SEIR-C: An epidemic model that includes contact tracing

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(Dated: April 26, 2020)

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 "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 4 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 exposed phase

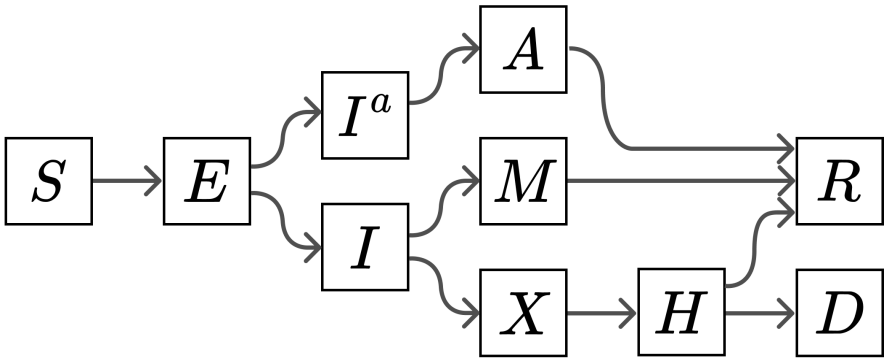

FIG. 1. Conceptual diagram for SEIR with asymptomatic individuals. The first population group are those who are susceptible (S), meaning they have not yet been infected. They can become infected through contact with someone who is infectious (I and I^a). Once infected, they move to the exposed group (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.

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 ($E_w \to I_t$). Instead they have to follow the path $E_w \to I_w \to I_t$.

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_u and stop quarantining. Similarily, 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:

$$J = \begin{bmatrix} J_u \\ J_w \\ J_t \end{bmatrix}, \tag{6}$$

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:

$$\sigma_t = \begin{bmatrix} -1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}. \tag{7}$$

The arrow corresponding to a positive test result is:

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

and a negative test result is:

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

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}, thos e who are in J_t can return back to J_u as their quarantine period is over. The matrix for this transition is:

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

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:

$$\frac{d\boldsymbol{S}}{dt} = (p_t \boldsymbol{\sigma_t} + f_{pos}\boldsymbol{\sigma_+} + (1 - f_{pos})\boldsymbol{\sigma_-} + \boldsymbol{\sigma_{iso}}) - \boldsymbol{T_{S\to E}}, \tag{11}$$

$$\boldsymbol{T_{S\to E}} = \beta \begin{bmatrix} 1 & 0 & 0 \\ 0 & d_r & 0 \\ 0 & 0 & d_r \end{bmatrix}. \tag{12}$$

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:

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

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 quaranting is therefore reduced by a factor of $(d_r)^2$.

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

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

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:

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

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

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

Those who are aymptomatic 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 recoverning asymptomatic population A is given as:

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

Those who show symptoms while infectious will either transition to a mild recovery phase ($\boldsymbol{M}$) with probability p_m or a severe recovery phase ($\boldsymbol{X}$) 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 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:

$$\frac{d\boldsymbol{M}}{dt} = \left(p_t^n \boldsymbol{\sigma_t} + (1 - f_{neg})\boldsymbol{\sigma_+} + f_{neg}\boldsymbol{\sigma_-} + \boldsymbol{\sigma_{iso}} - \frac{1}{\tau_{mild}}\mathbb{1} \right) \cdot \boldsymbol{M} + \frac{p_m}{\tau_{inf}}\mathbb{1} \cdot \boldsymbol{I}. \tag{18}$$

$$\frac{d\boldsymbol{X}}{dt} = \left(p_t^{sev} \boldsymbol{\sigma_t} + (1 - f_{neg})\boldsymbol{\sigma_+} + f_{neg}\boldsymbol{\sigma_-} - \frac{1}{\tau_h}\mathbb{1} \right) \cdot \boldsymbol{X} + \frac{(1 - p_m)}{\tau_{inf}}\mathbb{1} \cdot \boldsymbol{I}. \tag{19}$$

