SEIR-OPT Description

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1 Introduction

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3 SEIR Model

We first present an epidemiological model describing the dynamics of the pandemic for a given allocation of vaccines. Differential equations describe the movement of people through Susceptible, Exposed, Infectious, and Recovered (SEIR) states. We add additional states for vaccinated and hospitalized individuals, making it a "SEIR-V" model. The model will be used at a global scale with a small number of interacting geographic areas. They interact through virus mutation: a more contagious variant emerges after a given amount of infections and then spreads to the other areas. It is also aggregate in that age groups or risk groups are not considered. At the beginning of a pandemic, transmission between areas due to international travel significantly impacts its trajectory. However, later in the pandemic when all areas have a large number of cases, travel is less important. For this reason, our model does not include travel. First we present the model for a single area.

3.1 Single-area SEIR Model with Vaccination

For each geographic area, people move through the following states.

State Variables

S	Susceptible
E	Exposed
I	Infectious
H	Hospitalized
D	Dead
R	Recovered
S^V	Susceptible and vaccinated
E^V	Exposed and vaccinated
I^V	Infectious and vaccinated

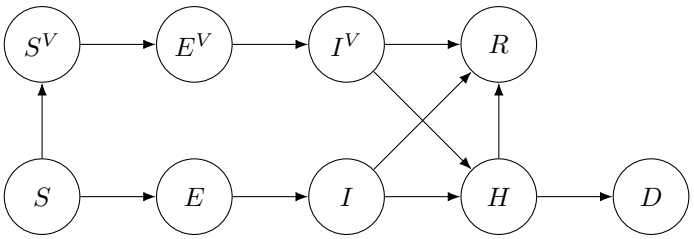

Figure 1: State diagram for the single-area SEIR-V model

State interactions are shown in Figure 1. The states at the bottom of the diagram show the usual progression of an infection. State I (infectious) creates further cases. States H and D are added to track results, though they have no impact on future cases. To model partial vaccine effectiveness, three vaccinated states are added at the top of the diagram. When people in state S are vaccinated, they move to S^V. States E^V and I^V allow the vaccinated track to have different rates of receiving and transmitting infection, hospitalization, and death. Let $S(t)$ be the number of people in state S at time t, etc. Also let $W(t)$ be the number in state S at time t who are willing to be vaccinated. We make the following assumptions about dynamics.

- *Vaccinations:* Vaccines are partially effective: individuals vaccinated at time t are brought to a susceptible and vaccinated state S^V. Individuals in this state are less likely to become infected. State I^V has a lower hospitalization proportion (and therefore mortality) than I. Similarly, vaccinated individuals are less contagious than an unvaccinated individual.

- *Vaccine willingness:* A proportion ρ of the population is willing to be vaccinated. Because only individuals in state S, not those who have had the virus, can be vaccinated, fewer than this proportion can actually be vaccinated. We assume that "willingness" is independent of risk of infection (e.g., age or behavior), so that individuals in state S who are willing to be vaccinated move to state E at the same rate as unwilling individuals. When there are no more willing in state S, vaccinations are stopped.

- *Infection:* Testing and isolation reduce the time spent infectious in states I and I^V. An infected person enters state R when their contagious period ends or when they self-isolate after noticing symptoms. They can also receive a positive test result and self-isolate in response. Thus the rate out of infectious states depends on testing.

- *Mortality:* Because there is only one H state, the proportion of hospitalized patients who die is the same with and without vaccination. Also, there are no deaths due to infection without hospitalization first.

- *Reproduction rate and mutation:* The reproduction rate of the new variant is larger than the previously dominant variant. The timing of when the variant appears and spreads to other areas is addressed in the next section.

- *Reinfection:* Individuals cannot be infected twice. This assumption is reasonable because the time horizon is assumed to be short enough that recovered individuals do not lose their immunity and re-enter the susceptible class.

- *Time dependence:* All parameters are assumed constant over time except for the amount of vaccine available and the infection rate, which changes due to mutation.

The parameters of the model are listed in Tables 1 and 2. More discussion of their values is given in Section 5. Also define the rate out of states I and I^V as $r^d = r_0 + \Delta r$, where Δr is due to testing and can depend on the area.

