Lecture 1: An introduction to stochastic modelling in continuous time – Epidemic!

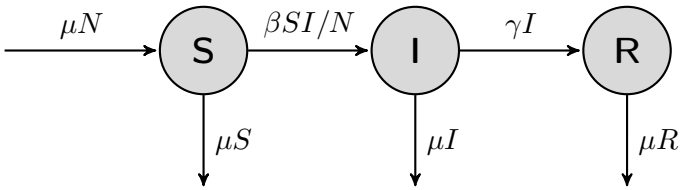
Concepts checklist

At the end of this lecture, you should be able to:

- Describe the difference between *deterministic* and *stochastic* models;
- Understand *why we wish to model* (i.e., understand model *outputs*);
- Appreciate *why stochasticity can be important in modelling*; and,
- Appreciate *why discreteness and stochasticity together can be important in modelling.*

Let's start by considering an outbreak of a disease in a population. For some diseases, each individual in the population can be thought of as being *susceptible* to the disease, *infectious* with the disease, or *recovered* from the disease. For many diseases, for example measles, there is a long period of immunity following infection, meaning that once recovered you can no longer be infected.

This structure can be represented in a *(state) transition diagram* (this is technically not a state transition diagram – you will see why next lecture), with *compartments* representing the number of susceptible (S), infectious (I) and recovered (R) individuals, arrows representing the *events* – additions to, deletions from, or transitions between compartments – and the (instantaneous) *rates* of these events. This (state) transition diagram represents a so-called *compartmental model* of the *process/system.*



One compartmental model that you might specify for this system is a set of ordinary differential equations:

$$\frac{dS}{dt} = \mu(N - S) - \beta SI/N,$$
$$\frac{dI}{dt} = \beta SI/N - (\mu + \gamma)I,$$
$$\frac{dR}{dt} = \gamma I - \mu R,$$

where μ is the per-capita birth/death rate, β is the (effective) transmission rate parameter, γ is the per-capita recovery rate, and N is the population size (i.e., $N = S(0) + I(0) + R(0)$).

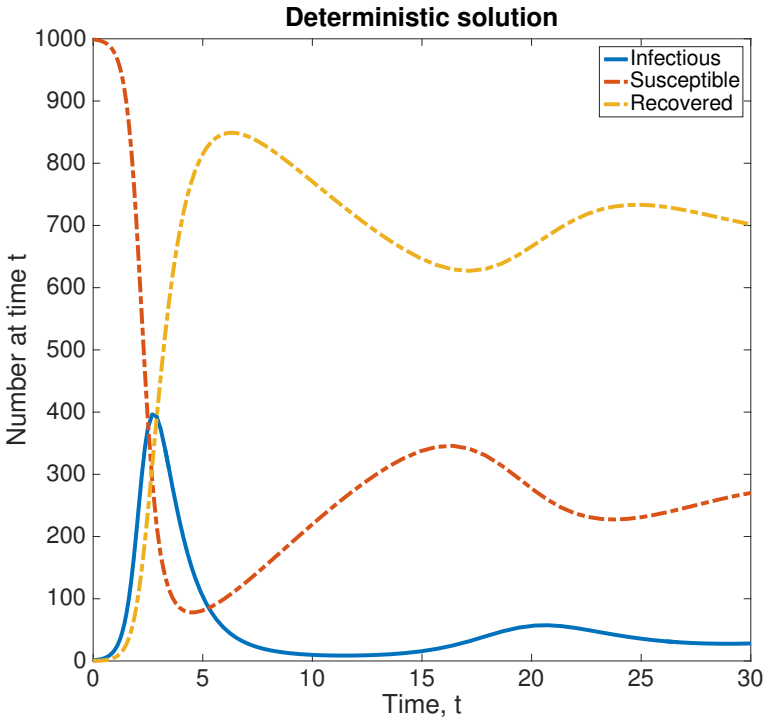


Figure 1: Numerical solution to ODE epidemic model with $\mu = 0.05$, $\beta = 4$, $\gamma = 1$, $N = 1000$, $S(0) = N - 1$, $I(0) = 1$ and $R(0) = 0$ over the period $t = 0$ to $t = 30$.

This is an example of a *deterministic* model of the system. **A deterministic model of a system will predict a single certain outcome, given *inputs* to the system.** Here the inputs are values for the parameters and an initial condition $(S(0), I(0), R(0))$.

The outcome for $\mu = 0.05$, $\beta = 4$, $\gamma = 1$, $N = 1000$, $S(0) = N - 1$, $I(0) = 1$ and $R(0) = 0$ is plotted in Figure 1, from *numerical solution* in MATLAB.

Another compartmental model that one might specify for this system – the type of model that will be the focus of this course – is a *continuous-time Markov chain* (CTMC). This is an example of a *stochastic* model of the system. **A stochastic model of a system will predict a set of possible outcomes, along with their probabilities of occurrence, given the inputs to the system.**

Stochastic, from the Greek *οτόχος* ("stokhos") for *target*, *aim* or *guess*, means *random*; its antonym is *sure*, *certain*, or *deterministic*.

A set of five independent outcomes (*realisations*) for the same parameters as for the deterministic model are plotted in Figure 2, from *numerical simulation* in MATLAB.

Some important features of these realisations, and particularly in comparison to the deterministic (ODE) model outcome, should be noted:

- In some realisations, the infection *fades out*, whereas in the deterministic model we have persistence of the disease. This is important for informing disease management.

