Structured compartment models of infection in Python

In this document we describe the implementations of age-structured epidemiological compartment models in PyRoss. The basic variable in this class of models is a metapopulation labeled by its epidemiological state (susceptible, infectious, removed, etc) and additional attributes like age, gender, geographic location and so on. The additional attributes are what comprise the "structure" of the model. Currently, PyRoss supports the models with susceptible (S), infected (I), exposed (E), activated (A), quarantined (Q) and removed (R) epidemiological states. Additionally, the infectious class can be subdivided into k-stages. The progress of these variables in time are described by chemical master equations and, when compartmental fluctuations (CME) are small, by ordinary differential equations (ODE). A hybrid method is also possible which switches from CME to ODE when the population reaches a user defined threshold, at which point it is assumed that random fluctuations are a negligible percentage of the total population. These integration methods build the foundation of PyRoss, upon which investigation into the effects of control such as self-isolation or forecasting made from real world data can be performed.

PyRoss takes the inputs - age, contact structure and an epidemiological compartment model - to simulate the deterministic and stochastic trajectories. The age [1] and contact structures [2] can be obtained from published data. The demographic parameters which determine contact matrices, together with their uncertainties, will be discussed elsewhere. In this work, we assumed they are user-supplied. In what follows, I-11, we describe various models available in PyRoss with increasing complexity. We also provide a class to implement a generic user-defined compartment model in XII.

I. SIR

We first present the well studied SIR model, where 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, $N_i = S_i + I_i + R_i$ [3–7]. 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

$$N = \sum_{i=1}^{M} N_i \tag{1}$$

remain constant in time. With these assumptions the progress of the epidemic is governed by the age-structured SIR model. Figure 1 shows the schematic. The deterministic limit of the SIR model is given by the ODE:

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

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

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

where β is the probability of infection on contact (assumed intrinsic to the pathogen) . We take the age-independent removal 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 SIR model can be improved by adding more epidemiological states as we describe below. Addition epidemiological states, like exposed (E), where the individual has contracted the diseases but is not infectious, or quarantined (Q), where the individual has contracted the disease, is infectious, but cannot spread contagion because of confinement, may be necessary for a better-resolved description. Despite these limitations, the SIR model and its age-structured variant provide the most parsimonious description of infectious disease and provide a null model against which all others must be compared.

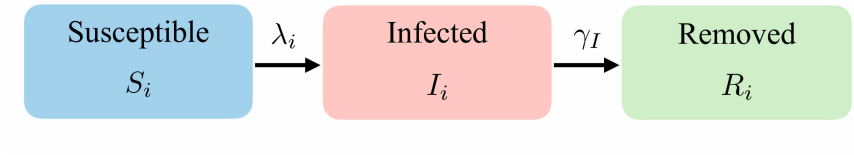

Figure 1. **Schematic of the SIR model.** The parameters for this model are: $\boldsymbol{\theta} = (\beta, \gamma_I)$. The class SIR can be instantiated in PyRoss using `pyross.deterministic.SIR`.

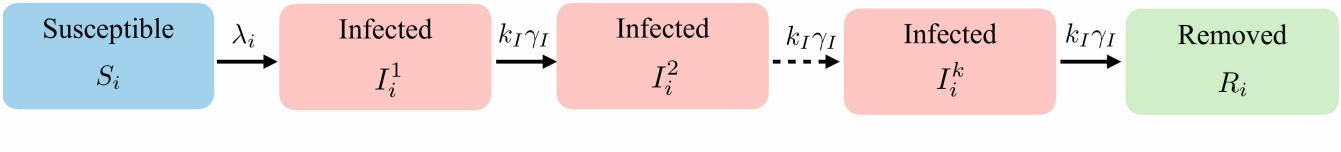

Figure 2. **Schematic of the SIR with stages (SIkR) model.** The parameters for this model are: $\boldsymbol{\theta} = (k_I, \beta, \gamma_I)$. The class SIkR can be instantiated in PyRoss using `pyross.deterministic.SIkR`.