Table 1: Parameters of SEIR-V that depend on the area

Parameter	Description	Source
N	Initial population	Assumed
ρ	Proportion willing to be vaccinated	??
ρ^V	Initial proportion vaccinated	Vaccination totals for June 1, 2021 and population by country from Our World In Data [1]
$\rho^I N$	Initial cases per day	New cases per day, smoothed over seven days, for June 1, 2021 by country from Our World In Data [1]
$V(t)$	Rate of vaccinations available at time t (people/day)	See Section 4

Δr	Contribution of testing to the rate out of the infectious state (proportion/day)	Assumed
γ	Behavior infection multiplier	??
$\alpha(t)$	Infection rate of out of the susceptible state into the exposed state (proportion/day)	Computed. See Section 3.2

Table 2: Other parameters of SEIR-V

Parameter	Value	Description	Source
r^I	1/5	Rate of out of the exposed (incubation) state into the infectious state (proportion/day)	Lauer et al. [7]
r_0	1/3.5	Rate out of the infectious state without testing, due to recovery, self-quarantine after noticing symptoms, or hospitalization (proportion/day)	Pre-symptomatic infection of about 2 days in Byrne et al. [3] plus an assumed 1.5 days of symptomatic infection until self-quarantine.
r^R	1/15	Rate of recovery or death out of the hospitalized state (proportion/day)	The value of T3 + T5 in Byrne et al. [3], estimated to be 18.1 days, less the time already spent infectious (3.5 days). The same value is used in Bertsimas et al. [2].
p^H	0.296	Proportion of infected unvaccinated people who are hospitalized	Death and hospitalization totals for June 1st, 2021 from the CDC [5] as well as hospitalazation risk ratios by vaccination status. USA vaccination totals for June 1st from Our World In Data [1].
p_V^H	0.0296	Proportion of infected vaccinated people who are hospitalized	Same as above.
p^D	0.1	In-hospital mortality rate, i.e., the proportion of those hospitalized who die	National Hospital Care Survey (NHCS) data for June 1st, 2021 accessed through In-hospital Mortality Among Hospital Confirmed COVID-19 Encounters.

a_0	0.6	Initial infection rate (proportion/day). See equation (4).	Assumed
Δa	0.6	Change in infection rate for a new variant (proportion/day). See equation (4).	Delta variant infectiousness divided by Alpha variant infectiousness is just over 2 in Hansen [6]. Set $\Delta a = a_0$ for a quotient of 2.
p^e	0.6	Transmission rate from a vaccinated person as a proportion of rate for an unvaccinated person; $1 - p^e$ is the vaccine effectiveness against transmitting the virus	Using the case counts from the supplementary material of Eyre et al. [4], we see that the positivity rate of contacts of partially vaccinated index cases is 0.60 times the positivity rate of contacts of unvaccinated index cases.
p^r	0.6	Infection rate for a vaccinated person as a proportion of rate for an unvaccinated person; $1-p^r$ is the vaccine effectiveness against receiving the virus	Data from Eyre et al. [4] show that vaccinated contacts were 0.62 as likely to test positive than unvaccinated contacts.
n	1000M	Unvaccinated person-days in the infectious state before new variant appears	Dominance date of new variants estimated from nextstrain.org to be April 1, 2021 (Alpha), August 1, 2021 (Delta), December 1, 20201 (Omicron.) The infectious duration (3.5 days) times the sum of cases between these dates gives 960m and 1005m respectively.
L	20	Lag for the variant to reach other areas (days)	Assumed
T_D	45	Time for a variant to dominate, i.e., represent half the new cases in an area (days)	Estimated from nextstrain.org for Omicron as approximately the duration from first cases (November 1) to dominance (December 15).

p	0.01	Proportion of people in state I and I^V that have the new variant when it is introduced in an area	Assumed

