SEIR-C: An epedemic 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

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.

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:

$$\frac{dS}{dt} = -\beta_0 \frac{I}{N} S, \tag{1}$$

$$\frac{dE}{dt} = \beta_0 \frac{I}{N} S - \frac{1}{\tau_{inc}} E, \tag{2}$$

$$\frac{dI}{dt} = \frac{1}{\tau_{inc}} E - \frac{1}{\tau_{inf}} I, \tag{3}$$

$$\frac{dR}{dt} = \frac{1}{\tau_{inf}} I. \tag{4}$$

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 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 infectous (I/N) multiplied by the number of people who are susceptible (S).

II. SEIR-C

Here we introduce a new layer to the model that incorporates contact tracing. Contact tracing is a method of epidemic control that relies on tracing who those infected were in contact with, and then having them self-isolate. This reduces the spread of the disease as it is possible to identify and isolate those who are infectious as well as those who could potentially become infectious. Contact tracing relies on a large portion of the population participating as well as testing a substatial fraction of the population. Here we model the dynamics of contact tracing where p_c is the fraction of the population who choose to participate, p_t is the probability of an individual getting tested in a time interval dt, the tests take some time τ_t to process, and it takes some time τ_n for someone who tests positive and chooses to participate to notify others they may have been in contact with. A certain percantage of the tests performed will result in either a false positive (f_{pos}) or a false negative (f_{neg}). A simplified model of SEIR-C is shown in figure 1.

To simply matters, we assume that those who are tested immediately isolate themselves while waiting for the results. We also assume that the isolation time, τ_{iso} is greater than sum of the incubation and infectious times in order to be effective. Finally, we assume that those in S who self-isolate either because they are waiting for a test result or because they come in contact with an infectious individual, can't become infected until they return to the general population. Those that are infectious (I_{iso}), but isolating, will have a much smaller rate of passing on the infection $\beta_{iso} = \frac{R_{iso}}{\tau_{inf}}$, while those who are infectious but have not isolating (I) will remain infectious at a rate of β_0 used in the SEIR model. Anyone who has been exposed, but is now isolating either through a contact tracing notification or because they have been tested will eventually join I_{iso} after an average time of τ_{inc}.
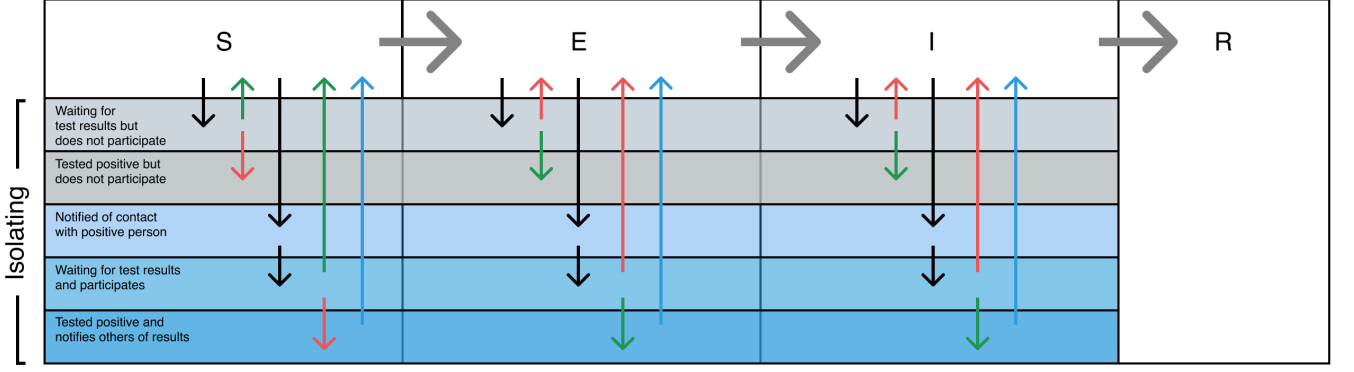
FIG. 1. Conceptual diagram for SEIR-C. Each of the four regions for sucesptible (S), exposed (E), infectious (I), and recovered (R) are separated, and the red arrows represent transitions between their respective populations simialr to SEIR. However, in S, E, and I there is a sub population of individuals who isolate, slowing the spread. The model assumes that during some dt there is a probability of being tested p_t. If someone tests positive and participates in contact tracing, then they notify those that they were in contact with so those individuals can begin isolation. Anyone who tests positive or who is waiting for a test is assumed to isolate. Also, it is assumed that the isolation period is longer thant the infectious and incubation period. The black and grey arrows represent the different dynamics as individuals are moved to isolation, and the blue arrows represent notifications from those who test positive and participate in contact tracing.

