MA3227 Numerical Analysis II

Lecture 9: Stochastic SIR Model

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Stochastic SIR Model

Disclaimer

The content of this lecture is not examinable. Its only purpose is to illustrate some of the material presented in Lecture 8.

Stochastic SIR Model

The deterministic SIR (dSIR) model

The *Susceptible-Infected-Recovered* or *SIR model* is a simple mathematical model describing the spread of a contagious disease.

At its simplest, this model takes the form of a system of ODEs

$$\dot{S} = -\tfrac{a}{N} SI, \qquad \dot{I} = \tfrac{a}{N} SI - bI, \qquad \dot{R} = bI,$$

$$S(0) = N - I_0, \qquad I(0) = I_0, \qquad R(0) = 0,$$

where

- $S, I, R : [0, \infty) \to [0, N]$ denote the number of people which are Susceptible to, Infected by and have Recovered from the disease,
- $a, b > 0$ denote the rate of infection and recovery,
- $N \in \mathbb{N}$ denotes the total population size, and
- I_0 denotes the number of initially infected individuals.

I will refer to these equations as the *deterministic* SIR (dSIR) model for reasons which will become clear in a moment.

This model can easily be solved using the `DifferentialEquations.jl` package, see `solve_ode()` and `plot_ode()`.

Stochastic SIR Model

Shortcomings of the deterministic SIR model

Like any model, the deterministic SIR model deviates from reality in some respects. For the purposes of this lecture, the most important of these *modelling errors* are the following.

- Infections and recoveries are assumed to occur at deterministic rates when actually they are random events.
- S, I and R are treated as continuous functions $[0, T] \to [0, N]$ when actually they are step functions $[0, T] \to \{0, \ldots, N\}$.

It turns out that these modelling errors are acceptable if S, I and R are large. The reasons for this are as follows.

- The randomness in each infection and recovery event averages out if many such events happen in a short amount of time.
- If S, I and R are large, then it becomes acceptable to ignore the less significant digits and instead treat these numbers as elements of $\mathbb{R}$.

  Example. We routinely abbreviate statements like "$I = 1532$" to "there are about 1.5 thousand infected individuals".

However, the converses of these arguments imply that the discrete and stochastic nature of infection and recovery events is important if at least one of S or I is small. We should therefore expect the deterministic SIR model to not be reliable in this regime.

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The stochastic SIR (sSIR) model

The shortcomings of the deterministic SIR model can be overcome by modifying the model as follows.

- Treat S, I and R as time-dependent and discrete random variables

$$S, I, R \quad : \quad [0, T] \times \Omega \quad \to \quad \{0, \ldots, n\}.$$

- Treat $\frac{a}{N} SI$ and bI as the *propensities* of the infection and recovery events, i.e. as an indication of how likely these events are to occur in an infinitesimally small time interval $[t, t + dt]$ (see next slide).

This model is known as the *stochastic* SIR (sSIR) model.

Stochastic SIR Model

Def: Propensity of random event

We say that a random event occurs with *propensity* $p \in (0, \infty)$ if the time until the next event is Exponential(p)-distributed.

The reason why "time until next event" is modelled using the exponential distribution is the following fact.

Thm: Exponential distribution is memoryless

If $T \sim \text{Exponential}(p)$, then

$$P\Big(T \in [t, t + \Delta t] \;\Big|\; T \geq t \Big) \quad \text{is independent of } t.$$

Proof. See next slide.

In terms of the SIR model, this property means that the time until the next infection/recovery depends only on the current values of S and I, but not on how long ago these values have been reached.

Another example of a memoryless random experiment is coin-flipping: the probability of obtaining heads is 0.5, even if you have just observed 10 tails in a row.

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Proof of memorylessness of Exponential(p).

$$
\begin{aligned}
P\Big(T \in [t, t+\Delta t] \;\Big|\; T \geq t \Big) &= \frac{\int_t^{t+\Delta t} p\, \exp(-p\tau)\, d\tau}{\int_t^{\infty} p\, \exp(-p\tau)\, d\tau} \\
&= \frac{\exp(-pt) - \exp\big(-p\,(t+\Delta t)\big)}{\exp(-pt)} \\
&= 1 - \exp(-p\,\Delta t).
\end{aligned}
$$

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Simulating the sSIR model

See `solve_sSIR()`, but ignore the lines `dt_infect = ...` and `dt_recover = ...` for now.

The problem with these lines is that they are supposed to sample the Exponential(p)-distributed times until the next infection and recovery events, and we do not know yet how to sample this distribution.

The following theorem will fill this gap.