II. SIR WITH STAGES (SIKR)

The SIR model considers only three mutually exclusive epidemiological states: S, I, R. This leads to an exponentially distributed residence time in the infectious state. Within the compartment framework, the simplest way to make infectious period distributions more realistic is to use stages (k stages of infectious) [8]. The model SIR with stages (SIkR) is obtained by allowing I class is the SIR to have k-stages [8]. The SIkR model then has an infectious period with Erlang, Gamma distributions with integer shape parameter, distribution [9–11]. The number of states k can be adjusted to match empirically observed infectious periods. Figure 2 shows the schematic. The deterministic limit of the SIkR model is given as

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t) S_i, \\
\dot{I}_i^1 &= \lambda_i(t) S_i - k_I\gamma_I I_i^1, \\
&\vdots \\
\dot{I}_i^k &= k_I\gamma_I I_i^{k-1} - k_I\gamma_I I_i^k, \\
\dot{R}_i &= k_I\gamma_I I_i^k.
\end{aligned} \tag{3}$$

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

$$\lambda_i(t) = \beta \sum_{j=1}^{M} \sum_{n=1}^{k} C_{ij}(t) \frac{I_j^n}{N_j}, \tag{4}$$

III. SIIR

We now extend the classic SIR model to an SIIR model, where the infective class has been divided in asymptomatic I_i^a and symptomatic I_i^s. We assume that the rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^{M} \left(C_{ij}^a(t) \frac{I_j^a}{N_j} + C_{ij}^s(t) \frac{I_j^s}{N_j} \right), \quad i, j = 1, \dots M \tag{5}$$

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 assume that symptomatic infectives reduce their contacts

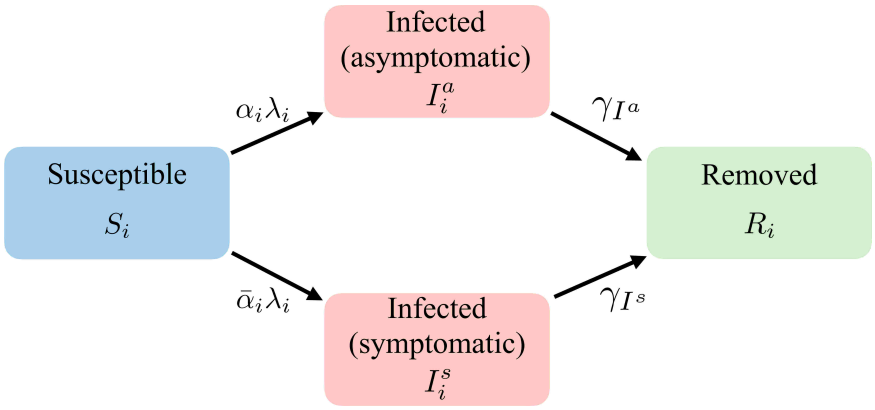

Figure 3. **Schematic of the SIIR model.** The parameters for this model are: $\boldsymbol{\theta} = (\alpha_i, \beta, \gamma_{I^a}, \gamma_{I^s})$. The class SIIR can be instantiated in PyRoss using `pyross.deterministic.SIR`. Please note that both SIIR and SIR have been implemented as `pyross.deterministic.SIR` in PyRoss, as it possible to go from one to another by correct choice of parameters.

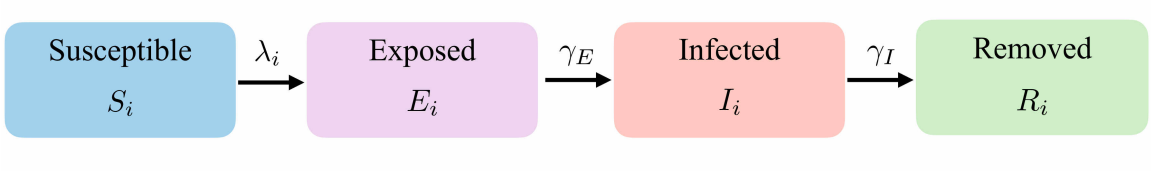

Figure 4. **Schematic of the SEIR model.** The parameters for this model are: $\boldsymbol{\theta} = (\beta, \gamma_I, \gamma_E)$. The class SEIR can be instantiated in PyRoss using `pyross.deterministic.SEIR`.

compared to asymptomatic infectives and set $C^s_{ij} = f^s C^a_{ij} \equiv f^s C_{ij}$, where $0 \leq f^s \leq 1$ is the proportion of contacts that are now avoided by these self-isolating individuals (allowing also for compliance rates)

With these assumptions the progress of the epidemic is governed by the age-structured SIIR model. Figure 3 shows the schematic. The deterministic limit is given as,

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t) S_i, \\
\dot{I}^a_i &= \alpha_i \lambda_i(t) S_i - \gamma_{I^a} I^a_i, \\
\dot{I}^s_i &= \bar{\alpha}_i \lambda_i(t) S_i - \gamma_{I^s} I^s_i, \\
\dot{R}_i &= \gamma_{I^a} I^a_i + \gamma_{I^s} I^s_i.
\end{aligned} \tag{6}$$

Here γ_{I^a} is the removal rate for asymptomatic infectives, γ_{I^s} is the removal rate for symptomatic infectives, α_i is the fraction of asymptomatic infectives.

