

SEIR-C: An epidemic model that includes contact tracing

Lynden K. Shalm¹ and Jasper Palfree¹

¹*Department of Physics, University of Colorado, Boulder, Colorado, USA*

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The SEIR model has been widely used to study the dynamics of pandemics. Here we update the model to include the effects of contact tracing as a means to control the outbreak. We call this new model SEIR-C.

I. INTRODUCTION TO SEIR

The SEIR model relies on a set of differential equations to model the transmission dynamics of an infectious disease. A susceptible population (S) has some probability of coming into contact with the infected population (I) while they are still infectious for some time (τ_{inf}). Those from S who have contracted the disease are then classified as having been exposed (E). Those who are exposed are not infectious, but rather the disease takes some time (τ_{inc}) to incubate, after which point they move to the infectious population. Individuals who are in I will eventually recover after a time τ_{inf} . At this point they are assumed to have achieved immunity or have died. For the situation considered here, we also assume that birth rates and death rates are equal so the total population remains constant. Therefore, the total population N is given by:

$$N = S + E + I + R. \quad (1)$$

In the standard SEIR model the rate of change for each of the different disease stages are given as a set of coupled differential equations:

$$\frac{dS}{dt} = -\beta_0 \frac{I}{N} S, \quad (2)$$

$$\frac{dE}{dt} = \beta_0 \frac{I}{N} S - \frac{1}{\tau_{inc}} E, \quad (3)$$

$$\frac{dI}{dt} = \frac{1}{\tau_{inc}} E - \frac{1}{\tau_{inf}} I, \quad (4)$$

$$\frac{dR}{dt} = \frac{1}{\tau_{inf}} I. \quad (5)$$

Here $\beta_0 = \frac{R_0}{\tau_{inf}}$, where R_0 is the average number of people an infectious person in I will infect and is known as the reproduction number. The rate at which the exposed population increases is therefore related to how fast an infectious person spreads the disease (β_0) times the fraction of the population that is infectious (I/N) multiplied by the number of people who are susceptible (S).

A modified SEIR model that is widely used also accounts for asymptomatic individuals, and can track hospitalizations and deaths. We will use this version of SEIR as our starting point, and then add in testing and contact tracing in a way that allows their effects to be studied somewhat independently (contact tracing is heavily dependent on testing, but it is possible to study the effects of testing independent of contact tracing). The modified model is shown in figure 1.

II. SEIR WITH TESTING (SEIR-T)

We will first extend the basic SEIR model described in the previous section to include testing. An important consideration is how long it takes to get test results on average (τ_t), as well as the percentage of tests that return a false positive (f_{pos}) or a false negative f_{neg} . In general, the probability that someone will be given a test is p_t , but it is possible to test those who show symptoms (p_t^i) as well as those who are hospitalized (p_t^{sev}) at a higher rate.

For each of the different populations S , E , I , I^a , A , M , X , and H , we consider three different subpopulations. There are those who have not yet been tested (which we denote with a “ u ” subscript, i.e. S_u), those who have been tested but are waiting for their results (denoted by a “ w ”, i.e. S_w), and finally those who have tested positive (denoted a “ t ” subscript, i.e. S_t). In figure XXX each of these not tested, waiting, and positive tests are represented as layers. To simplify matters, individuals can move between layers within their current population group, but when transitioning to a the next phase of the disease must stay within their layer. For example, someone who is in the

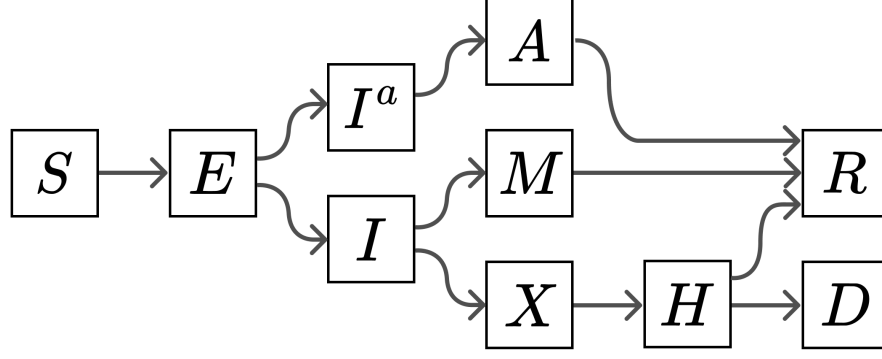


FIG. 1. Conceptual diagram for SEIR with asymptomatic individuals. The first population group are those who are susceptible (S), meaning they have not yet been infected. They can become infected through contact with someone who is infectious (I and I^a). Once infected, they move to the exposed group (E) for some incubation period τ_{inc} . During this time they cannot infect others. Next, they move to the infectious phase of the disease for an average time τ_{inf} where it can be spread to others through contact. There are two infectious populations, those who show symptoms (I), and those who are asymptomatic (I^a). Once the infectious phase is finished, those who are asymptomatic move to the population A where they are still sick but no longer infectious. After a time τ_a they recover (R), meaning they have developed immunity and can not be reinfected. Those who show symptoms will either progress to the mild population (M) where they will eventually recover after an average time τ_{mild} , or they will develop severe symptoms (X) that will eventually require hospitalization (H) after an average time τ_h . Those who are hospitalized will either recover after an average time τ_{sev} , or die (D) after an average time τ_d .

exposed phase and waiting for their test results, E_w can move to E_t if they test positive. They also have a chance of moving to the infectious phase I_w where they continue to wait for their test results. However, they cannot move to I_t directly from E_w ($E_w \rightarrow I_t$). Instead they have to follow the path $E_w \rightarrow I_w \rightarrow I_t$.

We assume that those who are waiting for their test results quarantine themselves. If an individual tests positive, then they continue to quarantine for an average time of τ_{iso} , after which they return to the general population. We assume that anyone who has tested positive will not be tested again unless their quarantine period ends before recovery and they return to the non-tested population. Those who develop severe symptoms and are hospitalized will remain quarantined. For those in the susceptible population who are quarantined, this leads to a reduction in their probability of infection by a factor d_r . For those in the infectious group who are quarantining, their ability to infect others (R_0) is reduced by a factor d_r . If an individual tests negative while in S_w they return to S_u and stop quarantining. Similarly, those who are infectious that test negative (through a false negative) will return to either I_u or I_u^a where they will resume infecting others at the original R_0 .

