the number of infections over time for each county in New Jersey State, the logistics cost, and the cost of vaccines.

A7.1 Population and Infection Data

Table A3 shows the population and the cumulative number of infections data for each county in New Jersey state, which is obtained from JHU (2020). For the number of infections, we only present three specific days of the total 90-day period, which are March 1, April 12, and May 24, 2021. The numbers of cumulative infections are rounded in thousands.

Source: (Aparadinar, 2021)

Figure A9: All the counties in New Jersey.

A7.2 Logistics and Operations Cost Data

Table A4 presents the vaccine cost and efficiency data for Pfizer, Moderna, and Janssen. The fixed cost of establishing the vaccination center includes planning and coordination cost, training cost, social mobilization cost, cold chain equipment cost, pharmacovigilance cost, as well as hand hygiene cost, and is estimated to be around $255,000 (WHO, 2021).

Table A3: Populations and the Number of Infections (in Thousands) for Each County in New Jersey

County	Population	March 1, 2021	April 12, 2021	May 24, 2021
Atlantic	274.5	24.9	29.7	31.5
Bergen	905.1	78	96.4	104.1
Burlington	448.7	35.5	41.9	44.1
Camden	513.5	44.3	51.1	55.4
Cape May	97.3	7.3	8.6	9.1
Cumberland	156.6	14.3	15.8	17
Essex	783.9	74	90.1	93.8
Gloucester	288.8	24.2	28.2	30.4
Hudson	634.3	69.6	83.7	87.8
Hunterdon	127.4	7	9	9.8
Mercer	367.5	27.9	32.1	33.8
Middlesex	810.0	72.8	87.8	91.9
Monmouth	630.4	57.2	71.5	75.3
Morris	492.3	37.7	47.4	50
Ocean	576.5	58.9	71.9	75.6
Passaic	501.6	57	67.5	72.7
Salem	66.1	4.7	5.5	6.1
Somerset	323.5	22.9	28.1	30
Sussex	148.9	9.2	12.7	13.9
Union	536.5	57	67.4	71.2
Warren	108.6	7.1	9	9.9

Table A4: COVID-19 Vaccine Cost ($) and Efficiency (Seladi-Schulman, 2021)

Vaccine Category	Cost per dose	First Dose Efficiency	Second Dose Efficiency
Pfizer	19.5	80%	95%
Moderna	15	80%	94.1%
Janssen	10	74.4%	-

A8 Model Validation

While OR models are extensively studied and used in practice, from transportation to production, the validation of optimization models, especially spatio-temporal ones, is inherently difficult since replicating the model decisions in real life and collecting observations might not be possible (Landry et al., 1983). Since our optimization model works with the agent-based simulation iteratively, where we fix the output of one in the other model as an input, as discussed in detail in Section 3.3, the results of each approach could validate the other. In this section, we present the validation approach and results for the simulation-optimization model. The government set up one Pfizer vaccination center in March at the New Jersey Institute of Technology in Essex County. The vaccination center can vaccinate up to 6,000 people each day. Thus, we use this actual vaccination center location in our model for validation. The number of Pfizer vaccine centers in our model is set to 1, and the location is in Essex County, while other types of vaccine centers are set to be 0 in the validation experiments. Similarly, the daily vaccine supply capacity upper bound for all local pharmacies and small vaccination sites in a region is set to 10,000 using real data from CDC (Heffernan, 2021). The optimization model decides how many vaccines of each type are allocated to each region, and these values are fixed as inputs in the simulation model. We use the data from JHU (2021) for the model

validation. We present the number of estimated infections throughout the 90-day planning horizon and compare it with the real outbreak data. The results of nine counties are shown in Figure A10.

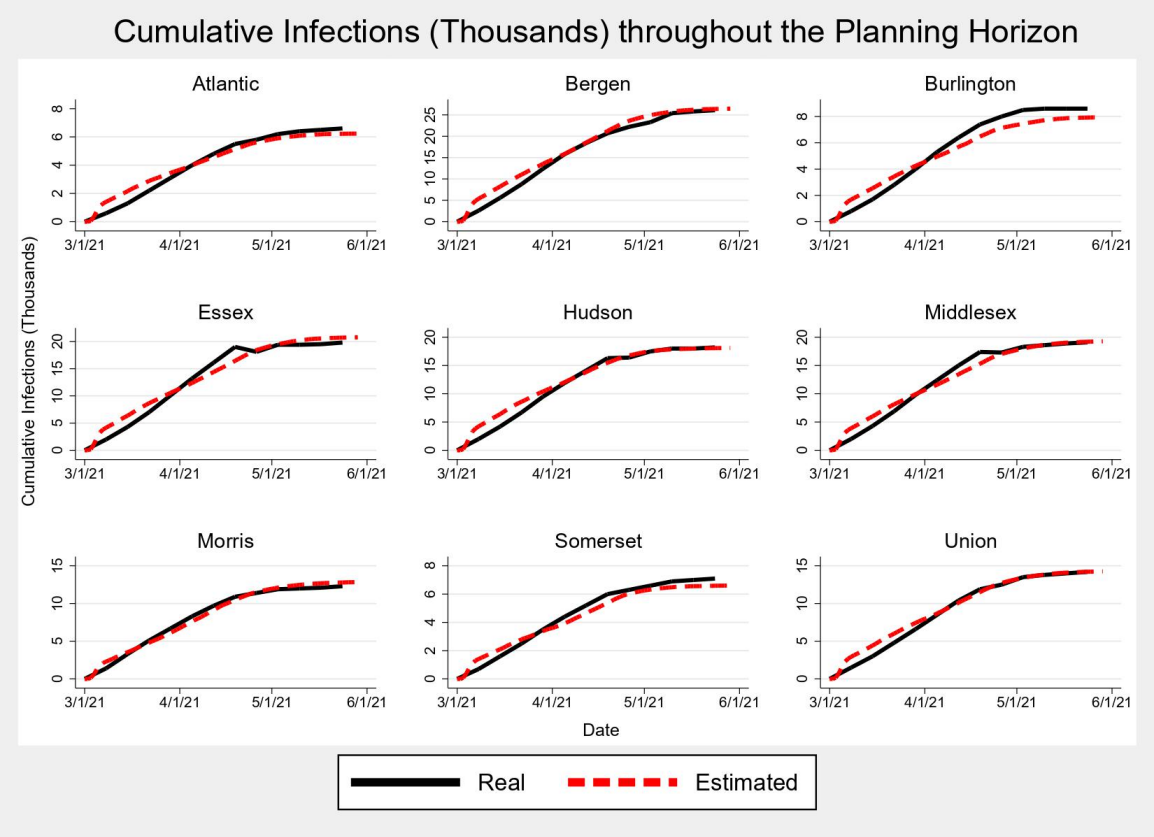

Figure A10: Model validation against real outbreak data in nine counties of New Jersey. The total cumulative infections are given only from March 1, 2021, to May 30, 2021.

According to the results, the estimation fits the real data well. A non-zero number of initial infections are considered, as shown in Appendix Table A3, while the total cumulative infections are given only between March 1, 2021 and May 30, 2021, in Figure A10. Covasim sharply increases the infections in the first few periods. However, since the real data starts from the mid-pandemic, on March 1, 2021, the simulation model predicts a slightly greater number of infections at the beginning of the time period. In the later periods, the predicted number may become less than the real data for some counties. In addition, we performed a paired t-test to analyze the difference between the weekly pairs of predicted new infections and the actual data in each period. As shown in Table A5, p-values corresponding to all counties are greater than 0.05, and thus our model provides statistically similar predictions with the real outbreak data from March 1 to May 30, 2021, for each

Table A5: Statistical Analysis Comparing Weekly Predicted New Cases and Real Outbreak Data

County	Mean		Two-tailed paired t-test		
	Outbreak	Predicted	t-stat	t-critical	p-value
Atlantic	508	479	0.21	2.20	0.73
Bergen	2008	2030	0.04		0.94
Burlington	662	609	0.28		0.61
Camden	854	860	0.03		0.96
Cape May	138	167	0.60		0.27
Cumberland	208	183	0.46		0.59
Essex	1523	1593	0.14		0.84
Gloucester	477	402	0.69		0.25
Hudson	1400	1391	0.02		0.97
Hunterdon	215	193	0.40		0.56
Mercer	454	449	0.03		0.95
Middlesex	1469	1477	0.02		0.98
Monmouth	1392	1405	0.03		0.96
Morris	946	984	0.14		0.74
Ocean	1285	1318	0.08		0.86
Passaic	1208	1300	0.33		0.62
Salem	108	117	0.40		0.54
Somerset	546	507	0.26		0.64
Sussex	362	484	1.24		0.27
Union	1092	1093	0.00		0.99
Warren	215	188	0.52		0.35

considered county in New Jersey.

