

Structured compartment models of infection in Python

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. We consider a structured metapopulation

$$\mathbf{n} = (n_1, \dots, n_{M \times L}) \quad (1)$$

consisting of M age-compartments and L classes of epidemiological states. The ξ -th reaction can be written down in its most general form as

$$\sum_{i=1}^{M \times L} f_i^\xi Y_i \rightarrow \sum_{i=1}^{M \times L} g_i^\xi Y_i$$

where \mathbf{Y}_i stands for an age-compartment of a epidemiological state (of dimension $M \times L$), and $\mathbf{f}^\xi, \mathbf{g}^\xi$ keeps track of the number of each participating in the ξ -th reaction. The change in the metapopulation as a result of the ξ -th reaction is,

$$\xi\text{-th transition step: } \mathbf{n} \xrightarrow{w_\xi} \mathbf{n} + \mathbf{r}_\xi \quad (2)$$

where \mathbf{r}^ξ is the vector of change for reaction ξ : $\mathbf{r}^\xi = \mathbf{g}^\xi - \mathbf{f}^\xi$, and the combinatorial forward rate constant is

$$w_\xi(t, \boldsymbol{\theta}, \mathbf{n}) = k_\xi(t) \prod_i \frac{x_i!}{(x_i - f_i^\xi)!}, \quad (3)$$

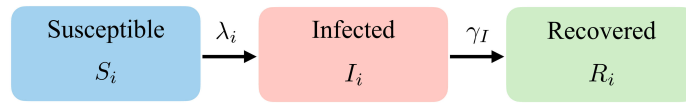
which gives the chemical master equation (CME) of interest:

$$\partial_t P(\mathbf{n}, t) = \sum_\xi [w_\xi(t, \boldsymbol{\theta}, \mathbf{n} - \mathbf{r}_\xi) P(\mathbf{n} - \mathbf{r}_\xi, t) - w_\xi(t, \boldsymbol{\theta}, \mathbf{n}) P(\mathbf{n}, t)]. \quad (4)$$

I. SIR

The population within age group i is partitioned into susceptibles S_i , infectives I_i , and removed individuals R_i . The sum of these is the size of the population in age group i , $N_i = S_i + I_i + R_i$ [1–5]. For this model, vital dynamics and the change in age structure on the time scale of the epidemic in this model is ignored. Therefore each N_i and, consequently, the total population size

$$N = \sum_{i=1}^M N_i \quad (5)$$



Step	\mathbf{r}_ξ	w_ξ
$S + I \rightarrow 2I$	$(-1, 1, 0)$	$\lambda_I n_S$
$I \rightarrow R$	$(0, -1, 1)$	$\gamma_I n_I$

Table I. **Schematics of the SIR model and elementary reaction steps and their rates.** The parameters for this model are: $\boldsymbol{\theta}(\beta, \gamma_I)$. The reaction takes the state $\mathbf{n} = (n_S, n_I, n_R)$ to the state $\mathbf{n} + \mathbf{r}_\xi$. For simplicity we consider $M = 1$, and thus, the sum in λ_i , (12), becomes trivial. we define $\lambda_I = \beta C n_I / N$.

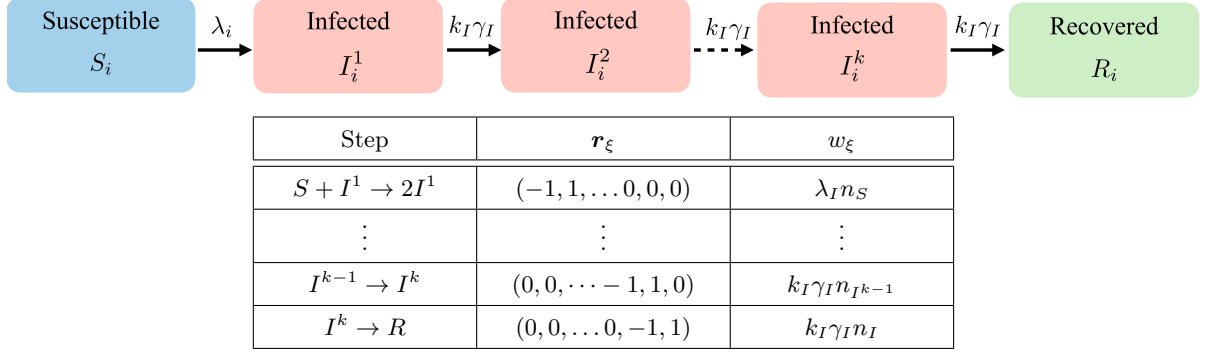


Table II. **Schematics of the SIkR model and elementary reaction steps and their rates.** The parameters for this model are: $\theta(k_I, \beta, \gamma_I)$. The reaction takes the state $\mathbf{n} = (n_S, n_{I^1}, \dots, n_{I^k}, n_R)$ to the state $\mathbf{n} + \mathbf{r}_\xi$. For simplicity we consider $M = 1$, and thus, the sum in λ_i , (12), becomes trivial. we define $\lambda_I = \beta C n_I / N$.

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

$$\lambda_i(t) = \beta \sum_{j=1}^M \left(C_{ij}(t) \frac{I_j}{N_j} \right), \quad i, j = 1, \dots, M \quad (6)$$

where β 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 γ to be identical for both asymptomatic and symptomatic individuals whose fractions are, respectively, α_i and $\bar{\alpha}_i = 1 - \alpha_i$. 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, $N_i C_{ij} = N_j C_{ji}$.

The above class SIR can be instantiated in PyRoss using `pyross.deterministic.SIR`. A detailed notebook is present in the examples folder of PyRoss [6].

II. SIkR

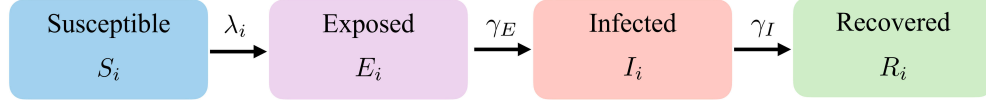
We now use method of stages to write an age-structured k -staged SIkR model $\dot{I}_k(t) = \gamma_I N_I (I_{k-1} - I_k)$

$$\begin{aligned} \dot{S}_i &= -\lambda_i(t) S_i, \\ \dot{I}_i^1 &= \lambda_i(t) S_i - k_I \gamma_I I_i^1, \\ \dot{I}_i^2 &= k_I \gamma_I I_i^1 - k_I \gamma_I I_i^2, \\ &\vdots \\ \dot{I}_i^k &= k_I \gamma_I I_i^{k-1} - k_I \gamma_I I_i^k, \\ \dot{R}_i &= k_I \gamma_I I_i^k. \end{aligned} \quad (7)$$

The rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^M \sum_{n=1}^k C_{ij} \frac{I_j^n}{N_j}, \quad (8)$$

The above class SIkR can be instantiated in PyRoss using `pyross.deterministic.SIkR`. A detailed notebook is present in the examples folder of PyRoss [6].



Step	\mathbf{r}_ξ	w_ξ
$S + I \rightarrow E + I$	$(-1, 1, 0, 0)$	$\lambda_I n_S$
$E \rightarrow I$	$(0, -1, 1, 0)$	$\gamma_E n_E$
$I \rightarrow R$	$(0, 0, -1, 1)$	$\gamma_I n_I$

Table III. **Schematics of the SEIR model and elementary reaction steps and their rates.** The parameters for this model are: $\theta(\beta, \gamma_I, \gamma_E)$. The reaction takes the state $\mathbf{n} = (n_S, n_E, n_I, n_R)$ to the state $\mathbf{n} + \mathbf{r}_\xi$. For simplicity we consider $M = 1$, and thus, the sum in λ_i , (12), becomes trivial. we define $\lambda_I = \beta C n_I / N$.

