SEIR-C: An epedemic model that includes contact tracing

Lynden K. Shalm[1]

[1] *National Institute of Standards and Technology, 325 Broadway, Boulder, CO 80305, USA*

(Dated: April 15, 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

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:

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

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

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

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

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. All tests are assumed to not have false negatives (someone who is either exposed or infectious that is tested will show a positive result). 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}.

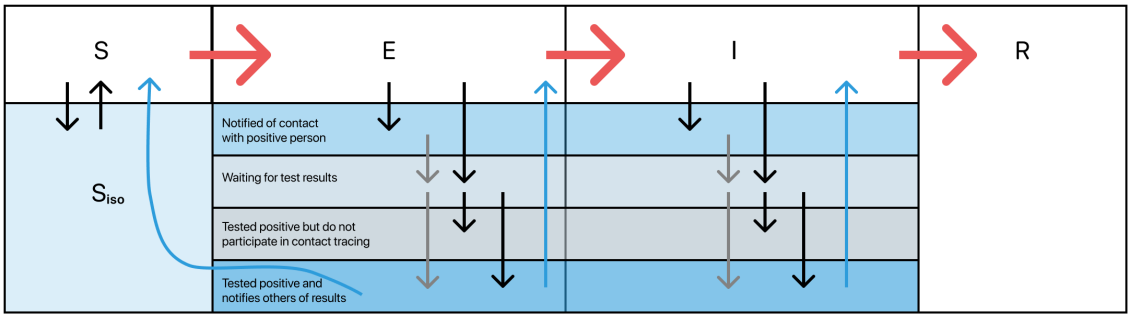

FIG. 1. Conceptual diagram for SEIR-C. Each of the four regions for sucesptible (S), exposed (E), infectious (I), and recovered (R) are separated, and the red arrows represent transitions between their respective populations simialr to SEIR. However, in S, E, and I there is a sub population of individuals 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}. Similarily, all those who are infectious ($I_{tot} = I + I_{tot}$) will eventually move to R after a time τ_{inf} regardless of their testing status or whether they are isolating. 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, now changes in the following way:

$$\frac{dS}{dt} = -[\beta_0 \frac{I}{N} + \beta_{iso}\frac{I_{iso}}{N} + \zeta p_c - p_t]S + [\frac{1}{\tau_{iso}} + \frac{1}{\tau_t}]S_{iso}. \tag{5}$$

The first two terms corresponds to people in S contracting the illness and moving to the exposed population. The third term corresponds to the population that is participating in contact tracing and has been notified of a possible contact. They will be isolated and be moved to S_{iso}. Here $\zeta = \beta_c \frac{N_c}{N}$, and $\beta_c = \frac{R_c}{\tau_n}$ where R_c is the average number of people an infectious person who has tested positive and is participating in contact tracing (N_c) has come into contact with over a time period where notification is required (τ_n). Those who who are selected for testing (p_t) are imediately moved to S_{iso} while they await for their test results an average of τ_t before moving back to S. After an average time τ_{iso}, those in S_{iso} can return to S.

The next term is:

$$\frac{dE_{tot}}{dt} = [\beta_0 \frac{I}{N} + \beta_{iso}\frac{I_{iso}}{N}]S - \frac{1}{\tau_{inc}}E_{tot}, \tag{6}$$

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,

$$\frac{dI_{tot}}{dt} = \frac{1}{\tau_{inc}}E_{tot} - \frac{1}{\tau_{inf}}I_{tot}, \tag{7}$$

$$\frac{dR_{tot}}{dt} = \frac{1}{\tau_{inf}}I_{tot}. \tag{8}$$

Now we must consider the rates involving the populations that are exposed (E) or infected (I) but have not been tested or notified that they need to isolate, the populations that know they need to isolate (S_{iso}, E_{iso}, and I_{iso}, the populations that have been notified they need to isolatebut have not been tested (E_c and I_c), and the population of those who test positive and participate in contact tracing and need to notify their recent contacts (N_c). For those who are in S_{iso}, we assume they can only be infected at the isolation rate β_{iso} no matter what class of infectious person they come in contact with. We therefore have:

$$\frac{dS_{iso}}{dt} = [\zeta p_c + p_t]S - [\frac{1}{\tau_{iso}} + \frac{1}{\tau_t} + \beta_{iso}\frac{I_{iso}}{N}]S_{iso}, \tag{9}$$