All of those who have been exposed ($E_{tot} = E + E_{iso}$) will move to the infectious stage after an average time of τ_{inc}. Similarly, all those who are infectious ($I_{tot} = I + I_{iso}$) will eventually move to R after a time τ_{inf} regardless of their testing status or whether they are isolating. For each stage (except R), we consider six different scenarios: Those that are not self isolating (S, E, and I), those who have been notified of a possible exposure through contact tracing but have not yet been tested (S^c, E^c, and I^c), those who are waiting for test results but are not involved in contact tracing (S_w, E_w, and I_w), those who are waiting for test results and are involved in contact tracing (S_w^c, E_w^c, those who tested positive but are not involved in contact tracing (S_t, E_t, and I_t). The final group are those who are involved in contact tracing and have received a positive test result, and then notify others in S, E, and I who might have been exposed. These are divided into two groups: those who receive a false positive test N_S^c and those whose tests are correct N_{EI}^c.

The initial set of differential equations closely follow the SEIR model, but now account for the different infectious rates between those who are isolating and those who are not. The sucesptible population, S, is given by:

$$S_{tot} = S + S_{iso}, \tag{5}$$
$$S_{iso} = S^c + S_w^c + S_w + S_t + N_S^c \tag{6}$$

where S_{tot} is the total susceptible population and S_{iso} is the susceptible population who are isolating. Individuals from S_{tot} can move to E after they come in contact with an infectious individual. The rate of infection transfer for those not in isolation (γ_0), and those in isolation (γ_{iso}) is given as:

$$\gamma_0 = \beta_0 \frac{I}{N} \tag{7}$$

$$\gamma_{iso} = \beta_{iso} \frac{I_{iso}}{N}. \tag{8}$$

The rate of change of S is determined by:

$$\frac{dS}{dt} = -[\gamma_0 + \gamma^c p_c + p_t]S + \frac{1}{\tau_{iso}}[S^c + S_t + N_S^c] + \frac{(1 - f_{pos})}{\tau_t}[S_w + S_w^c]. \tag{9}$$

The first term involve populations that leave S either through infection, a notification of a possible contact with an infectious person, or selection for testing. The second term represents those who have sucessfuly completed their isolation and return to S or who test negative and return to S. Here the parameter γ^c is a notification rate for those participating in contact tracing:

$$\gamma^c = \frac{R^c}{\tau_c} \frac{N_{Tot}^c}{N}, \tag{10}$$

$$N_{Tot}^c = (N_S^c + N_{EI}^c). \tag{11}$$

During contact tracing, the average number of contacts that have been made by an infectious person (N_{Tot}^c) with the the recent past (τ_c) are notified. The total population of individuals with a positive test who are participating in contact tracing is made up of those who are not infectious but received a false positive (N_S^c) and those who are infectious (N_{EI}^c).

The population of S_{iso} depends on five different populations. The rate of change of S_{iso} therefore depends on on the rate of change of its five constituent populations. First we consider those who go into isolation because they are tested but do not participate in contact tracing. The group waits for their test results. If the results are negative, they return to S but if they receive a false positive they are moved to S_t:

$$\frac{dS_w}{dt} = p_t(1 - p_c)S - [\frac{1}{\tau_t} + \gamma_{iso}]S_w, \tag{12}$$

$$\frac{dS_t}{dt} = \frac{f_{pos}}{\tau_t}S_w - [\frac{1}{\tau_{iso}} + \gamma_{iso}]S_t \tag{13}$$

While in S_w or S_t there is a chance of becoming infected and moving to the exposed stage. Since everyone that is susceptible is by definition not a carrier of the illness, any positive tests must be due to false positives. The remaing susceiptible populations are S^c, S_w^c, and N_S^c:

$$\frac{dS^c}{dt} = \gamma^c p_c S - [p_t + \frac{1}{\tau_{iso}} + \gamma_{iso}]S^c, \tag{14}$$

$$\frac{dS_w^c}{dt} = p_t p_c S + p_t S^c - [\frac{1}{\tau_t} + \frac{1}{\tau_{iso}} + \gamma_{iso}]S_w^c, \tag{15}$$

$$\frac{dN_S^c}{dt} = \frac{f_{pos}}{\tau_t}S_w^c - [\frac{1}{\tau_{iso}} + \gamma_{iso}]N_S^c. \tag{16}$$

Individuals who are notified through contact tracing to isolate are moved to S^c. Leaving S^c occurs when an individual is slected for testing (moved to S_w^c), they become infected (move to E^c), or they finish isolation and return to S. The final sucesptible population, N_S^c, are those who particpate in contact tracing and receive a false positive test. This group will self isolate, and may become infectious (moving them to E^c). Once their isolation is finished they return to S.