The initial conditions are defined by partitioning the initial population N. To estimate the exposed states, we use the steady state mean time in these states, $1/r^I$. Multiplying by the new cases per day,

$$E(0) + E^V(0) = \frac{1}{r^I}\rho^I N.$$

Similarly, for the infectious states

$$I(0) + I^V(0) = \frac{1}{r_0 + \Delta r}\rho^I N.$$

To allocate between vaccinated and unvaccinated states, use the initial proportion vaccinated and assume cases are only p^r as prevalent among vaccinated individuals. Then the initial conditions are

$$\begin{aligned}
E(0) &= \left(\frac{1-\rho^V}{p^r\rho^V + 1 - \rho^V}\right)\frac{1}{r^I}\rho^I N \\
E^V(0) &= \left(\frac{p^r\rho^V}{p^r\rho^V + 1 - \rho^V}\right)\frac{1}{r^I}\rho^I N \\
I(0) &= \left(\frac{1-\rho^V}{p^r\rho^V + 1 - \rho^V}\right)\frac{1}{r_0 + \Delta r}\rho^I N \\
I^V(0) &= \left(\frac{p^r\rho^V}{p^r\rho^V + 1 - \rho^V}\right)\frac{1}{r_0 + \Delta r}\rho^I N \\
S^V(0) &= \rho^V N - E^V(0) - I^V(0) \\
S(0) &= N - E(0) - E^V(0) - I(0) - I^V(0) - S^V(0).
\end{aligned} \tag{1}$$

Note that these initial values sum to N, so that $H(0) = D(0) = R(0) = 0$.

Because of the limit on vaccine willingness, vaccinations will stop when there are no more people in state S willing to be vaccinated, $W(t) = 0$. Thus, the rate of vaccinations *performed* is $V^*(t) = V(t)$ for t before $W(t) = 0$ and $V^*(t) = 0$ once $W(t) = 0$. Note that the limit could be hit at a noninteger t, so it is necessary for $V^*(t)$ to be defined on an interval. Even if everyone is willing to be vaccinated ($\rho = 1$), V^* may be needed to keep $S(t)$ nonnegative. We will show how to compute $W(t)$ when we solve SEIR-V in Section 3.3.

An infectious person who has been vaccinated is only p^e times as infectious as an unvaccinated individual. For notational convenience, define the effective number of (unvaccinated) infectious people at time t as

$$\mathcal{V}(t) = I(t) + p^e I^V(t). \tag{2}$$

The system of differential equations for the SEIR-V model is

$$
\begin{aligned}
\frac{\mathrm{d}S}{\mathrm{d}t} &= -V^*(t) - \alpha(t)\frac{S(t)}{N}\mathcal{V}(t) \\
\frac{\mathrm{d}S^V}{\mathrm{d}t} &= V^*(t) - p^r\alpha(t)\frac{S^V(t)}{N}\mathcal{V}(t) \\
\frac{\mathrm{d}E}{\mathrm{d}t} &= \alpha(t)\frac{S(t)}{N}\mathcal{V}(t) - r^I E(t) \\
\frac{\mathrm{d}E^V}{\mathrm{d}t} &= p^r\alpha(t)\frac{S^V(t)}{N}\mathcal{V}(t) - r^I E^V(t) \\
\frac{\mathrm{d}I}{\mathrm{d}t} &= r^I E(t) - r^d I(t) \\
\frac{\mathrm{d}I^V}{\mathrm{d}t} &= r^I E^V(t) - r^d I^V(t) \\
\frac{\mathrm{d}H}{\mathrm{d}t} &= r^d p^H I(t) + r^d p_V^H I^V(t) - r^R H(t) \\
\frac{\mathrm{d}D}{\mathrm{d}t} &= r^R p^D H(t) \\
\frac{\mathrm{d}R}{\mathrm{d}t} &= r^R(1-p^D)H(t) + r^d(1-p^H)I(t) + r^d(1-p_V^H)I^V(t).
\end{aligned}
\tag{3}
$$

A key characteristic of SEIR models is that the rate of new infections is proportional to the current number infectious. In the differential equation for S, the rate moving from S to E is the equivalent number of infectious, non-isolated people, $\mathcal{V}(t)$, times the potential number of new infections per day for each such person, $\alpha(t)$, times the proportion of people vulnerable to infection and unvaccinated, $S(t)/N$. The equation for S^V is similar, but vaccinated individuals are infected at a smaller rate because of the multiplier p^r.