It is convenient to represent the population for any stage in terms of a 3 element vector:

$$J = \begin{bmatrix} J_u \\ J_w \\ J_t \end{bmatrix}, \quad (6)$$

where J represents the populations S , E , I , I^a , A , M , X , H , D , and R . Then the different arrows representing population flow can be represented as transition matrices. The flow of population from those who are untested to those who have been tested and are now waiting for their results is:

$$\sigma_t = \begin{bmatrix} -1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}. \quad (7)$$

The arrow corresponding to a positive test result is:

$$\sigma_+ = \frac{1}{\tau_t} \begin{bmatrix} 0 & 0 & 0 \\ 0 & -1 & 0 \\ 0 & 1 & 0 \end{bmatrix}, \quad (8)$$

and a negative test result is:

$$\sigma_- = \frac{1}{\tau_t} \begin{bmatrix} 0 & 1 & 0 \\ 0 & -1 & 0 \\ 0 & 0 & 0 \end{bmatrix}. \quad (9)$$

Individuals will wait for an average for τ_t for their test results. Those who test positive quarantine (move to J_t), while those who test negative return to J_u .

After an average time τ_{iso} , those who are in J_t can return back to J_u as their quarantine period is over. The matrix for this transition is:

$$\sigma_{iso} = \frac{1}{\tau_{iso}} \begin{bmatrix} 0 & 0 & 1 \\ 0 & 0 & 0 \\ 0 & 0 & -1 \end{bmatrix}. \quad (10)$$

Finally, we also have the identity matrix, $\mathbb{1}$, which is needed to describe the transition between some of the disease phases. We can now describe the rate of change equations for those in the susceptible population as:

$$\frac{dS}{dt} = (p_t \sigma_t + f_{pos} \sigma_+ + (1 - f_{pos}) \sigma_- + \sigma_{iso}) - T_{S \rightarrow E}, \quad (11)$$

$$T_{S \rightarrow E} = \beta \begin{bmatrix} 1 & 0 & 0 \\ 0 & d_r & 0 \\ 0 & 0 & d_r \end{bmatrix}. \quad (12)$$

The final term represents the transition of population to the exposed stage. This occurs when someone who is susceptible comes into contact with someone who is infectious and is infected. This occurs at a rate β , where:

$$\beta = \frac{R_0}{\tau_{inf}} \left[\frac{I_u + I_u^a}{N} + d_r \left(\frac{I_{tot} + I_{tot}^a - I_u + I_u^a}{N} \right) \right], \quad (13)$$

where d_r is the fraction that R_0 is reduced to by those who are infectious but quarantining since they will make fewer contacts and infect fewer people in the susceptible category. Those who are susceptible and quarantining will also have a reduced chance d_r of being infected. The probability that someone who is infectious and quarantining infecting someone who is susceptible and quarantining is therefore reduced by a factor of $(d_r)^2$.

The rate of change of those in the exposed stage is:

$$\frac{dE}{dt} = \left(p_t \sigma_t + (1 - f_{neg}) \sigma_+ + f_{neg} \sigma_- + \sigma_{iso} - \frac{1}{\tau_{inc}} \mathbb{1} \right) \cdot E + T_{S \rightarrow E} \cdot S. \quad (14)$$

For those who are exposed (and those in all subsequent stages), a false negative in a test result will mistakenly return the individual to the untested subpopulation. Only the positive tests will correctly lead to a quarantine. After some time period τ_{inc} , individuals leave the exposed stage and move to the infectious stage. There are two populations in the infectious stage, those who display symptoms (I), and those who are asymptomatic (I^a). The probability of someone who is infectious but asymptomatic is p_a . The rate equations are:

$$\frac{dI}{dt} = \left(p_t^i \sigma_t + (1 - f_{neg}) \sigma_+ + f_{neg} \sigma_- + \sigma_{iso} - \frac{1}{\tau_{inf}} \mathbb{1} \right) \cdot I + \frac{(1 - p_a)}{\tau_{inc}} \mathbb{1} \cdot E, \quad (15)$$

$$\frac{dI^a}{dt} = \left(p_t^i \sigma_t + (1 - f_{neg}) \sigma_+ + f_{neg} \sigma_- + \sigma_{iso} - \frac{1}{\tau_{inf}} \mathbb{1} \right) \cdot I^a + \frac{p_a}{\tau_{inc}} \mathbb{1} \cdot E, \quad (16)$$

and after an average time of τ_{inf} the population transitions the next stage. Those who are infectious and show symptoms will be tested with a probability p_t^i .

Those who are asymptomatic leave the infectious phase where they are no longer infectious, but can still test positive. It takes an average time of τ_a before the disease runs its course and they develop immunity and move to R . The change in the recovering asymptomatic population A is given as:

$$\frac{dA}{dt} = \left(p_t \sigma_t + (1 - f_{neg}) \sigma_+ + f_{neg} \sigma_- + \sigma_{iso} - \frac{1}{\tau_a} \mathbb{1} \right) \cdot A + \frac{1}{\tau_{inf}} \mathbb{1} \cdot I^a. \quad (17)$$

$$(18)$$

Those who show symptoms while infectious will either transition to a mild recovery phase (M) with probability p_m or a severe recovery phase (X) with a probability $(1 - p_m)$. Those who display mild symptoms after the infectious phase will be tested with the same probability as those who display symptoms while infectious, p_t^i . However, those who show symptoms will be tested with a probability p_t^{sev} . It will take an average time τ_{mild} for these individuals to