Figures A11, A12, and A13 show the results of model validation against the real outbreak data for all the counties in New Jersey. In all figures and tables presented in this section, the total cumulative infections are given only from March 1, 2021, to May 30, 2021.

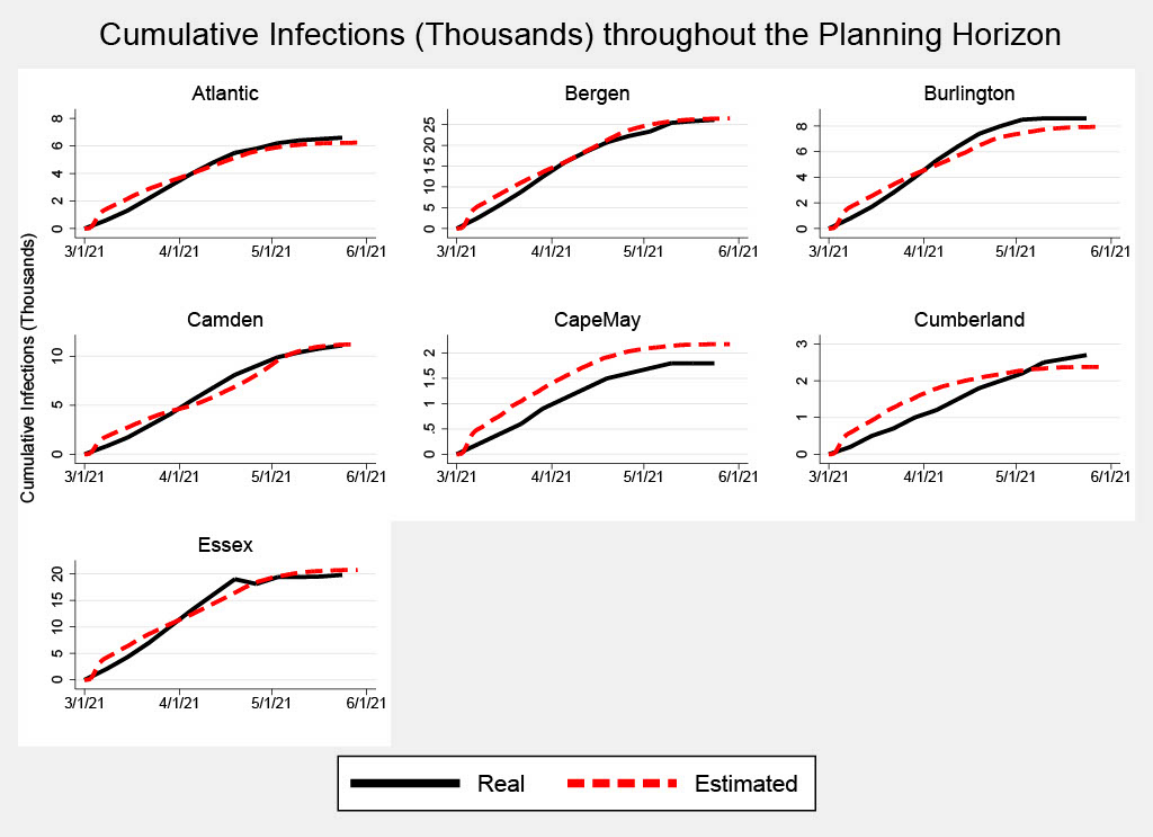

Figure A11: Cumulative infections (thousands) throughout the planning horizon for New Jersey counties - 1.

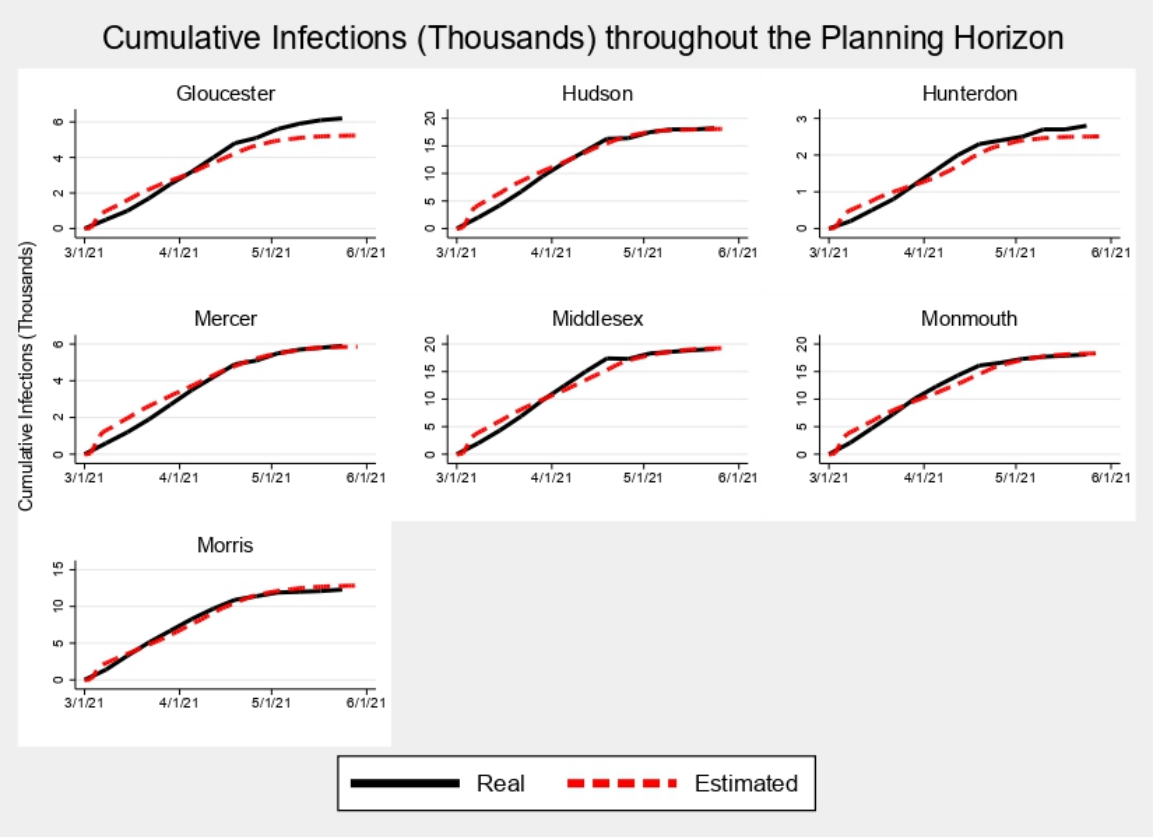

Figure A12: Cumulative infections (thousands) throughout the planning horizon for New Jersey counties - 2.

