SEIR-C: An epidemic model that includes contact tracing

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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 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:

$$N = S + E + I + R. \tag{1}$$

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:

$$\frac{dS}{dt} = -\beta_0 \frac{I}{N} S, \tag{2}$$

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

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

$$\frac{dR}{dt} = \frac{1}{\tau_{inf}} I. \tag{5}$$

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 if 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 "g" subscript, i.e. S_g), 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
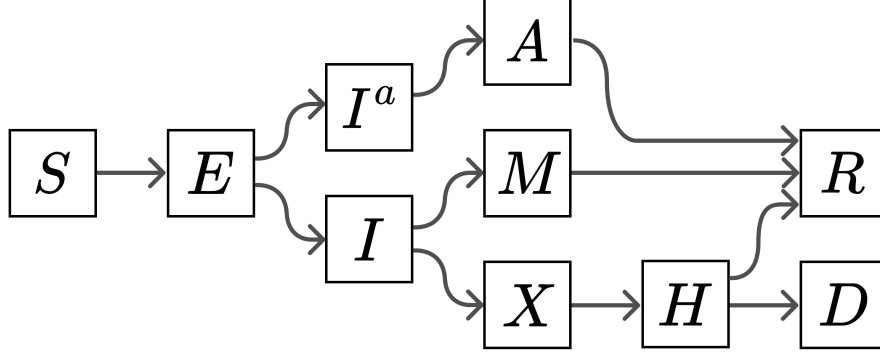
FIG. 1. Conceptual diagram for SEIR with asymptomatic individuals. The first population group are those who are susceptible (S), meaning they have not yet been infected. They can become infected through contact with someone who is infectious (I and I^a). Once infected, they move to the exposed group (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 infectous 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 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 infectous 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_g and stop quarantining. Similarly, those who are infectious that test negative (through a false negative) will return to either I_g or I_g^a where they will resume infecting others at the original R_0.

III. SEIR WITH CONTACT TRACING (SEIR-C)

We can further build on the SEIR model with testing to incorporate contact tracing. @TODO define contact tracing and what we consider.

The model assumes that a fraction of the population p_c chooses to particpate 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 particpate with a check accent (for example, $\check{E}$). We keep this notation throughout.

The flow of the population not particpating in contact tracing reduces to the case where we only have testing (as shown in figure XXXXX). However, those particpating in contact tracing have additional states that need to be considered as shown in figure XXXXX.

IV. DESCRIPTION OF MODEL

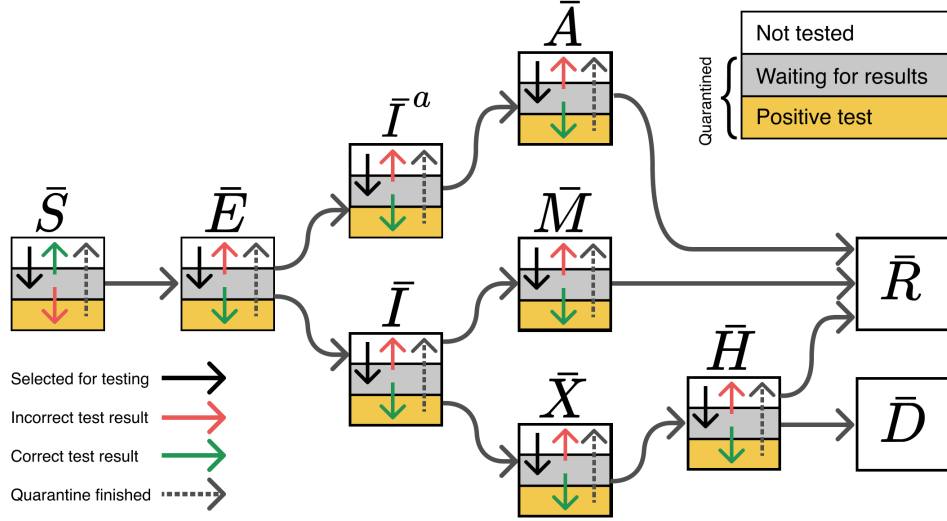Here we modify the SEIR model to include contact tracing and testing...