The next phase in the model are those who have been exposed (E_{tot}). The total exposed population grows based on the number of infections caused in thos susceptible, but is reduced by those who become infectious after the incubation period, τ_{inc}, is over.

$$E_{tot} = E + E_{iso}, \tag{17}$$

$$E_{iso} = E^c + E_w^c + E_w + E_t + N_E^c \tag{18}$$

The rate of change of E is determined by:

$$\frac{dE}{dt} = \gamma_0 S + \frac{1}{\tau_{iso}}[E^c + E_t + N_E^c] + \frac{f_{neg}}{\tau_t}[E_w + E_w^c] - [\gamma^c p_c + p_t + \frac{1}{\tau_{inc}}]E \tag{19}$$

The next term is:

$$\frac{dE_w}{dt} = \gamma_{iso}S_w + p_t(1 - p_c)E - [\frac{1}{\tau_t} + \frac{1}{\tau_{inc}}]E_w, \tag{20}$$

$$\frac{dE_t}{dt} = \gamma_{iso}S_t + \frac{(1 - f_{neg})}{\tau_t}E_w - [\frac{1}{\tau_{iso}} + \frac{1}{\tau_{inc}}]E_t \tag{21}$$

The next term is:

$$\frac{dE^c}{dt} = \gamma_{iso}S^c + \gamma^c p_c E - [p_t + \frac{1}{\tau_{iso}} + \frac{1}{\tau_{inc}}]E^c, \tag{22}$$

$$\frac{dE_w^c}{dt} = \gamma_{iso}[S_w^c + N_S^c] + p_t p_c E + p_t E^c - [\frac{1}{\tau_t} + \frac{1}{\tau_{iso}} + \frac{1}{\tau_{inc}}]E_w^c, \tag{23}$$

$$\frac{dN_E^c}{dt} = \frac{(1 - f_{neg})}{\tau_t}E_w^c - [\frac{1}{\tau_{iso}} + \frac{1}{\tau_{inc}}]N_E^c. \tag{24}$$

STARTING I phase

$$I_{tot} = I + I_{iso}, \tag{25}$$

$$I_{iso} = I^c + I_w^c + I_w + I_t + N_I^c + N_{I'}^c \tag{26}$$

The rate of change of I is determined by:

$$\frac{dI}{dt} = \frac{1}{\tau_{inc}}E + \frac{1}{\tau_{iso}}[I^c + I_t + N_I^c + N_{I'}^c] + \frac{f_{neg}}{\tau_t}[I_w + I_w^c] - [\gamma^c p_c + p_t + \frac{1}{\tau_{inf}}]I \tag{27}$$

The next term is:

$$\frac{dI_w}{dt} = \frac{1}{\tau_{inc}}E_w + p_t(1 - p_c)I - [\frac{1}{\tau_t} + \frac{1}{\tau_{inf}}]I_w, \tag{28}$$

$$\frac{dI_t}{dt} = \frac{1}{\tau_{inc}}E_t + \frac{(1 - f_{neg})}{\tau_t}I_w - [\frac{1}{\tau_{iso}} + \frac{1}{\tau_{inf}}]I_t \tag{29}$$

The next term is:

$$\frac{dI^c}{dt} = \frac{1}{\tau_{inc}}E^c + \gamma^c p_c I - [p_t + \frac{1}{\tau_{iso}} + \frac{1}{\tau_{inf}}]I^c, \tag{30}$$

$$\frac{dI_w^c}{dt} = \frac{1}{\tau_{inc}}E_w^c + p_t p_c I + p_t I^c - [\frac{1}{\tau_t} + \frac{1}{\tau_{iso}} + \frac{1}{\tau_{inf}}]I_w^c, \tag{31}$$

$$\frac{dN_I^c}{dt} = \frac{(1 - f_{neg})}{\tau_t}I_w^c - [\frac{1}{\tau_{iso}} + \frac{1}{\tau_{inf}}]N_I^c, \tag{32}$$

$$\frac{dN_{I'}^c}{dt} = \frac{1}{\tau_{inc}}E_I^c - \frac{1}{\tau_{inf}}N_{I'}^c. \tag{33}$$

Where the total exposed population grows based on the number of infections caused in thos susceptible, but is reduced by those who become infectious after the incubation period, τ_{inc}, is over. The total infectious rate and total recovered rate are identical to that from the standard SEIR model,

$$\frac{dI_{tot}}{dt} = \frac{1}{\tau_{inc}}E_{tot} - \frac{1}{\tau_{inf}}I_{tot}, \tag{34}$$

$$\frac{dR_{tot}}{dt} = \frac{1}{\tau_{inf}}I_{tot}. \tag{35}$$