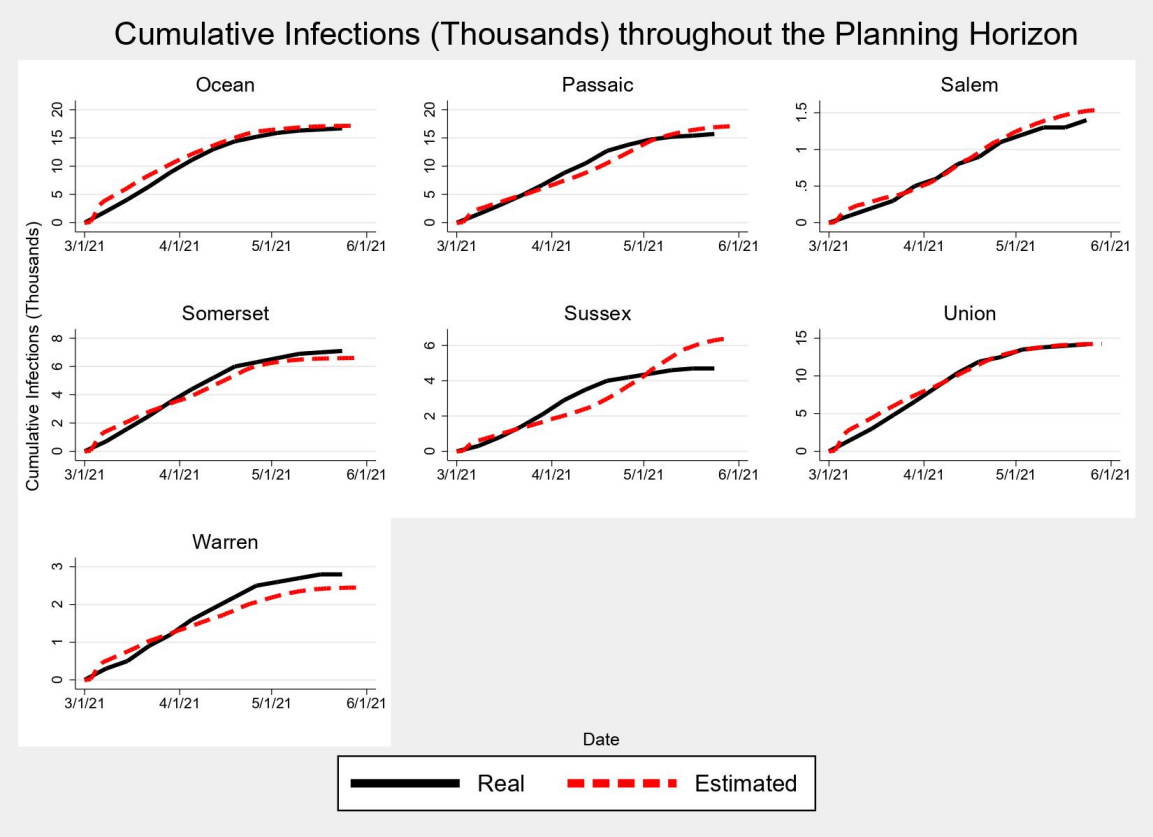

Figure A13: Cumulative infections (thousands) throughout the planning horizon for New Jersey counties - 3.

A9 Budget Impacts on Cumulative Infections

Figure A14 shows the number of cumulative infections under different budget levels for the nine most populated counties in New Jersey. Figures A15, A16, and A17 show the results of the cumulative number of infections under different budget levels for all the counties in New Jersey. According to the results, the number of cumulative infections stays the same under different budget levels at the initial stages. This is because it takes time for people to develop symptoms after being infected. Thus, the difference in the number of cumulative infections becomes more significant after a certain time period. For almost all the counties shown in Figure A14, the ample budget level generates the least number of cumulative infections due to the high number of vaccines allocated, followed by the medium budget level. However, for some counties, the cumulative number of infected individuals under different budget levels is similar, especially for the medium and ample budget levels. Not

surprisingly, we find that these counties either have high populations or high initial infections. Thus, the model gives priority to allocating more vaccines to these counties when the budget is not ample.

We find that some counties do not have fewer infections under the ample budget level (e.g., CapeMay and Salem County). In this result, the randomness in the agent-based simulation plays a role. The agent-based simulation randomly allocates vaccination to different compartments, such as susceptible and recovered individuals. While more people are vaccinated under the medium and ample budget levels, more recovered people than susceptible people could be vaccinated in a random simulation. Thus, the number of cumulative infections may be slightly higher in some counties under medium and ample budget levels compared to the limited budget level.

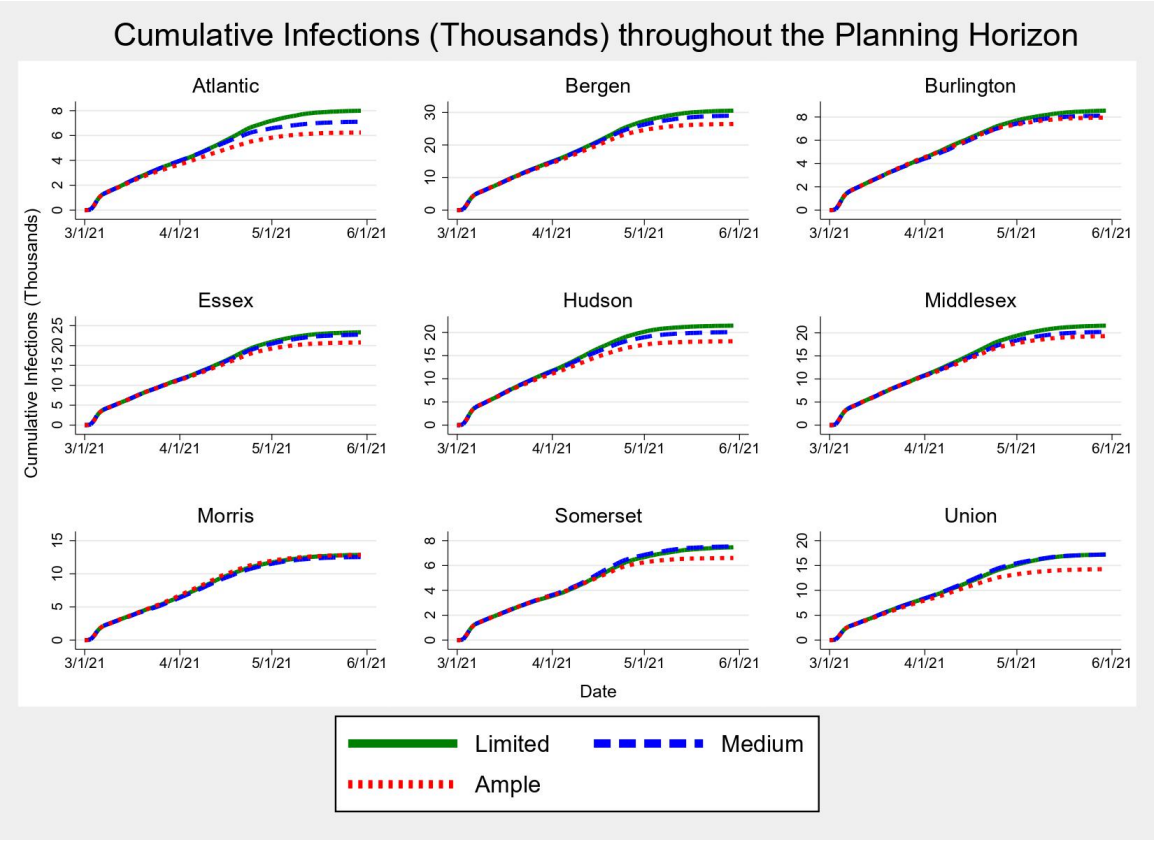

Figure A14: New Jersey cumulative infections under different budget levels. The total cumulative infections are given only from March 1, 2021, to May 30, 2021.

