

# Structured compartment models of infection in Python

## I. EPIDEMIOLOGICAL MODELS

We consider a population aggregated by age into  $M$  groups labelled by  $i = 1, 2, \dots, M$ . In what follows, we provide several mathematical models of infection which have been implemented in PyRoss.

### A. SIR

The population within age group  $i$  is partitioned into susceptibles  $S_i$ , asymptomatic infectives  $I_i^a$ , symptomatic infectives  $I_i^s$  and removed individuals  $R_i$ . The sum of these is the size of the population in age group  $i$ ,  $N_i = S_i + I_i^a + I_i^s + R_i$  [1–4]. We ignore vital dynamics and the change in age structure on the time scale of the epidemic in this model. Therefore each  $N_i$  and, consequently, the total population size

$$N = \sum_{i=1}^M N_i \quad (1)$$

remain constant in time. We assume that the rate of infection of a susceptible individual in age group  $i$  is

$$\lambda_i(t) = \beta \sum_{j=1}^M \left( C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} \right), \quad i, j = 1, \dots, M \quad (2)$$

where  $\beta$  is the probability of infection on contact (assumed intrinsic to the pathogen) and  $C_{ij}^a$  and  $C_{ij}^s$  are, respectively, the number of contacts between asymptomatic and symptomatic infectives in age-group  $j$  with susceptibles in age-group  $i$  (reflecting the structure of social contacts). We take the age-independent recovery rate  $\gamma$  to be identical for both asymptomatic and symptomatic individuals whose fractions are, respectively,  $\alpha$  and  $\bar{\alpha} = 1 - \alpha$ . The social contact matrix  $C_{ij}$  denotes the average number of contacts made per day by an individual in class  $i$  with an individual in class  $j$ . Clearly, the total number of contacts between group  $i$  to group  $j$  must equal the total number of contacts from group  $j$  to group  $i$ , and thus,  $N_i C_{ij} = N_j C_{ji}$ .

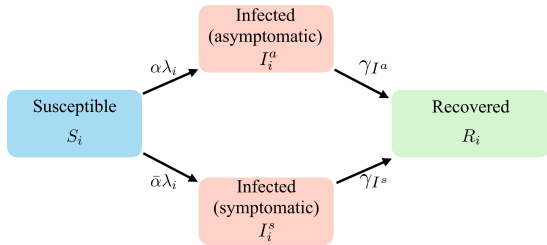


Figure 1: Schematics of the SIR model.

With these assumptions the progress of the epidemic is governed by the age-structured SIR model

$$\begin{aligned} \dot{S}_i &= -\lambda_i(t)S_i, \\ \dot{I}_i^a &= \alpha\lambda_i(t)S_i - \gamma I_i^a, \\ \dot{I}_i^s &= \bar{\alpha}\lambda_i(t)S_i - \gamma I_i^s, \\ \dot{R}_i &= \gamma I_i^a + \gamma I_i^s. \end{aligned} \quad (3)$$

The age structure of the population is specified the proportions  $N_i/N$  and the contact structure by the matrices  $C_{ij}^a$  and  $C_{ij}^s$ . We assume that symptomatic infectives reduce their contacts compared to asymptomatic infectives and set  $C_{ij}^s = f C_{ij}^a \equiv f C_{ij}$ , where  $0 \leq f \leq 1$  is the proportion by which this self-isolation takes place. Here

- $\gamma I_i^a$  is the recovery rate for asymptomatic infectives
- $\gamma I_i^s$  is the recovery rate for symptomatic infectives
- $\beta$  is the probability of infection on contact
- $\alpha$  is the fraction of asymptomatic infectives
- $f$  is the fraction for reduction in contacts of the symptomatic infectives