IV. SEIR

The SIR model does not model the incubation period of a virus. This can be included by adding to the SIR model an exposed E compartment (to give an age-structured SEIR model) [12–15]. Figure 4 shows the schematic of the SEIR model. The deterministic ODE giving its time-evolution is

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t) S_i, \\
\dot{E}_i &= \lambda_i(t) S_i - \gamma_E E_i \\
\dot{I}_i &= \gamma_E E_i - \gamma_I I_i, \\
\dot{R}_i &= \gamma_I I_i.
\end{aligned} \tag{7}$$

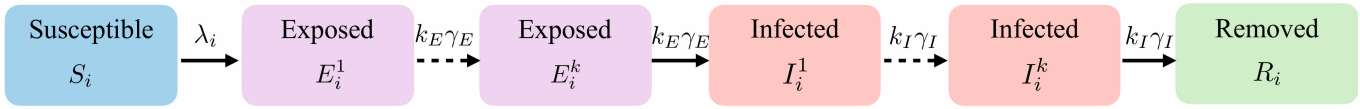

Figure 5. **Schematic of the SEIR with stages (SEkIkR) model.** The parameters for this model are: $\boldsymbol{\theta} = (k_I, k_E, \beta, \gamma_I, \gamma_E)$. The class SEkIkR can be instantiated in PyRoss using `pyross.deterministic.SEkIkR`.

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

$$\lambda_i(t) = \beta \sum_{j=1}^{M} \left(C_{ij}(t) \frac{I_j}{N_j} \right), \quad i, j = 1, \dots M \tag{8}$$

V. SEIR WITH STAGES (SEKIKR)

The SEIR model considers only four mutually exclusive epidemiological states: S, E, I, R. This leads to an exponentially distributed residence time in the incubating and infectious state. We use the same resolution as in SIkR model, see II, to obtain a more realistic distribution of incubation and infectious times. The SEIR model can be extended to an age-structured $k-$staged SEkIkR model. Figure 5 shows the schematic. The ODE describing SEIR is:

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

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

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

VI. SEIIR

We now extend the classic SIR model to an SIIR model, where the infective class has been divided in asymptomatic I_i^a and symptomatic I_i^s. We assume that the rate of infection of a susceptible individual in age group i is

$$\lambda_i(t) = \beta \sum_{j=1}^{M} \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} \right), \tag{11}$$

The deterministic dynamics is given by the following ODE:

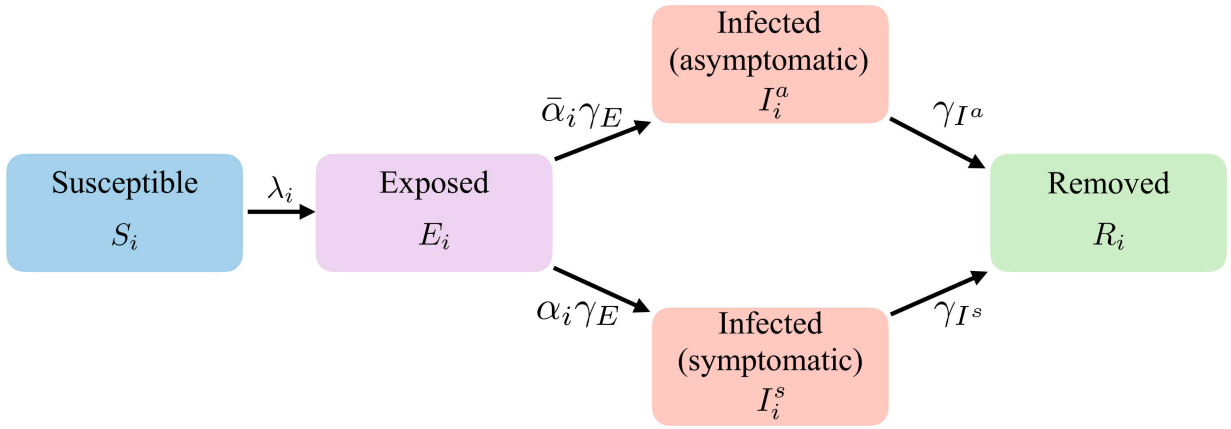

Figure 6. **Schematic of the SEIIR model.** The parameters for this model are: $\boldsymbol{\theta} = (\alpha_i, \beta, \gamma_E, \gamma_{I^a}, \gamma_{I^s})$. The class SEIIR can be instantiated in PyRoss using `pyross.deterministic.SEIR`. Please note that both SEIIR and SEIR have been implemented as `pyross.deterministic.SEIR` in PyRoss as it possible to go from one to another by correct choice of parameters.