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 $E_w \to I_w$ or $I_g \to M_g$). 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.
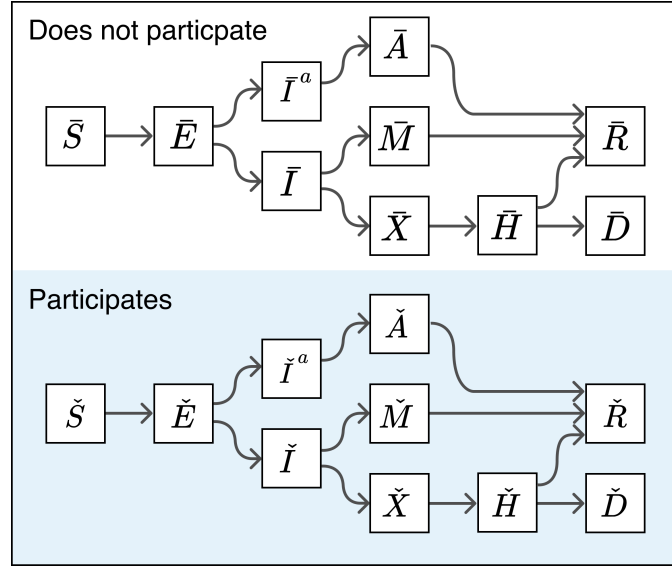

FIG. 3. Those who chose not to participate in contact tracing and those that do particpate in contact tracing are treated separately. Population can never flow between the top and bottom graphs, although infectious individuals, regardless of whether they contact trace or not, can infect anyone who is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

A. Conventions and notation

The populations are divided into those who particpate in contact tracing and those who do not. During each phase of the disease progression, there is never a transfer of popoulation from the group that is contact tracing and those who are not. We denote any population, J, that does not contact trace with a bar ($\bar{J}$) and those who do contact trace with a dot ($\check{J}$).

In this model, anyone who is notified of a potential exposure through contact tracing is quarantined for some
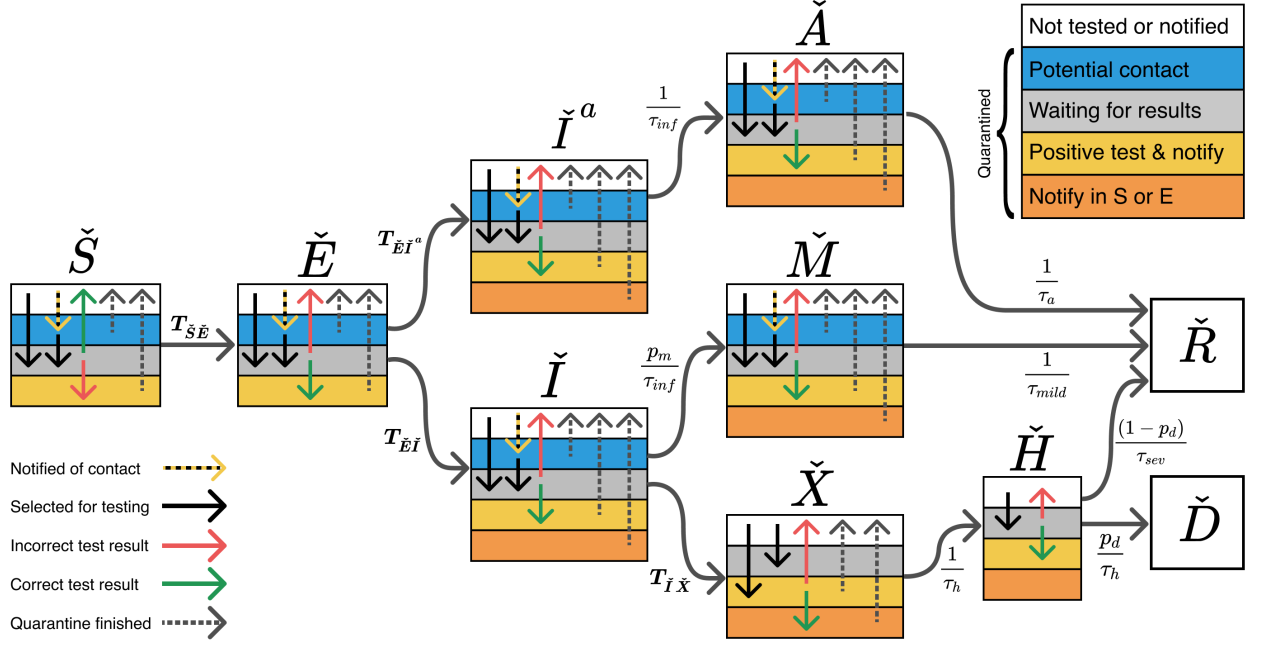
FIG. 4. Layers for contact tracing, as well as the transition rates between populations.