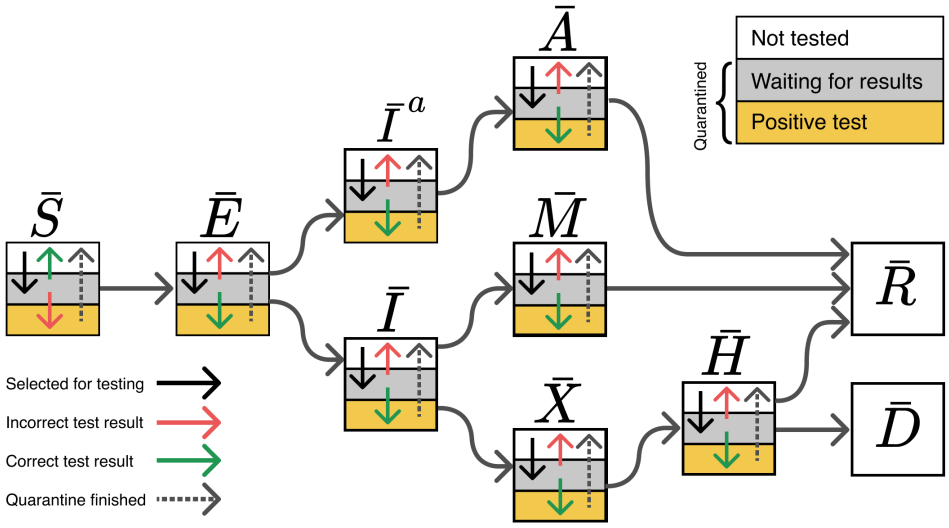

FIG. 2. SEIR with testing incorporated. It is convenient to divide each population into three subgroups, those who have not been tested (white), those who have been tested but are waiting for their results (grey), and those who have tested positive (yellow). Anyone in the white or yellow layers is quarantined. When transitioning between disease phases, individuals can only move to the same color layer (for example $E_w \to I_w$ or $I_u \to M_u$). 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.

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

$$\frac{d\boldsymbol{H}}{dt} = \left(p_t^{sev}\boldsymbol{\sigma_t} + (1-f_{neg})\boldsymbol{\sigma_+} + f_{neg}\boldsymbol{\sigma_-} - \frac{1}{\tau_{sev}}\mathbb{1}\right)\cdot\boldsymbol{H} + \frac{1}{\tau_h}\mathbb{1}\cdot\boldsymbol{X}. \tag{20}$$

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, 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:

$$p_d = \frac{C_{FR}}{(1-p_a)p_{sev}}. \tag{21}$$

The change in D is therefore given as:

$$\frac{d\boldsymbol{D}}{dt} = \frac{p_d}{\tau_{sev}}\mathbb{1}\cdot\boldsymbol{X}. \tag{22}$$

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

$$\frac{d\boldsymbol{R}}{dt} = \frac{1}{\tau_a}\mathbb{1}\cdot\boldsymbol{A} + \frac{1}{\tau_{mild}}\mathbb{1}\cdot\boldsymbol{M} + \frac{(1-p_d)}{\tau_{sev}}\mathbb{1}\cdot\boldsymbol{X}. \tag{23}$$

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 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.

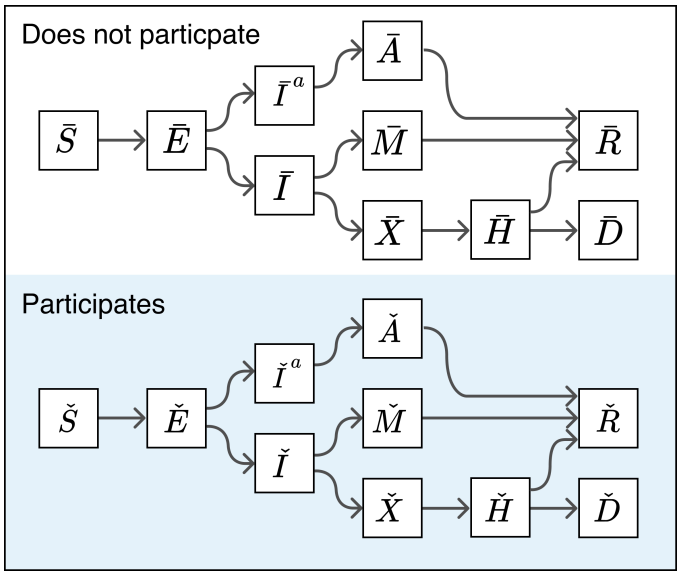

FIG. 3. Those who chose not to participate in contact tracing and those that do particpate in contact tracing are treated separately. Population can never flow between the top and bottom graphs, although infectious individuals, regardless of whether they contact trace or not, can infect anyone who is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

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. 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 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 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 notifiy all of their potential contacts to quarantine themselves (move from J_u to J_q). Individuals who are waiting for test, already quarantined, or have already tested positive are not affected by notifications. It takes a positive test at any stage to start the contact tracing process.