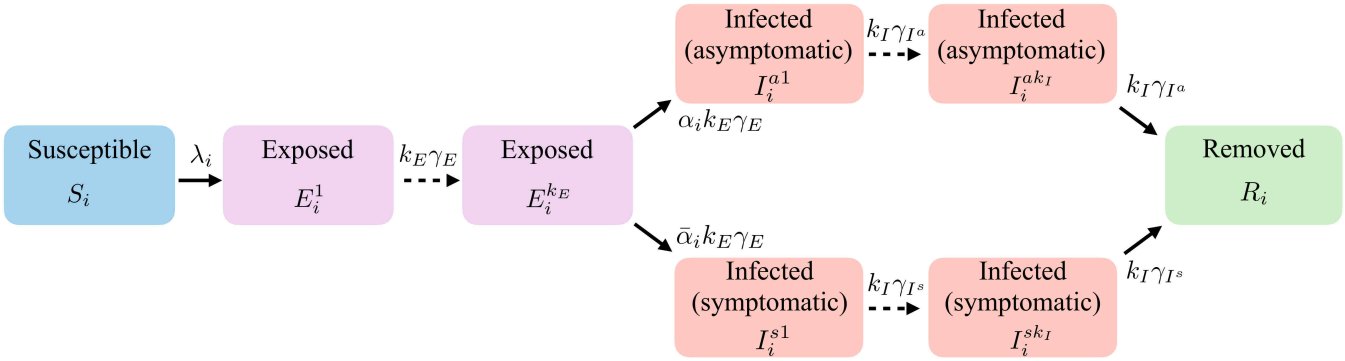

Figure 7. **Schematic of the SEIIR with stages (SEkIkIkR) model.** The parameters for this model are: $\boldsymbol{\theta} = (k_I, k_E, \alpha_i, \beta, \gamma_{I^a}, \gamma_{I^s}, \gamma_E)$. The class SEkIkIkR can be instantiated in PyRoss using `pyross.deterministic.SEkIkIkR`.

$$
\begin{aligned}
\dot{S}_i &= -\lambda_i(t) S_i, \\
\dot{E}_i &= \lambda_i(t) S_i - \gamma_E E_i \\
\dot{I}_i^a &= \alpha_i \gamma_E E_i - \gamma_{I^a} I_i^a, \\
\dot{I}_i^s &= \bar{\alpha}_i \gamma_E E_i - \gamma_{I^a} I_i^s, \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s.
\end{aligned}
\tag{12}
$$

VII. SEIIR WITH STAGES (SEKIKIKR)

We now extend the SEIIR model to have stages in exposed, asymptomatic infectives, and symptomatic infectives classes. This is the the same resolution as in SIkR model, see II, to obtain a more realistic distribution of incubation and infectious times. Figure 7 shows the schematic. The deterministic dynamics is given as