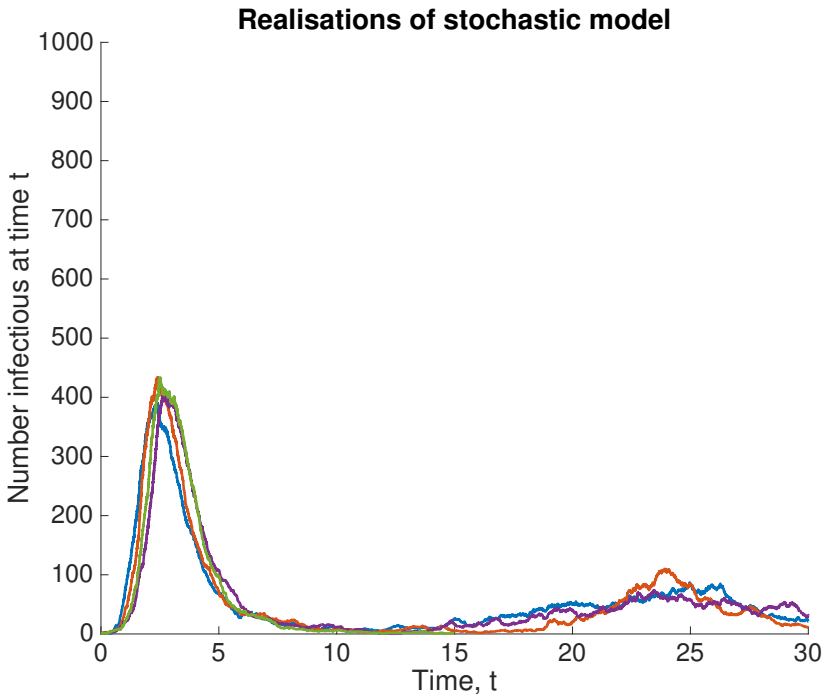


Figure 2: Five realisations of the continuous-time Markov chain epidemic model with $\mu = 0.05$, $\beta = 4$, $\gamma = 1$, $N = 1000$, $S(0) = N - 1$, $I(0) = 1$ and $R(0) = 0$ over the period $t = 0$ to $t = 30$.

- The realisations reflect *discrete* individuals, rather than being modelled as continuous variables. This is more accurate for this (and many other) systems. This also means that stochasticity can be more influential, in particular with respect to phenomena such as fade out.

Some questions that you might use this model to answer are:

- What is the probability of *initial fade out* (i.e., fade out before seeing a large peak)?;
- What is the probability of *epidemic fade out* (i.e., fade out in the trough following the first wave of the infection)?;
- What is the expected time until fade out?; and,
- What is the distribution of the number of infectious individuals at time $t, t \in \mathbb{R}^+$?

The answer to these questions are model *outputs* – the probabilities of the various fade out events, or the expected time to fade out, or the distribution of the number infectious at time $t, t \in \mathbb{R}^+$. Effectively model outputs are what we want to know, i.e., the purpose of modelling is to gain these outputs.

We build mathematical models to translate information that we know, or are willing to assume, into information that we want to know.

So, what is the algorithm used to produce the stochastic realisations? To explain this algorithm, it is helpful to consider the *Events*, their *Rates*, and the *Change in State* that results from each event. The state of this CTMC epidemic model at time t, is $X(t) = (S(t), I(t))$

being the number of susceptible and infectious individuals in the population at time t. The information discussed is given in Table 1.

Event	Rate	Change in State
Birth (of susceptible)	μN	$(S, I) \to (S + 1, I)$
Death of susceptible	μS	$(S, I) \to (S - 1, I)$
Infection	$\beta SI/N$	$(S, I) \to (S - 1, I + 1)$
Removal of infectious	$(\gamma + \mu)I$	$(S, I) \to (S, I - 1)$

Table 1: CTMC epidemic model Events, Rates and Changes in State.

Note, that we have not modelled the number of recovered individuals here, as we are primarily interested in the dynamics of infectious individuals and the rates are only dependent upon S, I and parameters (and not R). Also, note that the two events, death of an infectious and recovery of an infectious, have been combined into a single event – removal of infectious – as the Change in State is identical between these events, and that we have specified the Rate as the sum of the individual rates.

The algorithm essentially operates as follows. Given the current state (S, I), compute the rate of each event and sum these to also get the *total rate* (TR) of seeing an event. Wait an exponentially-distributed amount of time, with mean 1/TR; this is the time of the next event. Choose the event to occur with probability in proportion to the rate of each event; i.e., e.g., the event Death of Susceptible happens with probability (w.p.) $\mu N/\text{TR}$. Update the state according to which event occurs. Repeat until the infection dies out (i.e., $I = 0$), or the time surpasses the desired time period.

The name *random process* should now be clearer. We have considered a continuous series of events that involve randomness in their timing and type.

Some examples of systems which are typically best modelled with random processes are:

- **Engineering:** Telecommunications, computer networks, industrial processes, dams.
- **Biology:** Evolution, genetics, epidemics, species interaction.
- **Chemistry:** Polymerisation, reactions, bonding.
- **Physics:** Quantum mechanics, statistical mechanics.
- **Economics and Finance:** Portfolio management, financial instruments.
- **Management Science:** Call centres, queues and networks of queues.

The focus in this course is on random processes in continuous time ($t \in \mathbb{R}^+$, henceforth simplified to $t \geq 0$) and discrete in state.