Modelling with Matlab Assignment 4

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1 Question 1

Comes in two parts, Part A and Part B

1.1 Part A

This is an SIR model based on the Gillespie algorithm, which updates a Master Equation of transition probabilities for a set of variables. In this case there are six variables/events to model: birth, infection, recovery from infection, death of susceptible, death of infected, death of recovered.
The three files for the basic SIR model are:

- A41: renamed Run_Sim.m, as it sets up and initial values, passes them to subroutines, and plots results. It Runs the Simulation.
- A42: renamed Loop_Counter.m, since that's pretty much all it does
- A43: renamed ME_Update.m, since it does the actual work of updating the population vector for the loop counter according to a birth-death process. ME Stands for Master Equation.

1.2 Part B

To use the files: They are set up to run. Open Run_Sim.m in the matlab editor and click on the green arrow.

What they do: The files simulate an SIR (Susceptible, Infected, Recovered) model with three birth death processes working on three populations: Susceptibles(X), Infected(Y), and Recovered(Z) with rate parameters given in the file ME_Update.m

Notes on birth death processes can be found (among many other places) in the course notes for Stochastic Processes taught at the University of York. I will refer to the 2015/2016 version of those notes and the notation they use for this assignment. They can be found here:
https://maths.york.ac.uk/moodle/pluginfile.php/86069/mod_resource/content/1/notes.pdf
Using the definitions, results and notation in (87),(88),(89) on page 24 of this document, ME_Update.m could be said to describe three equations of the form:

$$\frac{d}{dt}P_{ij}(t) = \lambda_{j-1}P_{i,j-1} + \mu_{j+1}P_{i,j+1} - (\lambda_j + \mu_j)X_{i,j}$$

Where $P_{i,j}$ is the transition probability given in definition(87) applied to the populations $N(t) = X(t), Y(t)$ and $Z(t)$ and the rates are as follows:
For Susceptibles $X(t)$: "birth" rate $\lambda_j = CC * N$, where N is the total population, is the actual birth rate; the "death" rate here is the rate of infection **plus** the rate susceptibles die: $\mu_j = AA * X * Y/N + CC * X$.
For Infected $Y(t)$: "birth" rate $\lambda_j = AA * X * Y/N$ is the rate of infection. Death rate $\mu_j = (BB + CC)Y$ is the rate of recovery plus the rate infected die,
For Recovered$Z(t)$: "birth" rate $\lambda_j = BB * Y$ is the recovery rate. Death rate $\mu_j = CC * Z$ is the rate at which recovered individuals die.

The model can be written as three separate master equations with interconnected terms or combined into a single master equation. This is not a deterministic ODE model, the birth-death process it describes is a Markov process and the sample paths generated are different every time the model is run. Examples in figure 1:

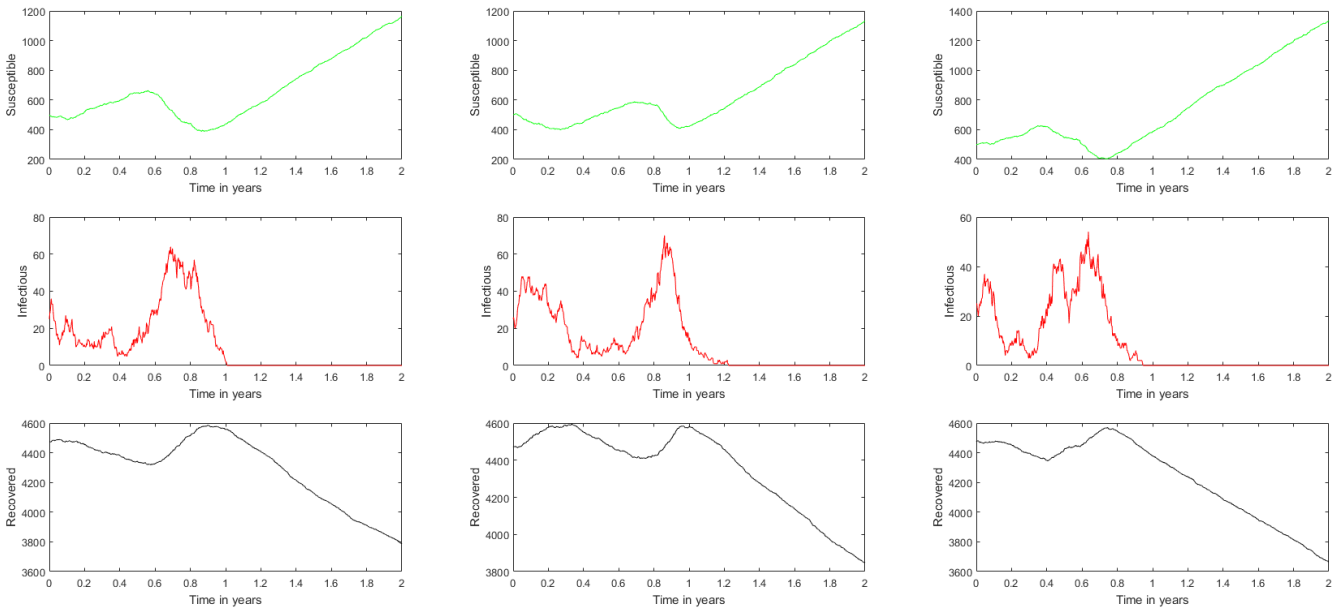

Figure 1: Three sample paths for Run_Sim.m showing the solution is nondeterministic.