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

$$\check{J} = \begin{bmatrix} \check{J}_u \\ \check{J}_q \\ \check{J}_w \\ \check{J}_t \end{bmatrix}, \tag{24}$$

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:

$$\boldsymbol{\check{\sigma}_c} = \begin{bmatrix} -1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \tag{25}$$

Similar to SEIR-T, we have transition matrices for those who are tested ($\boldsymbol{\check{\sigma}_t^u}$ and $\boldsymbol{\sigma\check{q}_t}$), positive tests ($\boldsymbol{\check{\sigma}_+}$), negative

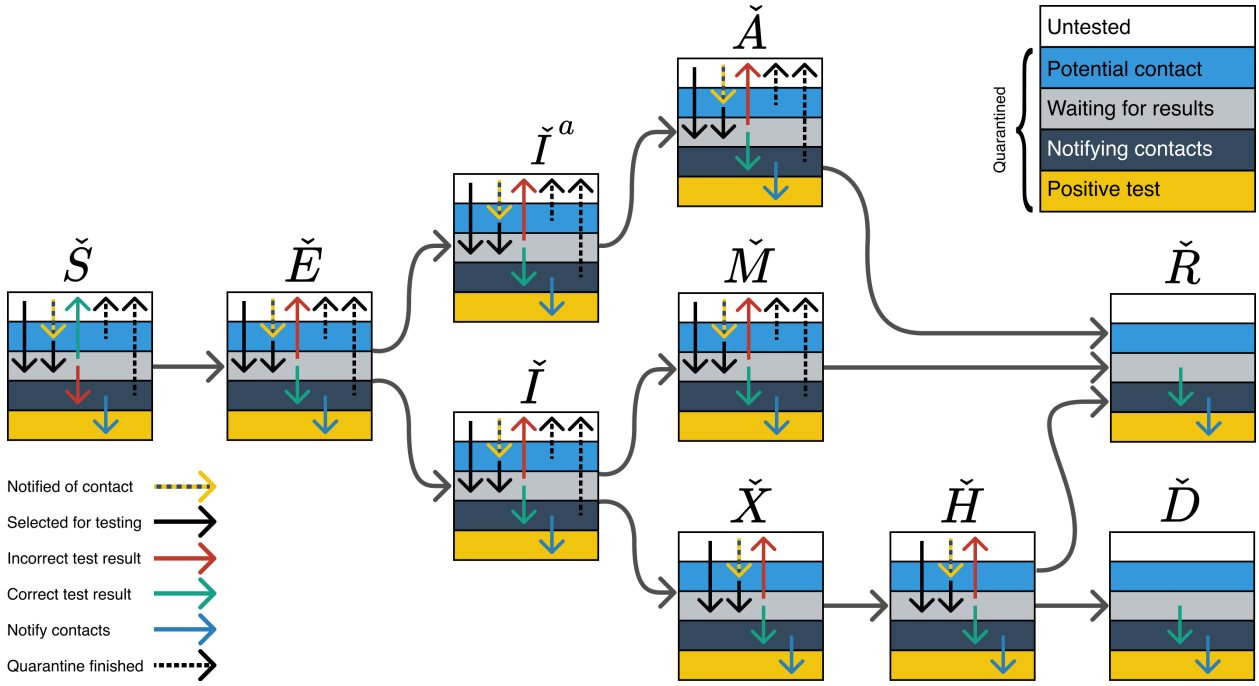

FIG. 4. Layers for contact tracing, as well as the transition rates between populations.