### B. SIRS

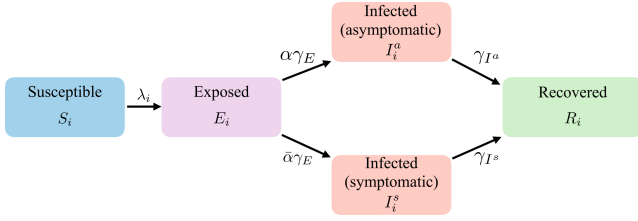
We now extend the age-structured SIR model to allow for recovered persons to be susceptible and change in population of each age group. The dynamics of the resulting SIRS model is:

$$\begin{aligned} \dot{S}_i &= -\lambda_i(t)S_i + \sigma_i + \epsilon(\gamma I_i^a + \gamma I_i^s) \\ \dot{I}_i^a &= \alpha\lambda_i(t)S_i - \gamma I_i^a \\ \dot{I}_i^s &= \bar{\alpha}\lambda_i(t)S_i - \gamma I_i^s \\ \dot{N}_i &= \sigma_i + l_i \end{aligned} \quad (4)$$

Here  $\epsilon$  is fraction of recovered who is susceptible.  $\sigma_i$  denotes of the arrival of new susceptibles, while  $l_i$  are new asymptomatic infectives. This means that  $N_i$  is now dynamical.

### C. SEIR

We can add an exposed class, that has caught the infection but is not infectious, to the SIR model to obtain an SEIR model. The rate of infection remains unchanged as before, but the equations now change to

Figure 2: **Schematics of the SEIR model.**

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t)S_i, \\
\dot{E}_i &= \lambda_i(t)S_i - \gamma_E E_i \\
\dot{I}_i^a &= \alpha\gamma_E E_i - \gamma_{I^a} I_i^a, \\
\dot{I}_i^s &= \bar{\alpha}\gamma_E E_i - \gamma_{I^s} I_i^s, \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s.
\end{aligned} \tag{5}$$

Assuming an exponentially distributed incubation time distribution,  $1/\gamma_E$  can be interpreted as the average incubation period. Here the population remains constant.

#### D. SEI5R

We now extend SEIR model to have five types of infectives ( $I_i^h$ : infectives who are hospitalized,  $I_i^c$ : infectives who are in ICU, and  $I_i^m$ : mortality) to obtain:

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t)S_i + \sigma_i, \\
\dot{E}_i &= \lambda_i(t)S_i - \gamma_E E_i \\
\dot{I}_i^a &= \alpha\gamma_E E_i - \gamma_{I^a} I_i^a, \\
\dot{I}_i^s &= \bar{\alpha}\gamma_E E_i - \gamma_{I^s} I_i^s, \\
\dot{I}_i^h &= h_i\gamma_{I^s} I_i^s - \gamma_{I^h} I_i^h, \\
\dot{I}_i^c &= c_i\gamma_{I^h} I_i^h - \gamma_{I^c} I_i^c, \\
\dot{I}_i^m &= m_i\gamma_{I^c} I_i^c, \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \bar{h}_i\gamma_{I^s} I_i^s + \bar{c}_i\gamma_{I^h} I_i^h + \bar{m}_i\gamma_{I^c} I_i^c. \\
\dot{N}_i &= \sigma_i - I_i^m - d_i
\end{aligned} \tag{6}$$

$$\lambda_i(t) = \beta \sum_{j=1}^M \left( C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} + C_{ij}^h \frac{I_j^h}{N_j} \right), \tag{7}$$

Here  $\bar{h}_i = 1 - h_i$ ,  $\bar{m}_i = 1 - m_i$ ,  $C_{ij}^s = f^s C_{ij}^a \equiv f^s C_{ij}$  and  $C_{ij}^s = f^h C_{ij}^a \equiv f^h C_{ij}$ .  $I^c$  is ICU cases and  $I^m$  is the mortality due to the infection and  $d_i$  is mortality die to natural causes.