III. 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.

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

The rate of infection remains unchanged as before, but the equations now change. The rate of infection of a susceptible individual in age group i is

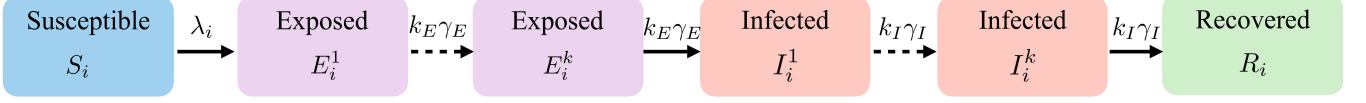
$$\lambda_i(t) = \beta \sum_{j=1}^M \left(C_{ij} \frac{I_j}{N_j} \right), \tag{10}$$

The above class SEIR can be instantiated in PyRoss using `pyross.deterministic.SEIR`. A detailed notebook is present in the examples folder of PyRoss [6].

IV. SEIKR

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

$$\begin{aligned}
 \dot{S}_i &= -\lambda_i(t) S_i, \\
 \dot{E}_i^1 &= \lambda_i(t) S_i - k_E \gamma_E E_i^1 \\
 \dot{E}_i^2 &= k_E \gamma_E E_i^1 - k_E \gamma_E E_i^2 \\
 &\vdots \\
 \dot{E}_i^k &= k_E \gamma_E E_i^{k-1} - k_E \gamma_E E_i^k \\
 \dot{I}_i^1 &= k_E \gamma_E E_i^k - k_I \gamma_I I_i^1, \\
 \dot{I}_i^2 &= k_I \gamma_I I_i^1 - k_I \gamma_I I_i^2, \\
 &\vdots \\
 \dot{I}_i^k &= k_I \gamma_I I_i^{(k-1)} - k_I \gamma_I I_i^k, \\
 \dot{R}_i &= k_I \gamma_I I_i^k.
 \end{aligned} \tag{11}$$



Step	\mathbf{r}_ξ	w_ξ
$S + I^1 \rightarrow E^1 + I^1$	$(-1, 1, 0, \dots, 0, 0, 0, \dots, 0, 0)$	$\lambda_I n_S$
$E^1 \rightarrow E^2$	$(0, -1, 1, \dots, 0, 0, 0, \dots, 0, 0)$	$k_E \gamma_E n_E$
\vdots	\vdots	\vdots
$E^{k-1} \rightarrow E^k$	$(0, 0, 0, \dots, -1, 1, 0, \dots, 0, 0)$	$k_E \gamma_E n_E$
$E^k \rightarrow I^1$	$(0, 0, 0, \dots, 0, -1, 1, \dots, 0, 0)$	$k_E \gamma_E n_E$
\vdots	\vdots	\vdots
$I^k \rightarrow R$	$(0, 0, 0, \dots, 0, 0, 0, \dots, -1, 1)$	$k_I \gamma_I n_I$

Table IV. **Schematics of the SEkIkR model and elementary reaction steps and their rates.** The parameters for this model are: $\theta(k_I, k_E, \beta, \gamma_I, \gamma_E)$. The reaction takes the state $\mathbf{n} = (n_S, n_{E^1}, \dots, n_{E^k}, n_{I^1}, \dots, n_{I^k}, n_R)$ to the state $\mathbf{n} + \mathbf{r}_\xi$. For simplicity we consider $M = 1$, and thus, the sum in λ_i , (12), becomes trivial. we define $\lambda_I = \beta C n_I / N$.

The rate of infection of a susceptible individual in age group i is as in SIkR. The above class SEkIkR can be instantiated in PyRoss using `pyross.deterministic.SEkIkR`. A detailed notebook is present in the examples folder of PyRoss [6].

V. SIIR

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

$$\lambda_i(t) = \beta \sum_{j=1}^M \left(C_{ij}^a(t) \frac{I_j^a}{N_j} + C_{ij}^s(t) \frac{I_j^s}{N_j} \right), \quad i, j = 1, \dots, M \quad (12)$$

where β 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).

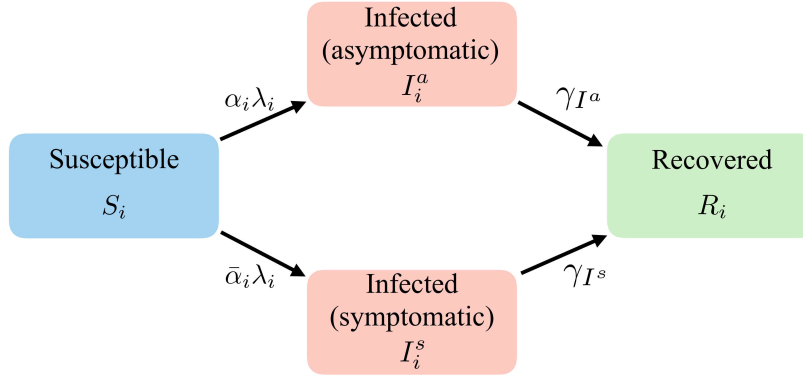
With these assumptions the progress of the epidemic is governed by the age-structured SIR model

$$\begin{aligned} \dot{S}_i &= -\lambda_i(t) S_i, \\ \dot{I}_i^a &= \alpha_i \lambda_i(t) S_i - \gamma_{I^a} I_i^a, \\ \dot{I}_i^s &= \bar{\alpha}_i \lambda_i(t) S_i - \gamma_{I^s} I_i^s, \\ \dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s. \end{aligned} \quad (13)$$

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 $C_{ij}^s = f^s C_{ij}^a \equiv f^s C_{ij}$, where $0 \leq f^s \leq 1$ is the proportion by which this self-isolation takes place. Here

The rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^M \left(C_{ij}^a(t) \frac{I_j^a}{N_j} + C_{ij}^s(t) \frac{I_j^s}{N_j} \right), \quad i, j = 1, \dots, M \quad (14)$$



Step	\mathbf{r}_ξ	w_ξ
$S + I^a \rightarrow 2I^a$	$(-1, 1, 0, 0)$	$\alpha \lambda_I^a n_S$
$S + I^a \rightarrow I^s + I^a$	$(-1, 0, 1, 0)$	$\bar{\alpha} \lambda_I^a n_S$
$S + I^s \rightarrow I^a + I^s$	$(-1, 1, 0, 0)$	$\alpha \lambda_I^s n_S$
$S + I^s \rightarrow 2I^s$	$(-1, 0, 1, 0)$	$\bar{\alpha} \lambda_I^s n_S$
$I^a \rightarrow R$	$(0, -1, 0, 1)$	$\gamma_{I^a} n_{I^a}$
$I^s \rightarrow R$	$(0, 0, -1, 1)$	$\gamma_{I^s} n_{I^s}$

Table V. **Schematics of the SIIR model and elementary reaction steps and their rates.** The parameters for this model are: $\theta(\alpha_i, \beta, \gamma_{I^a}, \gamma_{I^s})$. The reaction takes the state $\mathbf{n} = (n_S, n_{I^a}, n_{I^s}, n_R)$ to the state $\mathbf{n} + \mathbf{r}_\xi$. For simplicity we consider $M = 1$, and thus, the sum in λ_i , (12), becomes trivial. we define $\lambda_I^a = \beta C^a n_{I^a} / N$ and $\lambda_I^s = \beta C^s n_{I^s} / N$ such that $\lambda = \lambda_I^a + \lambda_I^s$. This can be easily generalized to the age-structured model.