Where the population of S_{iso} is increased by either people in S being informed of potential exposure through contact tracing or by individuals waiting for test results. Once the isolation period or the negative test results are obtained (these are individuals who have not yet been infected, and we are assuming there are no false positives), people return to S. There is also the chance that someone could become infected and moves to the exposed group that is isolating, E_{iso}. It is important to note the the population of E and I, those who have the disease but are not isolating, is given by:

$$E = E_{tot} - E_{iso}, \tag{10}$$
$$I = I_{tot} - I_{iso}. \tag{11}$$

The rate of change in the expose population that is isolating is given by:

$$\frac{dE_{iso}}{dt} = \beta_{iso}\frac{I_{iso}}{N}S_{iso} + [\zeta p_c + p_t - \zeta p_c p_t]E, \tag{12}$$

here the isolating population S_{iso} that become exposed continue to isolate in E_{iso}. Also, anyone in E who is participating in contact tracing and notifyied to self isolate, or have been selected for testing are moved to E_{iso}. Finally, to avoid double-counting we account for those who have been notified to isolate through contact tracing and being selected for testing (the $-\zeta p_c p_t E$ term).

Next we have the dynamics of the population E_c who are exposed, participate in contact tracing, and have been told to isolate due to a potential interaction with an infectious person, but have not yet been tested. These numbers are already included in E_{iso}, but we need to separate out this sub population to properly account for who gets notified. The changes to these rates do not directly affect E_{tot}, but do have an effect on N_c.

$$\frac{dE_c}{dt} = \beta_{iso}\frac{I_{iso}}{N}\zeta p_c S + \zeta p_c E - p_t E_c, \tag{13}$$

where those in S_{iso} due to being notified of possible exposure through contact tracing ($\zeta p_c S$) and then subsequently infected while isolating ($\beta_{iso}\frac{I_{iso}}{N}$) are moved to E_c. Additionally, anyone in E who is notified of potential exposure is moved to E_c, but anyone in E_c who is chosen for testing is removed while they wait their eventual positive result (at which point they are moved to N_c).

The infectious phase follows a similar set of dynamics as the exposure phase. The rate of change in the I_{iso} population is:

$$\frac{dI_{iso}}{dt} = \frac{1}{\tau_{inc}}E_{iso} + [\zeta p_c + p_t - \zeta p_c p_t]I, \tag{14}$$

where those who start in E_{iso} are moved to I_{iso} as we are assuming τ_{iso} is longer than the incubation of infectious phases of the illness. Similar to the dynamics of $\frac{dE_{iso}}{dt}$, population can move from I through either contact notification or testing. Again we add a term to prevent double counting. We also need to account for the dynamics of the population I_c who are infectious and have been notified to isolate, but have not yet been tested. This does not affect directly I_{tot}, but is needed for N_c. The rate of change of I_c depends on the population of those originally in E_c that become infectious, as well as those in I who are notified to isolate. Anyone in I_c selected for testing is removed as they wait for their eventual positive test results and subsequent inclusion into N_c:

$$\frac{dI_c}{dt} = \frac{1}{\tau_{inc}}E_{iso} + \zeta p_c I - p_t I_c. \tag{15}$$

Finally, the dynamics of the N_c notification group that test positive and are part of contact tracing is described by:

$$\frac{dN_c}{dt} = \frac{p_t}{\tau_t}[p_c E + E_c + p_c I + I_c]. \tag{16}$$