average time τ_{iso}. During this time, their R_0 is reduced by a fraction d_r, making them far less likely to be exposed to the virus if they are susceptible, or much less likely to infect others if they are infectious. Testing can also take place. The average probability that someone in the general population is selected for testing is p_t. Later on we will allow for different testing rates for those who have been identified as being potentially exposed through contact tracing (p_t^c), those who show symptoms while infectious(p_t^i), and those who develop severe symptoms (p_t^{sev}). We can also account for tests that return false positives (f_{pos}) and false negatives (f_{neg}), as well as the time it takes to get the test results (τ_t) As in the basic SEIR model, the average time spent in the exposure phase is τ_{inc}, and the time spend in the infectious phase is τ_{inf}. Instead of a monolithic recovery phase, we consider several different subpopulations. There are those who are asymptomatic, those with mild infections, those with severe infections that lead to hospitalizations, and those who die after being hospitalized.

V. SUSCEPTIBLE

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

$$\frac{d\bar{S}}{dt} = \bar{\boldsymbol{S}}_{\boldsymbol{m}} \cdot \bar{S}, \tag{6}$$

where:

$$\bar{\boldsymbol{S}}_{\boldsymbol{m}} = \begin{bmatrix} -\gamma' - p_t & \frac{(1-f_{pos})}{\tau_t} & \frac{1}{\tau_{iso}} \\ p_t & -\frac{1}{\tau_t} - d_r\gamma' & 0 \\ 0 & \frac{f_{pos}}{\tau_t} & -d_r\gamma' \end{bmatrix} \tag{7}$$

$$\bar{S} = \begin{bmatrix} \bar{S}_g \\ \bar{S}_w \\ \bar{S}_t \end{bmatrix} \tag{8}$$

$$\tag{9}$$

Here @TODO explain terms.

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

$$\frac{d\check{S}}{dt} = \check{\boldsymbol{S}}_{\boldsymbol{m}} \cdot \check{S}, \tag{10}$$

where:

$$\check{\boldsymbol{S}}_{\boldsymbol{m}} = \begin{bmatrix} -\gamma' - \gamma_{false}^c - p_t & \frac{1}{\tau_{iso}} & \frac{(1-f_{pos})}{\tau_t} & \frac{1}{\tau_{iso}} \\ \gamma_{false}^c & -p_t^c - \frac{1}{\tau_{iso}} - d_r\gamma' & 0 & 0 \\ p_t & p_t^c & -\frac{1}{\tau_t} - d_r\gamma' & 0 \\ 0 & 0 & \frac{f_{pos}}{\tau_t} & -\frac{1}{\tau_{iso}} - d_r\gamma' \end{bmatrix}, \tag{11}$$

$$\check{S} = \begin{bmatrix} \check{S}_g \\ \check{S}_q \\ \check{S}_w \\ \check{S}_n \end{bmatrix} \tag{12}$$