From E (or E^V), the rate into I (or I^V) is r^I and the rate out of I (or I^V) is r^d. The units of these rates are per day, so that in steady state the time spent in the infectious state is $1/r^d$ days. To model the splitting out of state I, the total rate out is r^d and the proportion hospitalized is p^H. The remaining proportion $1 - p^H$ move to the recovered state. Vaccinated individuals have the same rate rate out but a smaller proportion hospitalized, p_V^H. Similarly, the total rate r^R out of state H is split with proportion p^D dying and the rest recovering. Note that the case mortality rate is $p^H p^D$ for unvaccinated and $p_V^H p^D$ for vaccinated.

3.2 Mutation Model

To describe the spread of new variants, now consider a set of geographic areas $a \in \mathcal{A}$. A separate SEIR-V model will be used for each area, but they will be linked by the spread of variants of the virus and by vaccine availability. State variables and some parameters vary by area; this will be indicated by an area subscript. The infection rate depends on the characteristics of an area, such as population density, behavioral changes such as masking and distancing, and demographics such as the age distribution. It also depends on the

intrinsic reproduction rate of the current variant(s) of the virus. We assume the behavior is constant over time. Thus, the infection rate $\alpha_a(t)$ in area a at time t is proportional to γ_a, which adjusts for characteristics of the area.

Initially, the same variant is assumed to be dominant in all areas, with reproduction rate $\alpha_a(0) = a_0$. The reproduction rate of the new variant is larger by Δa. We assume that a variant appears after a certain number n of unvaccinated infectious person-days are accumulated over all areas. Thus, we are assuming that each person in state I contributes the same mutation risk (per day), while vaccinated people in state I^V do not contribute to mutation. Furthermore, the amount of mutation risk until a new variant appears is deterministic. For a given scenario and a_0, the mutation threshold of n person-days is reached at some time t_n. However, since mutations may be more likely in poorer areas with less access to modern medicine, we assume that the mutation appears in an area that is not the donor area.

We assume that the mutation occurs in the area with the largest number of infected person-days, which we call area m for mutation. In this area the variant is some small proportion p of infections occurring on day t_n and becomes dominant (half of infections) after a delay of T_D days. The infection rate induced by the mixture of the two variants changes over time according to

$$a(t) = a_0 + \frac{\Delta a}{1 + e^{-k(t-(t_n+T_D))}}. \tag{4}$$

Here $k = \ln[(1-p)/p]/T_D$. This value of k ensures that the definition of p is satisfied, that is, $\alpha_m(t_n) = a_0 + \Delta a p$. See Figure 2. The new variant is assumed to reach other areas with a lag of L days. Including the behavior factor, the infection rate by area is

$$\begin{aligned} \alpha_m(t) &= a(t)\gamma_m, \quad t \geq t_n \\ \alpha_a(t) &= a_m(\,\max\{t-L,\,0\}\,)\gamma_a \text{ for } a \neq m. \end{aligned} \tag{5}$$

3.3 Simulating SEIR-V with Vaccination Limits

To solve SEIR-V numerically over a time horizon of T days, the differential equations are replaced by difference equations with a time step of one day. The model parameters from Tables 1 and 2 and equations (2), (4), and (5) are used. All of the areas are solved simultaneously to find t_n, the time when the new variant appears. However, we omit the area subscript when it is not needed.

The state variables are initialized by (1). Because the vaccination schedule $V(t)$ might not be feasible,