#### E. SIkR

We now use method of stages to write an age-structured  $k$ -staged SIkR model  $\dot{I}_k(t) = \gamma_I N_I (I_{k-1} - I_k)$

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t)S_i, \\
\dot{I}_i^1 &= \lambda_i(t)S_i - k\gamma_I I_i^1, \\
\dot{I}_i^2 &= k\gamma_I I_i^1 - k\gamma_I I_i^2, \\
&\vdots \\
\dot{I}_i^k &= k\gamma_I I_i^{k-1} - k\gamma_I I_i^k, \\
\dot{R}_i &= k\gamma_I I_i^k.
\end{aligned} \tag{8}$$

#### F. SEkIkR

The above method of stages for SIR can be extended to SEIR model to obtain an age-structured  $k$ -staged SEkIkR model to obtain

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t)S_i, \\
\dot{E}_i^1 &= \lambda_i(t)S_i - k\gamma_E E_i^1 \\
\dot{E}_i^2 &= k\gamma_E E_i^1 - k\gamma_E E_i^2 \\
&\vdots \\
\dot{E}_i^k &= k\gamma_E E_i^{k-1} - k\gamma_E E_i^k \\
\dot{I}_i^1 &= \lambda_i(t)S_i - k\gamma_I I_i^1, \\
\dot{I}_i^2 &= k\gamma_I I_i^1 - k\gamma_I I_i^2, \\
&\vdots \\
\dot{I}_i^k &= k\gamma_I I_i^{k-1} - k\gamma_I I_i^k, \\
\dot{R}_i &= k\gamma_I I_i^k.
\end{aligned} \tag{9}$$

#### G. SEAIR

This model is an extension of the SEIR model, introducing the additional class A, which is both asymptomatic and infectious. In other words, this model shows what ensues if *everyone* who gets infected, undergoes a latency period where they are both asymptomatic and infectious. This class is potentially quite important, as there is some evidence that people are infectious before they start showing symptoms

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t)S_i \\
\dot{E}_i &= \lambda_i(t)S_i - \gamma_E E_i \\
\dot{A}_i &= \gamma_E E_i - (\alpha\gamma_{A \rightarrow I^a} + \bar{\alpha}\gamma_{A \rightarrow I^s})A_i \\
\dot{I}_i^a &= \alpha\gamma_{A \rightarrow I^a} A_i - \gamma_{I^a} I_i^a \\
\dot{I}_i^s &= \bar{\alpha}\gamma_{A \rightarrow I^s} A_i - \gamma_{I^s} I_i^s \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s
\end{aligned} \tag{10}$$

