How to implement deterministic & stochastic SEIR models

This brief description gives some details on how to implement the various SEIR models described in the practical exercises. Given some programming experience there should be enough detail here to get the models up and running! Once you have simulated the examples described below it should be more or less straightforward (depending on your application) to modify the code to implement your own models.

1 The ODE model

One of the most commonly used models of childhood disease is the simple SEIR model presented below. People are considered to be born into a class labeled susceptible (S). On contact with a person who has the disease and is infectious (I), or at some background rate \( \nu \), the susceptible moves into a category which contains those who have the disease but are not yet infectious (E). After a short number of days the person then leaves this exposed category (E) and becomes infectious (I). After another short period the person recovers and moves to the category (R) where they remain until death. The population as a whole is assumed to be constant (N), with births matching deaths. This system is described by the following equations:

\[
\begin{align*}
\frac{dS}{dt} &= mN - mS - bSI - \nu S \\
\frac{dE}{dt} &= bSI + \nu S - mE - aE \\
\frac{dI}{dt} &= aE - mI - gI \\
\frac{dR}{dt} &= gI - mR
\end{align*}
\]

where the total population is

\[N = S + E + I + R\]

and the force of infection is time-varying

\[b = b_0(1 + b_1 \cos(2\pi t)) , \]

where \( t \) is the time in years.

For a sufficiently small time-step \( \delta t \) this system can be solved using the Euler scheme, which simply iterates,

\[
\begin{align*}
S(t + \delta t) &= S(t) + (mN - mS - bSI - \nu S)\delta t \\
E(t + \delta t) &= E(t) + (bSI + \nu S - mE - aE)\delta t \\
I(t + \delta t) &= I(t) + (aE - mI - gI)\delta t \\
R(t + \delta t) &= R(t) + (gI - mR)\delta t
\end{align*}
\]

starting from the initial values \( S(0), E(0), I(0) \& R(0) \) to obtain values at subsequent times.

A typical population is \( N = 10^6 \) and the best fit values of these parameters to a measles data set are \( m = 0.02 , g = 55.0 , a = 50.0 , b_0 = 0.001 , b_1 = 0.28 , \nu = 0.0001 \).
2 The Markovian model

The stochastic version of the SEIR model is defined by the following events and rates (with N=S+E+I+R):

<table>
<thead>
<tr>
<th>Description</th>
<th>Event</th>
<th>Rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth of susceptibles</td>
<td>S → S + 1</td>
<td>mN</td>
</tr>
<tr>
<td>Death of susceptibles</td>
<td>S → S − 1</td>
<td>mS</td>
</tr>
<tr>
<td>Infection</td>
<td>S → S − 1 &amp; E → E + 1</td>
<td>bSI + νS</td>
</tr>
<tr>
<td>Death in exposed class</td>
<td>E → E − 1</td>
<td>mE</td>
</tr>
<tr>
<td>End of latent stage</td>
<td>E → E − 1 &amp; I → I + 1</td>
<td>aE</td>
</tr>
<tr>
<td>Death in infective class</td>
<td>I → I − 1</td>
<td>mI</td>
</tr>
<tr>
<td>End of infectious stage</td>
<td>I → I − 1 &amp; R → R + 1</td>
<td>gI</td>
</tr>
<tr>
<td>Death from recovered class</td>
<td>R → R − 1</td>
<td>mR</td>
</tr>
</tbody>
</table>

Starting from the now integer valued initial conditions S(0), E(0), I(0) & R(0) simulate the process by iterating the following:

(i) Calculate the total event Rate = 2mN + bSI + νS + aE + gI

(ii) Draw a random number from the unit interval y ∼ U(0, 1)

(iii) Set the time increment to be δt = min{(1 − 0.05)/Rate, δt_min}

(iv) The next event is chosen as follows:

Birth of susceptibles if \( y \leq mN\delta t \)

Death of susceptibles else if \( y \leq (mN + mS)\delta t \)

Infection else if \( y \leq (mN + mS + bSI + νS)\delta t \)

Death in exposed class else if \( y \leq (mN + mS + bSI + νS + mE)\delta t \)

End of latent stage else if \( y \leq (mN + mS + bSI + νS + mE + aE)\delta t \)

Death in infective class else if \( y \leq (mN + mS + bSI + νS + mE + aE + mI)\delta t \)

End of infectious stage else if \( y \leq (mN + mS + bSI + νS + mE + aE + mI + gI)\delta t \)

Death from recovered class else if \( y \leq (mN + mS + bSI + νS + mE + aE + mI + gI + mR)\delta t \)

No event occurs otherwise

(v) Update state-space (S(t), E(t), I(t) & R(t)) accordingly and increment time \( t = t + \delta t \)