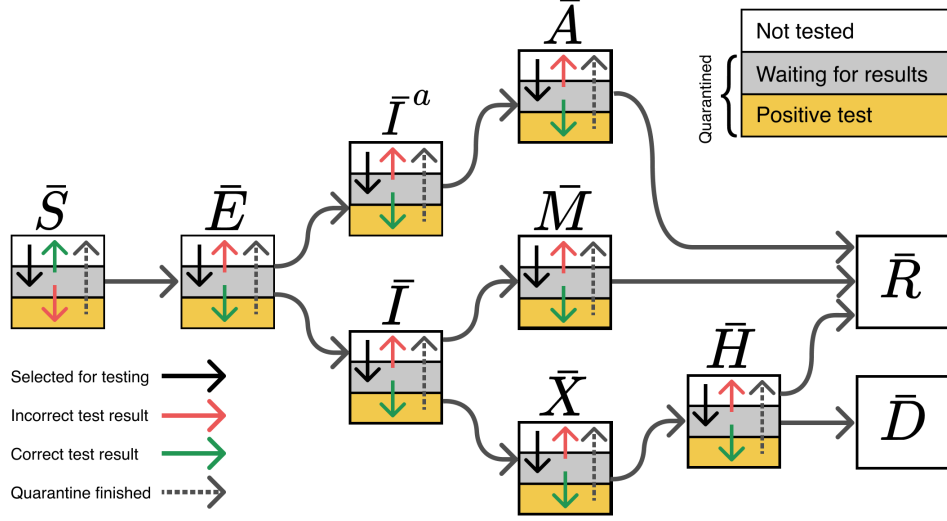


FIG. 2. SEIR with testing incorporated. It is convenient to divide each population into three subgroups, those who have not been tested (white), those who have been tested but are waiting for their results (grey), and those who have tested positive (yellow). Anyone in the white or yellow layers is quarantined. When transitioning between disease phases, individuals can only move to the same color layer (for example $E_w \rightarrow I_w$ or $I_u \rightarrow M_u$). Vertical arrows represent the transitions that can occur within a population group. Black arrows represent movement due to testing, red arrows represent movement due to an incorrect test result (false positive for those in susceptible, false negative for all other populations), green arrows show movement due to a correct test result, and the dashed arrow show individuals who have finished their quarantine period.

make a full recovery and develop immunity, while those who are in the severe phase will be admitted to the hospital after an average time τ_h :

$$\frac{dM}{dt} = \left(p_t^i \sigma_t + (1 - f_{neg}) \sigma_+ + f_{neg} \sigma_- + \sigma_{iso} - \frac{1}{\tau_{mild}} \mathbb{1} \right) \cdot M + \frac{p_m}{\tau_{inf}} \mathbb{1} \cdot I. \quad (19)$$

$$\frac{dX}{dt} = \left(p_t^{sev} \sigma_t + (1 - f_{neg}) \sigma_+ + f_{neg} \sigma_- - \frac{1}{\tau_h} \mathbb{1} \right) \cdot X + \frac{(1 - p_m)}{\tau_{inf}} \mathbb{1} \cdot I. \quad (20)$$

It is also assumed that those who show severe symptoms or are hospitalized will remain quarantined, hence the lack of a σ_{iso} term. The rate of change of those in the hospital is:

$$\frac{dH}{dt} = \left(p_t^{sev} \sigma_t + (1 - f_{neg}) \sigma_+ + f_{neg} \sigma_- - \frac{1}{\tau_{sev}} \mathbb{1} \right) \cdot H + \frac{1}{\tau_h} \mathbb{1} \cdot X. \quad (21)$$

A fraction p_d of those who are hospitalized will die after an average time τ_d , or recover after a time τ_{sev} . To find p_d , we must use the case fatality rate, C_{FR} to figure out the percentage of those hospitalized that will die. Since the case fatality rate applies to all infections, we need to determine the average fraction of the population that will end up in the hospital. Since those can only come from those who were infectious with symptoms that later developed into severe symptoms, we have:

$$p_d = \frac{C_{FR}}{(1 - p_a) p_{sev}}. \quad (22)$$

The change in D is therefore given as:

$$\frac{dD}{dt} = \frac{p_d}{\tau_{sev}} \mathbb{1} \cdot X. \quad (23)$$

Finally, the rate of change of those who recover is:

$$\frac{dR}{dt} = \frac{1}{\tau_a} \mathbb{1} \cdot A + \frac{1}{\tau_{mild}} \mathbb{1} \cdot M + \frac{(1 - p_d)}{\tau_{sev}} \mathbb{1} \cdot X. \quad (24)$$

III. SEIR WITH CONTACT TRACING (SEIR-C)

We can further build on the SEIR model with testing to incorporate contact tracing. We first consider automatic contact tracing facilitated through technology. There are many proposed methods for carrying this out, with many center around defining contacts made through bluetooth enabled devices. Here we take a technology agnostic approach, and consider some fraction of the population p_c that chooses to participate in contact tracing. We therefore divide the population in those who do not contact trace and those that do, and treat their population dynamics separately. Someone who starts in the contact tracing group cannot migrate to the non contact tracing population, but someone who is contact tracing can infect someone who is not (and vice-versa). As shown in figure XXXX, we now have two separate sets of population transfer dynamics to consider. We label all the population groups who do not participate in contact tracing with a bar accent (for example, \bar{S}), and those who do participate with a check accent (for example, \check{E}). We keep this notation throughout. Those who do not participate in contact tracing have dynamics described by the SEIR-T model described in the previous section.

The flow of the population not participating in contact tracing reduces to the case where we only have testing (as shown in figure XXXXX). However, those participating in contact tracing have one additional state that needs to be accounted for. Those who are untested in a group now have a chance to quarantine themselves when they are notified of a past contact with someone who is infectious. These individuals move from the population J_u to J_q . Those who are in J_q are tested at a rate of r_t^c . Anyone chosen for testing in J_u or J_q move to the waiting state J_w until their test results come back. If the test is negative, they return to J_u , but if it is positive, the move to J_n . As individuals move from J_w to J_n they notify all of their potential contacts to quarantine themselves (move from J_u to J_q).

As in the testing section, we consider a population J to be represented by the vector:

$$\check{J} = \begin{bmatrix} \check{J}_u \\ \check{J}_q \\ \check{J}_w \\ \check{J}_t \end{bmatrix}, \quad (25)$$

Notifications can identify individuals that the infectious person has infected as well as those they had contact with but did not infect. We can describe the notification transition with the following matrix:

$$\check{\sigma}_c = \begin{bmatrix} -1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad (26)$$

Similar to SEIR-T, we have transition matrices for those who are tested ($\check{\sigma}_t$), positive tests ($\check{\sigma}_+$), negative tests ($\check{\sigma}_-$), and those who return from isolation ($\check{\sigma}_{iso}$):

$$\check{\sigma}_t = \begin{bmatrix} -1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad (27)$$

$$\check{\sigma}_+ = \frac{1}{\tau_t} \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 \\ 0 & 0 & 1 & 0 \end{bmatrix} \quad (28)$$

$$\check{\sigma}_- = \frac{1}{\tau_t} \begin{bmatrix} 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad (29)$$

$$\check{\sigma}_{iso} = \frac{1}{\tau_{iso}} \begin{bmatrix} 0 & 1 & 0 & 1 \\ 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 \end{bmatrix} \quad (30)$$

IV. DESCRIPTION OF MODEL

Here we modify the SEIR model to include contact tracing and testing...