VI. EXPOSURE

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

$$\frac{d\bar{E}}{dt} = \bar{\boldsymbol{E}}_{\boldsymbol{m}} \cdot \bar{E} + \boldsymbol{T}_{\bar{\boldsymbol{S}}\bar{\boldsymbol{E}}}\bar{S}, \tag{13}$$

where:

$$\bar{\boldsymbol{E}}_{\boldsymbol{m}} = \begin{bmatrix} -p_t - \frac{1}{\tau_{inc}} & \frac{(1-f_{neg})}{\tau_t} & \frac{1}{\tau_{iso}} \\ p_t & -\frac{1}{\tau_t} - \frac{1}{\tau_{inc}} & 0 \\ 0 & \frac{f_{neg}}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{inc}} \end{bmatrix} \tag{14}$$

$$\bar{E} = \begin{bmatrix} \bar{E}_g \\ \bar{E}_w \\ \bar{E}_t \end{bmatrix} \tag{15}$$

$$\boldsymbol{T}_{\bar{\boldsymbol{S}}\bar{\boldsymbol{E}}} = \begin{bmatrix} \gamma' & 0 & 0 \\ 0 & d_r\gamma' & 0 \\ 0 & 0 & d_r\gamma' \end{bmatrix}. \tag{16}$$

For the exposedß population particpating in contact tracing we have:

$$\frac{d\check{E}}{dt} = \check{\boldsymbol{E}}_{\boldsymbol{m}} \cdot \check{E} + \boldsymbol{T}_{\check{\boldsymbol{S}}\check{\boldsymbol{E}}}\check{S}, \tag{17}$$

where:

$$\check{\boldsymbol{E}}_{\boldsymbol{m}} = \begin{bmatrix} -\gamma_{false}^c - \gamma_{true}^c - p_t - \frac{1}{\tau_{inc}} & \frac{1}{\tau_{iso}} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} \\ \gamma_{false}^c + \gamma_{true}^c & -p_t^c - \frac{1}{\tau_{iso}} - \frac{1}{\tau_{inc}} & 0 & 0 \\ p_t & p_t^c & -\frac{1}{\tau_t} - \frac{1}{\tau_{inc}} & 0 \\ 0 & 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{inc}} \end{bmatrix}, \tag{18}$$

$$\check{E} = \begin{bmatrix} \check{E}_g \\ \check{E}_q \\ \check{E}_w \\ \check{E}_n \end{bmatrix}, \tag{19}$$

$$\boldsymbol{T}_{\check{\boldsymbol{S}}\check{\boldsymbol{E}}} = \begin{bmatrix} \gamma' & 0 & 0 & 0 \\ 0 & d_r\gamma' & 0 & 0 \\ 0 & 0 & d_r\gamma' & 0 \\ 0 & 0 & 0 & d_r\gamma' \end{bmatrix}. \tag{20}$$

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:

$$\frac{d\bar{I}}{dt} = \bar{\boldsymbol{I}}_{\boldsymbol{m}} \cdot \bar{I} + \frac{(1-p_a)}{\tau_{inc}} \mathbb{1} \cdot \bar{E}, \tag{21}$$

where:

$$\bar{\boldsymbol{I}}_{\boldsymbol{m}} = \begin{bmatrix} -p_t^i - \frac{1}{\tau_{inf}} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} \\ p_t^i & -\frac{1}{\tau_t} - \frac{1}{\tau_{inf}} & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{inf}} \end{bmatrix}, \tag{22}$$

$$\bar{I} = \begin{bmatrix} \bar{I}_g \\ \bar{I}_w \\ \bar{I}_t \end{bmatrix}, \tag{23}$$

$$\tag{24}$$

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

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

$$\frac{d\check{I}}{dt} = \check{\boldsymbol{I}}_{\boldsymbol{m}}\check{I} + \boldsymbol{T}_{\check{\boldsymbol{E}}\check{\boldsymbol{I}}} \cdot \check{E}, \tag{25}$$

where:

$$\check{\boldsymbol{I}}_{\boldsymbol{m}} = \begin{bmatrix} -\gamma_{false}^c - \gamma_{true}^c - p_t^i - \frac{1}{\tau_{inf}} & \frac{1}{\tau_{iso}} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} & \frac{1}{\tau_{iso}} \\ \gamma_{false}^c + \gamma_{true}^c & -p_t^n - \frac{1}{\tau_{iso}} - \frac{1}{\tau_{inf}} & 0 & 0 & 0 \\ p_t^i & p_t^n & -\frac{1}{\tau_t} - \frac{1}{\tau_{inf}} & 0 & 0 \\ 0 & 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{inf}} & 0 \\ 0 & 0 & 0 & 0 & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{inf}} \end{bmatrix}, \tag{26}$$