Note that \( \delta t_{min} \) is chosen so that \( b = b_0(1 + b_1 \cos (2\pi t)) \) remains approximately constant over the interval \( (t, t + \delta t) \)

3 A non-Markovian model

The assumption in the Markovian case described above is that the time an individual spends in a given state is exponentially distributed. However, this is unlikely to be true and is particularly unrealistic in the case of the latent period (the time taken to move from class E to I). To remedy this we will assume that the time spent in the exposed state E is distributed according to \( p(t_{res}) \). When an individual enters the exposed state E at time t we draw its residence time \( t_{res} \sim p(t_{res}) \) and calculate the time it will move to the infective state I as \( t_{end} = t + t_{res} \). Now we proceed as before but setting the parameter \( a = 0 \). In order to implement the transition from the exposed to infectious states we simply check (at each time step) to see when \( t \geq t_{end} \) for each individual in state E, and then update \( (E → E − 1 & I → I + 1) \).
The simplest possible latent period distribution is when every individual spends a fixed time \( t_{\text{lat}} = 1/50 \) in the exposed state. In this case an individual entering the exposed state \( E \) at time \( t \) will leave it a fixed time \( t_{\text{lat}} \) later at \( t_{\text{end}} = t + t_{\text{lat}} \).

4 A simple meta-population model

Consider a lattice \( L \) with \( |L| \) sites. With each site \( k \in L \) we associate a non-spatial (Markovian or non-Markovian) SEIR model, with state variables \( S_k(t), E_k(t), I_k(t) \), and \( R_k(t) \). To connect sites assume that, in addition to within-site infections, externally induced infections at site \( k \) occur due to contact between susceptibles at site \( k \) and infectives at all other sites:

<table>
<thead>
<tr>
<th>Description Event</th>
<th>Rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>External Infection at site ( k ) ( S_k \rightarrow S_k - 1 ) &amp; ( \phi b S_k \sum_{j \neq i} I_j )</td>
<td></td>
</tr>
<tr>
<td>( E_k \rightarrow E_k + 1 )</td>
<td></td>
</tr>
</tbody>
</table>

The parameter \( \phi \) thus controls the relative level of contact within and between sites: \( \phi = 1 \) means uniform contact between and within sites; and \( \phi = 0 \) means no contact between sites.

The spatial process is simulated as before except that now the total rate is calculated by summing over all events at each site (i.e. now including \( \phi b S_k \sum_{j \neq i} I_j \)) and over all sites.

5 A more general spatial Markovian model

A spatially explicit stochastic version of the SEIR model is defined by the following events and rates with sites indexed by \( k = 1, \ldots, |L| \), and state variables \( N_k = S_k + E_k + I_k + R_k \)

<table>
<thead>
<tr>
<th>Description Event</th>
<th>Rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth of susceptibles ( S_k \rightarrow S_k + 1 )</td>
<td>( m N_k )</td>
</tr>
<tr>
<td>Death of susceptibles ( S_k \rightarrow S_k - 1 )</td>
<td>( \mu_s S_k )</td>
</tr>
<tr>
<td>Infection ( S_k \rightarrow S_k - 1 &amp; E_k \rightarrow E_k + 1 )</td>
<td>( b S_k I_k + \nu S_k + \phi b S_k \sigma_{j=1}^{[L]} I_j F_{jk} )</td>
</tr>
<tr>
<td>Death in exposed class ( E_k \rightarrow E_k - 1 )</td>
<td>( \mu_E E_k )</td>
</tr>
<tr>
<td>End of latent stage ( E_k \rightarrow E_k - 1 &amp; I_k \rightarrow I_k + 1 )</td>
<td>( a E_k )</td>
</tr>
<tr>
<td>Death in infective class ( I_k \rightarrow I_k - 1 )</td>
<td>( \mu_I I_k )</td>
</tr>
<tr>
<td>End of infectious stage ( I_k \rightarrow I_k - 1 &amp; R_k \rightarrow R_k + 1 )</td>
<td>( g I_k )</td>
</tr>
<tr>
<td>Death from recovered class ( R_k \rightarrow R_k - 1 )</td>
<td>( \mu_R R_k )</td>
</tr>
</tbody>
</table>

Thus in this model infection can occur due to a background contamination at rate \( \nu \), within a site due to secondary infection, or by secondary infection at a distance and governed by the infection dispersal kernel \( F_{jk} \). Where \( F_{jk} = F(|x_j - x_k|) = F(y_{jk}) \) is typically a function of the distance between sites \( j \) and \( k \) which can be located at arbitrary points in space denoted by \( x_j \) and \( x_k \) respectively. \( F(y) \) is often assumed to decay exponentially, or as a power-law with distance; the latter producing a more patchy distribution of clusters of infected sites.

Now, as noted above this system can be simulated by extending the algorithm described earlier for the non-spatial process, where now the summation runs over all events and over each site.