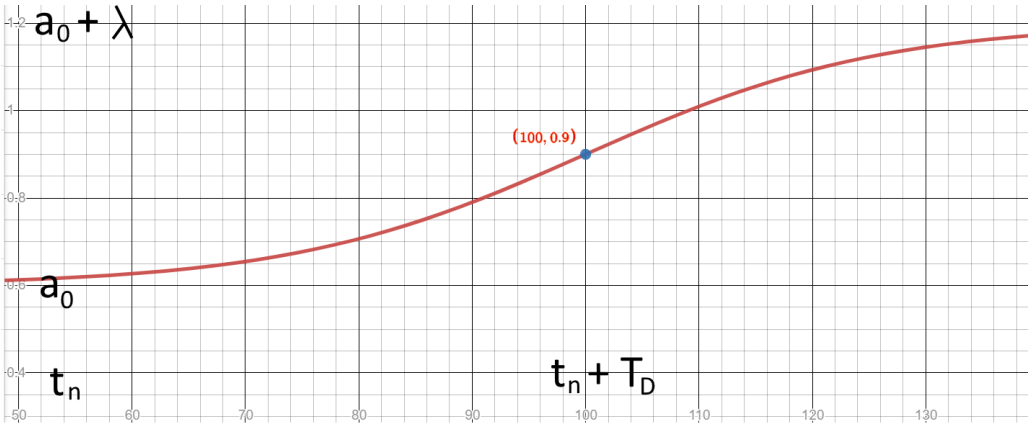

Figure 2: Equation (4) with $t_n = 55$, $T_D = 45$, $a_0 = 0.6$, $\Delta a = 0.6$, $p = 0.01$.

we also need to compute $W(t)$. Initially,

$$W(0) = \rho N - S^V(0) - E^V(0) - I^V(0) - \rho E(0) - \rho I(0). \tag{6}$$

Here ρN is the number willing to be vaccinated and we assume that those initially in states E and I are representative of the population. To enforce nonnegativity, the maximum one-day number moving from S to E is

$$\Delta E(t) = \min\{S(t), \alpha(t)\frac{S(t)}{N}\mathcal{V}(t)\}. \tag{7}$$

The number of vaccinations performed on day t is

$$V^*(t) = \min\{W(t) - \frac{W(t)}{S(t)}\Delta E(t), V(t)\}. \tag{8}$$

The first expression is the number in state S willing to vaccinate before the vaccinations occur. Also subtracting the vaccinations,

$$W(t+1) = W(t) - \frac{W(t)}{S(t)}\Delta E(t) - V^*(t). \tag{9}$$

Note that if $S(t) = 0$, then $\Delta E(t) = 0$ and this term should be interpreted as 0 in (8) and (9).

Using these quantities, the difference equations are

$$\begin{aligned}
S(t+1) &= S(t) - \Delta E(t) - V^*(t) && t = 0, \cdots, T-1 \\
S^V(t+1) &= S^V(t) + V^*(t) - p^r \alpha(t) \tfrac{S^V(t)}{N} \mathcal{V}(t) && t = 0, \cdots, T-1 \\
E(t+1) &= E(t) + \Delta E(t) - r^I E(t) && t = 0, \cdots, T-1 \\
E^V(t+1) &= E^V(t) + p^r \alpha(t) \tfrac{S^V(t)}{N} \mathcal{V}(t) - r^I E^V(t) && t = 0, \cdots, T-1 \\
I(t+1) &= I(t) + r^I E(t) - r^d I(t) && t = 0, \cdots, T-1 \\
I^V(t+1) &= I^V(t) + r^I E^V(t) - r^d I^V(t) && t = 0, \cdots, T-1 \\
H(t+1) &= H(t) + r^d p^H I(t) + r^d p_V^H I^V(t) - r^R H(t) && t = 0, \cdots, T-1 \\
D(t+1) &= D(t) + r^R p^D H(t) && t = 0, \cdots, T-1 \\
R(t+1) &= R(t) + r^R (1-p^D) H(t) + r^d (1-p^H) I(t) + r^d (1-p_V^H) I^V(t) && t = 0, \cdots, T-1
\end{aligned}$$

These equations must be solved iteratively over t for all areas to find t_n and the area m where the variant emerges. The variant appears in day t^*, which is the smallest integer for which

$$\sum_{a \in \mathcal{A}} \sum_{t=0}^{t^*} I_a(t) \geq n. \tag{10}$$

The variant emerges in the area m with the largest number of unvaccinated infection-days $\sum_{t=0}^{t^*} I_a(t)$. It will be useful to interpolate between days, setting

$$t_n = t^* - 1 + \frac{\sum_{a \in \mathcal{A}} \sum_{t=0}^{t^*} I_a(t) - n}{\sum_{a \in \mathcal{A}} I_a(t^*)}. \tag{11}$$

The following sequence of calculations is used to simulate SEIR-V.