$$\check{I} = \begin{bmatrix} \check{I}_g \\ \check{I}_q \\ \check{I}_w \\ \check{I}_n \\ \check{I}_{n'} \end{bmatrix}, \tag{27}$$

$$\boldsymbol{T}_{\check{\boldsymbol{E}}\check{\boldsymbol{I}}} = \frac{(1-p_a)}{\tau_{inc}} \begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \end{bmatrix}. \tag{28}$$

B. Asymptomatic

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

$$\frac{d\bar{I}^a}{dt} = \bar{\boldsymbol{I}}_{\boldsymbol{m}}^{\boldsymbol{a}} \cdot \bar{I}^a + \frac{p_a}{\tau_{inc}} \mathbb{1} \cdot \bar{E}, \tag{29}$$

$$\bar{\boldsymbol{I}}_{\boldsymbol{m}}^{\boldsymbol{a}} = \bar{\boldsymbol{I}}_{\boldsymbol{m}}, \tag{30}$$

$$\bar{I}^a = \begin{bmatrix} \bar{I}_g^a \\ \bar{I}_w^a \\ \bar{I}_t^a \end{bmatrix}, \tag{31}$$

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

$$\frac{d\check{I}^a}{dt} = \check{\boldsymbol{I}}_{\boldsymbol{m}}^{\boldsymbol{a}} \cdot \check{I}^a + \boldsymbol{T}_{\check{\boldsymbol{E}}\check{\boldsymbol{I}}^{\boldsymbol{a}}} \cdot \check{E}, \tag{32}$$

$$\check{\boldsymbol{I}}_{\boldsymbol{m}}^{\boldsymbol{a}} = \check{\boldsymbol{I}}_{\boldsymbol{m}}, \tag{33}$$

$$\boldsymbol{T}_{\check{\boldsymbol{E}}\check{\boldsymbol{I}}^{\boldsymbol{a}}} = \boldsymbol{T}_{\bar{\boldsymbol{E}}\bar{\boldsymbol{I}}^{\boldsymbol{a}}} \tag{34}$$

$$\check{I} = \begin{bmatrix} \check{I}_g^a \\ \check{I}_q^a \\ \check{I}_w^a \\ \check{I}_n^a \\ \check{I}_{n'}^a \end{bmatrix} \tag{35}$$

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 intermetiate states where someone is in the recovery process O for outcomes.

A.   Asymptomatic

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

$$\frac{d\bar{A}}{dt} = \bar{\boldsymbol{A}}_{\boldsymbol{m}} \cdot \bar{A} + \frac{1}{\tau_{inf}} \mathbb{1} \cdot \bar{I}^a, \tag{36}$$

where:

$$\bar{\boldsymbol{A}}_{\boldsymbol{m}} = \begin{bmatrix} -p_t - \frac{1}{\tau_a} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} \\ p_t & -\frac{1}{\tau_t} - \frac{1}{\tau_a} & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_a} \end{bmatrix}, \tag{37}$$

$$\bar{A} = \begin{bmatrix} \bar{A}_g \\ \bar{A}_w \\ \bar{A}_t \end{bmatrix}. \tag{38}$$

$$\tag{39}$$

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

$$\frac{d\check{A}}{dt} = \check{\boldsymbol{A}}_{\boldsymbol{m}} \cdot \check{A} + \frac{1}{\tau_{inf}} \mathbb{1} \cdot \check{I}^a, \tag{40}$$

where:

$$\check{\boldsymbol{A}}_{\boldsymbol{m}} = \begin{bmatrix} -\gamma_{false}^c - \gamma_{true}^c - p_t - \frac{1}{\tau_a} & \frac{1}{\tau_{iso}} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} & \frac{1}{\tau_{iso}} \\ \gamma_{false}^c + \gamma_{true}^c & -p_t^c - \frac{1}{\tau_{iso}} - \frac{1}{\tau_a} & 0 & 0 & 0 \\ p_t & p_t^c & -\frac{1}{\tau_t} - \frac{1}{\tau_a} & 0 & 0 \\ 0 & 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_a} & 0 \\ 0 & 0 & 0 & 0 & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_a} \end{bmatrix}, \tag{41}$$