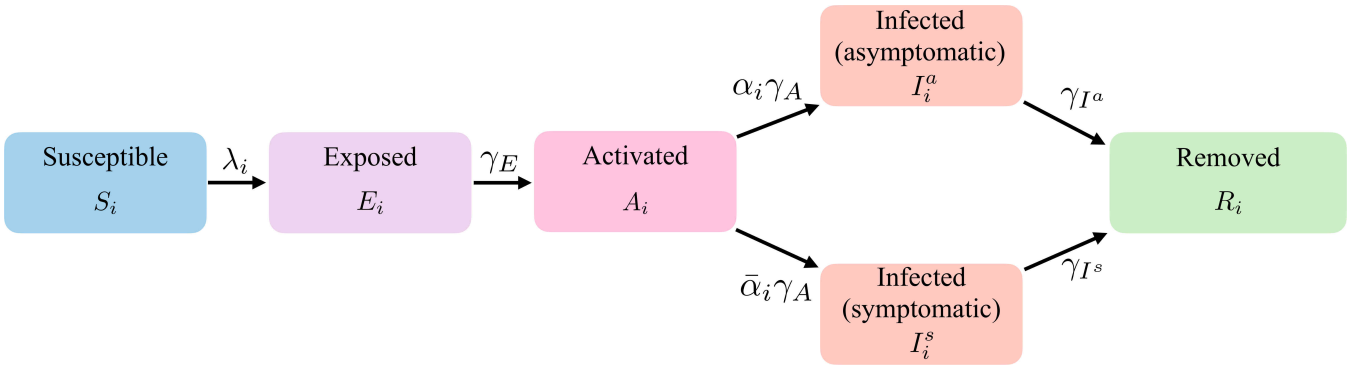

Figure 8. **Schematic of the SEAIIR model.** The parameters for this model are: $\boldsymbol{\theta} = (\alpha_i, \beta, \gamma_E, \gamma_A, \gamma_{I^a}, \gamma_{I^s})$. The class SEAIIR can be instantiated in PyRoss using `pyross.deterministic.SEAIR`.

$$
\begin{aligned}
\dot{S}_i &= -\lambda_i(t) S_i, \\
\dot{E}_i^1 &= \lambda_i(t) S_i - k_E \gamma_E E_i^1 \\
&\vdots \\
\dot{E}_i^{k_E} &= k_E \gamma_E E_i^{k_E - 1} - k_E \gamma_E E_i^{k_E} \qquad (13) \\
\dot{I}_i^{a1} &= \alpha_i k_E \gamma_E E_i^k - k_I \gamma_{I^a} I_i^{a1}, \\
&\vdots \\
\dot{I}_i^{ak_I} &= k_{I^a} \gamma_{I^a} I_i^{a(k_I - 1)} - k_I \gamma_{I^a} I_i^{ak_I}, \\
\dot{I}_i^{s1} &= \bar{\alpha}_i k_E \gamma_E E_i^{k_E} - k_I \gamma_{I^s} I_i^{a1}, \qquad (14) \\
&\vdots \qquad (15) \\
\dot{I}_i^{sk_I} &= k_I \gamma_{I^s} I_i^{s(k_I - 1)} - k_I \gamma_{I^s} I_i^{sk_I}, \qquad (16) \\
\dot{R}_i &= k_I \gamma_{I^a} I_i^{ak_I} + k_I \gamma_{I^s} I_i^{sk_I}.
\end{aligned}
$$

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

$$
\lambda_i(t) = \beta \sum_{j=1}^{M} \sum_{n=1}^{k_I} \left(C_{ij}^a \frac{I_j^{an}}{N_j} + C_{ij}^s \frac{I_j^{sn}}{N_j} \right), \qquad (17)
$$

VIII. SEAIIR

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. The deterministic limit of this case

