

A model of epidemics with time since infection (TSI)

June 18, 2020

As a complement to the pyRoss project, pyRossTSI provides a dedicated set of tools for modelling epidemics in which the characteristics of a disease (infectiousness, case outcomes, etc.) are defined explicitly as a function of time since infection (TSI). The governing equations are given below.

Suppose a population is divided into M classes based on demographic characteristics such as age, gender, geographic location, etc. Each population is then further divided into susceptibles and infecteds. In a model with time since infection, we describe the infected population in terms of the number density of persons (per unit time) whose infections began at a time s prior to the current time t , $I_i(t, s)$. Thus, the total number of persons in class i infected in the narrow interval between s and $s + \delta s$ prior to time t is given by $I_i(t, s)\delta s$. The time since infection for all infected persons evolves in time due to the passage of time:

$$\frac{\partial}{\partial t} I_i(t, s) + \frac{\partial}{\partial s} I_i(t, s) = 0 \quad (1)$$

The number density of new infections, $I_i(t, 0)$, is set by the rate at which susceptible persons in the same class are becoming infected:

$$I_i(t, 0) = -\frac{dS_i}{dt} \quad (2)$$

Given $I_i(t, s)$, one can calculate the rate at which susceptible persons become infected:

$$\frac{dS_i}{dt} = -S_i \sum_{j=1}^M \frac{C_{ij}}{N_j} \int_0^T ds \beta_j(s) I_j(t, s) \quad (3)$$

Here, S_i is the susceptible population in class i , C_{ij} describes the frequency of potentially transmissive contacts between classes i and j , and $\beta_j(s)$ describes how infectious an infected person from class j is as a function of their time since infection. Here we have assumed that infections older than time T are no longer transmitting, $\beta_j(s > T) = 0$, which allows the integral to be truncated at time T . We have also ignored the possibility of re-infection for the time being.

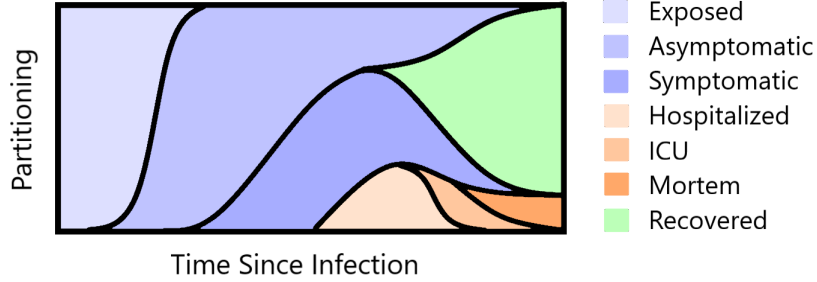


Figure 1: A graphical representation of how an infected population might be partitioned into different categories.

As with the standard SIR model, the equations for susceptibles and infecteds are closed. However, for practical applications of an epidemic model one may also need to describe the various sub-classes of the infected population (e.g. infectious, recovered, hospitalized, deceased, quarantined, asymptomatic, etc), with each sub-class α representing a fraction $\Phi_i^\alpha(s)$ of the total with number density of infecteds, $I_i^\alpha(t, s) = \Phi_i^\alpha(s)I_i(t, s)$. The total population in each sub-class at any time is then given by:

$$I_i^\alpha(t) = \int_0^\infty ds \Phi_i^\alpha(s) I_i(t, s) \quad (4)$$

This partitioning is also represented graphically in Figure.

Taking a time derivative of equation 4 and defining $\phi_i^\alpha = d\Phi_i^\alpha/ds$, we can also write:

$$\frac{dI_i^\alpha}{dt} = \int_0^T ds \phi_i^\alpha(s) I_i^\alpha(t, s) \quad (5)$$

Note that the equations for S_i and I_i remain closed no matter how many sub-classes one decides to resolve within the infected population. If each sub-class has a rate constant for infection $\beta_\alpha(s)$, then equation 3 accounts for interactions with all sub-classes via the mean value $\beta(s)$ which can be pre-computed by:

$$\beta(s) = \sum_\alpha \Phi_\alpha(s) \beta_\alpha(s) \quad (6)$$

The governing PDE model can be discretized and solved in any number of ways, including via compartment models like those found in pyRoss. While TSI models can be implemented in pyRoss, the user interface and numerical methods in pyRossTSI are much better suited to the TSI modelling framework. Details on the different numerical methods can be found in our longer report.

A final note on the input functions $\beta_i(s)$ and $\phi_i^\alpha(s)$. At this time, there is insufficient data to robustly show that $\beta_i(s)$ is different for different sectors of the population (there's barely even a consensus on the bare reproduction

number!). Therefore, to simplify the burden of user inputs pyRossTSI assumes $\beta_i(s) = \beta(s)$ for the whole population. Likewise, while it's known that infection outcomes vary by demographic (e.g. older people are more likely to be hospitalized), we will assume that demographic characteristics simply rescale an underlying transition probability, $\phi_i^\alpha(s) = p_i \phi^\alpha(s)$. Support for more general functions $\beta_i(s)$ and $\phi_i^\alpha(s)$ may appear in future implementations of pyRossTSI.