$$\check{A} = \begin{bmatrix} \check{A}_g \\ \check{A}_q \\ \check{A}_w \\ \check{A}_n \\ \check{A}_{n'} \end{bmatrix}. \tag{42}$$

$$\tag{43}$$

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:

$$p_m = \frac{p_{mild}}{(1 - p_a)}. \tag{44}$$

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

$$\frac{d\bar{M}}{dt} = \bar{\boldsymbol{M}}_{\boldsymbol{m}} \cdot \bar{M} + \frac{p_m}{\tau_{inf}} \mathbb{1} \cdot \bar{I}, \tag{45}$$

where:

$$\bar{\boldsymbol{M}}_{\boldsymbol{m}} = \begin{bmatrix} -p_t - \frac{1}{\tau_{mild}} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} \\ p_t & -\frac{1}{\tau_t} - \frac{1}{\tau_{mild}} & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{mild}} \end{bmatrix}, \tag{46}$$

$$\bar{M} = \begin{bmatrix} \bar{M}_g \\ \bar{M}_w \\ \bar{M}_t \end{bmatrix}. \tag{47}$$

$$\tag{48}$$

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

$$\frac{d\check{M}}{dt} = \check{\boldsymbol{M}}_{\boldsymbol{m}} \cdot \check{M} + \frac{p_m}{\tau_{inf}} \mathbb{1} \cdot \check{I}, \tag{49}$$

where:

$$\check{\boldsymbol{M}}_{\boldsymbol{m}} = \begin{bmatrix} -\gamma^c_{false} - \gamma^c_{true} - p_t - \frac{1}{\tau_{mild}} & \frac{1}{\tau_{iso}} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} & \frac{1}{\tau_{iso}} \\ \gamma^c_{false} + \gamma^c_{true} & -p_t^c - \frac{1}{\tau_{iso}} - \frac{1}{\tau_{mild}} & 0 & 0 & 0 \\ p_t & p_t^c & -\frac{1}{\tau_t} - \frac{1}{\tau_{mild}} & 0 & 0 \\ 0 & 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{mild}} & 0 \\ 0 & 0 & 0 & 0 & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_{mild}} \end{bmatrix}, \tag{50}$$

$$\check{M} = \begin{bmatrix} \check{M}_g \\ \check{M}_q \\ \check{M}_w \\ \check{M}_n \\ \check{M}_{n'} \end{bmatrix}. \tag{51}$$

$$\tag{52}$$

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:

$$p_{sev} = 1 - p_m, \tag{53}$$

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 particpate in contact tracing can be descibed by the following dynamics:

$$\frac{d\bar{X}}{dt} = \bar{\boldsymbol{X}}_{\boldsymbol{m}} \cdot \bar{X} + \frac{p_{sev}}{\tau_{inf}} \mathbb{1} \cdot \bar{I}, \tag{54}$$

where:

$$\bar{\boldsymbol{X}}_{\boldsymbol{m}} = \begin{bmatrix} -p_t^{sev} - \frac{1}{\tau_h} & \frac{f_{neg}}{\tau_t} & \frac{1}{\tau_{iso}} \\ p_t^{sev} & -\frac{1}{\tau_t} - \frac{1}{\tau_h} & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_{iso}} - \frac{1}{\tau_h} \end{bmatrix}, \tag{55}$$

$$\bar{X} = \begin{bmatrix} \bar{X}_g \\ \bar{X}_w \\ \bar{X}_t \end{bmatrix}. \tag{56}$$

$$\tag{57}$$

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

$$\frac{d\check{X}}{dt} = \check{\boldsymbol{X}}_{\boldsymbol{m}} \cdot \check{X} + \frac{p_{sev}}{\tau_{inf}} \mathbb{1} \cdot \check{I}, \tag{58}$$

where:

$$\check{\boldsymbol{X}}_{\boldsymbol{m}} = \begin{bmatrix} -p_t^{sev} - \frac{1}{\tau_h} & \frac{f_{neg}}{\tau_t} & 0 & 0 \\ p_t^{sev} & -\frac{1}{\tau_t} - \frac{1}{\tau_h} & 0 & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\frac{1}{\tau_h} & 0 \\ 0 & 0 & 0 & -\frac{1}{\tau_h} \end{bmatrix}, \tag{59}$$

$$\check{X} = \begin{bmatrix} \check{X}_g \\ \check{X}_w \\ \check{X}_n \\ \check{X}_{n'} \end{bmatrix}, \tag{60}$$

$$\boldsymbol{T}_{\check{I}\check{X}} = \frac{p_{sev}}{\tau_{inf}} \begin{bmatrix} 1 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix} \tag{61}$$

1. Hospitalized

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

$$\frac{d\bar{H}}{dt} = \bar{\boldsymbol{H}}_{\boldsymbol{m}} \cdot \bar{H} + \frac{1}{\tau_h} \mathbb{1} \cdot \bar{X}, \tag{62}$$

where:

$$\bar{\boldsymbol{H}}_{\boldsymbol{m}} = \begin{bmatrix} -p_t^{sev} - \gamma^{sev} & \frac{f_{neg}}{\tau_t} & 0 \\ p_t^{sev} & -\frac{1}{\tau_t} - \gamma^{sev} & 0 \\ 0 & \frac{(1-f_{neg})}{\tau_t} & -\gamma^{sev} \end{bmatrix}, \tag{63}$$

$$\bar{H} = \begin{bmatrix} \bar{H}_g \\ \bar{H}_w \\ \bar{H}_t \end{bmatrix}. \tag{64}$$

$$\tag{65}$$

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 percantage of those hospitalized that will die. Since the case fatality rate applies to all infections, the probability of those who are hospitalized dying is:

$$p_d = \frac{C_{FR}}{1 - p_a - p_{mild}}. \tag{66}$$

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

$$\gamma^{sev} = \frac{p_d}{\tau_d} + \frac{(1 - p_d)}{\tau_{sev}}. \tag{67}$$

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.

$$\frac{d\check{H}}{dt} = \check{\boldsymbol{H}}_{\boldsymbol{m}} \cdot \check{H} + \frac{1}{\tau_h} \mathbb{1} \cdot \check{X}, \tag{68}$$

$$\check{\boldsymbol{H}}_{\boldsymbol{m}} = \begin{bmatrix} -p_t^{sev} - \gamma^{sev} & \frac{f_{neg}}{\tau_t} & 0 & 0 \\ p_t^{sev} & -\frac{1}{\tau_t} - \gamma^{sev} & 0 & 0 \\ 0 & \frac{(1 - f_{neg})}{\tau_t} & -\gamma^{sev} & 0 \\ 0 & 0 & 0 & -\gamma^{sev} \end{bmatrix}, \tag{69}$$

$$\check{H} = \begin{bmatrix} \check{H}_g \\ \check{H}_w \\ \check{H}_n \\ \check{H}_{n'} \end{bmatrix}, \tag{70}$$

$$\tag{71}$$

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:

$$\frac{d\bar{D}}{dt} = \frac{p_d}{\tau_d} \mathbb{1} \cdot \bar{H}, \tag{72}$$

$$\frac{d\check{D}}{dt} = \frac{p_d}{\tau_d} \mathbb{1} \cdot \check{H}. \tag{73}$$

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:

$$\frac{d\bar{R}}{dt} = \frac{(1 - p_d)}{\tau_{sev}} \mathbb{1} \cdot \bar{H} + \frac{1}{\tau_{mild}} \mathbb{1} \cdot \bar{M} + \frac{1}{\tau_a} \mathbb{1} \cdot \bar{A}, \tag{74}$$