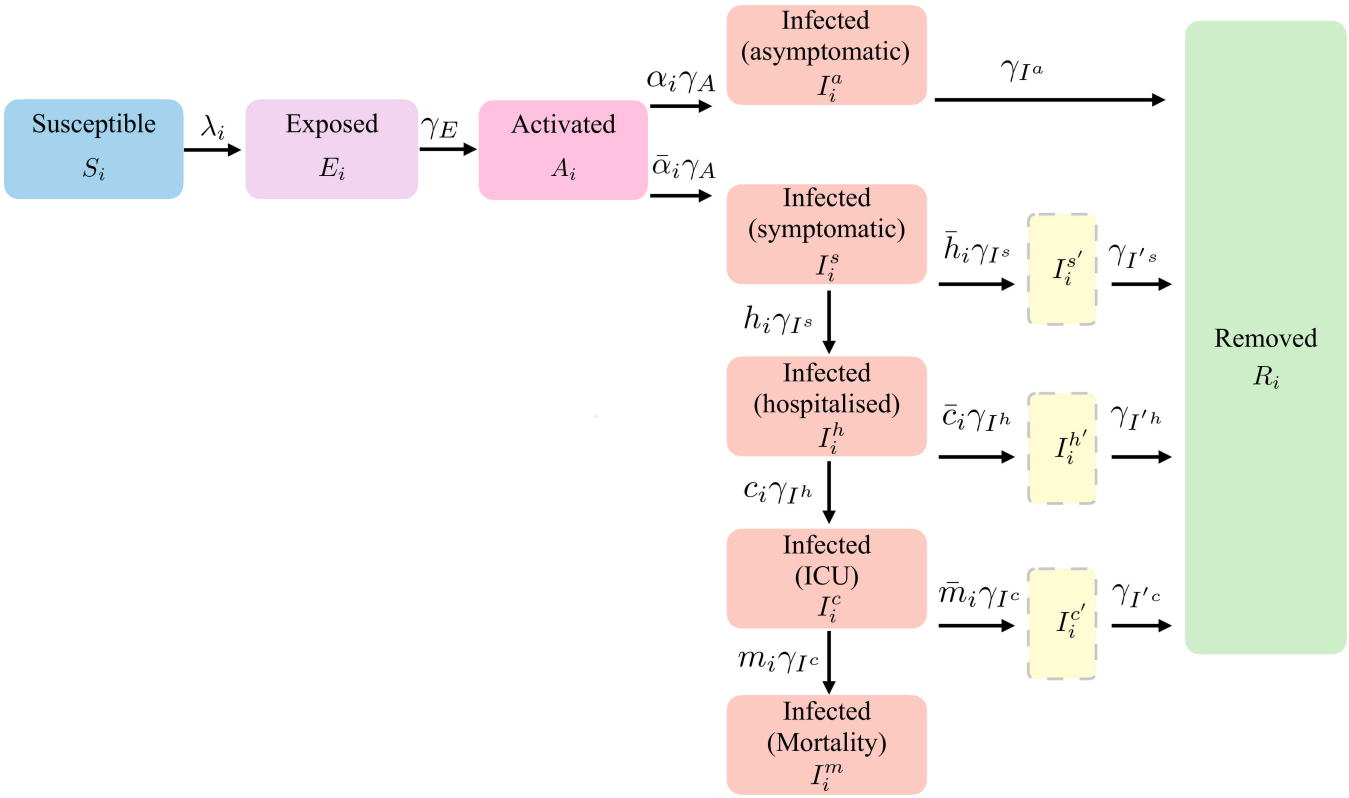

Figure 9. **Schematic of the SEAI8R model.** The class SEAI8R can be instantiated in PyRoss using `pyross.deterministic.SEAI8R`.

$$
\begin{aligned}
\dot{S}_i &= -\lambda_i(t) S_i \\
\dot{E}_i &= \lambda_i(t) S_i - \gamma_E E_i \\
\dot{A}_i &= \gamma_E E_i - \gamma_A A_i \\
\dot{I}_i^a &= \alpha_i \gamma_A A_i - \gamma_{I^a} I_i^a \\
\dot{I}_i^s &= \bar{\alpha}_i \gamma_A A_i - \gamma_{I^s} I_i^s \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s
\end{aligned}
\tag{18}
$$

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

$$
\lambda_i(t) = \beta \sum_{j=1}^{M} \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^a \frac{A_j}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} \right), \tag{19}
$$

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.

IX. SEAI8R

This model is an extension of the SEAIIR model. There are now six more types of infectives (I_i^h: infectives who are hospitalized, I_i^c: infectives who are in ICU, I_i^m: mortality due to the infection from ICU, $I_i^{s'}$: intermediate stage between symptomatic and removed, $I_i^{c'}$: intermediate stage between hospitalized and removed, and $I_i^{c'}$: intermediate stage between ICU and removed). The intermediate stages are needed to allow for a fast progression of the disease