1. Compute the intial states and W using (1) and (6). Set the infection rates to the constant, pre-variant rates

$$\alpha_a(t) = a_0 \gamma_a. \tag{12}$$

2. For $t = 0, \ldots, T-1$,

   a) Solve the difference equations along with (2), (7), (9), and (8) for all areas at the current t.

   b) Check (10); if it is satisfied, the variant has appeared: compute t_n and the variant area m, and the time-varying infection rates (4) and (5). Switch to these rates for the remaining t.

We propose one more refinement to SEIR-V. Thus far, (8) discards vaccine planned for an area that cannot be used. It is conceivable that these could be reallocated to another area, particularly if vaccination rates are being tracked and it can be anticipated that an area will soon reach saturation. Rather than

finding a reallocation that minimizes the number of unused vaccinations, we consider the simpler option of reallocating vaccines from one donor area to other areas that are not saturated, in proportion to their population. We call this *proportional reallocation*. It modifies the computations in this section as follows. Assume that $a = 1$ is the donor area. First, compute $V_a^*(t)$ and $W_a(t+1)$ as before using (8) and (9). The total population in areas being reallocated to is

$$N_\bullet(t) = \sum_{a:a\neq 1, W_a(t+1)>0} N_a. \tag{13}$$

The planned plus reallocated vaccinations on day t are

$$V_a^+(t) = V_a(t) + \frac{N_a}{N_\bullet(t)}[V_1(t) - V_1^*(t)], \quad a \neq 1, W_a(t+1) > 0. \tag{14}$$

For other areas, $V_a^+(t) = V_a(t)$. If $N_\bullet(t) = 0$, then no areas can receive reallocations. In this case, (14) is undefined, so set $V_a^+(t) = V_a(t)$. Next recompute $V_a^*(t)$ and $W_a(t+1)$ for $a \neq 1$ as in (8) and (9) but using V^+ in place of V. Then compute the state variables as before using the difference equations.

4 Optimization Framework

In this section we formulate a nonlinear program that considers multiple areas: Given the vaccines available each day, find the allocation of vaccines to areas that minimizes deaths in the donor areas $\mathcal{D}$. The constraints are the difference equations, (9) to compute W, and the vaccination budget of $B(t)$ doses available for day

t. The nonlinear program, called SEIR-OPT, is

$$
\begin{aligned}
\min \ & \sum_{a\in\mathcal{D}} D_a(T) && && && && \text{(Donor deaths)}\\
\text{s.t.} \ & \sum_{a\in A} V_a(t) && \le B(t) && t=0,\cdots,T-1 && && \text{(Vacc. budget)}\\
& W_a(t+1) && = W_a(t) - \alpha_a(t)\tfrac{W_a(t)}{N_a}\mathcal{V}_a(t) - V_a(t) && t=0,\cdots,T-1, && a\in A && \text{(Vacc. willingness)}\\
& S_a(t+1) && = S_a(t) - V_a(t) - \alpha_a(t)\tfrac{S_a(t)}{N_a}\mathcal{V}_a(t) && t=0,\cdots,T-1, && a\in A && \text{(Diff. Equations)}\\
& S_a^V(t+1) && = S_a^V(t) + V_a(t) - p^r\alpha_a(t)\tfrac{S_a^V(t)}{N_a}\mathcal{V}_a(t) && t=0,\cdots,T-1, && a\in A &&\\
& E_a(t+1) && = E_a(t) + \alpha_a(t)\tfrac{S_a(t)}{N_a}\mathcal{V}_a(t) - r^I E_a(t) && t=0,\cdots,T-1, && a\in A &&\\
& E_a^V(t+1) && = E_a^V(t) + p^r\alpha_a(t)\tfrac{S_a^V(t)}{N_a}\mathcal{V}_a(t) - r^I E_a^V(t) && t=0,\cdots,T-1, && a\in A &&\\
& I_a(t+1) && = I_a(t) + r^I E_a(t) - r^d I_a(t) && t=0,\cdots,T-1, && a\in A &&\\
& I_a^V(t+1) && = I_a^V(t) + r^I E_a^V(t) - r^d I_a^V(t) && t=0,\cdots,T-1, && a\in A &&\\
& H_a(t+1) && = H_a(t) + r^d p^H I_a(t) + r^d p_V^H I_a^V(t) - r^R H_a(t) && t=0,\cdots,T-1, && a\in A &&\\
& D_a(t+1) && = D_a(t) + r^R p^D H_a(t) && t=0,\cdots,T-1, && a\in A &&\\
& R_a(t+1) && = R_a(t) + r^R(1-p^D)H_a(t) && && && \\
& && \quad + r^d(1-p^H)I_a(t) + r^d(1-p_V^H)I_a^V(t) && t=0,\cdots,T-1, && a\in A &&\\
& \mathcal{V}_a(t) && = I_a(t) + p^e I_a^V(t) && t=0,\cdots,T-1, && a\in A && \text{(Def. of } \mathcal{V}_a(t))\\
& && W_a(t), S_a(t), E_a(t), I_a(t), S_a^V(t), E_a^V(t), && && && \\
& && I_a^V(t), H_a(t), V_a(t) \ge 0 && t=0,\cdots,T, && a\in A. && \text{(Nonnegativity)}
\end{aligned}
$$