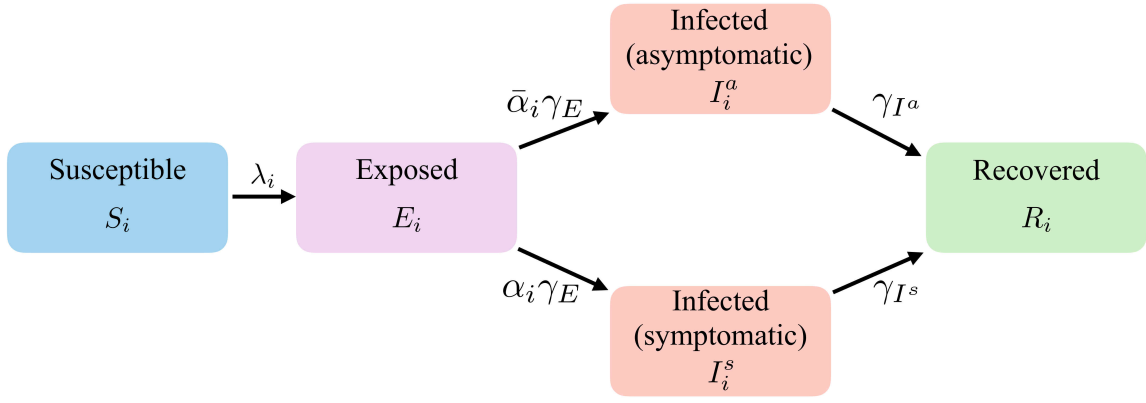
where β is the probability of infection on contact (assumed intrinsic to the pathogen) and C_{ij}^a and C_{ij}^s are, respectively, the number of contacts between asymptomatic and symptomatic infectives in age-group j with susceptibles in age-group i (reflecting the structure of social contacts). We take the age-independent recovery rate γ to be identical for both asymptomatic and symptomatic individuals whose fractions are, respectively, α_i and $\bar{\alpha}_i = 1 - \alpha_i$. 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, $N_i C_{ij} = N_j C_{ji}$.

- γ_{I^a} is the recovery rate for asymptomatic infectives
- γ_{I^s} is the recovery rate for symptomatic infectives
- β is the probability of infection on contact
- α_i is the fraction of asymptomatic infectives
- f^s is the fraction for reduction in contacts of the symptomatic infectives

In what follows, we add more features to SIR model and derive more detailed models. The above class SIIR can be instantiated in PyRoss using `pyross.deterministic.SIR`. A detailed notebook is present in the examples folder of PyRoss [6].

VI. SEIIR

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



Step	\mathbf{r}_ξ	w_ξ
$S + I^a, I^s \rightarrow E + I^a, I^s$	$(-1, 1, 0, 0, 0)$	$\lambda_I^a n_S, \lambda_I^s n_S$
$E \rightarrow I^a$	$(0, -1, 1, 0, 0)$	$\alpha \gamma_E n_E$
$E \rightarrow I^s$	$(0, -1, 0, 1, 0)$	$\bar{\alpha} \gamma_E n_E$
$I^a \rightarrow R$	$(0, 0, -1, 0, 1)$	$\gamma_{I^a} n_{I^a}$
$I^s \rightarrow R$	$(0, 0, 0, -1, 1)$	$\gamma_{I^s} n_{I^s}$

Table VI. **Schematics of the SEIIR model, elementary reaction steps and their rates.** The parameters for this model are: $\theta(\alpha_i, \beta, \gamma_E, \gamma_{I^a}, \gamma_{I^s})$. The reaction takes the state $\mathbf{n} = (n_S, n_E, n_{I^a}, n_{I^s}, n_R)$ to the state $\mathbf{n} + \mathbf{r}_\xi$. The infection rates λ_I^a and λ_I^s are defined in V.

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t) S_i, \\
\dot{E}_i &= \lambda_i(t) S_i - \gamma_E E_i \\
\dot{I}_i^a &= \alpha_i \gamma_E E_i - \gamma_{I^a} I_i^a, \\
\dot{I}_i^s &= \bar{\alpha}_i \gamma_E E_i - \gamma_{I^s} I_i^s, \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s.
\end{aligned} \tag{15}$$

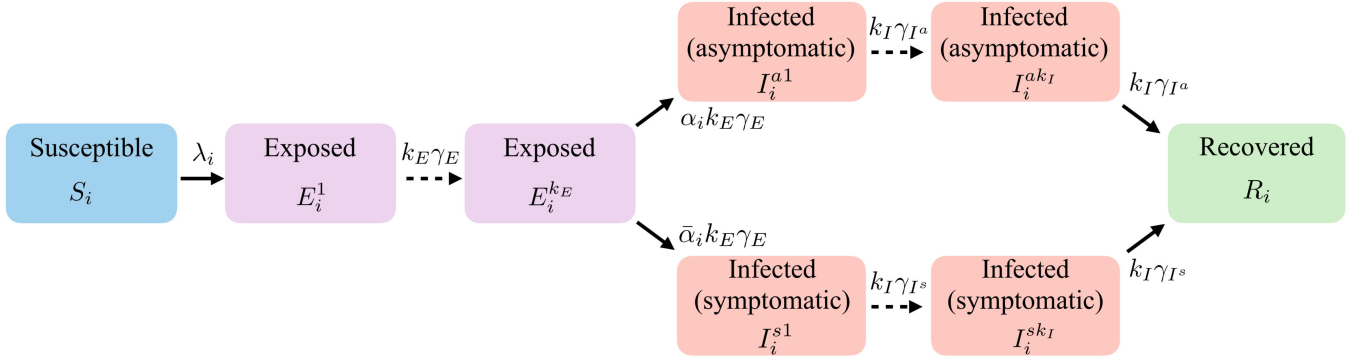
The rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^M \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} \right), \tag{16}$$

Assuming an exponentially distributed incubation time distribution, $1/\gamma_E$ can be interpreted as the average incubation period. Here the population remains constant. The above class SEIIR can be instantiated in PyRoss using `pyross.deterministic.SEIR`. A detailed notebook is present in the examples folder of PyRoss [6].

VII. SEKIKIKR

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



Step	\mathbf{r}_ξ	w_ξ
$S + I^1 \rightarrow E^1 + I^1$	$(-1, 1, 0, \dots, 0, 0, 0, \dots, 0, 0, 0, \dots, 0, 0)$	$\lambda_I n_S$
$E^1 \rightarrow E^2$	$(0, -1, 1, \dots, 0, 0, 0, \dots, 0, 0, 0, \dots, 0, 0)$	$k_E \gamma_E n_E$
\vdots	\vdots	\vdots
$E^{k-1} \rightarrow E^k$	$(0, 0, 0, \dots, -1, 1, 0, \dots, 0, 0, 0, \dots, 0, 0)$	$k_E \gamma_E n_E$
$E^k \rightarrow I^{a1}$	$(0, 0, 0, \dots, 0, -1, 1, \dots, 0, 0, 0, \dots, 0, 0)$	$\alpha k_E \gamma_E n_E$
\vdots	\vdots	\vdots
$E^k \rightarrow I^{s1}$	$(0, 0, 0, \dots, 0, -1, 0, \dots, 0, 0, 1, \dots, 0, 0)$	$\bar{\alpha} k_E \gamma_E n_E$
\vdots	\vdots	\vdots

Table VII. **Schematics of the SEIkR model and elementary reaction steps and their rates.** The parameters for this model are: $\theta(k_I, k_E, \alpha_i, \beta, \gamma_{I^a}, \gamma_{I^s}, \gamma_E)$. The reaction takes the state $\mathbf{n} = (n_S, n_{E^1}, \dots, n_{E^{k_E}}, n_{I^{a1}}, \dots, n_{I^{a k_I}}, n_{I^{s1}}, \dots, n_{I^{s k_I}}, n_R)$ to the state $\mathbf{n} + \mathbf{r}_\xi$. For simplicity we consider $M = 1$, and thus, the sum in λ_i , (12), becomes trivial. we define $\lambda_I = \beta C n_I / N$.

