MA3227 Numerical Analysis II

Lecture 24: Stochastic SIR Model

Simon Etter

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Stochastic SIR Model

Disclaimer

This lecture illustrates the theory developed in Lectures 22 and 23 by means of a concrete, real-world example.

The deterministic SIR model

Consider a population of N people which are exposed to a novel disease. We assume that at any given moment, the population can be split into three groups:

$$\text{Susceptible,} \qquad \text{Infected,} \qquad \text{Recovered.}$$

Let us denote by $S(t)$, $I(t)$ and $R(t)$ the number of people in each group, and let us assume that these quantities satisfy the system of ODEs

$$\dot{S} = -\frac{k}{N} SI, \qquad \dot{I} = \frac{k}{N} SI - I, \qquad \dot{R} = I \qquad \text{for some } k > 0.$$

These equations are known as the (deterministic) SIR model.

We will see later why sometimes we need the "deterministic" qualifier to refer to the above model.

Stochastic SIR Model

The deterministic SIR model (continued)

SIR model copied from above:

$$\dot{S} = -\frac{k}{N} SI, \qquad \dot{I} = \frac{k}{N} SI - I, \qquad \dot{R} = I \qquad \text{for some } k > 0.$$

The SIR model is a very crude approximation to a complicated real-world process, but it captures the correct qualitative behaviour. In particular:

- The $\pm \frac{k}{N} SI$ terms say that people move from the Susceptible to the Infected group as long as there are both susceptible and infected people in the population. Moreover, the disease spreads faster the more susceptible and infected people there are.

- The $\pm I$ terms say that the number of people recovering during a small time interval is proportional to the number of infected people.

- Once people reach the Recovered group, they are immune to the disease and cannot be infected anymore.

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Shortcomings of the deterministic SIR model

SIR model copied from above:

$$\dot{S} = -\frac{k}{N} SI, \qquad \dot{I} = \frac{k}{N} SI - I, \qquad \dot{R} = I \qquad \text{for some } k > 0.$$

Some noticeable shortcomings of the SIR model are:

- The recovery terms $\pm I$ should include a rate constant analogous to the k in the infection terms $\pm \frac{k}{N} SI$. This would be easy to add, but I omitted this generality since from a qualitative point of view, the only thing which matters is whether the rate of infection is faster ($k > 1$) or slower ($k < 1$) than the rate of recovery.

- There is no lag between getting infected, infecting other people and recovering.

- S, I and R are all treated as real numbers when actually they should be integers. Implicitly, this assumes that S and I are sufficiently large that we can afford to ignore the less significant digits of S and I.

- The model does not take into account fluctuations in how fast people infect each other and recover.

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Numerical simulation of the deterministic SIR model

See `sir_ode()` and `simulate()`. Also, note that Julia has a function

The stochastic SIR model

The stochastic SIR model addresses the last two of the shortcomings of the deterministic model listed above.

The idea is to treat S, I and R as time-dependent random variables,

$$S, I, R : [0, T] \times \Omega \to \{0, \dots, N\},$$

and interpret the terms $\pm \frac{k}{N} SI$ and $\pm I$ as a probability density that a person gets infected or recovers in an infinitely small time interval.

The easiest way to present the details of the stochastic model is to present the algorithm which generates samples of the model.

This algorithm is known as the Gillespie algorithm and described on the next slide.

Stochastic SIR Model

The stochastic SIR model (continued)

Algorithm 1 Gillespie algorithm for the stochastic SIR model

1: Input: N, I_0, k, T

2: Set $\quad \ell = 0, \quad t_0 = 0, \quad S_0 = N - I_0, \quad R_0 = 0$

3: **while** $t_\ell < T$ **do**

4: $\quad$ Draw $\Delta t_\ell \sim \text{Exp}\big(\frac{k}{N} S_\ell I_\ell + I_\ell\big)$ and set $t_{\ell+1} = t_\ell + \Delta t_\ell$

5: $\quad$ Draw $P_\ell \sim \text{Bernoulli}\Big(\frac{k}{N} S_\ell I_\ell / \big(\frac{k}{N} S_\ell I_\ell + I_\ell\big)\Big)$.