The figures are easy to read and speak for themselves: notice that once an individual is recovered in this model they become immune and cannot be reinfected. This could be altered easily for other models.
Addendum: After a quick look at Allen(2017) which I reference in question 2 below, it occurs to me that you *could approximate* the above birth-death process by a deterministic ODE model. If you were to do that, the model would look like this:

$$N = X + Y + Z$$

$$\frac{dX}{dt} = CC * N - CC * X - \frac{AA * X * Y}{N}$$

$$\frac{dY}{dt} = \frac{AA * X * Y}{N} - (BB + CC) * Y$$

$$\frac{dZ}{dt} = BB * Y - CC * Z$$

2 Question 2

Comes in two subsections, Part A and Part B

2.1 Part A

We Now wish to update the model to incorporate the phenomenon known as superspreading, which happens when certain infected individuals, possibly because of compromised immune systems or genetic defects or a secondary infection, are able to cause unusually large numbers of secondary cases.
If $N_1(t)$ is a Poisson process with rate λ_1 and $N_2(t)$ is a Poisson process with rate λ_2, then their sum $N(t) = N_1 + N_2$ is also a Poisson process with rate $\lambda = \lambda_1 + \lambda_2$. We can take advantage of this fact and split the mean rate of infection into two events: average infected individuals with rate $R1$, and superspreading individuals with rate $R2$.
Naively, make 10 percent of the population superspreaders who become infected at 10 times the normal rate. For simplicity, have them recover and die at the same rate as the "average infected".
To implement this, create a new variable Y_s, for the superspreader infected, and an associated increased infection rate R. The best way to illustrate what this looks like mathematically would be to show the deterministic ODE model this now represents:

$$N = X + (Y - Y_s) + Y_s + Z$$

$$\frac{dX}{dt} = CC * N - CC * X - \frac{AA * X * (Y - Ys)}{N} - \frac{R * X * (Ys)}{N}$$

$$\frac{dY}{dt} = \frac{AA * X * (Y - Y_s)}{N} + \frac{R * X * (Y_s)}{N} - (BB + CC) * Y$$

$$\frac{dZ}{dt} = BB * Y - CC * Z$$

2.2 Part B

The modified files are Run_Sim2.m, Loop_Counter2.m and ME_Update2.m all of which were submitted. I've increased the runtime from two years to five years so that you can see we now get periodic outbreak/epidemics for some sample paths (it's difficult to demonstrate more effectively than a single example because the output is still stochastic, if/where the outbreaks will occur vary for each sample path and so plotting several sample paths would simply create an unintelligible mess).

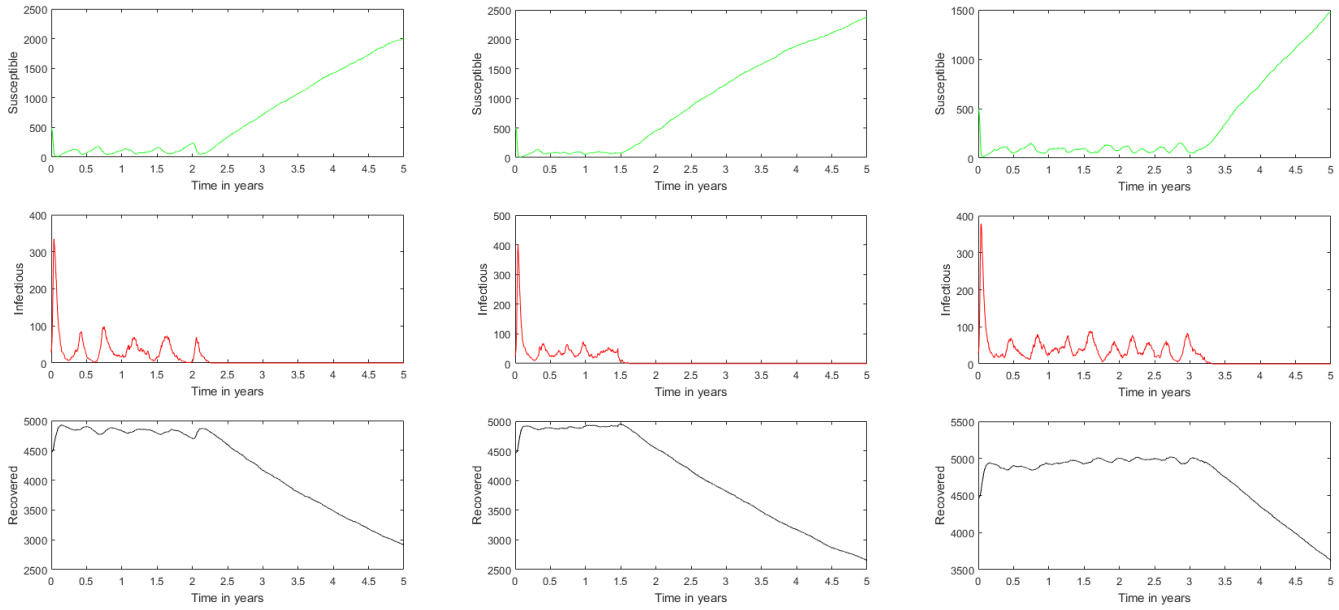

Figure 2: Three sample paths for Run_Sim2.m showing outbreak-like behaviour. Note that the Y axis is much larger than previously, and almost all sample paths begin with a huge spike in infected near t_0