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

$$\frac{d\check{R}}{dt} = \frac{(1 - p_d)}{\tau_{sev}} \mathbb{1} \cdot \check{H} + \frac{1}{\tau_{mild}} \mathbb{1} \cdot \check{M} + \frac{1}{\tau_a} \mathbb{1} \cdot \check{A}, \tag{75}$$

$$\frac{d\check{P}}{dt} =$$

$$
\begin{bmatrix}
\check{S}_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
T_{\check{S}\check{E}} & \check{E}_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & T_{\check{E}\check{I}} & \check{I}_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & T_{\check{E}\check{I}^a} & 0 & \check{I}_m^a & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & \frac{1}{\tau_{inf}} & \check{A}_m & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \frac{p_m}{\tau_{inf}} & 0 & 0 & \check{M}_m & 0 & 0 & 0 & 0 \\
0 & 0 & T_{\check{I}\check{X}} & 0 & 0 & 0 & \check{X}_m & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\tau_h} & \check{H}_m & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{p_d}{\tau_d} & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\tau_a} & \frac{1}{\tau_{mild}} & \frac{(1-p_d)}{\tau_{sev}} & 0 & 0
\end{bmatrix}
\cdot
\begin{bmatrix}
\check{S} \\
\check{E} \\
\check{I} \\
\check{I}^a \\
\check{A} \\
\check{M} \\
\check{X} \\
\check{H} \\
\check{D} \\
\check{R}
\end{bmatrix},
\tag{76}
$$

$$\frac{d\bar{P}}{dt} = \tag{77}$$

$$
\begin{bmatrix}
\bar{S}_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
T_{\bar{S}\bar{E}} & \bar{E}_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & \frac{p_a}{\tau_{inc}} & \bar{I}_m & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & \frac{(1-p_a)}{\tau_{inc}} & 0 & \bar{I}_m^a & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & \frac{1}{\tau_{inf}} & \bar{A}_m & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \frac{p_m}{\tau_{inf}} & 0 & 0 & \bar{M}_m & 0 & 0 & 0 & 0 \\
0 & 0 & \frac{p_{sev}}{\tau_{inf}} & 0 & 0 & 0 & \bar{X}_m & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\tau_h} & \bar{H}_m & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{p_d}{\tau_d} & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\tau_a} & \frac{1}{\tau_{mild}} & \frac{(1-p_d)}{\tau_{sev}} & 0 & 0
\end{bmatrix}
\cdot
\begin{bmatrix}
\bar{S} \\
\bar{E} \\
\bar{I} \\
\bar{I}^a \\
\bar{A} \\
\bar{M} \\
\bar{X} \\
\bar{H} \\
\bar{D} \\
\bar{R}
\end{bmatrix},
\tag{78}
$$

$$\frac{dP}{dt} = \begin{bmatrix} \bar{P}_m & 0 \\ 0 & \check{P}_m \end{bmatrix} \cdot \begin{bmatrix} \bar{P} \\ \check{P} \end{bmatrix}, \tag{79}$$

$$\gamma_{false}^c = \beta_c(\check{S}_n + \check{E}_n + \check{I}_{n'} + \check{I}_{n'}^a + \check{\boldsymbol{R}}_{\boldsymbol{n'}}) + \frac{(R_c - R_0)}{\tau_c}(\check{I}_n + \check{I}_n^a + \check{\boldsymbol{R}}_{\boldsymbol{n}}), \tag{80}$$

$$\gamma_{true}^c = \beta_0(\check{I}_n + \check{I}_n^a + \check{\boldsymbol{R}}_{\boldsymbol{n}}), \tag{81}$$

$$\check{\boldsymbol{R}}_{\boldsymbol{n'}} = \check{A}_{n'} + \check{M}_{n'} + \check{X}_{n'} + \check{H}_{n'}, \tag{82}$$

$$\check{\boldsymbol{R}}_{\boldsymbol{n}} = \check{A}_n + \check{M}_n + \check{X}_n + \check{H}_g + \check{H}_w + \check{H}_n \tag{83}$$

TABLE I. Parameter List

Parameter	Definition
Average time parameters	
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.
Testing parameters	
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.
Population percentages	
p_c	Fraction of the population participating in contact tracing.
p_a	Fraction of the population that is asymptomatic
Infectious Rates	
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).