The variables in SEIR-OPT are all of the state variables, W, and $\mathcal{V}$ at times $t = 1, \cdots, T$. Their values at $t = 0$ are the initial conditions, computed in (1) and (6). Also, α is a variable because the time at which the variant appears, t_n, depends on the state variable I; see (4), (5), and (10)-(11). Unfortunately, this complex dependence on t_n makes SEIR-OPT difficult to solve. It also has quadratic bilinear terms, such as $W_a(t)\mathcal{V}_a(t)$, in the constraint for W and the first four difference equations. The difference equations differ from those in Section 3.3 because V contains the actual vaccinations; it does not need to be corrected to be feasible, so V^* and ΔE are not used. The constraint for W is obtained from (9) by replacing $\Delta E(t)$ with the second term in (7) (which is feasible) and $V^*(t)$ with $V_a(t)$, which is the actual vaccinations.

SEIR-OPT assumes self-interest: the donor area(s) minimize their deaths. We can also add fairness policy constraints. The simplest is a single constraint

$$\sum_{a\in\mathcal{D}} V_a(t) \le p^k B(t) \qquad t = 0, \cdots, T-1 \tag{15}$$

for each day requiring the proportion of the vaccinations available that are used in the donor areas to be at most p^k.

Because we cannot directly solve SEIR-OPT, we iteratively solve a simpler problem that does not have the complex dependence on t_n, seeking to converge to the optimal t_n. If we had an explicit equation for t_n, we could solve a Lagrangian relaxation with Lagrange multiplier λ. For some value of λ, the optimal solution of the relaxation is optimal for the original problem. As an approximation, we use the unvaccinated infectious-days up to the current $\lceil t_n \rceil$ as the "Lagrangian" term in the objective with multiplier λ. This term incentivizes reducing the number of unvaccinated infectious people before (and a fraction of a day after) the variant appears. The new objective is

$$\min \sum_{a \in \mathcal{D}} D_a(T) + \lambda \sum_{a \in \mathcal{A}} \sum_{t=0}^{\lceil t_n \rceil} I_a(t). \tag{16}$$

We fix t_n: instead of depending on I in (11), it is a constant. Call this problem the *Lagrangian*. The Lagrangian interpretation motivates using (16) and searching for the value of λ that minimizes the original objective.

Even without t_n, the constraints are quadratic. A method is proposed in Bertsimas, et. al [2] to solve a similar problem by solving a sequence of linear approximations. At each iteration, given the current vaccine allocation V, we solve the difference equations to get the current infectious population estimates $\hat{I}_a(t)$ and $\hat{I}_a^V(t)$ as well as t_n. The terms containing $\mathcal{V}$ in the constraints for W, S, S^V, and E are nonlinear. We replace the variables I and I^V in $\mathcal{V}$ with the constants $\hat{I}$ and $\hat{I}^V$; see (2). We add the regularization constraints

$$\begin{aligned} \mid I_a(t) - \hat{I}_a(t) \mid \leq \epsilon \qquad & t = 1, \cdots, T, \quad a \in A \\ \mid I_a^V(t) - \hat{I}_a^V(t) \mid \leq \epsilon \qquad & t = 1, \cdots, T, \quad a \in A. \end{aligned} \tag{17}$$

To summarize, the linear program is SEIR-OPT with the objective (16), constant t_n, constant $\mathcal{V}$, and added constraints (17). Here, ϵ is an error tolerance. This linear program can be solved to find the best solution V^{new} that gives infection dynamics I and I^V that are close to $\hat{I}$ and $\hat{I}^V$, i.e., close to those of the current solution. The current solution V is updated and the process repeated until the objective function value converges.