tests ($\boldsymbol{\sigma}^{\check{}}_{-}$), and those who return from isolation ($\boldsymbol{\sigma}^{\check{}}_{\boldsymbol{iso}}$):

$$\boldsymbol{\sigma}^{\check{u}}_{t} = \begin{bmatrix} -1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \tag{26}$$

$$\boldsymbol{\sigma}^{\check{q}}_{t} = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & -1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \tag{27}$$

$$\boldsymbol{\sigma}^{\check{}}_{+} = \frac{1}{\tau_t} \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 \\ 0 & 0 & 1 & 0 \end{bmatrix} \tag{28}$$

$$\boldsymbol{\sigma}^{\check{}}_{-} = \frac{1}{\tau_t} \begin{bmatrix} 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \tag{29}$$

$$\boldsymbol{\sigma}^{\check{}}_{\boldsymbol{iso}} = \frac{1}{\tau_{iso}} \begin{bmatrix} 0 & 1 & 0 & 1 \\ 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 \end{bmatrix} \tag{30}$$

We can now write down the rate equations for each of the disease phases that particpate in contact tracing. Their

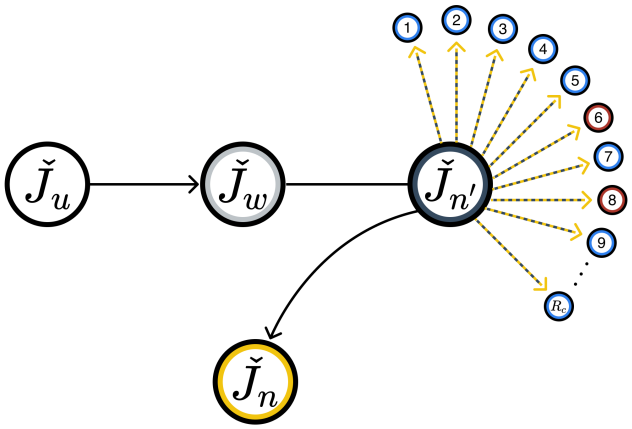

FIG. 5. Those who test positive and move to J_n from J_w will notify (blue arrows) on average R_c of the people they have contacted. If the individual is or was infectious, then on average R_0 of those contacts will have become infected (red arrows). If the notified indiduals are in an untested layer, they will then move to a quarantine layer J_q

general form is nearly identical to those used in SEIR-T, and they are given by:

$$\frac{d\check{\boldsymbol{S}}}{dt} = \left(p_t\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{u}} + p_t^c\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{q}} + \gamma_F^c\check{\boldsymbol{\sigma}}_{\boldsymbol{c}} + f_{pos}\check{\boldsymbol{\sigma}}_{+} + (1-f_{pos})\check{\boldsymbol{\sigma}}_{-} + \check{\boldsymbol{\sigma}}_{\boldsymbol{iso}}\right)\check{\boldsymbol{S}} - \check{\boldsymbol{T}}_{\boldsymbol{S\to E}}, \tag{31}$$

$$\check{\boldsymbol{T}}_{\boldsymbol{S\to E}} = \beta\begin{bmatrix}1 & 0 & 0 & 0\\ 0 & d_r & 0 & 0\\ 0 & 0 & d_r & 0\\ 0 & 0 & 0 & d_r\end{bmatrix} \tag{32}$$

$$\beta = \frac{R_0}{N\tau_{inf}}\left[I_{tot}^u + d_r(I_{tot} - I_{tot}^u)\right], \tag{33}$$

$$I_{tot}^u = \check{I}_u + \check{I}_u^a + I_u + I_u^a \tag{34}$$

$$\tag{35}$$

For both the $\frac{d\check{\boldsymbol{S}}}{dt}$ and $\frac{d\bar{\boldsymbol{S}}}{dt}$ terms, the value of β needs to be modified to include the populations of those who particpate in contact tracing, and those who do no. Anyone who is infectious can infect someone who is susceptibe regardless of whether they participate in contact tracing or not. We also have the value of γ_F^c which represents the individuals who are notified to quarantine through a contact that did not infect them. The total number of contacts an infected person makes on average is R_c, however only R_0 of those contacts will lead to an infection. Those who are in the susceptible and exposed populations cannot infect others, so all of their contacts self quarantine without being infected. For those in the other phases (except recovered and death), $(R_c - R_0)$ will quarantine without being infected. The notifications take on average time τ_n to carry out, and occur whenever population transfers from $J_w \to J_n$, with an average rate of change of $\frac{J_w}{\tau_t}$ goverened by the time it takes to get a test result. Here we have:

$$\begin{aligned}\gamma_F^c = &\frac{R_c}{(1+\tau_n)}\frac{(f_{pos}\check{S}_w + (1-f_{neg})\check{E}_w)}{N\tau_t}\\ &+\frac{(R_c-R_0)}{(1+\tau_n)}(1-f_{neg})\frac{(\check{I}_w + \check{I^a}_w + \check{A}_w + \check{M}_w + \check{X}_w + \check{H}_w + \check{D}_w + \check{R}_w)}{N\tau_t}.\end{aligned} \tag{36}$$

The next rate equations again closely follow the form of their counterparts in SEIR-R, and are given as:

$$\frac{d\check{\boldsymbol{E}}}{dt} = \left(p_t\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{u}} + p_t^c\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{q}} + (\gamma_F^c + \gamma_E^c)\check{\boldsymbol{\sigma}}_{\boldsymbol{c}} + (1-f_{neg})\check{\boldsymbol{\sigma}}_{\boldsymbol{+}} + f_{neg}\check{\boldsymbol{\sigma}}_{\boldsymbol{-}} + \check{\boldsymbol{\sigma}}_{\boldsymbol{iso}} - \frac{1}{\tau_{inc}}\mathbb{1}\right)\cdot\check{\boldsymbol{E}} + \check{\boldsymbol{T}}_{\boldsymbol{S\to E}}\cdot\check{\boldsymbol{S}}, \tag{37}$$

$$\frac{d\check{\boldsymbol{I}}}{dt} = \left(p_t^i\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{u}} + p_t^n\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{q}} + (\gamma_F^c + \gamma_I^c)\check{\boldsymbol{\sigma}}_{\boldsymbol{c}} + (1-f_{neg})\check{\boldsymbol{\sigma}}_{\boldsymbol{+}} + f_{neg}\check{\boldsymbol{\sigma}}_{\boldsymbol{-}} + \check{\boldsymbol{\sigma}}_{\boldsymbol{iso}} - \frac{1}{\tau_{inf}}\mathbb{1}\right)\cdot\check{\boldsymbol{I}} + \frac{(1-p_a)}{\tau_{inc}}\mathbb{1}\cdot\check{\boldsymbol{E}}, \tag{38}$$

$$\frac{d\check{\boldsymbol{I}}^{\boldsymbol{a}}}{dt} = \left(p_t^i\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{u}} + p_t^n\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{q}} + (\gamma_F^c + \gamma_I^c)\check{\boldsymbol{\sigma}}_{\boldsymbol{c}} + (1-f_{neg})\check{\boldsymbol{\sigma}}_{\boldsymbol{+}} + f_{neg}\check{\boldsymbol{\sigma}}_{\boldsymbol{-}} + \check{\boldsymbol{\sigma}}_{\boldsymbol{iso}} - \frac{1}{\tau_{inf}}\mathbb{1}\right)\cdot\check{\boldsymbol{I}}^{\boldsymbol{a}} + \frac{p_a}{\tau_{inc}}\mathbb{1}\cdot\check{\boldsymbol{E}}, \tag{39}$$

$$\frac{d\check{\boldsymbol{A}}}{dt} = \left(p_t\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{u}} + p_t^c\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{q}} + \gamma_F^c\check{\boldsymbol{\sigma}}_{\boldsymbol{c}} + (1-f_{neg})\check{\boldsymbol{\sigma}}_{\boldsymbol{+}} + f_{neg}\check{\boldsymbol{\sigma}}_{\boldsymbol{-}} + \check{\boldsymbol{\sigma}}_{\boldsymbol{iso}} - \frac{1}{\tau_a}\mathbb{1}\right)\cdot\check{\boldsymbol{A}} + \frac{1}{\tau_{inf}}\mathbb{1}\cdot\check{\boldsymbol{I}}^{\boldsymbol{a}}, \tag{40}$$