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t) S_i, \\
\dot{E}_i^1 &= \lambda_i(t) S_i - k_E \gamma_E E_i^1 \\
\dot{E}_i^2 &= k_E \gamma_E E_i^1 - k_E \gamma_E E_i^2 \\
&\vdots \\
\dot{E}_i^{k_E} &= k_E \gamma_E E_i^{k_E-1} - k_E \gamma_E E_i^{k_E} \\
\dot{I}_i^{a1} &= \alpha_i k_E \gamma_E E_i^{k_E} - k_I \gamma_{I^a} I_i^{a1}, \\
\dot{I}_i^{a2} &= k_I \gamma_{I^a} I_i^{a1} - k_I \gamma_{I^a} I_i^{a2}, \\
&\vdots \\
\dot{I}_i^{a k_I} &= k_I \gamma_{I^a} I_i^{a(k_I-1)} - k_I \gamma_{I^a} I_i^{a k_I}, \\
\dot{I}_i^{s1} &= \bar{\alpha}_i k_E \gamma_E E_i^{k_E} - k_I \gamma_{I^s} I_i^{s1}, \\
\dot{I}_i^{s2} &= k_I \gamma_{I^s} I_i^{s1} - k_I \gamma_{I^s} I_i^{s2}, \\
&\vdots \\
\dot{I}_i^{s k_I} &= k_I \gamma_{I^s} I_i^{s(k_I-1)} - k_I \gamma_{I^s} I_i^{s k_I}, \\
\dot{R}_i &= k_I \gamma_{I^a} I_i^{a k_I} + k_I \gamma_{I^s} I_i^{s k_I}.
\end{aligned} \tag{17}$$

The rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^M \sum_{n=1}^{k_I} \left(C_{ij}^a \frac{I_j^{an}}{N_j} + C_{ij}^s \frac{I_j^{sn}}{N_j} \right), \quad (18)$$

The above class SEkIkIkR can be instantiated in PyRoss using `pyross.deterministic.SEkIkIkR`. A detailed notebook is present in the examples folder of PyRoss [6].

VIII. SEI5R

We now extend SEIR model to have fives 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:

$$\begin{aligned} \dot{S}_i &= -\lambda_i(t)S_i + \sigma_i, \\ \dot{E}_i &= \lambda_i(t)S_i - \gamma_E E_i \\ \dot{I}_i^a &= \alpha_i \gamma_E E_i - \gamma_{I^a} I_i^a, \\ \dot{I}_i^s &= \bar{\alpha}_i \gamma_E E_i - \gamma_{I^s} I_i^s, \\ \dot{I}_i^h &= h_i \gamma_{I^s} I_i^s - \gamma_{I^h} I_i^h, \\ \dot{I}_i^c &= c_i \gamma_{I^h} I_i^h - \gamma_{I^c} I_i^c, \\ \dot{I}_i^m &= m_i \gamma_{I^c} I_i^c, \\ \dot{R}_i &= \gamma_{I^a} I_i^a + \bar{h}_i \gamma_{I^s} I_i^s + \bar{c}_i \gamma_{I^h} I_i^h + \bar{m}_i \gamma_{I^c} I_i^c. \\ \dot{N}_i &= \sigma_i - m_i \gamma_{I^c} I_i^c \end{aligned} \quad (19)$$

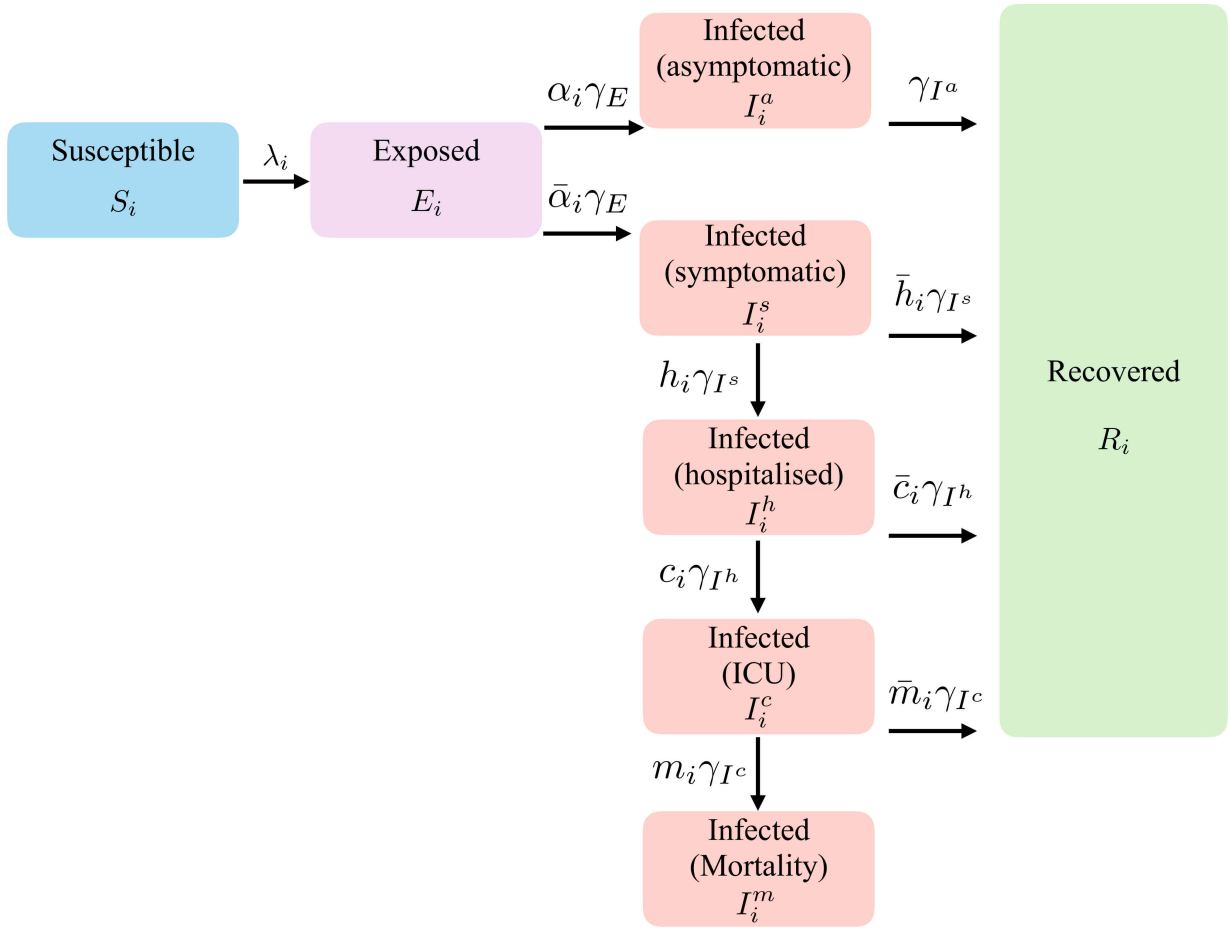
The rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^M \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} + C_{ij}^h \frac{I_j^h}{N_j} \right), \quad (20)$$

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. The above class SEI5R can be instantiated in PyRoss using `pyross.deterministic.SEI5R`. A detailed notebook is present in the examples folder of PyRoss [6].