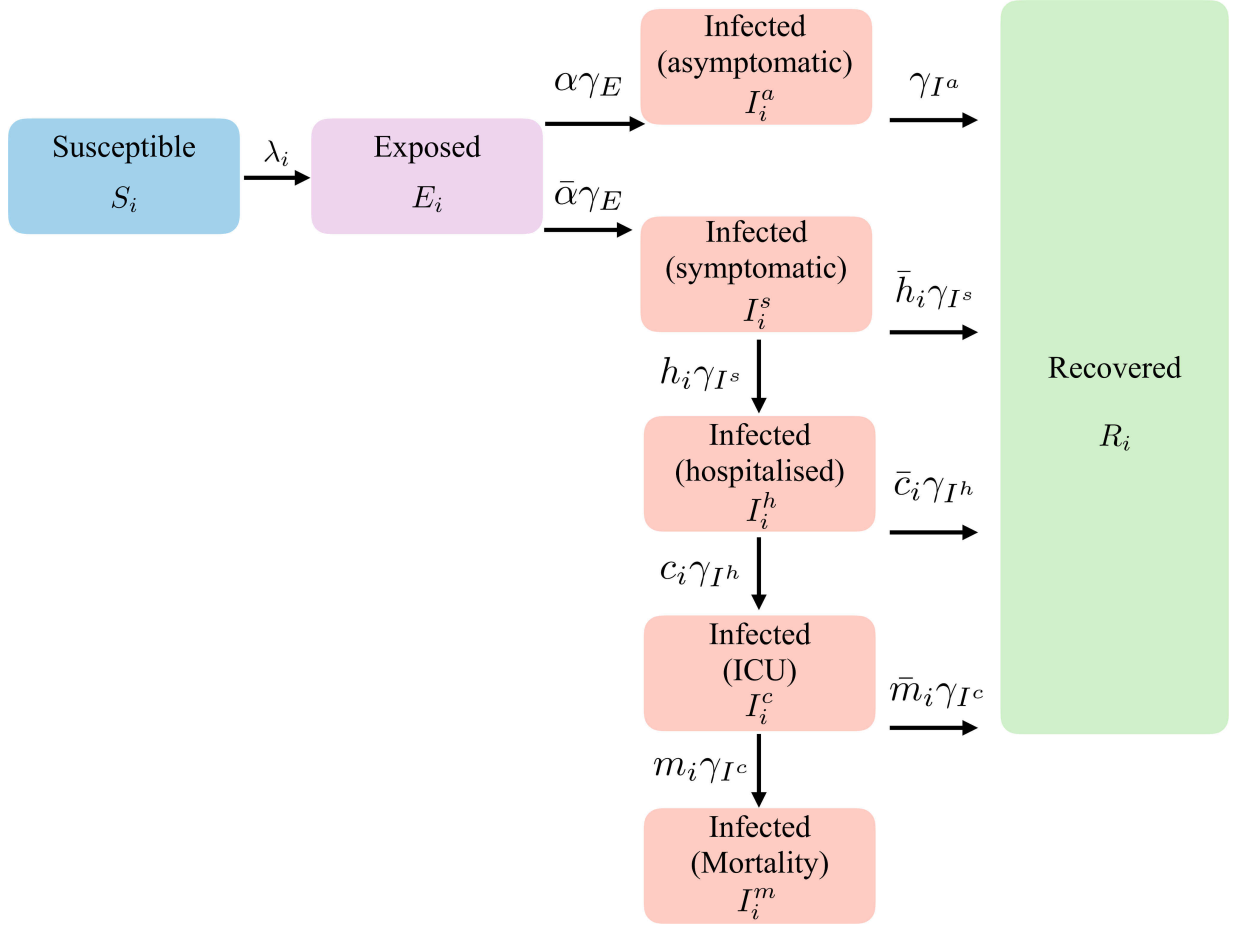


Figure 3: Schematics of the SEI5R model.

The  $A$  and  $I^a$  classes should behave virtually the same (so their contact matrices should be equal). The two are kept distinct to keep track of the fact that some people remain asymptomatic even in the  $I$  stage. Since it's difficult to find data on the ratio of  $I^s$  to  $I^a$ , it is possible to disregard the distinction and simply use  $I$  instead.

## H. SEAIRQ

We now introduce the  $Q$ -class, which represents people who have been tested and put into quarantine (and can therefore not infect anyone else). The dynamics of the SEAIR model is:

$$\begin{aligned}
 \dot{S}_i &= -\lambda_i(t)S_i - \tau_S S_i \\
 \dot{E}_i &= \lambda_i(t)S_i - (\gamma_E + \tau_E)E_i \\
 \dot{A}_i &= \gamma_E E_i - (\alpha\gamma_{A \rightarrow I^s} + \bar{\alpha}\gamma_{A \rightarrow I^a} + \tau_A)A_i \\
 \dot{I}_i^a &= \alpha\gamma_{A \rightarrow I^a}A_i - (\gamma_{I^a} + \tau_{I^a})I_i^a \\
 \dot{I}_i^s &= \bar{\alpha}\gamma_{A \rightarrow I^s}A_i - (\gamma_{I^s} + \tau_{I^s})I_i^s \\
 \dot{R}_i &= \gamma_{I^a}I_i^a + \gamma_{I^s}I_i^s \\
 \dot{Q}_i &= \tau_S S_i + \tau_E E + \tau_A A + \tau_{I^s}I_i^s + \tau_{I^a}I_i^a
 \end{aligned} \tag{11}$$

Here  $\tau_{E,A,I^s,I^a}$  is the testing rate in the population, these are in general different for different classes. We have presumed that people in the incubation stage  $E$  can also be tested. The  $\tau_S$  terms model the effects of false-positives, resulting in susceptibles being put into quarantine. Note that this model does not keep track of what happens to people once they're put into  $Q$  (which is especially important to do if  $\tau_S > 0$ ). Since  $Q$  is a closed system, this can all be done after the initial SEAIR simulation has been completed.

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