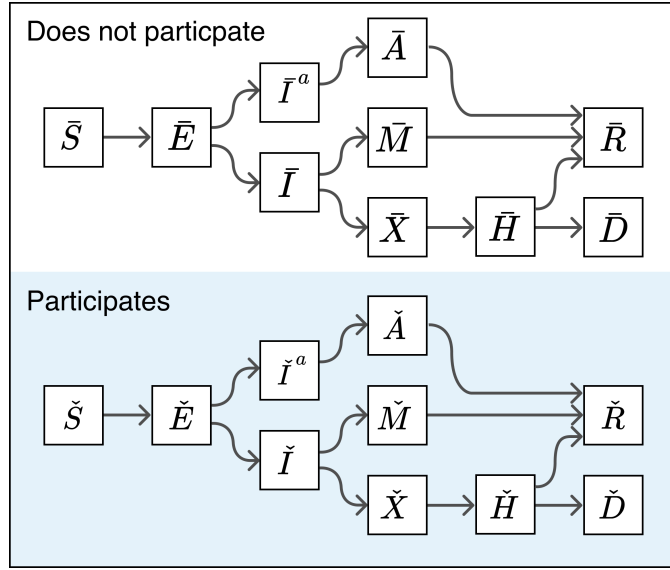


FIG. 3. Those who chose not to participate in contact tracing and those that do participate in contact tracing are treated separately. Population can never flow between the top and bottom graphs, although infectious individuals, regardless of whether they contact trace or not, can infect anyone who is susceptible.

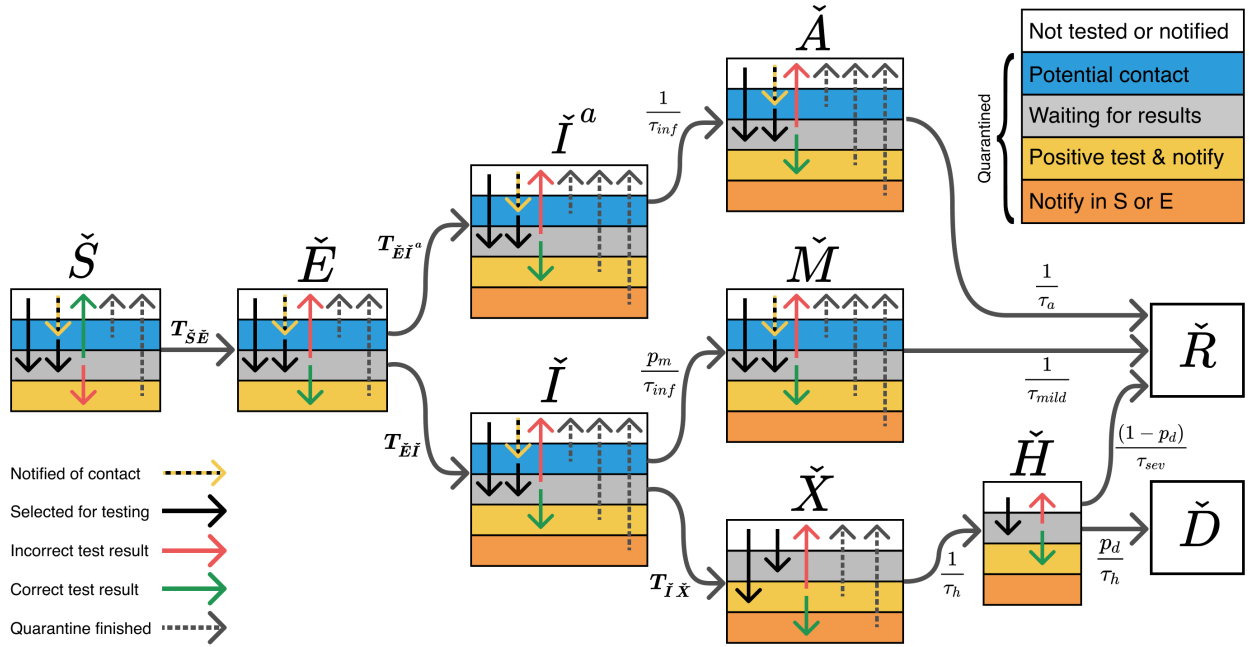


FIG. 4. Layers for contact tracing, as well as the transition rates between populations.

V. SUSCEPTIBLE

The rate of change equations for the susceptible populations that are not contact tracing (\bar{S}) are given as:

$$\frac{d\bar{S}}{dt} = \bar{S}_m \cdot \bar{S}, \quad (31)$$

where:

$$\bar{\mathbf{S}}_{\mathbf{m}} = \begin{bmatrix} -\gamma' - p_t & \frac{(1-f_{pos})}{\tau_t} & \frac{1}{\tau_{iso}} \\ p_t & -\frac{1}{\tau_t} - d_r\gamma' & 0 \\ 0 & \frac{f_{pos}}{\tau_t} & -d_r\gamma' \end{bmatrix} \quad (32)$$

$$\bar{\mathbf{S}} = \begin{bmatrix} \bar{S}_u \\ \bar{S}_w \\ \bar{S}_t \end{bmatrix} \quad (33)$$

$$(34)$$

Here @TODO explain terms.