IX. SEI8R

We now extend SEIR model to have eight 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:



Step	\mathbf{r}_ξ	w_ξ
$S + I^a, I^s \rightarrow E + I^a, I^s$	$(-1, 1, 0, 0, 0, 0, 0, 0)$	$\lambda_I^a n_S, \lambda_I^s n_S$
$E \rightarrow I^a$	$(0, -1, 1, 0, 0, 0, 0, 0)$	$\alpha \gamma_E n_E$
$I^a \rightarrow R$	$(0, 0, -1, 0, 0, 0, 0, 1)$	$\gamma_{I^a} n_{I^a}$
$E \rightarrow I^s$	$(0, -1, 0, 1, 0, 0, 0, 0)$	$\bar{\alpha} \gamma_E n_E$
$I^s \rightarrow R$	$(0, 0, 0, -1, 0, 0, 0, 1)$	$\bar{h} \gamma_{I^s} n_{I^s}$
$I^s \rightarrow I^h$	$(0, 0, 0, -1, 1, 0, 0, 0)$	$h \gamma_{I^s} n_{I^s}$
$I^h \rightarrow R$	$(0, 0, 0, 0, -1, 0, 0, 1)$	$\bar{c} \gamma_{I^h} n_{I^h}$
$I^h \rightarrow I^c$	$(0, 0, 0, 0, -1, 1, 0, 0)$	$c \gamma_{I^h} n_{I^h}$
$I^c \rightarrow R$	$(0, 0, 0, 0, 0, -1, 0, 1)$	$\bar{m} \gamma_{I^c} n_{I^c}$
$I^c \rightarrow I^m$	$(0, 0, 0, 0, 0, -1, 1, 1)$	$m \gamma_{I^c} n_{I^c}$

Table VIII. **Schematics of the SEI5R model, elementary reaction steps and their rates.** The parameters for this model are: $\theta(\alpha_i, \beta, \gamma_E, \gamma_{I^a}, \gamma_{I^s}, \gamma_{I^h}, \gamma_{I^c}, h_i, c_i, m_i)$. The reaction takes the state $\mathbf{n} = (n_S, n_E, n_{I^a}, n_{I^s}, n_{I^h}, n_{I^c}, n_{I^m}, n_R)$ to the state $\mathbf{n} + \mathbf{r}_\xi$. The infection rates λ_I^a and λ_I^s are defined in V.

Table IX. **Schematics of the SEI8R model, elementary reaction steps and their rates.** The parameters for this model are: $\theta(\alpha_i, \beta, \gamma_E, \gamma_{I^a}, \gamma_{I^s}, \gamma_{I^h}, \gamma_{I^c}, \gamma_{I^{s'}}, \gamma_{I^{h'}}, \gamma_{I^{c'}}, h_i, c_i, m_i)$. Elementary reaction steps and their rates for the SEAI8R model for $M = 1$. The reaction takes the state $\mathbf{n} = (n_S, n_E, n_{I^a}, n_{I^s}, n_{I^{s'}}, n_{I^h}, n_{I^{h'}}, n_{I^c}, n_{I^{c'}}, n_{I^m}, n_R)$ to the state $\mathbf{n} + \mathbf{r}_\xi$. The infection rates λ_I^a and λ_I^s are defined in .

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t)S_i + \sigma_i, \\
\dot{E}_i &= \lambda_i(t)S_i - \gamma_E E_i \\
\dot{I}_i^a &= \alpha_i \gamma_E E_i - \gamma_{I^a} I_i^a, \\
\dot{I}_i^s &= \bar{\alpha}_i \gamma_E E_i - \gamma_{I^s} I_i^s, \\
\dot{I}_i^{s'} &= \bar{h}_i \gamma_{I^s} I_i^s - \gamma_{I^{s'}} I_i^{s'} \\
\dot{I}_i^h &= h_i \gamma_{I^s} I_i^s - \gamma_{I^h} I_i^h, \\
\dot{I}_i^{h'} &= \bar{c}_i \gamma_{I^h} I_i^h - \gamma_{I^{h'}} I_i^{h'} \\
\dot{I}_i^c &= c_i \gamma_{I^h} I_i^h - \gamma_{I^c} I_i^c, \\
\dot{I}_i^{c'} &= \bar{m}_i \gamma_{I^c} I_i^c - \gamma_{I^{c'}} I_i^{c'} \\
\dot{I}_i^m &= m_i \gamma_{I^c} I_i^c, \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^{s'}} I_i^{s'} + \gamma_{I^{h'}} I_i^{h'} + \gamma_{I^{c'}} I_i^{c'} \\
\dot{N}_i &= \sigma_i - m_i \gamma_{I^c} I_i^c
\end{aligned} \tag{21}$$

The rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^M \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} + C_{ij}^h \frac{I_j^h}{N_j} \right), \tag{22}$$

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. The above class SEI8R can be instantiated in PyRoss using `pyross.deterministic.SEI8R`. A detailed notebook is present in the examples folder of PyRoss [6].

X. SEAIR

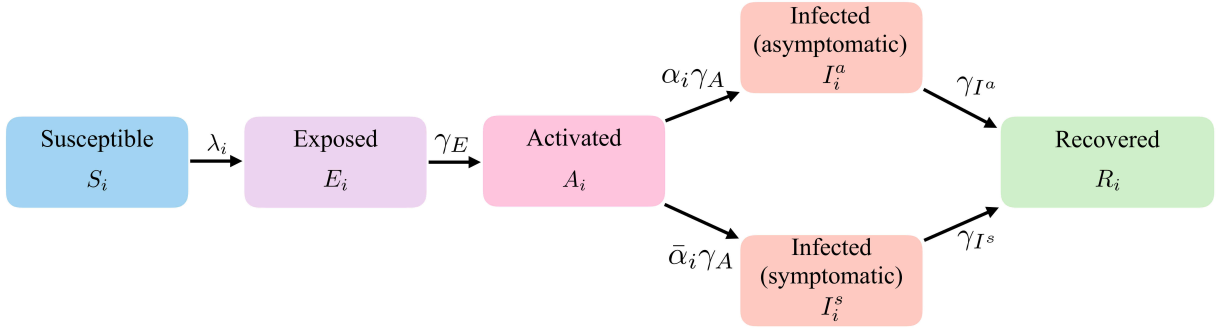
This model is an extension of the SEIR model, introducing the additional class A, which is both asymptomatic and infectious. In other words, this models shows what ensues if *everyone* who gets infected, undergoes a latency period where they are both asymptomatic and infectious. This class is potentially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

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t)S_i \\
\dot{E}_i &= \lambda_i(t)S_i - \gamma_E E_i \\
\dot{A}_i &= \gamma_E E_i - \gamma_A A_i \\
\dot{I}_i^a &= \alpha_i \gamma_A A_i - \gamma_{I^a} I_i^a \\
\dot{I}_i^s &= \bar{\alpha}_i \gamma_A A_i - \gamma_{I^s} I_i^s \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s
\end{aligned} \tag{23}$$

The rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^M \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^a \frac{A_j}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} \right), \tag{24}$$

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. The above class SEI5R can be instantiated in PyRoss using `pyross.deterministic.SEAIR`. A detailed notebook is present in the examples folder of PyRoss [6].



Step	\mathbf{r}_ξ	w_ξ
$S + A, I^a, I^s \rightarrow E + A, I^a, I^s$	$(-1, 1, 0, 0, 0)$	$\lambda_A^a n_S, \lambda_I^a n_S, \lambda_I^s n_S$
$E \rightarrow A$	$(0, -1, 1, 0, 0)$	$\gamma_E n_E$
$A \rightarrow I^a$	$(0, 0, -1, 1, 0)$	$\alpha \gamma_A n_A$
$A \rightarrow I^s$	$(0, 0, -1, 0, 1)$	$\bar{\alpha} \gamma_A n_A$
$I^a \rightarrow R$	$(0, 0, 0, -1, 0)$	$\gamma_{I^a} n_{I^a}$
$I^s \rightarrow R$	$(0, 0, 0, 0, -1)$	$\gamma_{I^s} n_{I^s}$

Table X. **Schematics of the SEAIIR model, elementary reaction steps and their rates.** The parameters for this model are: $\theta(\alpha_i, \beta, \gamma_E, \gamma_A, \gamma_{I^a}, \gamma_{I^s})$. Elementary reaction steps and their rates for the SEAIIR model. The reaction takes the state $\mathbf{n} = (n_S, n_E, n_A, n_{I^a}, n_{I^s})$ to the state $\mathbf{n} + \mathbf{r}_\alpha$ for $M = 1$. In addition to the infection rates λ_I^a and λ_I^s , we define $\lambda_A^a = \beta C^a n_A / N$. Thus, for this simplified model we can write for the total rate of infection, $(??)$, $\lambda = \lambda_A^a + \lambda_I^a + \lambda_I^s$.