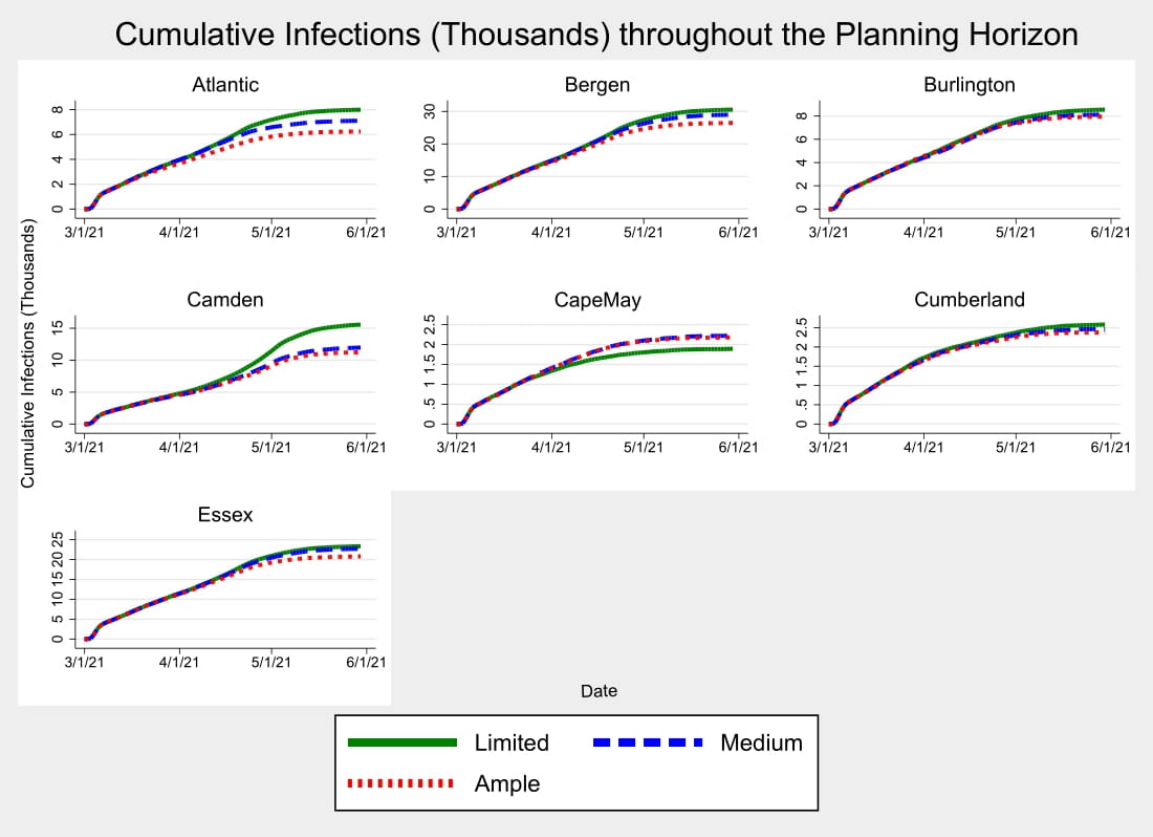

Figure A15: New Jersey cumulative infections under different budget levels - 1.

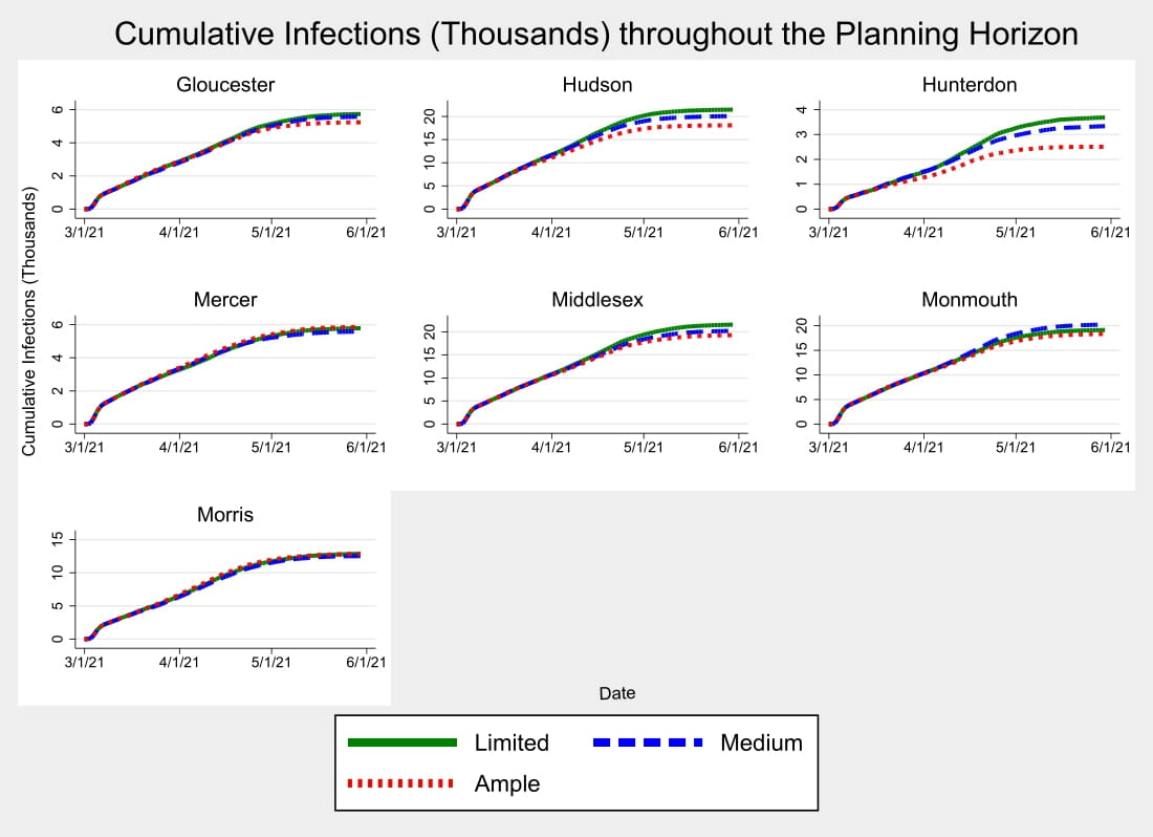

Figure A16: New Jersey cumulative infections under different budget levels - 2.

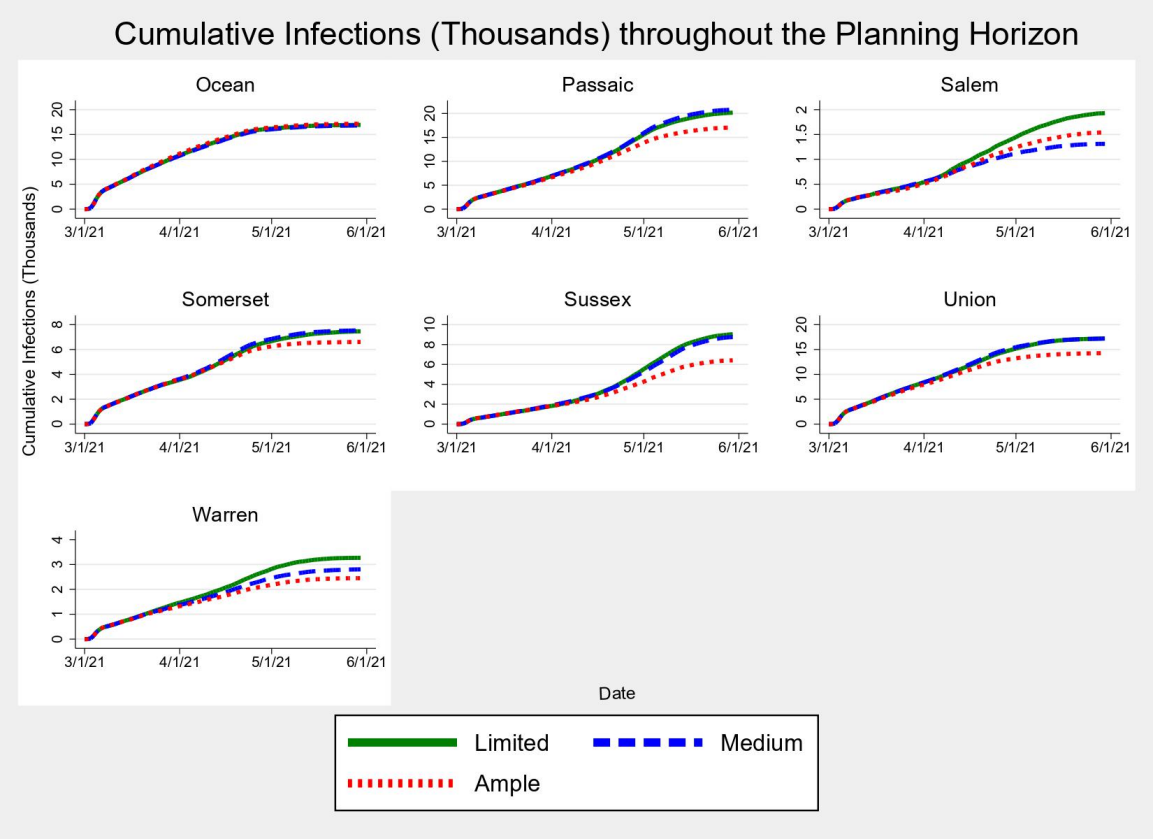

Figure A17: New Jersey cumulative infections under different budget levels - 3.

Tables A6, A7, and A8 present the statistical results comparing cumulative infections for each county under each combination of budget levels, limited and medium, limited and ample, and medium and ample, respectively. Since p values are less than 0.01, we can say that the number of cumulative infections in each region is statistically different under different budget levels.