The rate of change of the susceptible populations that are participating in contact tracing (\check{S}) are given as:

$$\frac{d\check{S}}{dt} = \check{\mathbf{S}}_{\mathbf{m}} \cdot \check{\mathbf{S}}, \quad (35)$$

where:

$$\check{\mathbf{S}}_{\mathbf{m}} = \begin{bmatrix} -\gamma' - \gamma_{false}^c - p_t & \frac{1}{\tau_{iso}} & \frac{(1-f_{pos})}{\tau_t} & \frac{1}{\tau_{iso}} \\ \gamma_{false}^c & -p_t^c - \frac{1}{\tau_{iso}} - d_r\gamma' & 0 & 0 \\ p_t & p_t^c & -\frac{1}{\tau_t} - d_r\gamma' & 0 \\ 0 & 0 & \frac{f_{pos}}{\tau_t} & -\frac{1}{\tau_{iso}} - d_r\gamma' \end{bmatrix}, \quad (36)$$

$$\check{\mathbf{S}} = \begin{bmatrix} \check{S}_u \\ \check{S}_q \\ \check{S}_w \\ \check{S}_n \end{bmatrix} \quad (37)$$

VI. EXPOSURE

The rate of change equations for the exposed populations that are not contact tracing (\bar{S}) are given as:

$$\frac{d\bar{E}}{dt} = \bar{\mathbf{E}}_{\mathbf{m}} \cdot \bar{\mathbf{E}} + \mathbf{T}_{\bar{\mathbf{S}}\bar{\mathbf{E}}} \bar{\mathbf{S}}, \quad (38)$$

where:

$$\bar{\mathbf{E}}_{\mathbf{m}} = \begin{bmatrix} -p_t - \frac{1}{\tau_{inc}} & \frac{(1-f_{neg})}{\tau_t} & \frac{1}{\tau_{iso}} \\ p_t & -\frac{1}{\tau_t} - \frac{1}{\tau_{inc}} & 0 \\ 0 & \frac{f_{neg}}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{inc}} \end{bmatrix} \quad (39)$$

$$\bar{\mathbf{E}} = \begin{bmatrix} \bar{E}_u \\ \bar{E}_w \\ \bar{E}_t \end{bmatrix} \quad (40)$$

$$\mathbf{T}_{\bar{\mathbf{S}}\bar{\mathbf{E}}} = \begin{bmatrix} \gamma' & 0 & 0 \\ 0 & d_r\gamma' & 0 \\ 0 & 0 & d_r\gamma' \end{bmatrix}. \quad (41)$$

For the exposed population participating in contact tracing we have:

$$\frac{d\check{E}}{dt} = \check{\mathbf{E}}_{\mathbf{m}} \cdot \check{\mathbf{E}} + \mathbf{T}_{\check{\mathbf{S}}\check{\mathbf{E}}} \check{\mathbf{S}}, \quad (42)$$

where:

$$\check{\mathbf{E}}_{\mathbf{m}} = \begin{bmatrix} -\gamma_{false}^c - \gamma_{true}^c - p_t - \frac{1}{\tau_{inc}} & -p_t^c - \frac{1}{\tau_{iso}} - \frac{1}{\tau_{inc}} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} \\ \gamma_{false}^c + \gamma_{true}^c & p_t^c & 0 & 0 \\ p_t & 0 & -\frac{1}{\tau_t} - \frac{1}{\tau_{inc}} & 0 \\ 0 & 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{inc}} \end{bmatrix}, \quad (43)$$

$$\check{\mathbf{E}} = \begin{bmatrix} \check{E}_u \\ \check{E}_q \\ \check{E}_w \\ \check{E}_n \end{bmatrix}, \quad (44)$$

$$\mathbf{T}_{\check{\mathbf{S}}\check{\mathbf{E}}} = \begin{bmatrix} \gamma' & 0 & 0 & 0 \\ 0 & d_r \gamma' & 0 & 0 \\ 0 & 0 & d_r \gamma' & 0 \\ 0 & 0 & 0 & d_r \gamma' \end{bmatrix}. \quad (45)$$

VII. INFECTIOUS

In the infectious population, we must consider that a certain percentage of those infected (p_a) will be asymptomatic. Those who display no symptoms will not be as likely to be tested, and will be more difficult to quarantine. The asymptomatic individuals will be split between those who contact trace and those who do not. We denote those who are asymptomatic with a superscript a .

A. Individuals who are infectious and display symptoms

First we consider those who display symptoms, but don't contact trace:

$$\frac{d\bar{I}}{dt} = \bar{\mathbf{I}}_{\mathbf{m}} \cdot \bar{I} + \frac{(1-p_a)}{\tau_{inc}} \mathbb{1} \cdot \bar{E}, \quad (46)$$

where:

$$\bar{\mathbf{I}}_{\mathbf{m}} = \begin{bmatrix} -p_t^i - \frac{1}{\tau_{inf}} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} \\ p_t^i & -\frac{1}{\tau_t} - \frac{1}{\tau_{inf}} & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{inf}} \end{bmatrix}, \quad (47)$$

$$\bar{I} = \begin{bmatrix} \bar{I}_u \\ \bar{I}_w \\ \bar{I}_t \end{bmatrix}, \quad (48)$$

$$(49)$$

and the identity matrix is represented as $\mathbb{1}$.

Those who participate in contact tracing, are infectious, and display symptoms:

$$\frac{d\check{I}}{dt} = \check{\mathbf{I}}_{\mathbf{m}} \check{I} + \mathbf{T}_{\check{\mathbf{E}}\check{I}} \cdot \check{E}, \quad (50)$$

where:

$$\check{\mathbf{I}}_m = \begin{bmatrix} -\gamma_{false}^c - \gamma_{true}^c - p_t^i - \frac{1}{\tau_{inf}} & -\frac{1}{\tau_{iso}} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} & \frac{1}{\tau_{iso}} \\ \gamma_{false}^c + \gamma_{true}^c & -p_t^n - \frac{1}{\tau_{iso}} - \frac{1}{\tau_{inf}} & 0 & 0 & 0 \\ p_t^i & p_t^n & -\frac{1}{\tau_t} - \frac{1}{\tau_{inf}} & 0 & 0 \\ 0 & 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{inf}} & 0 \\ 0 & 0 & 0 & 0 & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{inf}} \end{bmatrix}, \quad (51)$$

$$\check{\mathbf{I}} = \begin{bmatrix} \check{I}_u \\ \check{I}_q \\ \check{I}_w \\ \check{I}_n \\ \check{I}_{n'} \end{bmatrix}, \quad (52)$$

$$\mathbf{T}_{\check{\mathbf{E}}\check{\mathbf{I}}} = \frac{(1-p_a)}{\tau_{inc}} \begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \end{bmatrix}. \quad (53)$$