XI. SEAI5R

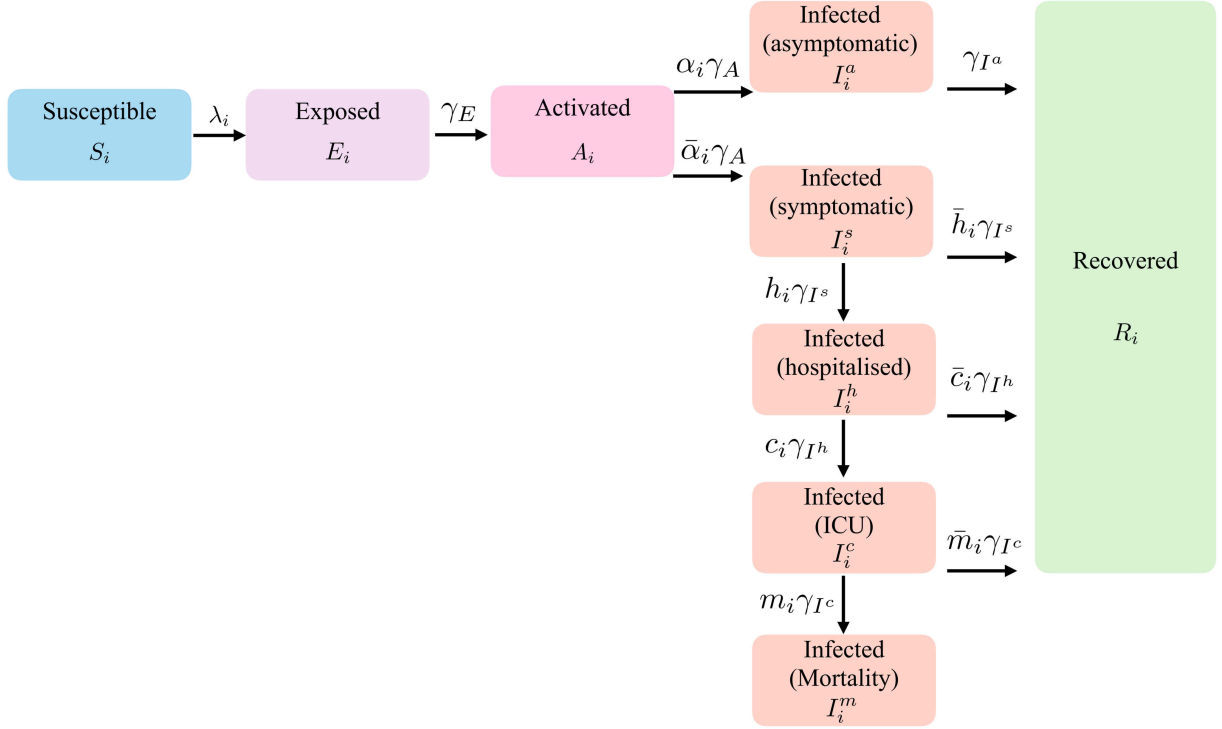
We now extend SEIR model to have five types of infectives (I_i^h : infectives who are hospitalized, I_i^c : infectives who are in ICU, and I_i^m : mortality) to obtain:

$$\begin{aligned}
 \dot{S}_i &= -\lambda_i(t) S_i + \sigma_i, \\
 \dot{E}_i &= \lambda_i(t) S_i - \gamma_E E_i \\
 \dot{A}_i &= \gamma_E E_i - \gamma_A A_i \\
 \dot{I}_i^a &= \alpha_i \gamma_A A_i - \gamma_{I^a} I_i^a, \\
 \dot{I}_i^s &= \bar{\alpha}_i \gamma_A A_i - \gamma_{I^s} I_i^s, \\
 \dot{I}_i^h &= h_i \gamma_{I^s} I_i^s - \gamma_{I^h} I_i^h, \\
 \dot{I}_i^c &= c_i \gamma_{I^h} I_i^h - \gamma_{I^c} I_i^c, \\
 \dot{I}_i^m &= m_i \gamma_{I^c} I_i^c, \\
 \dot{R}_i &= \gamma_{I^a} I_i^a + \bar{h}_i \gamma_{I^s} I_i^s + \bar{c}_i \gamma_{I^h} I_i^h + \bar{m}_i \gamma_{I^c} I_i^c. \\
 \dot{N}_i &= \sigma_i - m_i \gamma_{I^c} I_i^m
 \end{aligned} \tag{25}$$

The rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^M \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^s \frac{A_j}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} + C_{ij}^h \frac{I_j^h}{N_j} \right), \tag{26}$$

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. The above class SEAI5R can be instantiated in PyRoss using `pyross.deterministic.SEAI5R`. A detailed notebook is present in the examples folder of PyRoss [6].