Table A6: Statistical Analysis Comparing Limited and Medium Budget Levels

County	Cumulative Infections		Two-tailed paired-t-test		
	Limited	Medium	t-stat	t-critical	p-value
Atlantic	7993	7104	8.54	1.99	3.13E-13
Bergen	30555	29034	9.26		9.76E-15
Burlington	8545	8117	11.84		4.66E-20
Camden	15573	11976	8.99		3.55E-14
Cape May	1890	2222	12.13		1.22E-20
Cumberland	2580	2466	13.33		5.13E-23
Essex	23337	22730	10.32		6.32E-17
Gloucester	5733	5574	14.65		1.49E-25
Hudson	21478	20086	10.63		1.41E-17
Hunterdon	3682	3338	9.26		9.72E-15
Mercer	5785	5585	5.01		2.73E-06
Middlesex	21564	20207	10.09		1.83E-16
Monmouth	19122	20224	9.95		3.55E-16
Morris	12851	12524	17.23		2.98E-30
Ocean	16938	16821	13.11		1.40E-22
Passaic	20173	20803	8.46		4.51E-13
Salem	1930	1312	8.62		2.16E-13
Somerset	7463	7535	12.35		4.52E-21
Sussex	9036	8753	6.18		1.80E-08
Union	17216	17208	6.99		4.57E-10
Warren	3269	2806	11.24		8.06E-19

Table A7: Statistical Analysis Comparing Limited and Ample Budget Levels

County	Cumulative Infections		Two-tailed paired-t-test		
	Limited	Ample	t-stat	t-critical	p-value
Atlantic	7993	6240	11.45	1.99	2.99E-19
Bergen	30555	26461	10.22		1.00E-16
Burlington	8545	7946	8.13		2.23E-12
Camden	15573	11241	8.78		9.85E-14
Cape May	1890	2179	11.98		2.53E-20
Cumberland	2580	2378	12.73		7.75E-22
Essex	23337	20778	9.76		8.83E-16
Gloucester	5733	5238	7.68		1.82E-11
Hudson	21478	18106	12.02		2.06E-20
Hunterdon	3682	2508	11.86		4.29E-20
Mercer	5785	5852	14.65		1.49E-25
Middlesex	21564	19294	10.11		1.69E-16
Monmouth	19122	18340	9.77		8.68E-16
Morris	12851	12844	10.79		6.65E-18
Ocean	16938	17167	20.81		3.72E-36
Passaic	20173	17071	9.57		2.20E-15
Salem	1930	1543	9.95		3.60E-16
Somerset	7463	6607	7.78		1.14E-11
Sussex	9036	6414	8.11		2.44E-12
Union	17216	14273	10.91		3.82E-18
Warren	3269	2451	11.22		8.84E-19

Table A8: Statistical Analysis Comparing Medium and Ample Budget Levels

County	Cumulative Infections		Two-tailed paired-t-test		
	Medium	Ample	t-stat	t-critical	p-value
Atlantic	7104	6240	14.15	1.99	1.30E-24
Bergen	29034	26461	10.78		7.07E-18
Burlington	8117	7946	1.24		2.17E-01
Camden	11976	11241	7.64		2.23E-11
Cape May	2222	2179	9.43		4.38E-15
Cumberland	2466	2378	11.08		1.69E-18
Essex	22730	20778	9.54		2.56E-15
Gloucester	5574	5238	4.65		1.13E-05
Hudson	20086	18106	13.01		2.14E-22
Hunterdon	3338	2508	13.06		1.76E-22
Mercer	5585	5852	12.72		8.10E-22
Middlesex	20207	19294	10.07		2.01E-16
Monmouth	20224	18340	9.94		3.88E-16
Morris	12524	12844	16.98		8.30E-30
Ocean	16821	17167	19.56		3.59E-34
Passaic	20803	17071	9.38		5.48E-15
Salem	1312	1543	6.55		3.50E-09
Somerset	7535	6607	9.49		3.33E-15
Sussex	8753	6414	8.34		8.10E-13
Union	17208	14273	11.41		3.49E-19
Warren	2806	2451	11.16		1.16E-18

A10 Number of Vaccines Allocated to Each County under Medium and Ample Budget

Table A9: Vaccine Allocation under Medium Budget Level

County	Population Proportion	Vaccine Proportion	Difference	Total Vaccine Dose	Pfizer First Dose	Pfizer Second Dose	Moderna First Dose	Moderna Second	Janssen
Atlantic	3.1%	3.2%	-0.1%	61,169	4,500	1,080	26,005	13,683	15,901
Bergen	10.3%	9.9%	0.4%	188,279	4,500	1,080	84,927	47,770	50,002
Burlington	5.1%	5.2%	-0.1%	98,378	4,500	1,080	41,796	22,671	28,331
Camden	5.8%	5.9%	-0.1%	112,200	4,501	1,081	49,253	27,279	30,086
Cape May	1.1%	1.3%	-0.2%	24,961	4,504	1,084	8,905	3,680	6,788
Cumberland	1.8%	1.9%	-0.1%	36,933	4,501	1,080	14,368	6,814	10,170
Essex	8.9%	8.6%	0.3%	163,455	4,500	1,080	72,965	40,689	44,221
Gloucester	3.3%	3.4%	-0.1%	65,606	4,504	1,084	27,469	14,543	18,006
Hudson	7.2%	7.0%	0.2%	134,295	4,500	1,080	60,535	33,883	34,297
Hunterdon	1.4%	1.6%	-0.2%	31,162	4,500	1,080	11,837	5,398	8,347
Mercer	4.2%	4.3%	-0.1%	82,226	4,500	1,080	35,112	19,013	22,521
Middlesex	9.2%	9.0%	0.2%	170,680	4,504	1,084	77,708	43,924	43,460
Monmouth	7.2%	7.0%	0.2%	133,654	4,500	1,080	60,232	33,703	34,139
Morris	5.6%	5.5%	0.1%	105,676	4,500	1,080	46,992	25,992	27,112
Ocean	6.6%	6.4%	0.2%	122,502	4,500	1,080	54,960	30,630	31,332
Passaic	5.7%	5.6%	0.1%	107,558	4,500	1,080	47,909	26,496	27,573
Salem	0.8%	1.0%	-0.2%	18,657	4,500	1,080	5,932	1,946	5,199
Somerset	3.7%	3.7%	0.0%	71,320	4,500	1,080	30,800	16,489	18,451
Sussex	1.7%	1.9%	-0.2%	35,542	4,504	1,084	13,902	6,600	9,452
Union	6.1%	6.0%	0.1%	114,559	4,500	1,080	51,216	28,433	29,330
Warren	1.2%	1.4%	-0.2%	27,316	4,500	1,080	10,020	4,334	7,382
Total	**100.0%**	**100.0%**	**3.4%***	**1,906,128**	**94,518**	**22,697**	**832,843**	**453,970**	**502,100**

*The sum of the absolute value of the difference between the population and vaccination proportions.

Under the medium budget level (Table A9), the total number of Janssen vaccines allocated is decreased, while more Moderna vaccines are allocated (which is also shown in Figure 7). This is because the model starts to consider the vaccine efficacy when the budget increases and the expected number of people saved by the vaccines with higher efficacy is more than the number of people saved

by the vaccines with a lower efficacy. Nevertheless, since Pfizer is still much more expensive than Moderna and Janssen, the model allocates more Moderna vaccines instead of Pfizer. Observing the population and vaccination proportions, the counties with a higher population receive even more vaccines. For example, the percentage of vaccines distributed to Bergen county increases from 9.5% to 9.9% when the budget is increased from limited to medium. This is because the total number of vaccines allocated is still not enough to satisfy the people's vaccination needs, and the model gives priority to distributing more vaccines to the regions with high populations and high initial infections. Under the medium budget, we also observe less deviation between the population and vaccination proportions compared to the limited budget case.