B. Asymptomatic

For those who are asymptomatic, we first look at the group that does not participate in contact tracing:

$$\frac{d\bar{I}^a}{dt} = \bar{\mathbf{I}}_m^a \cdot \bar{I}^a + \frac{p_a}{\tau_{inc}} \mathbb{1} \cdot \bar{E}, \quad (54)$$

$$\bar{\mathbf{I}}_m^a = \bar{\mathbf{I}}_m, \quad (55)$$

$$\bar{I}^a = \begin{bmatrix} \bar{I}_u^a \\ \bar{I}_q^a \\ \bar{I}_w^a \\ \bar{I}_t^a \end{bmatrix}, \quad (56)$$

Finally, we have those who are asymptomatic but are participating in contact tracing:

$$\frac{d\check{I}^a}{dt} = \check{\mathbf{I}}_m^a \cdot \check{I}^a + \mathbf{T}_{\check{\mathbf{E}}\check{\mathbf{I}}}^a \cdot \check{E}, \quad (57)$$

$$\check{\mathbf{I}}_m^a = \check{\mathbf{I}}_m, \quad (58)$$

$$\mathbf{T}_{\check{\mathbf{E}}\check{\mathbf{I}}}^a = \mathbf{T}_{\check{\mathbf{E}}\check{\mathbf{I}}} \quad (59)$$

$$\check{I}^a = \begin{bmatrix} \check{I}_u^a \\ \check{I}_q^a \\ \check{I}_w^a \\ \check{I}_n^a \\ \check{I}_{n'}^a \end{bmatrix} \quad (60)$$

VIII. OUTCOMES

This is part of the R section in a traditional $SEIR$ model. We divide this into several transition times as it make take a patient some time to recover after they are infectious (and therefore still test positive). We divide these up into those who are asymptomatic, mild, and severe. Those who are severe have a chance p_h of needing hospitalization or making a recovery R . Those who are hospitalized can recover R or die D . We denote the intermediate states where someone is in the recovery process O for outcomes.

A. Asymptomatic

Those who are asymptomatic, but not participating in contact tracing, have a population that changes:

$$\frac{d\bar{A}}{dt} = \bar{\mathbf{A}}_{\mathbf{m}} \cdot \bar{A} + \frac{1}{\tau_{inf}} \mathbb{1} \cdot \bar{I}^a, \quad (61)$$

where:

$$\bar{\mathbf{A}}_{\mathbf{m}} = \begin{bmatrix} -p_t - \frac{1}{\tau_a} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} \\ p_t & -\frac{1}{\tau_t} - \frac{1}{\tau_a} & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_a} \end{bmatrix}, \quad (62)$$

$$\bar{A} = \begin{bmatrix} \bar{A}_u \\ \bar{A}_w \\ \bar{A}_t \end{bmatrix}. \quad (63)$$

$$(64)$$

Those who are participating in contact tracing, but are asymptomatic have the following population change as a function of time:

$$\frac{d\check{A}}{dt} = \check{\mathbf{A}}_{\mathbf{m}} \cdot \check{A} + \frac{1}{\tau_{inf}} \mathbb{1} \cdot \check{I}^a, \quad (65)$$

where:

$$\check{\mathbf{A}}_{\mathbf{m}} = \begin{bmatrix} -\gamma_{false}^c - \gamma_{true}^c - p_t - \frac{1}{\tau_a} & \frac{1}{\tau_{iso}} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} & \frac{1}{\tau_{iso}} \\ \gamma_{false}^c + \gamma_{true}^c & -p_t^c - \frac{1}{\tau_{iso}} - \frac{1}{\tau_a} & 0 & 0 & 0 \\ p_t & p_t^c & -\frac{1}{\tau_t} - \frac{1}{\tau_a} & 0 & 0 \\ 0 & 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_a} & 0 \\ 0 & 0 & 0 & 0 & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_a} \end{bmatrix}, \quad (66)$$

$$\check{A} = \begin{bmatrix} \check{A}_u \\ \check{A}_q \\ \check{A}_w \\ \check{A}_n \\ \check{A}_{n'} \end{bmatrix}. \quad (67)$$

$$(68)$$

We must track each of these subpopulations. Even though no one in A is still infectious, they can still test positive and thereby notify others that they need to quarantine themselves (including those who they may have infected).

1. Mild

We now deal with the infectious population who develop a mild case (show symptoms), but do not need hospitalization and do not die. These individual recover in a time τ_{mild} , and make up p_{mild} fraction of total infectious cases. Asymptomatic individuals cannot be included in this group. Since we are looking at a subpopulation who aren't asymptomatic, we must account for this. The fraction of nonasymptomatic individuals who develop mild cases is given as:

$$p_m = \frac{p_{mild}}{(1 - p_a)}. \quad (69)$$

For those who develop mild cases and do not participate in contact tracing we have:

$$\frac{d\bar{M}}{dt} = \bar{\mathbf{M}}_{\mathbf{m}} \cdot \bar{M} + \frac{p_m}{\tau_{inf}} \mathbb{1} \cdot \bar{I}, \quad (70)$$

where:

$$\bar{\mathbf{M}}_{\mathbf{m}} = \begin{bmatrix} -p_t - \frac{1}{\tau_{mild}} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} \\ p_t & -\frac{1}{\tau_t} - \frac{1}{\tau_{mild}} & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{mild}} \end{bmatrix}, \quad (71)$$

$$\bar{\mathbf{M}} = \begin{bmatrix} \bar{M}_u \\ \bar{M}_w \\ \bar{M}_t \end{bmatrix}. \quad (72)$$

$$(73)$$

Finally, for those who develop mild cases and contact trace:

$$\frac{d\check{\mathbf{M}}}{dt} = \check{\mathbf{M}}_{\mathbf{m}} \cdot \check{\mathbf{M}} + \frac{p_m}{\tau_{inf}} \mathbb{1} \cdot \check{\mathbf{I}}, \quad (74)$$

where:

$$\check{\mathbf{M}}_{\mathbf{m}} = \begin{bmatrix} -\gamma_{false}^c - \gamma_{true}^c - p_t - \frac{1}{\tau_{mild}} & \frac{1}{\tau_{iso}} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} & \frac{1}{\tau_{iso}} \\ \gamma_{false}^c + \gamma_{true}^c & -p_t^c - \frac{1}{\tau_{iso}} - \frac{1}{\tau_{mild}} & 0 & 0 & 0 \\ p_t & p_t^c & -\frac{1}{\tau_t} - \frac{1}{\tau_{mild}} & 0 & 0 \\ 0 & 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{mild}} & 0 \\ 0 & 0 & 0 & 0 & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{mild}} \end{bmatrix}, \quad (75)$$