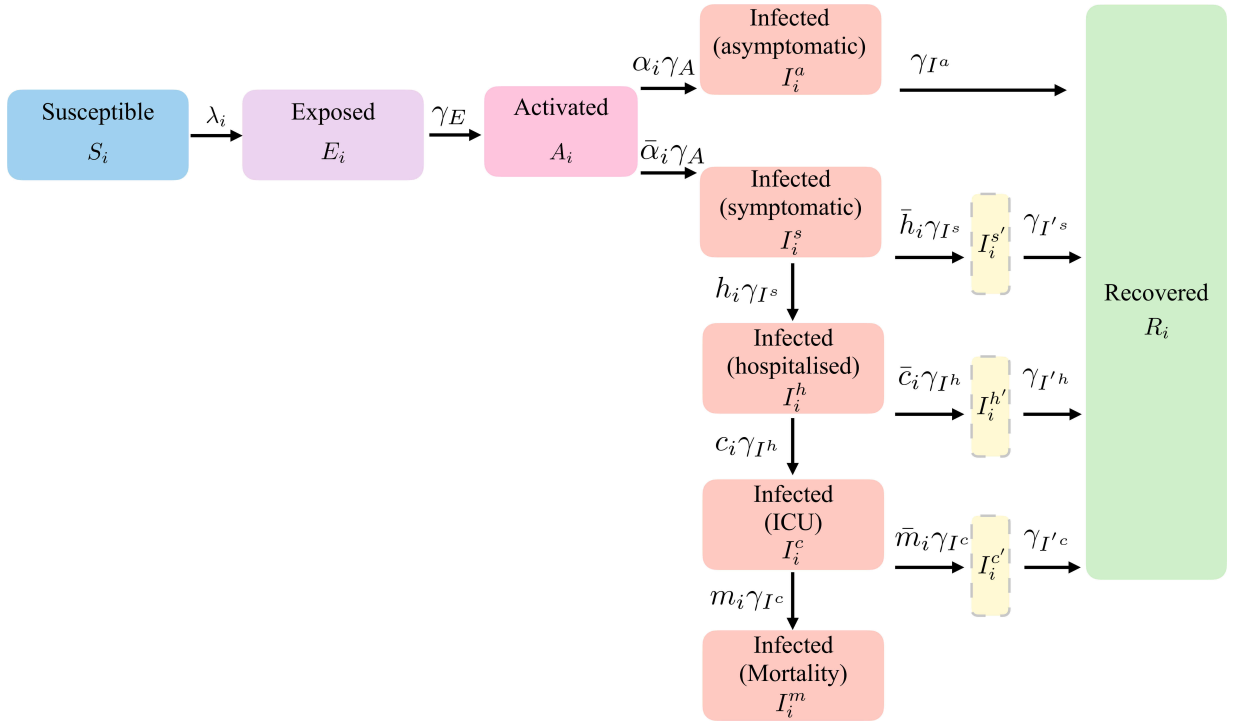


Step	\mathbf{r}_ξ	w_ξ
$S + I^a, I^s \rightarrow E + I^a, I^s$	$(-1, 1, 0, 0, 0, 0, 0, 0, 0, 0)$	$\lambda_I^a n_S, \lambda_I^s n_S$
$E \rightarrow A$	$(0, -1, 1, 0, 0, 0, 0, 0, 0, 0)$	$\gamma_E n_E$
$A \rightarrow I^a$	$(0, 0, -1, 1, 0, 0, 0, 0, 0, 0)$	$\alpha \gamma_A n_E$
$I^a \rightarrow R$	$(0, 0, 0, -1, 0, 0, 0, 0, 0, 1)$	$\gamma_{I^a} n_{I^a}$
$A \rightarrow I^s$	$(0, 0, -1, 0, 1, 0, 0, 0, 0, 0)$	$\bar{\alpha} \gamma_A n_E$
$I^s \rightarrow R$	$(0, 0, 0, 0, -1, 0, 0, 0, 0, 1)$	$\bar{h} \gamma_{I^s} n_{I^s}$
$I^s \rightarrow I^h$	$(0, 0, 0, 0, -1, 1, 0, 0, 0, 0)$	$h \gamma_{I^s} n_{I^s}$
$I^h \rightarrow R$	$(0, 0, 0, 0, 0, -1, 0, 0, 0, 1)$	$\bar{c} \gamma_{I^h} n_{I^h}$
$I^h \rightarrow I^c$	$(0, 0, 0, 0, 0, -1, 1, 0, 0, 0)$	$c \gamma_{I^h} n_{I^h}$
$I^c \rightarrow R$	$(0, 0, 0, 0, 0, 0, -1, 0, 0, 1)$	$m \gamma_{I^c} n_{I^c}$
$I^c \rightarrow I^m$	$(0, 0, 0, 0, 0, 0, -1, 1, 1, 0)$	$m \gamma_{I^c} n_{I^c}$

Table XI. **Schematics of the SEAI5R model, elementary reaction steps and their rates.** The parameters for this model are: $\theta(\alpha_i, \beta, \gamma_E, \gamma_A, \gamma_{I^a}, \gamma_{I^s}, \gamma_{I^h}, \gamma_{I^c}, h_i, c_i, m_i)$. Elementary reaction steps and their rates for the SEAI5R model for $M = 1$. The reaction takes the state $\mathbf{n} = (n_S, n_E, n_A, n_{I^a}, n_{I^s}, n_{I^h}, n_{I^c}, n_{I^m}, n_R)$ to the state $\mathbf{n} + \mathbf{r}_\xi$. The infection rates λ_I^a and λ_I^s are defined in .

XII. SEAI8R

We now extend SEIR model to have eight 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:



$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t)S_i + \sigma_i, \\
\dot{E}_i &= \lambda_i(t)S_i - \gamma_E E_i \\
\dot{A}_i &= \gamma_E E_i - \gamma_A A_i \\
\dot{I}_i^a &= \alpha_i \gamma_A A_i - \gamma_{I^a} I_i^a, \\
\dot{I}_i^s &= \bar{\alpha}_i \gamma_A A_i - \gamma_{I^s} I_i^s, \\
\dot{I}_i^{s'} &= \bar{h}_i \gamma_{I^s} I_i^s - \gamma_{I^{s'}} I_i^{s'} \\
\dot{I}_i^h &= h_i \gamma_{I^s} I_i^s - \gamma_{I^h} I_i^h, \\
\dot{I}_i^{h'} &= \bar{c}_i \gamma_{I^h} I_i^h - \gamma_{I^{h'}} I_i^{h'} \\
\dot{I}_i^c &= c_i \gamma_{I^h} I_i^h - \gamma_{I^c} I_i^c, \\
\dot{I}_i^{c'} &= \bar{m}_i \gamma_{I^c} I_i^c - \gamma_{I^{c'}} I_i^{c'} \\
\dot{I}_i^m &= m_i \gamma_{I^c} I_i^c, \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^{s'}} I_i^{s'} + \gamma_{I^{h'}} I_i^{h'} + \gamma_{I^{c'}} I_i^{c'}. \\
\dot{N}_i &= \sigma_i - m_i \gamma_{I^c} I_i^c
\end{aligned} \tag{27}$$

The rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^M \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} + C_{ij}^h \frac{I_j^h}{N_j} \right), \tag{28}$$

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. The above class SEAI8R can be instantiated in PyRoss using `pyross.deterministic.SEAI8R`. A detailed notebook is present in the examples folder of PyRoss [6].

XIII. SEAIRQ

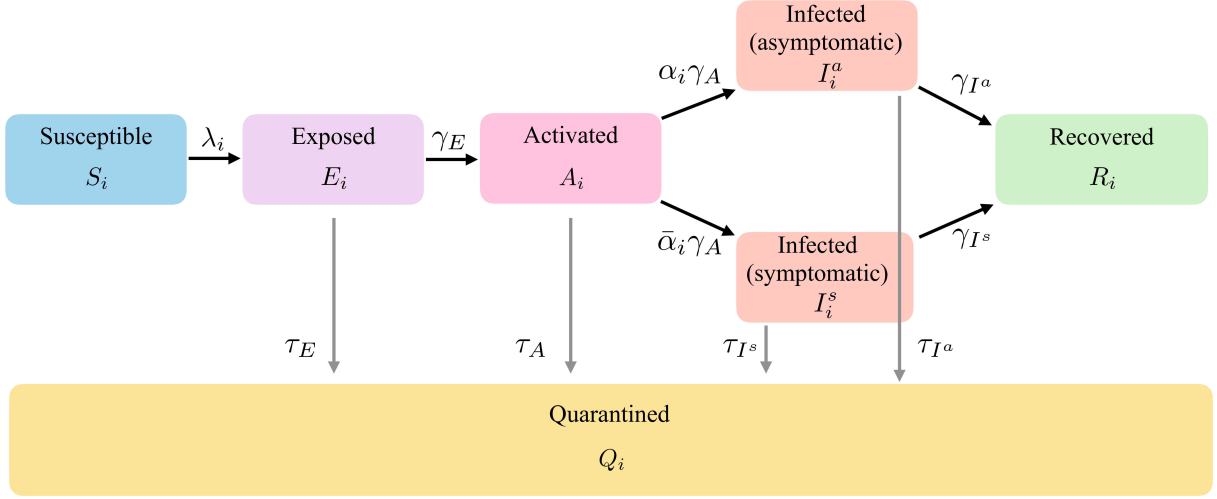
We now introduce the Q -class, which represents people who have been tested and put into quarantine (and can therefore not infect anyone else). This point of Q -class is to model proper contact tracing. The dynamics of the SEAIRQ model is given as:

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t)S_i \\
\dot{E}_i &= \lambda_i(t)S_i - (\gamma_E + \tau_E)E_i \\
\dot{A}_i &= \gamma_E E_i - (\gamma_A + \tau_A)A_i \\
\dot{I}_i^a &= \alpha_i \gamma_A A_i - (\gamma_{I^a} + \tau_{I^a})I_i^a \\
\dot{I}_i^s &= \bar{\alpha}_i \gamma_A A_i - (\gamma_{I^s} + \tau_{I^s})I_i^s \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s \\
\dot{Q}_i &= \tau_S S_i + \tau_E E_i + \tau_A A_i + \tau_{I^s} I_i^s + \tau_{I^a} I_i^a
\end{aligned} \tag{29}$$

The rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^M \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^a \frac{A_j}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} \right), \tag{30}$$

Here τ_{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 τ_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