6: $\quad$ If $P_\ell = 1$, set $\quad S_{\ell+1} = S_\ell - 1, \quad I_{\ell+1} = I_\ell - 1$.

7: $\quad$ If $P_\ell = 0$, set $\quad I_{\ell+1} = I_\ell - 1, \quad R_{\ell+1} = R_\ell - 1$.

8: $\quad$ Set $\ell = \ell + 1$.

9: **end while**

Remarks:

- $\text{Exp}(\lambda)$ denotes the distribution with PDF $f(x) = \lambda \exp(-\lambda x)$.
- $X \sim \text{Bernoulli}(p)$ means $\quad P(X = 1) = p, \quad P(X = 0) = 1 - p$.
- The next slide will discuss how to sample these distributions.

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Sampling the exponential distribution

The $\text{Exp}(\lambda)$ distribution can easily be sampled using transformation sampling. The CDF is given by

$$F(x) = \int_0^x \lambda \exp(-\lambda y)\, dy = 1 - \exp(-\lambda x);$$

hence if $U \sim \text{Uniform}[0, 1]$, then

$$X = F^{-1}(U) = -\tfrac{1}{\lambda} \log(1 - U) \sim \text{Exp}(\lambda).$$

See `exp_sampling()`. Also, note that Julia has a function `randexp()` in the `Random` package.

Sampling the Bernoulli distribution

Let $U \sim \text{Uniform}[0, 1]$ and set

$$X(U) = \begin{cases} 1 & \text{if } U < p, \\ 0 & \text{otherwise.} \end{cases}$$

Then,

$$P(X = 1) = P(U < p) = p \qquad \Longleftrightarrow \qquad X \sim \text{Bernoulli}(p).$$

See `bernoulli_sampling()`.

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Numerical simulation of the stochastic SIR model

See `sir_gillespie()` and `simulate()`.

Discussion: scaling of the SIR model

It is easy to see that the deterministic SIR model is invariant under scaling of the population: if we fix $\alpha > 0$ and set

$$\tilde{N} = \alpha N, \qquad \tilde{S}(t) = \alpha S(t), \qquad \tilde{I}(t) = \alpha I(t), \qquad \tilde{R}(t) = \alpha R(t),$$

then

$$\dot{\tilde{S}} = \alpha \dot{S} = -\alpha \frac{k}{N} SI = -\frac{k}{\alpha N} (\alpha S)(\alpha I) = -\frac{k}{\tilde{N}} \tilde{S}\tilde{I},$$

$$\dot{\tilde{I}} = \alpha \dot{I} = \alpha \frac{k}{N} SI - \alpha I = \frac{k}{\alpha N} (\alpha S)(\alpha I) - \alpha I = \frac{k}{\tilde{N}} \tilde{S}\tilde{I} - \tilde{I},$$

$$\dot{\tilde{R}} = \alpha \dot{R} = \alpha I = \tilde{I},$$

and

$$\tilde{S}(0) = \alpha S(0) = \alpha (N - I_0) = \tilde{N} - \tilde{I}_0,$$

$$\tilde{I}(0) = \alpha I(0) = \alpha I_0 = \tilde{I}_0,$$

$$\tilde{R}(0) = \alpha R(0) = 0.$$

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Discussion: scaling of the SIR models (continued)

The above means that $\tilde{S}, \tilde{I}, \tilde{R}$ satisfy the same ODEs as S, I, R but with scaled initial conditions. Since solutions to ODEs are unique (assuming the ODE is Lipschitz continuous, which is the case here), this conversely means that we can get the solution for scaled initial conditions simply by scaling the solution.

To see this numerically, replace `N = 1000` in `simulate()` with e.g. `N = 10_000` or `N = 100`. We observe that the solution to the deterministic model looks the same in each case on appropriately scaled axes.

The same is not true for the stochastic model: for large population sizes N, the stochastic solutions closely follow the deterministic solutions, but for small population sizes there is significant randomness in the stochastic solutions.

This confirms that using the deterministic model is justified if the population is large, but stochastic models should be used otherwise.