Table A10: Vaccine Allocation under Ample Budget Level

County	Population Proportion	Vaccine Proportion	Difference	Total Vaccine Dose	Pfizer First Dose	Pfizer Second Dose	Moderna First Dose	Moderna Second	Janssen
Atlantic	3.1%	3.1%	0.0%	88,854	34,143	17,744	29,833	2,634	4,500
Bergen	10.3%	10.3%	0.0%	294,610	161,094	66,391	58,775	3,850	4,500
Burlington	5.1%	5.1%	0.0%	145,735	70,577	31,296	36,846	2,514	4,502
Camden	5.8%	5.9%	-0.1%	167,620	104,750	38,124	18,890	1,352	4,504
Cape May	1.1%	1.1%	0.0%	30,842	13,383	4,596	6,619	1,744	4,500
Cumberland	1.8%	1.8%	0.0%	50,308	21,690	9,031	13,131	1,956	4,500
Essex	8.9%	8.9%	0.0%	254,718	136,864	55,362	53,241	4,751	4,500
Gloucester	3.3%	3.3%	0.0%	93,755	56,344	20,229	11,328	1,352	4,502
Hudson	7.2%	7.2%	0.0%	205,278	101,315	45,020	51,386	3,057	4,500
Hunterdon	1.4%	1.4%	0.0%	40,817	18,793	6,749	8,766	2,009	4,500
Mercer	4.2%	4.2%	0.0%	119,530	56,846	24,608	30,394	3,178	4,504
Middlesex	9.2%	9.3%	-0.1%	264,130	136,834	61,506	59,940	1,350	4,500
Monmouth	7.2%	7.2%	0.0%	204,867	104,985	42,127	46,883	6,372	4,500
Morris	5.6%	5.6%	0.0%	160,023	70,210	33,748	47,679	3,886	4,500
Ocean	6.6%	6.5%	0.1%	186,872	95,527	38,248	42,705	5,892	4,500
Passaic	5.7%	5.7%	0.0%	162,595	76,867	35,180	43,377	2,671	4,500
Salem	0.8%	0.7%	0.1%	20,749	6,852	2,420	5,502	1,475	4,500
Somerset	3.7%	3.7%	0.0%	105,050	47,109	20,604	29,120	3,717	4,500
Sussex	1.7%	1.7%	0.0%	47,786	19,483	8,233	13,374	2,196	4,500
Union	6.1%	6.1%	0.0%	174,383	86,554	36,975	42,214	4,140	4,500
Warren	1.2%	1.2%	0.0%	34,624	13,765	5,579	9,104	1,676	4,500
Total	**100.0%**	**100.0%**	**0.4%***	**2,853,146**	**1,433,985**	**603,770**	**659,107**	**61,772**	**94,512**

*The sum of absolute value of the difference between the population and vaccination proportions.

* The sum of absolute value of the difference between the population and vaccination proportions

As shown in Table A10, the total number of Pfizer vaccines allocated under the ample budget level increases significantly. When there is no budget limitation on the vaccine allocation, vaccine efficacy is the only consideration for the vaccine administration. Thus, Pfizer vaccines have the priority to be allocated compared with Moderna and Janssen. Under the ample budget level, the vaccine allocation proportion is almost the same as the population proportion. For example, Bergen county receives 10.3% of the total vaccines, which is equivalent to its population proportion. This is because all people who are willing to be vaccinated receive the vaccine shots when the budget is ample and as long as there is a sufficient vaccine supply. Furthermore, we assume the same vaccine acceptance rate in each county of New Jersey.

A11 Vaccination Center Locations for Multiple Vaccine Types

We also study vaccination center locations for multiple types of vaccines. Figure A18 presents the vaccination center locations when the numbers of Moderna centers and Janssen centers are set to one, while the number of Pfizer centers remains to be two. On the left side of Figure A18, we allow each county to have different types of vaccine centers. On the right side of Figure A18, each region can only have one type of vaccine center. For the first case, Essex County has the Pfizer and Moderna centers allocated, while Union County has another Pfizer center allocated. This is because the vaccine warehouses for Pfizer and Moderna are located in Essex County. Somerset County has the Janssen vaccination center allocated since the Janssen manufacturer and the warehouse are located in Somerset. Here, the distance from the warehouse to the vaccination centers is the main factor that influences the vaccination center locations. Therefore, the model chooses the closest county to the supply warehouse for each type of vaccine as the corresponding vaccination center. For the second case, the Moderna vaccination center is moved to Hudson County since each county can only have one vaccination center, and Hudson County is the third closest county to the warehouse after Essex County and Union County. We do not show the vaccine centers' service decisions in Figure A18 for clarity. In this figure, the service decision for the Pfizer center is the same as on the right side of Figure A9. We find that Union County is geographically the closest county to Essex County, where the Pfizer warehouse is allocated. Thus, the locations of vaccination centers for New Jersey counties are ordered by their distance from the warehouse from low to high.

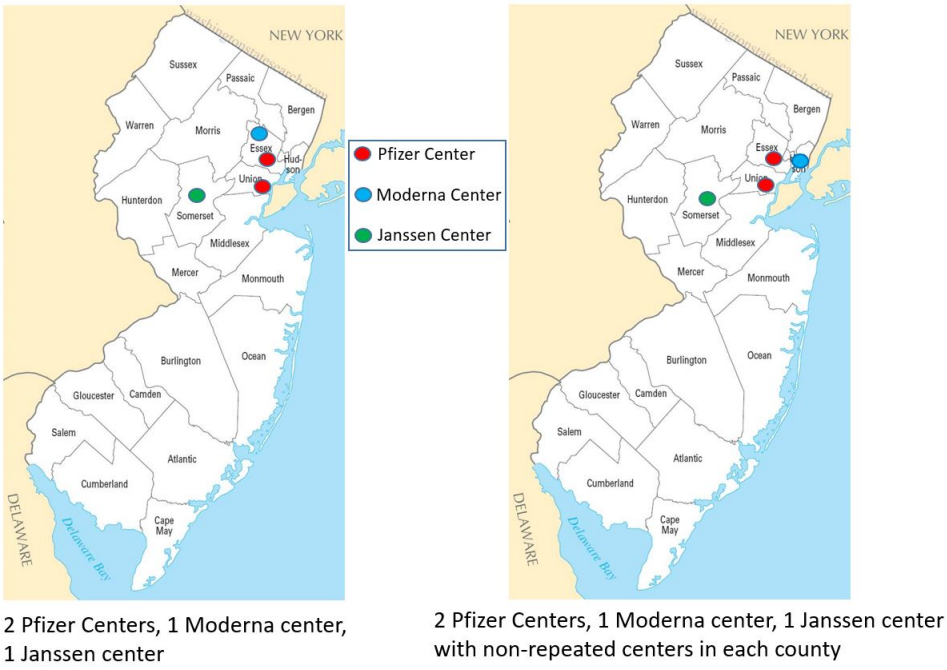

Figure A18: Vaccination center locations for all types of vaccines.

A12 Vaccine Allocation between Centers and Pharmacies

Table A11 presents the results of vaccine allocation between the vaccination centers and local pharmacies (and small vaccination sites) when only one Pfizer center is located. Under the limited budget level, the model allocates all the Pfizer vaccines to the vaccination centers. This is because the number of Pfizer vaccines distributed is relatively low, and vaccine allocation to the vaccination center costs lower than that to local pharmacies and small vaccination sites. Under the medium budget level, the number of vaccines allocated to the vaccination center decreases. But still, the total number of vaccines allocated to the vaccination center is much more than the local pharmacies and small vaccination sites. Under an ample budget level, the model allocates the majority of the vaccines to local pharmacies and small vaccination sites since the number of Pfizer vaccines is significantly increased, and the vaccination capacity provided by pharmacies and small vaccination sites in total is larger than that of the vaccination centers.

Table A11: Vaccine Allocation with Only One Pfizer Center

		Budget					
		Limited		Medium		Ample	
Pfizer	Center	117,180	100%	141,959	73%	310,134	15%
	Pharmacy	0	0%	51,916	27%	1,727,621	85%
	Total	117,180	100%	193,875	100%	2,037,755	100%

Table A12 shows the vaccine allocation results between vaccination centers and local pharmacies (and small vaccination sites) with different types of vaccination centers. In this case, the number of Pfizer vaccination centers is fixed to two, and the number of Moderna and Janssen vaccination centers is set to one each. Similar to Table A11, the number of vaccines allocated to the vaccination centers shows a decreasing trend for each type of vaccine when the budget is increased from limited to ample. Under the medium budget level, Pfizer vaccination centers receive all the vaccines, while Moderna and Janssen's vaccines are mostly sent to pharmacies and small vaccine centers due to their higher volume compared to the Pfizer vaccine. At an ample budget level, almost all vaccines are given in pharmacies and small vaccine sites, reducing the need for vaccine centers, which may come with a high fixed cost and limited capacity for vaccination. This result is also consistent with what happened in the real case. When vaccines were newly available and limited, most people had to travel to the vaccine centers for mass vaccination. As vaccines become more available, then most vaccines are distributed to local pharmacies so that people are able to get immunization in their own counties (Gharpure et al., 2021; Paudyal et al., 2021).