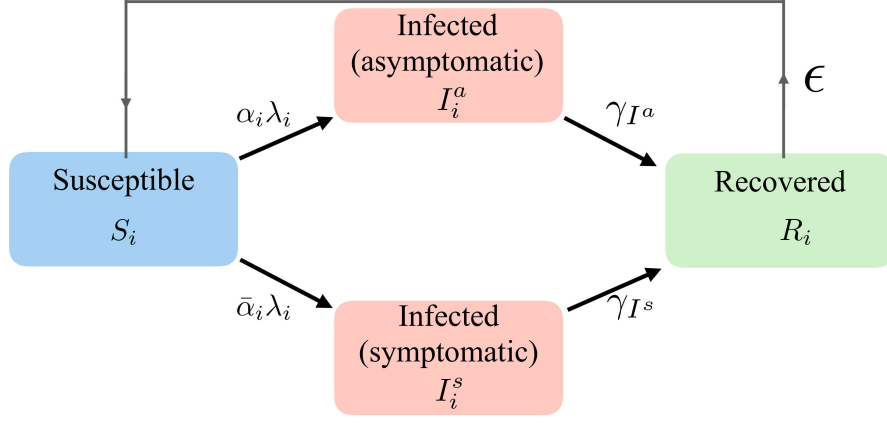


Step	\mathbf{r}_ξ	w_ξ
$S + A, I^a, I^s \rightarrow E + A, I^a, I^s$	$(-1, 1, 0, 0, 0, 0, 0)$	$\lambda_A^a n_S, \lambda_I^a n_S, \lambda_I^s n_S$
$S \rightarrow Q$	$(-1, 0, 0, 0, 0, 1, 0)$	$\tau_S n_S$
$E \rightarrow A$	$(0, -1, 1, 0, 0, 0, 0)$	$\gamma_E n_E$
$E \rightarrow Q$	$(0, -1, 0, 0, 0, 1, 0)$	$\tau_E n_E$
$A \rightarrow I^a$	$(0, 0, -1, 1, 0, 0, 0)$	$\alpha \gamma_A n_A$
$A \rightarrow I^s$	$(0, 0, -1, 0, 1, 0, 0)$	$\bar{\alpha} \gamma_A n_A$
$A \rightarrow Q$	$(0, 0, -1, 0, 0, 1, 0)$	$\tau_A n_A$
$I^a \rightarrow Q$	$(0, 0, 0, -1, 0, 1, 0)$	$\tau_{I^a} n_{I^a}$
$I^a \rightarrow R$	$(0, 0, 0, -1, 0, 0, 1)$	$\gamma_{I^a} n_{I^a}$
$I^s \rightarrow Q$	$(0, 0, 0, 0, -1, 1, 0)$	$\tau_{I^s} n_{I^s}$
$I^s \rightarrow R$	$(0, 0, 0, 0, -1, 0, 1)$	$\gamma_{I^s} n_{I^s}$

Table XIII. **Schematics of the SEAIRQ model, elementary reaction steps and their rates.** The parameters for this model are: $\theta(\alpha_i, \beta, \gamma_E, \gamma_A, \gamma_{I^a}, \gamma_{I^s}, \tau_E, \tau_A, \tau_{I^a}, \tau_{I^s})$. Elementary reaction steps and their rates for the SEAIRQ model. The reaction takes the state $\mathbf{n} = (n_S, n_E, n_A, n_{I^a}, n_{I^s}, n_Q, n_R)$ to the state $\mathbf{n} + \mathbf{r}_\xi$ for $M = 1$. In addition to the infection rates λ_I^a and λ_I^s , see Table V on page 5, we define $\lambda_A^a = \beta C^a n_A / N$. Thus, for this simplified model we can write for the total rate of infection, $(??)$, $\lambda = \lambda_A^a + \lambda_I^a + \lambda_I^s$.

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.

Here τ_{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 τ_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. The above class SEAIRQ can be instantiated in PyRoss using `pyross.deterministic.SEAIRQ`. A detailed notebook is present in the examples folder of PyRoss [6].



Step	\mathbf{r}_ξ	w_ξ
$S + I^a \rightarrow 2I^a$	$(-1, 1, 0, 0)$	$\alpha \lambda_I^a n_S$
$S + I^a \rightarrow I^s + I^a$	$(-1, 0, 1, 0)$	$\bar{\alpha} \lambda_I^a n_S$
$S + I^s \rightarrow I^a + I^s$	$(-1, 1, 0, 0)$	$\alpha \lambda_I^s n_S$
$S + I^s \rightarrow 2I^s$	$(-1, 0, 1, 0)$	$\bar{\alpha} \lambda_I^s n_S$
$I^a \rightarrow R$	$(0, -1, 0, 1)$	$\gamma_{I^a} n_{I^a}$
$I^s \rightarrow R$	$(0, 0, -1, 1)$	$\gamma_{I^s} n_{I^s}$
$R \rightarrow S$	$(1, 0, 0, -1)$	ϵn_R

Table XIV. **Schematics of the SIRS model, elementary reaction steps and their rates.** The parameters for this model are: $\theta(\alpha_i, \beta, \gamma_{I^a}, \gamma_{I^s}, \epsilon)$. Elementary reaction steps and their rates for the non-age-structured SIRS model. The reaction takes the state $\mathbf{n} = (n_S, n_{I^a}, n_{I^s}, n_R)$ to the state $\mathbf{n} + \mathbf{r}_\xi$. For this simplified model the sum in λ_i , (6), becomes trivial. Thus, let's define $\lambda_I^a = \beta C^a n_{I^a} / N$ and $\lambda_I^s = \beta C^s n_{I^s} / N$ such that $\lambda = \lambda_I^a + \lambda_I^s$. This can be easily generalized to the age-structured model.

XIV. SIIRS

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:

$$\begin{aligned}
 \dot{S}_i &= -\lambda_i(t) S_i + \sigma_i + \epsilon(\gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s) \\
 \dot{I}_i^a &= \alpha_i \lambda_i(t) S_i - \gamma_{I^a} I_i^a + l_i \\
 \dot{I}_i^s &= \bar{\alpha}_i \lambda_i(t) S_i - \gamma_{I^s} I_i^s \\
 \dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s \\
 \dot{N}_i &= \sigma_i + l_i
 \end{aligned} \tag{31}$$

Here ϵ is fraction of recovered who is susceptible. σ_i denotes of the arrival of new susceptibles, while l_i are new asymptomatic infectives. This means that N_i is now dynamical. The rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^M \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} \right), \tag{32}$$

The above class SIRS can be instantiated in PyRoss using `pyross.deterministic.SIRS`. A detailed notebook is present in the examples folder of PyRoss [6].

XV. WHAT ELSE ?

If the plethora of models described in the preceding sections are not enough, then PyRoss provides the additional class `pyross.deterministic.Spp` (pronounced “*S plus plus*”), which has the ability to simulate any generic compartmental model. The model is specified by providing a Python dictionary, and supports age-differentiated parameters. For example the SIR model would be:

```
model_spec = {
    "classes" : ["S", "I", "R"],

    "S" : {
        "linear" : [],
        "infection" : [ ["I", "-beta"] ]
    },

    "I" : {
        "linear" : [ ["I", "-gamma"] ],
        "infection" : [ ["I", "beta"] ]
    },

    "R" : {
        "linear" : [ ["I", "gamma"] ],
        "infection" : []
    }
}
```

Currently, the `Spp` class supports the two types of terms which all the compartmental models above share: linear terms and infection terms. Future incarnations of the class could be extended to simulate any generic model of the form

$$\sum_{i=1}^{M \times L} f_i^\xi Y_i \rightarrow \sum_{i=1}^{M \times L} g_i^\xi Y_i$$

where the rates could be both time and state dependent.

Note that `pyross.deterministic.Spp` is designed with generality rather than optimality in mind. A model implemented using `pyross.deterministic.Spp` will in general perform worse than any of the corresponding hard-coded classes above.

-
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 - [2] M. J. Keeling and P. Rohani, *Modeling infectious diseases in humans and animals* (Princeton University Press, 2011).
 - [3] S. Towers and Z. Feng, “Social contact patterns and control strategies for influenza in the elderly,” *Math. Biosci.* **240**, 241–249 (2012).
 - [4] N. M. Ferguson *et al.*, “Strategies for mitigating an influenza pandemic,” *Nature* **442**, 448–452 (2006).
 - [5] Rajesh Singh and R Adhikari, “Age-structured impact of social distancing on the covid-19 epidemic in india,” arXiv preprint arXiv:2003.12055 (2020).
 - [6] “<https://github.com/rajeshrinet/pyross>,” .