$$\frac{d\check{\boldsymbol{M}}}{dt} = \left(p_t^i\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{u}} + p_t^n\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{q}} + \gamma_F^c\check{\boldsymbol{\sigma}}_{\boldsymbol{c}} + (1-f_{neg})\check{\boldsymbol{\sigma}}_{\boldsymbol{+}} + f_{neg}\check{\boldsymbol{\sigma}}_{\boldsymbol{-}} + \check{\boldsymbol{\sigma}}_{\boldsymbol{iso}} - \frac{1}{\tau_{mild}}\mathbb{1}\right)\cdot\check{\boldsymbol{M}} + \frac{p_m}{\tau_{inf}}\mathbb{1}\cdot\check{\boldsymbol{I}}, \tag{41}$$

$$\frac{d\check{\boldsymbol{X}}}{dt} = \left(p_t^{sev}\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{u}} + p_t^{sev}\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{q}} + \gamma_F^c\check{\boldsymbol{\sigma}}_{\boldsymbol{c}} + (1-f_{neg})\check{\boldsymbol{\sigma}}_{\boldsymbol{+}} + f_{neg}\check{\boldsymbol{\sigma}}_{\boldsymbol{-}} - \frac{1}{\tau_h}\mathbb{1}\right)\cdot\check{\boldsymbol{X}} + \frac{(1-p_m)}{\tau_{inf}}\mathbb{1}\cdot\check{\boldsymbol{I}}, \tag{42}$$

$$\frac{d\check{\boldsymbol{H}}}{dt} = \left(p_t^{sev}\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{u}} + p_t^{sev}\check{\boldsymbol{\sigma}}_{\boldsymbol{t}}^{\boldsymbol{q}} + \gamma_F^c\check{\boldsymbol{\sigma}}_{\boldsymbol{c}} + (1-f_{neg})\check{\boldsymbol{\sigma}}_{\boldsymbol{+}} + f_{neg}\check{\boldsymbol{\sigma}}_{\boldsymbol{-}} - \frac{1}{\tau_{sev}}\mathbb{1}\right)\cdot\check{\boldsymbol{H}} + \frac{1}{\tau_h}\mathbb{1}\cdot\check{\boldsymbol{X}}. \tag{43}$$

Those who are infectious (or were infectious but have moved on to A, X, M, H, D, or R) all infect on average R_0 individuals. We need to consider the notification rates for those who are able to sucessfully identify someone they infected and have them quarantine. We assume here that those who are in I or I^a can only notify those who are in E, and that those who are in A, X, M, H, D, or R can only notify those in I or I^a of a true infection. The notification rate for those in E is therefore given as:

$$\gamma_E^c = \frac{R_0}{(1+\tau_n)}(1-f_{neg})\frac{(\check{I}_w + \check{I^a}_w)}{N\tau_t}, \tag{44}$$

and the true notification rates for those in I_u and I_u^a are:

$$\gamma_I^c = \frac{R_0}{(1+\tau_n)}(1-f_{neg})\frac{(\check{A}_w + \check{M}_w + \check{X}_w + \check{H}_w + \check{D}_w + \check{R}_w)}{N\tau_t}. \tag{45}$$

As before, 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, we need to determine the average fraction of the population that will end up in the hospital. Anyone who who gets tested while in the hospital, but dies before their results are returned still need to trigger a round of notifications. Therefore, we need to track the dynamic of $D_w \to D_n$. This leads to a rate of change of the death population of:

$$\frac{d\check{\boldsymbol{D}}}{dt} = (1-f_{neg})\check{\boldsymbol{\sigma}}_{\boldsymbol{+}}\check{\boldsymbol{D}} + \frac{p_d}{\tau_d}\mathbb{1}\cdot\check{\boldsymbol{X}}. \tag{46}$$

Similarly, we must also track the dynamics of those who recover while waiting for their test results so the proper notifications can be sent out. This leads to:

$$\frac{d\check{\boldsymbol{R}}}{dt} = (1-f_{neg})\check{\boldsymbol{\sigma}}_{\boldsymbol{+}}\check{\boldsymbol{R}} + \frac{1}{\tau_a}\mathbb{1}\cdot\check{\boldsymbol{A}} + \frac{1}{\tau_{mild}}\mathbb{1}\cdot\check{\boldsymbol{M}} + \frac{(1-p_d)}{\tau_{sev}}\mathbb{1}\cdot\check{\boldsymbol{X}}. \tag{47}$$

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).