Table A12: Vaccine Allocation When Vaccine Center Types and Locations are Fixed

		Budget					
		Limited		Medium		Ample	
Pfizer	Center	117,180	100%	117,173	100%	5,310	0.3%
	Pharmacy	0	0%	19	0%	1,657,658	99.7%
	Total	117,180	100%	117,192	100%	1,662,968	100%
Moderna	Center	117,180	100%	150,834	14%	0	0%
	Pharmacy	0	0%	949,523	86%	1,098,128	100%
	Total	117,180	100%	1,100,357	100%	1,098,128	100%
Janssen	Center	120,156	18%	122,988	21%	0	0%
	Pharmacy	550,425	82%	452,209	79%	94,500	100%
	Total	670,581	100%	575,197	100%	94,500	100%

A13 Additional Sensitivity Analysis

A13.1 Vaccination priority of different age groups

We have performed a sensitivity analysis on the vaccination of different age groups. We re-defined the probability of being vaccinated for each age group for all three types of vaccines. Those revised probabilities are 0.1 for people with age < 50, 0.3 for people with age between 50 and 75, and 0.6 for people with age ≥ 75. We compared the results of cumulative infections with previous results (with an equal probability of vaccination for different age groups) and presented the results in Table A13. The cumulative infections are similar to the original vaccination strategy (equal probability of vaccination for different age groups). However, when we look at the detailed data, the vaccination of different age groups has hundreds of fewer infections for most of the counties compared with the original strategy. Thus, it is still a large improvement in the infection number. According to the results, giving priority to vaccinating people of higher ages leads to fewer cumulative infections throughout the planning horizon. Similar conclusions are also reported in the existing literature (see, e.g., Sadarangani et al. (2021)).

Table A13: Number of cumulative infections under each vaccination strategy: Non-old priority (equal probability of vaccination for different age groups) and Old priority (higher probability for older age groups)

County	Mean	
	Non-old priority	Old priority
Atlantic	6,791	6,010
Bergen	27,047	23,862
Burlington	7,888	7,233
Camden	14,334	11,106
Cape May	2,027	1,943
Cumberland	2,532	2,199
Essex	21,052	17,903
Gloucester	5,195	4,966
Hudson	18,805	18,752
Hunterdon	2,782	2,199
Mercer	5,945	5,434
Middlesex	19,945	17,736
Monmouth	17,891	16,647
Morris	13,247	11,760
Ocean	16,708	14,929
Passaic	17,275	14,442
Salem	1,297	1,212
Somerset	7,363	7,410
Sussex	6,107	5,830
Union	14,058	12,907
Warren	2,546	2,152

A13.2 Incorporating vaccine storage costs

We perform sensitivity analysis on the vaccine storage cost. We obtained the information on vaccine storing conditions from CDC (2022). Through online searches and our communications with experts whose research focuses on the COVID-19 vaccines, we found out that those vaccines are often stored in super refrigerators. Those refrigerators have a large capacity and can store all the vaccines supplied in each time period, as considered in this study. In addition, they can change the temperature according to the need (INDUSTRIAL, 2023). Therefore, the cost of vaccine storage includes the fixed cost of purchasing super refrigerators and the electricity cost, which is typically low compared to

the fixed cost. Since adding the fixed cost would unnecessarily complicate the model, instead of using a fixed cost, we perform sensitivity analysis by adding an approximate 10% extra cost on vaccine prices to reflect the impact of different storage conditions on their distribution. Since Pfizer and Moderna require similar and stricter storage conditions than Janssen, we add more costs ($2 for Pfizer and Moderna and $1 for Janssen). We use $\$5M$ (limited) and $\$10M$ (medium) budget levels for the sensitivity analysis. According to Figure A19, more Janssen vaccines are allocated under limited budget levels, consistent with the previous results. When adding the vaccine storage cost, even more Janssen vaccines are allocated since the storage cost of Janssen vaccines is less than Pfizer and Moderna. Due to lower bounds imposed on the number of each type of vaccine distributed, the allocation of the Pfizer vaccine gets slightly closer to the lower bound when storage costs are added. Thus, the vaccine storage cost influences the portion of Moderna allocated more than Pfizer.

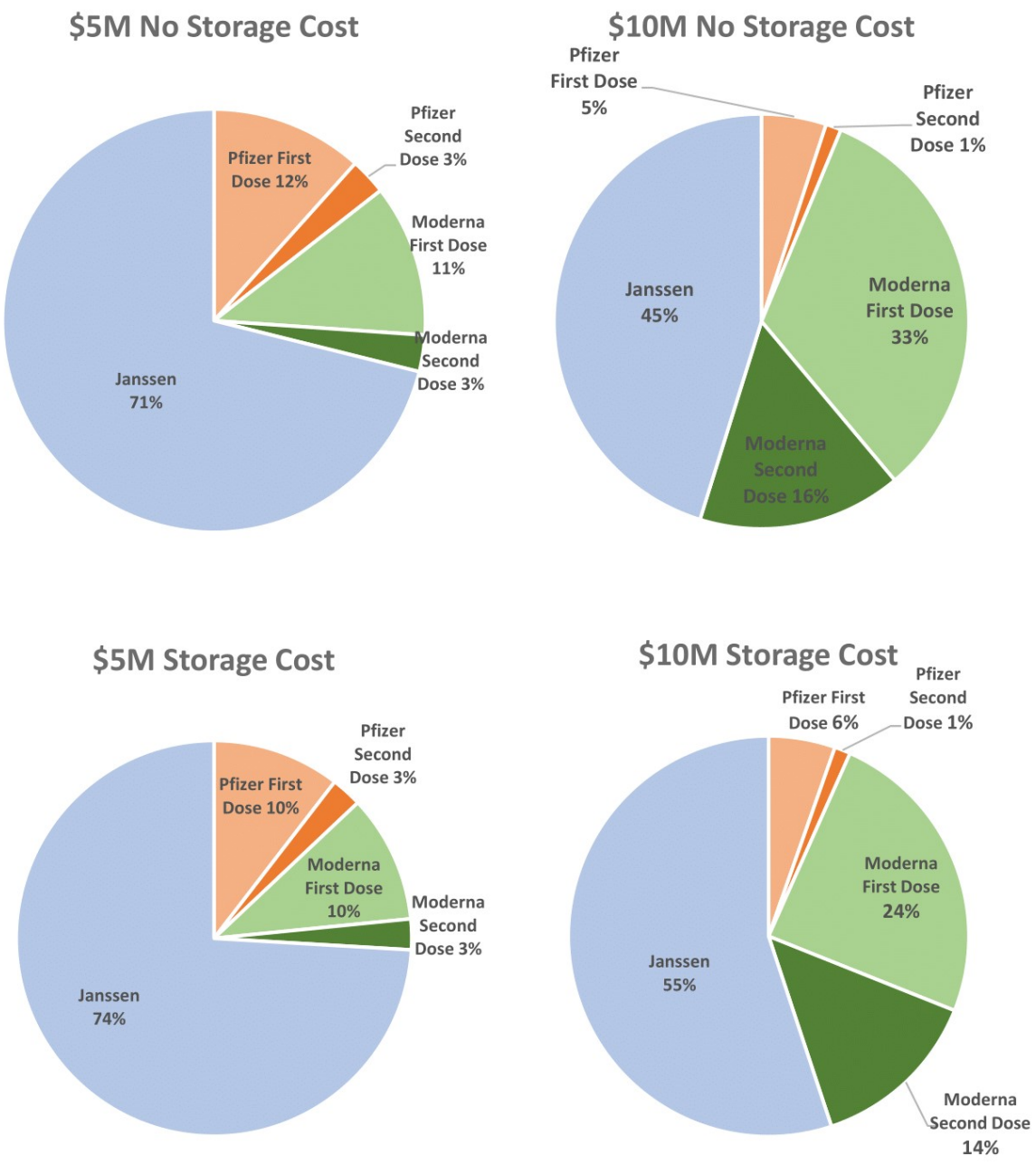

Figure A19: Proportion of each type of vaccine allocated under different budget levels with and without adding the vaccine storage cost.

References

Aparadinar (2021). N.J. U.S. map. https://5thworldadventures.blogspot.com/2018/07/nj-us-map.html. Accessed July 10, 2021.

Bilinski, A., Salomon, J. A., Giardina, J., Ciaranello, A., and Fitzpatrick, M. C. (2021). Passing the test: a model-based analysis of safe school-reopening strategies. *Annals of Internal Medicine*, 174(8):1090–1100.

CDC (2022). U.S. COVID-19 vaccine product information. https://www.cdc.gov/vaccines/covid-19/info-by-product/index.html. Accessed March 5, 2023.