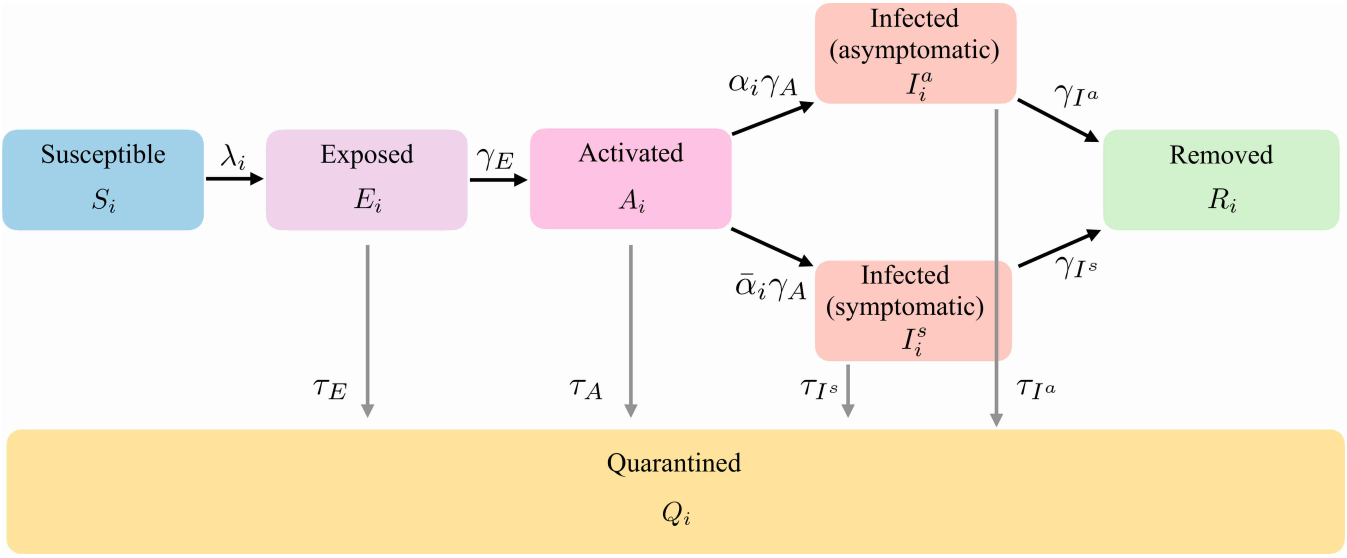

Figure 10. **Schematic of the SEAIIRQ model.** The parameters for this model are: $\boldsymbol{\theta} = (\alpha_i, \beta, \gamma_E, \gamma_A, \gamma_{I^a}, \gamma_{I^s}, \tau_E, \tau_A, \tau_{I^a}, \tau_{I^s})$. The class SEAIIRQ can be instantiated in PyRoss using `pyross.deterministic.SEAIRQ`.

while retaining the longer recovery time and the ratios of people experiencing different levels of severity of the disease. Figure 9 shows the schematic. The deterministic dynamics if given by the following ODE:

$$\begin{aligned}
\dot{S}_i &= -\lambda_i(t)S_i + \sigma_i, \qquad \dot{E}_i = \lambda_i(t)S_i - \gamma_E E_i, \qquad \dot{A}_i = \gamma_E E_i - \gamma_A A_i \\
\dot{I}_i^a &= \alpha_i\gamma_A A_i - \gamma_{I^a} I_i^a, \qquad \dot{I}_i^s = \bar{\alpha}_i\gamma_A A_i - \gamma_{I^s} I_i^s, \qquad \dot{I}_i^{s'} = \bar{h}_i\gamma_{I^s} I_i^s - \gamma_{I^{s'}} I_i^{s'} \\
\dot{I}_i^h &= h_i\gamma_{I^s} I_i^s - \gamma_{I^h} I_i^h, \qquad \dot{I}_i^{h'} = \bar{c}_i\gamma_{I^h} I_i^h - \gamma_{I^{h'}} I_i^{h'}, \qquad \dot{I}_i^c = c_i\gamma_{I^h} I_i^h - \gamma_{I^c} I_i^c, \\
\dot{I}_i^{c'} &= \bar{m}_i\gamma_{I^c} I_i^c - \gamma_{I^{c'}} I_i^{c'}, \qquad \dot{I}_i^m = m_i\gamma_{I^c} I_i^c, \qquad \dot{N}_i = \sigma_i - m_i\gamma_{I^c} I_i^c \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^{s'}} I_i^{s'} + \gamma_{I^{h'}} I_i^{h'} + \gamma_{I^{c'}} I_i^{c'}.
\end{aligned} \tag{20}$$

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

$$\lambda_i(t) = \beta \sum_{j=1}^{M} \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^a \frac{A_j}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} + C_{ij}^s \frac{I_j^{s'}}{N_j} \right), \tag{21}$$

Here $\bar{h}_i = 1 - h_i$, $\bar{m}_i = 1 - m_i$, $C_{ij}^s = f^s C_{ij}^a \equiv f^s C_{ij}$. We note the individuals can be removed at any stage from either of the eight infection classes.

X. SEAIIRQ

This model is an extension of the SEAIIR model. We introduce the Q_i class, which may model individuals who have been tested and put into quarantine (and can therefore not infect anyone else). This point of Q_i class is to model a possible an implementation of contact tracing in PyRoss. Figure 10 shows the schematic. The deterministic dynamics of the SEAIRQ model is given as:

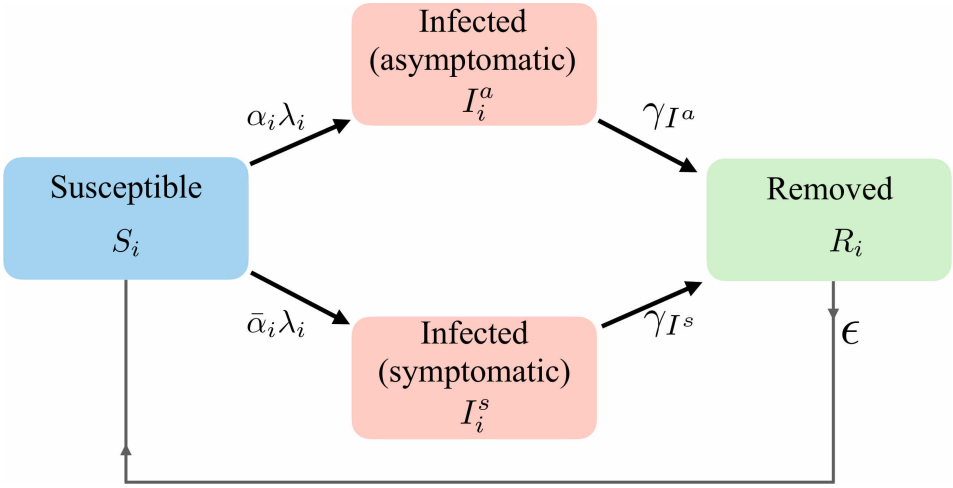

Figure 11. **Schematic of the SIIRS model.** The parameters for this model are: $\boldsymbol{\theta} = (\alpha_i, \beta, \gamma_{I^a}, \gamma_{I^s}, \epsilon)$. The class SIIRS can be instantiated in PyRoss using `pyross.deterministic.SIRS`.

$$
\begin{aligned}
\dot{S}_i &= -\lambda_i(t) S_i \\
\dot{E}_i &= \lambda_i(t) S_i - (\gamma_E + \tau_E) E_i \\
\dot{A}_i &= \gamma_E E_i - (\gamma_A + \tau_A) A_i \\
\dot{I}_i^a &= \alpha_i \gamma_A A_i - (\gamma_{I^a} + \tau_{I^a}) I_i^a \\
\dot{I}_i^s &= \bar{\alpha}_i \gamma_A A_i - (\gamma_{I^s} + \tau_{I^s}) I_i^s \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s \\
\dot{Q}_i &= \tau_S S_i + \tau_E E_i + \tau_A A_i + \tau_{I^s} I_i^s + \tau_{I^a} I_i^a
\end{aligned}
\tag{22}
$$

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

$$
\lambda_i(t) = \beta \sum_{j=1}^{M} \left(C_{ij}^a \frac{I_j^a}{N_j} + C_{ij}^a \frac{A_j}{N_j} + C_{ij}^s \frac{I_j^s}{N_j} \right), \tag{23}
$$

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.

XI. SIIRS

We now extend the age-structured SIR model to allow for removed persons to be susceptible and for change in the population of each age group. Figure 11 shows the schematic. The deterministic dynamics of the resulting SIRS model is:

$$
\begin{aligned}
\dot{S}_i &= -\lambda_i(t) S_i + \sigma_i + \epsilon(\gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s) \\
\dot{I}_i^a &= \alpha_i \lambda_i(t) S_i - \gamma_{I^a} I_i^a + l_i \\
\dot{I}_i^s &= \bar{\alpha}_i \lambda_i(t) S_i - \gamma_{I^a} I_i^s \\
\dot{R}_i &= \gamma_{I^a} I_i^a + \gamma_{I^s} I_i^s . \\
\dot{N}_i &= \sigma_i + l_i
\end{aligned}
\tag{24}
$$

Here ϵ is fraction of removed 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 same as in the SIIR model.

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


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

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

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

Figure 12. **Definition of the *Spp* class.** The *Spp* class can be instantiated in PyRoss using `pyross.deterministic.Spp`.

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


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

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

  "test_pos"  : [ "p_falsepos", "p_truepos", "p_falsepos"] ,

  "test_freq" : [ "tf", "tf", "tf"]
}
```

Figure 13. **Definition of the *SppQ* class.** The *SppQ* class can be instantiated in PyRoss using `pyross.deterministic.SppQ`.

XII. GENERIC USER-DEFINED MODEL

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. As an example, the SIR model, defined in the Spp class, is given in Fig.12.

Currently, the *Spp* class supports the two types of terms which all the compartmental models above share: linear terms and infection terms. The class could be used to simulate any generic age-structured epidemiological compartment model, 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. We also have a class `pyross.deterministic.SppQ` to model constant influx, random testing (without false positives/negatives), and quarantine

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