Thm: Inverse transform sampling for Exponential(p)

$$U \sim \text{Uniform}[0,1] \quad \Longrightarrow \quad -\log(1-U)/p \sim \text{Exponential}(p)$$

Proof. The claim is an immediate consequence of the inverse transform sampling theorem: the CDF of the Exponential(p) distribution is given by

$$C(x) = 1 - \exp(-p\,x),$$

(see Wikipedia), and one easily verifies that $C^{-1}(U) = -\log(1-U)/p$.

Numerical demonstration. See `exp_sampling()`.

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The `randexp()` function

It turns out that instead of coming up with our own algorithm for sampling Exponential(p), we could have googled "how to sample the exponential distribution in Julia", and we would have learned that Julia provides a `randexp()` function which samples Exponential(1).

These samples can then be transformed into samples of Exponential(p) using the following result.

Thm: Transforming Exponential(1) into Exponential(p)

$$X \sim \text{Exponential}(1) \quad \Longrightarrow \quad X/p \sim \text{Exponential}(p)$$

Proof.

$$P(X/p \leq x) = P(X \leq px) = 1 - \exp(-px).$$

`randexp()` turns out to be slightly faster than our own code, see `exp_benchmarks()`. I therefore use this function in `solve_sSIR()`.

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Simulating the sSIR model (continued)

Now that our implementation of `solve_sSIR()` is complete, we can simulate the stochastic SIR model and compare its predictions against those of the deterministic SIR model.

I do so in `plot_sSIR()`, and observe:

- The predictions of the sSIR model are qualitatively similar to those of the dSIR model, but there are significant quantitative deviations.
- The difference between the dSIR and sSIR models is larger the smaller the population size N, as expected.
- If the recovery rate b is larger than the infection rate a (set `regime = false`), then the deterministic model predicts that the disease dies out monotonically, but the stochastic model shows that there is a nonzero probability of the disease first spreading both wildly and over long periods of time before eventually dying out (uncomment the `Random.seed!(1)` line).

Stochastic SIR Model

Max / distribution

Let us now imagine that we are health officials in charge of managing the pandemic in the last of the above scenarios, i.e. in the case where the disease will eventually vanish but we are not sure how exactly this will play out.

We may then be pondering the following question:

What is the largest number of simultaneously infected people,
i.e. how large can $\max_t I(t)$ possibly be?

Being able to answer this question would help us determine how many hospital beds, quarantine facilities and contact tracers we should prepare.

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Max I distribution (continued)

In the stochastic SIR model, it is of course possible to obtain any answer

$$\max_t I(t) \ \in \ [I_0, \infty),$$

but not all of these answers are equally likely. The best way to address the above question is hence to create a plot of

$$I_{\text{max}} \quad \mapsto \quad P\big(\max_t I(t) = I_{\text{max}}\big).$$

Doing so is straightforward using our `solve_sSIR()` function; see `max_I_distribution()`.

Stochastic SIR Model

Max I distribution (continued)

We observe that for small values of $I_{\max}$, the resulting plot looks smooth and changes little between successive runs, but the opposite is true for large values of $I_{\max}$.

The explanation for this phenomenon goes as follows.

- Small values of $\max_t I(t)$ are more likely.
- Hence they are simulated more often.
- Hence we have a better understanding of how likely they really are.

The ultimate reason for the lack of accuracy in $P\big(\max_t I(t) = I_{\max}\big)$ for large values of $I_{\max}$ is hence the following rule-of-thumb which appears frequently both in Monte Carlo simulations and in real life.

> Determining the likelihood of an event requires observing said event at least a couple of times.

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Max / distribution (continued)

The observations on the previous slide lead us to the following questions:

- Can we quantify the accuracy of our Monte Carlo estimates?
- Can we modify our code so we obtain more accurate estimates for the likelihoods of rare events?

The answer to both of these questions is yes, and the remainder of this lecture will explain how.

Stochastic SIR Model

Estimating Monte Carlo errors

It turns out that we can estimate Monte Carlo errors simply by combining some of the ideas presented in Lecture 8:

- We have seen in Lecture 8 that the Monte Carlo estimate $\tilde{\mathbb{E}}_N[X]$ is within a distance $3\sqrt{\mathrm{Var}[X]/N}$ of the true expectation $\mathbb{E}[X]$ with a probability of about 99.8%.
- Estimating the error in $\tilde{\mathbb{E}}_N[X]$ hence amounts to estimating $\mathrm{Var}[X]$.
- We have

$$\mathrm{Var}[X] \;=\; \mathbb{E}\big[(X - \mathbb{E}[X])^2\big];$$

  hence we can estimate $\mathrm{Var}[X]$ by computing

$$\mathrm{Var}_N[X] \;=\; \tilde{\mathbb{E}}_N\big[(X - \tilde{\mathbb{E}}_N[X])^2\big].$$

Numerical demonstration. Rerun `max_I_distribution()`, but set `errors = true`.

Stochastic SIR Model

More accurate likelihood estimates for rare events

See `solve_isSIR()` and