$$\check{\mathbf{M}} = \begin{bmatrix} \check{M}_u \\ \check{M}_q \\ \check{M}_w \\ \check{M}_n \\ \check{M}_{n'} \end{bmatrix}. \quad (76)$$

$$(77)$$

B. Severe

The final group we must consider are those who are severe cases. These represent the following fraction of the symptomatic cases that are severe:

$$p_{sev} = 1 - p_m, \quad (78)$$

and lead to hospitalization some time τ_h after they cease to be infectious. We also assume that anyone in the severe category will be tested at a rate p_t^{sev} regardless of whether they have been notified of a potential contact Those hospitalized will either recover or die. Those who do not participate in contact tracing can be described by the following dynamics:

$$\frac{d\bar{\mathbf{X}}}{dt} = \bar{\mathbf{X}}_{\mathbf{m}} \cdot \bar{\mathbf{X}} + \frac{p_{sev}}{\tau_{inf}} \mathbb{1} \cdot \bar{\mathbf{I}}, \quad (79)$$

where:

$$\bar{\mathbf{X}}_{\mathbf{m}} = \begin{bmatrix} -p_t^{sev} - \frac{1}{\tau_h} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} \\ p_t^{sev} & -\frac{1}{\tau_t} - \frac{1}{\tau_h} & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_h} \end{bmatrix}, \quad (80)$$

$$\bar{\mathbf{X}} = \begin{bmatrix} \bar{X}_u \\ \bar{X}_w \\ \bar{X}_t \end{bmatrix}. \quad (81)$$

$$(82)$$

For those who do participate in contact tracing but develop severe symptoms we have:

$$\frac{d\check{\mathbf{X}}}{dt} = \check{\mathbf{X}}_{\mathbf{m}} \cdot \check{\mathbf{X}} + \frac{p_{sev}}{\tau_{inf}} \mathbb{1} \cdot \check{\mathbf{I}}, \quad (83)$$

where:

$$\check{\mathbf{X}}_{\mathbf{m}} = \begin{bmatrix} -p_t^{sev} - \frac{1}{\tau_h} & \frac{f_{neg}}{\tau_t} & 0 & 0 \\ p_t^{sev} & -\frac{1}{\tau_t} - \frac{1}{\tau_h} & 0 & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_h} & 0 \\ 0 & 0 & 0 & -\frac{1}{\tau_h} \end{bmatrix}, \quad (84)$$

$$\check{\mathbf{X}} = \begin{bmatrix} \check{X}_u \\ \check{X}_w \\ \check{X}_n \\ \check{X}_{n'} \end{bmatrix}, \quad (85)$$

$$\mathbf{T}_{I\check{\mathbf{X}}} = \frac{p_{sev}}{\tau_{inf}} \begin{bmatrix} 1 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix} \quad (86)$$

1. Hospitalized

Those that are hospitalized The population dynamics for those hospitalized who are not contact tracing is given as:

$$\frac{d\bar{\mathbf{H}}}{dt} = \bar{\mathbf{H}}_{\mathbf{m}} \cdot \bar{\mathbf{H}} + \frac{1}{\tau_h} \mathbb{1} \cdot \bar{\mathbf{X}}, \quad (87)$$

where:

$$\bar{\mathbf{H}}_{\mathbf{m}} = \begin{bmatrix} -p_t^{sev} - \gamma^{sev} & \frac{f_{neg}}{\tau_t} & 0 \\ p_t^{sev} & -\frac{1}{\tau_t} - \gamma^{sev} & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\gamma^{sev} \end{bmatrix}, \quad (88)$$

$$\bar{\mathbf{H}} = \begin{bmatrix} \bar{H}_u \\ \bar{H}_w \\ \bar{H}_t \end{bmatrix}. \quad (89)$$

A fraction p_d of those who are hospitalized will die after an average time τ_d , or recover after a time τ_{sev} . To find p_d , we must use the case fatality rate, C_{FR} to figure out the percentage of those hospitalized that will die. Since the case fatality rate applies to all infections, the probability of those who are hospitalized dying is:

$$p_d = \frac{C_{FR}}{1 - p_a - p_{mild}}. \quad (91)$$

The effective rate at which individuals leave the hospital is given as:

$$\gamma^{sev} = \frac{p_d}{\tau_d} + \frac{(1 - p_d)}{\tau_{sev}}. \quad (92)$$

Those who participate in contact tracing and are hospitalized automatically notify all of their prior contacts regardless if they have been tested. There is no effect if they are notified of a potential contact.

$$\frac{d\check{\mathbf{H}}}{dt} = \check{\mathbf{H}}_{\mathbf{m}} \cdot \check{\mathbf{H}} + \frac{1}{\tau_h} \mathbb{1} \cdot \check{\mathbf{X}}, \quad (93)$$

$$\check{\mathbf{H}}_{\mathbf{m}} = \begin{bmatrix} -p_t^{sev} - \gamma^{sev} & \frac{f_{neg}}{\tau_t} & 0 & 0 \\ p_t^{sev} & -\frac{1}{\tau_t} - \gamma^{sev} & 0 & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\gamma^{sev} & 0 \\ 0 & 0 & 0 & -\gamma^{sev} \end{bmatrix}, \quad (94)$$

$$\check{\mathbf{H}} = \begin{bmatrix} \check{H}_u \\ \check{H}_w \\ \check{H}_n \\ \check{H}_{n'} \end{bmatrix}, \quad (95)$$

$$(96)$$

C. Deaths

In this model, only those who are hospitalized have a probability p_d of dying. We will split the population of potential deaths into those who died and were contact tracing and those who died but were not. The two equations describing the death rate are:

$$\frac{d\bar{D}}{dt} = \frac{p_d}{\tau_d} \mathbb{1} \cdot \bar{H}, \quad (97)$$

$$\frac{d\check{D}}{dt} = \frac{p_d}{\tau_d} \mathbb{1} \cdot \check{H}. \quad (98)$$