To start the algorithm an initial solution V is needed. We assume there is only one donor area, $a = 1$. If there is no policy constraint (15), allocate all vaccine to the donor: $V_1(t) = B(t)$. With (15), allocate the

vaccine that cannot be kept by the donor proportional to $S_a(0)$:

$$\begin{aligned} V_1(t) &= p^k B(t) \\ V_a(t) &= (1-p^k)(S_a(0)/S_\bullet)B(t), \qquad a \neq 1, \end{aligned} \tag{18}$$

where $S_\bullet = \sum_{a \neq 1} S_a(0)$.

"Simulate" refers to solving the difference equations to find I, I^V, t_n, and m as in Section 3.3 and using them to update $\hat{I}$ and $\hat{I}^V$. Algorithm 1 has an outer loop that updates λ and an inner loop that solves the linear program to update V, then simulates. It uses the the parameters listed in Table 3. Let $z^{(i)}$ be the donor deaths found when solving the ith Lagrangian problem with objective function weight $\lambda^{(i)}$ and $z_{\text{LP}}^{(j)}$ be the optimal objective value of the jth linear program (for a given λ).

Algorithm 1 Algorithm for SEIR-OPT.

Initialization: $i \leftarrow 0, \lambda^{(1)} \leftarrow \lambda, \lambda^{(2)} \leftarrow \lambda\phi$, phase $\leftarrow 1$, V from (18).
Simulate. Update t_n and m. $\hat{I} \leftarrow I$, $\hat{I}^V \leftarrow I^V$.
while $|z^{(i)} - z^{(i-1)}| > \delta$ or $i < 2$ or phase $= 1$ **do**
  $i \leftarrow i+1, \lambda \leftarrow \lambda^{(i)}, j \leftarrow 0, \epsilon \leftarrow \epsilon_0$
  while $|z_{\text{LP}}^{(j)} - z_{\text{LP}}^{(j-1)}| > \delta_I$ or $j < 2$ **do**
    $j \leftarrow j+1$
    Solve the linear program using t_n, m, $\hat{I}$, $\hat{I}^V$, λ and ϵ. $V \leftarrow V^{\text{new}}$, $z_{\text{LP}}^{(j)} \leftarrow$ optimal objective value.
    Simulate. Update t_n and m. $\hat{I} \leftarrow I$, $\hat{I}^V \leftarrow I^V$.
    $\epsilon \leftarrow \beta\epsilon$
  end while
  Compute $z^{(i)}$ from $D_a(T)$ in the current linear program solution.
  If $i > 2$ find the next multiplier $\lambda^{(i+1)}$
  If an interval containing the optimal λ was found, phase $\leftarrow 2$
end while
output: Vaccine allocation V and donor deaths $z^{(i)}$

Table 3: Parameters for optimization model

Parameter	Value	Description	Source
$\mathcal{D}$	1	Donor area(s)	By definition
$B(t)$	Varies	Vaccine doses available on day t	World vaccination totals after June 1st, 2021 from Our World In Data [1].
p^k	Varies	Policy constraint: maximum proportion of available vaccinations each day that may be used in donor areas	Assumed

λ	Varies	Initial "Lagrange multiplier" for infection	Based on numerical tests
ϕ	2	Exploration multiplier for λ (Lagrange multiplier for infection)	Based on numerical tests
ϵ_0	100	Exploration tolerance around infection counts	Based on numerical tests (when $N_a = 100,000$)
δ_I	100	Termination tolerance for linear program	Assumed
δ	0.1	Termination tolerance	Assumed
β	0.9	Convergence parameter for linear program	Based on numerical tests

5 Parameter Estimation

6 Results

7 Future Work and Conclusions

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