Chen, J., Qi, T., Liu, L., Ling, Y., Qian, Z., Li, T., Li, F., Xu, Q., Zhang, Y., Xu, S., et al. (2020). Clinical progression of patients with COVID-19 in shanghai, china. *Journal of Infection*, 80(5):e1–e6.

Contreras, S., Dehning, J., Loidolt, M., Zierenberg, J., Spitzner, F. P., Urrea-Quintero, J. H., Mohr, S. B., Wilczek, M., Wibral, M., and Priesemann, V. (2021). The challenges of containing SARS-CoV-2 via test-trace-and-isolate. *Nature Communications*, 12(1):1–13.

Du, Z., Xu, X., Wu, Y., Wang, L., Cowling, B. J., and Meyers, L. A. (2020). Serial interval of COVID-19 among publicly reported confirmed cases. *Emerging Infectious Diseases*, 26(6):1341.

Gharakhanlou, N. M. and Hooshangi, N. (2020). Spatio-temporal simulation of the novel Coronavirus COVID-19 outbreak using the agent-based modeling approach (case study: Urmia, Iran). *Informatics in Medicine Unlocked*, 20:100403.

Gharpure, R., Guo, A., Bishnoi, C. K., Patel, U., Gifford, D., Tippins, A., Jaffe, A., Shulman, E., Stone, N., Mungai, E., et al. (2021). Early COVID-19 first-dose vaccination coverage among residents and staff members of skilled nursing facilities participating in the pharmacy partnership for long-term care program—United States, December 2020–January 2021. *Morbidity and Mortality Weekly Report*, 70(5):178.

He, X., Lau, E. H., Wu, P., Deng, X., Wang, J., Hao, X., Lau, Y. C., Wong, J. Y., Guan, Y., Tan, X., et al. (2020). Temporal dynamics in viral shedding and transmissibility of COVID-19. *Nature Medicine*, 26(5):672–675.

Heffernan, E. (2021). COVID-19 vaccine distribution allocations by jurisdiction - Pfizer. https://data.cdc.gov/Vaccinations/COVID-19-Vaccine-Distribution-Allocations-by-Juris/saz5-9hgg. Accessed June 10, 2021.

INDUSTRIAL, G. (2023). American biotech supply ultra low temperature freezer, 25 cu. ft. 230v. https://www.globalindustrial.com/p/ultra-low-temperature-freezer-230v-abt-230v-2586-25-cu-ft?infoParam. Accessed March 5, 2023.

JHU (2020). COVID-19 United States Cases by County. https://coronavirus.jhu.edu/us-map. Accessed November 30, 2020.

JHU (2021). COVID-19 dashboard. https://coronavirus.jhu.edu/map.html. Accessed July 10, 2021.

Kerr, C. C., Mistry, D., Stuart, R. M., Rosenfeld, K., Hart, G. R., Núñez, R. C., Cohen, J. A., Selvaraj, P., Abeysuriya, R. G., Jastrzębski, M., et al. (2021a). Controlling COVID-19 via test-trace-quarantine. *Nature Communications*, 12(1):1–12.

Kerr, C. C., Stuart, R. M., Mistry, D., Abeysuriya, R. G., Rosenfeld, K., Hart, G. R., Núñez, R. C., Cohen, J. A., Selvaraj, P., Hagedorn, B., et al. (2021b). Covasim: an agent-based model of COVID-19 dynamics and interventions. *PLOS Computational Biology*, 17(7):e1009149.

Landry, M., Malouin, J.-L., and Oral, M. (1983). Model validation in operations research. *European Journal of Operational Research*, 14(3):207–220.

Lauer, S. A., Grantz, K. H., Bi, Q., Jones, F. K., Zheng, Q., Meredith, H. R., Azman, A. S., Reich, N. G., and Lessler, J. (2020). The incubation period of coronavirus disease 2019 (COVID-19) from publicly reported confirmed cases: estimation and application. *Annals of Internal Medicine*, 172(9):577–582.

Linton, N. M., Kobayashi, T., Yang, Y., Hayashi, K., Akhmetzhanov, A. R., Jung, S.-m., Yuan, B., Kinoshita, R., and Nishiura, H. (2020). Incubation period and other epidemiological characteristics of 2019 novel Coronavirus infections with right truncation: a statistical analysis of publicly available case data. *Journal of Clinical Medicine*, 9(2):538.

Nishiura, H., Linton, N. M., and Akhmetzhanov, A. R. (2020). Serial interval of novel Coronavirus (COVID-19) infections. *International Journal of Infectious Diseases*, 93:284–286.

Panovska-Griffiths, J., Kerr, C. C., Stuart, R. M., Mistry, D., Klein, D. J., Viner, R. M., and Bonell, C. (2020). Determining the optimal strategy for reopening schools, the impact of test and trace interventions, and the risk of occurrence of a second COVID-19 epidemic wave in the uk: a modelling study. *The Lancet Child & Adolescent Health*, 4(11):817–827.

Paudyal, V., Fialová, D., Henman, M. C., Hazen, A., Okuyan, B., Lutters, M., Cadogan, C., Da Costa, F. A., Galfrascoli, E., Pudritz, Y. M., et al. (2021). Pharmacists' involvement in COVID-19 vaccination across europe: a situational analysis of current practice and policy. *International Journal of Clinical Pharmacy*, 43(4):1139–1148.

Pham, Q. D., Stuart, R. M., Nguyen, T. V., Luong, Q. C., Tran, Q. D., Pham, T. Q., Phan, L. T., Dang, T. Q., Tran, D. N., Do, H. T., et al. (2021). Estimating and mitigating the risk of COVID-19 epidemic rebound associated with reopening of international borders in vietnam: a modelling study. *The Lancet Global Health*, 9(7):e916–e924.

Pung, R., Chiew, C. J., Young, B. E., Chin, S., Chen, M. I., Clapham, H. E., Cook, A. R., Maurer-Stroh, S., Toh, M. P., Poh, C., et al. (2020). Investigation of three clusters of COVID-19 in singapore: implications for surveillance and response measures. *The Lancet*, 395(10229):1039–1046.

Sadarangani, M., Raya, B. A., Conway, J. M., Iyaniwura, S. A., Falcao, R. C., Colijn, C., Coombs, D., and Gantt, S. (2021). Importance of COVID-19 vaccine efficacy in older age groups. *Vaccine*, 39(15):2020–2023.

Scott, N., Palmer, A., Delport, D., Abeysuriya, R., Stuart, R., Kerr, C. C., Mistry, D., Klein, D. J., Sacks-Davis, R., Heath, K., et al. (2020). Modelling the impact of reducing control measures on the COVID-19 pandemic in a low transmission setting. *The Medical Journal of Australia*, 214(2):79–83.

Seladi-Schulman, J. (2021). What we know about the effectiveness of the Johnson & Johnson COVID-19 vaccine. https://www.healthline.com/health/adult-vaccines/johnson-and-johnson-vaccine-efficacy. Accessed June 10, 2021.

Stuart, R. M., Abeysuriya, R. G., Kerr, C. C., Mistry, D., Klein, D. J., Gray, R. T., Hellard, M., and Scott, N. (2021). Role of masks, testing and contact tracing in preventing COVID-19 resurgences: a case study from new south wales, australia. *BMJ open*, 11(4):e045941.

Verity, R., Okell, L. C., Dorigatti, I., Winskill, P., Whittaker, C., Imai, N., Cuomo-Dannenburg, G., Thompson, H., Walker, P. G., Fu, H., et al. (2020). Estimates of the severity of Coronavirus disease 2019: a model-based analysis. *The Lancet Infectious Diseases*, 20(6):669–677.

Wang, D., Hu, B., Hu, C., Zhu, F., Liu, X., Zhang, J., Wang, B., Xiang, H., Cheng, Z., Xiong, Y., et al. (2020). Clinical characteristics of 138 hospitalized patients with 2019 novel Coronavirus–infected pneumonia in Wuhan, China. *Jama*, 323(11):1061–1069.

WHO (2021). Costs of delivering COVID-19 vaccine in 92 AMC countries. https://www.who.int/publications/m/item/costs-of-delivering-covid-19-vaccine-in-92-amc-countries. Accessed June 10, 2021.

Wölfel, R., Corman, V. M., Guggemos, W., Seilmaier, M., Zange, S., Müller, M. A., Niemeyer, D., Jones, T. C., Vollmar, P., Rothe, C., et al. (2020). Virological assessment of hospitalized patients with COVID-2019. *Nature*, 581(7809):465–469.