D. Recovery

Finally, we consider those who recover and are now considered immune. Again we consider those who recover and contact trace and those who abstain. For the non participants we have:

$$\frac{d\bar{R}}{dt} = \frac{(1-p_d)}{\tau_{sev}} \mathbb{1} \cdot \bar{H} + \frac{1}{\tau_{mild}} \mathbb{1} \cdot \bar{M} + \frac{1}{\tau_a} \mathbb{1} \cdot \bar{A}, \quad (99)$$

and for those who do participate in contact tracing the recovery rate is:

$$\frac{d\check{R}}{dt} = \frac{(1-p_d)}{\tau_{sev}} \mathbb{1} \cdot \check{H} + \frac{1}{\tau_{mild}} \mathbb{1} \cdot \check{M} + \frac{1}{\tau_a} \mathbb{1} \cdot \check{A}, \quad (100)$$

$$\frac{d\check{P}}{dt} = \begin{bmatrix} \check{S}_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ T_{\check{S}\check{E}} & \check{E}_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & T_{\check{E}\check{I}} & \check{I}_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & T_{\check{E}\check{I}^a} & 0 & \check{I}_m^a & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{1}{\tau_{inf}} \check{A}_m & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{p_m}{\tau_{inf}} & 0 & 0 & \check{M}_m & 0 & 0 & 0 & 0 \\ 0 & 0 & T_{I\check{X}} & 0 & 0 & 0 & \check{X}_m & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\tau_h} \check{H}_m & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{p_d}{\tau_d} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\tau_a} & \frac{1}{\tau_{mild}} & \frac{(1-p_d)}{\tau_{sev}} & 0 \end{bmatrix} \cdot \begin{bmatrix} \check{S} \\ \check{E} \\ \check{I} \\ \check{I}^a \\ \check{A} \\ \check{M} \\ \check{X} \\ \check{H} \\ \check{D} \\ \check{R} \end{bmatrix}, \quad (101)$$

$$\frac{d\bar{P}}{dt} = \begin{bmatrix} \bar{S}_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ T_{\bar{S}\bar{E}} & \bar{E}_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{p_a}{\tau_{inc}} & \bar{I}_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{(1-p_a)}{\tau_{inc}} & 0 & \bar{I}_m^a & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{1}{\tau_{inf}} \bar{A}_m & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{p_m}{\tau_{inf}} & 0 & 0 & \bar{M}_m & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{p_{sev}}{\tau_{inf}} & 0 & 0 & 0 & \bar{X}_m & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\tau_h} \bar{H}_m & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{p_d}{\tau_d} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\tau_a} & \frac{1}{\tau_{mild}} & \frac{(1-p_d)}{\tau_{sev}} & 0 \end{bmatrix} \cdot \begin{bmatrix} \bar{S} \\ \bar{E} \\ \bar{I} \\ \bar{I}^a \\ \bar{A} \\ \bar{M} \\ \bar{X} \\ \bar{H} \\ \bar{D} \\ \bar{R} \end{bmatrix}, \quad (102)$$

$$\frac{dP}{dt} = \begin{bmatrix} \bar{P}_m & 0 \\ 0 & \check{P}_m \end{bmatrix} \cdot \begin{bmatrix} \bar{P} \\ \check{P} \end{bmatrix}, \quad (104)$$

TABLE I. Parameter List

Parameter	Definition
<i>Average time parameters</i>	
τ_{iso}	Time spent in isolation after a contact or positive test
τ_{inc}	Incubation time. Length of time spent in the exposed phase.
τ_{inf}	Amount of time spent infectious.
τ_a	Amount of time it takes someone asymptomatic to recover after leaving infectious phase
τ_{mild}	Amount of time it takes someone with mild symptoms to recover after leaving infectious phase
τ_h	Average time before someone with severe symptoms enters the hospital.
τ_{sev}	Amount of time it takes someone with severe symptoms to recover after entering the hospital.
τ_d	Amount of time it takes someone to die who is in the hospital.
τ_c	Average time over which to consider notifying those who someone infectious has made contact with.
<i>Testing parameters</i>	
τ_t	Average time it takes to return a test result.
f_{neg}	Fraction of tests that return a false negative.
f_{pos}	Fraction of tests that return a false positive.
p_t	Probability that someone in the general population gets tested (not showing symptoms or isolating)
p_t^c	Probability that someone who is notified of a possible infectious contact event is tested.
p_t^i	Probability that someone in the infectious phase showing symptoms is tested.
p_t^n	The greater of p_t^c , p_t^i , or p_t .
p_t^{sev}	Probability that someone who is showing severe symptoms or is hospitalized is tested.
<i>Population percentages</i>	
p_c	Fraction of the population participating in contact tracing.
p_a	Fraction of the population that is asymptomatic
<i>Infectious Rates</i>	
R_0	Reproduction rate
β_0	$= \frac{R_0}{\tau_{inf}}$
d_r	The fraction that R_0 is reduced by those who are isolating through contact tracing or testing.
d_q	The fraction that R_0 is reduced due to stay-at-home orders.
γ	$= \beta_0(\bar{I}_{tot} + d_r \check{I}_{tot})$ The probability someone infectious spreads
R_c	Average number of individuals an infectious person has come in contact with in the past τ_c days.
β_c	Average number of total daily contacts someone infectious has made.
γ_{false}^c	Rate of false notifications of individuals who aren't infected.
γ_{true}^c	Rate of true notifications of individuals who have become infectious (contact tracing works).

$$\gamma_{false}^c = \beta_c(\check{S}_n + \check{E}_n + \check{I}_{n'} + \check{I}_{n'}^a + \check{\mathbf{R}}_{\mathbf{n}'}) + \frac{(R_c - R_0)}{\tau_c}(\check{I}_n + \check{I}_n^a + \check{\mathbf{R}}_{\mathbf{n}}), \quad (105)$$

$$\gamma_{true}^c = \beta_0(\check{I}_n + \check{I}_n^a + \check{\mathbf{R}}_{\mathbf{n}}), \quad (106)$$

$$\check{\mathbf{R}}_{\mathbf{n}'} = \check{A}_{n'} + \check{M}_{n'} + \check{X}_{n'} + \check{H}_{n'}, \quad (107)$$

$$\check{\mathbf{R}}_{\mathbf{n}} = \check{A}_n + \check{M}_n + \check{X}_n + \check{H}_u + \check{H}_w + \check{H}_n \quad (108)$$