Continuous-time stochastic models

Modern Techniques in Modelling

LONDON SCHOOL of HYGIENE &TROPICAL MEDICINE

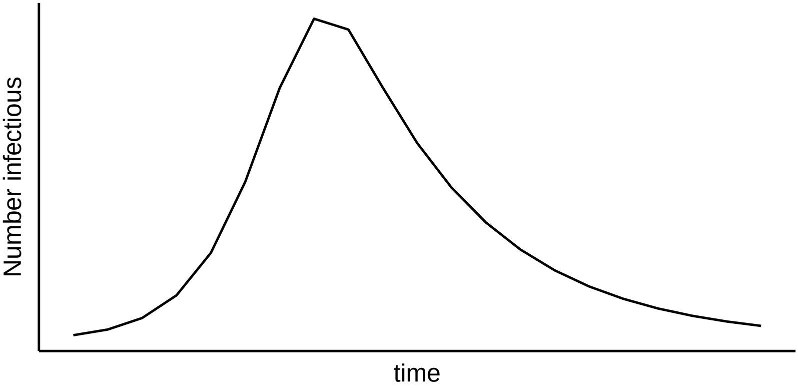
Introduction

Overview

- Introduce continuous-time stochastic models (~20 minutes)
- Implement the Gillespie algorithm and analyse stochastic model output (~60 minutes)
- Implement a stochastic model with the `adaptivetau` package (~20 minutes)
- Discussion and concluding remarks (~20 minutes)

Deterministic models

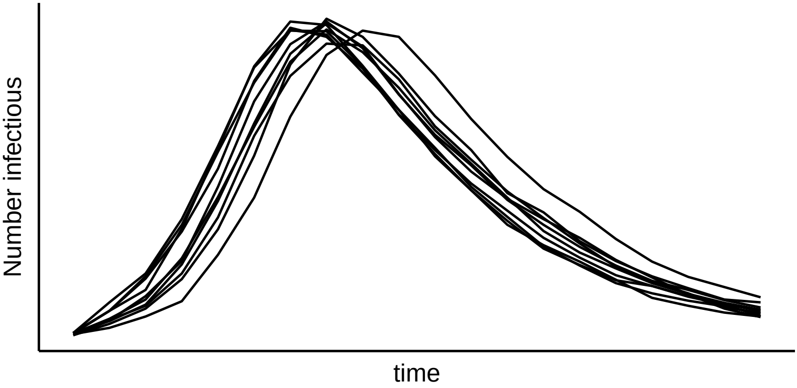
SIR model with $I_0 = 10, \beta = 1.3, \gamma = 0.3$



One set of parameters $\rightarrow$ one trajectory

Stochastic models

SIR model with $I_0 = 10, \beta = 1.3, \gamma = 0.3$



One set of parameters $\rightarrow$ many trajectories

Types of model

- *discrete* vs *continuous* time
- *compartment*- vs *individual*-based
- *deterministic* vs *stochastic* dynamics

Session 3: Discrete-time deterministic models

- *discrete* vs *continuous* time
- *compartment*- vs *individual*-based
- *deterministic* vs *stochastic* dynamics

$$
\begin{aligned}
S(t+1) &= S(t) - \beta S(t) I(t) \\
I(t+1) &= I(t) + \beta S(t) I(t) - \gamma I(t) \\
R(t+1) &= R(t) + \gamma I(t)
\end{aligned}
$$

Session 3: Discrete-time deterministic models

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Session 4: Ordinary differential equations

- *discrete* vs *continuous* time
- *compartment*- vs *individual*-based
- *deterministic* vs *stochastic* dynamics

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\begin{aligned}
dS/dt &= -\beta SI/N \\
dI/dt &= \beta SI/N - \gamma I \\
dR/dt &= \gamma I
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Session 4: Ordinary differential equations

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Session 8: Stochastic individual-based models

- *discrete* vs *continuous* time
- *compartment-* vs *individual*-based
- *deterministic* vs *stochastic* dynamics

```
For each ts from 1 to T {
  lambda <- beta * I/N
  For each i from 1 to N {
    If individual i is susceptible:
      with prob 1-exp(-lambda· t) make infected.
    Else-if individual i is infected:
      with prob 1-exp(-gamma· t) make susceptible.
  }
  Record population state
}
```

Session 8: Stochastic individual-based models

- **discrete** vs ~~continuous~~ time
- ~~compartment-~~ vs **individual-**based
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}
```

Continuous-time stochastic models

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Continuous-time stochastic models

- ~~discrete~~ vs **continuous** time
- *compartment*- vs *individual*-based
- ~~deterministic~~ vs **stochastic** dynamics

Stochastic differential equations (SDEs)

- ~~discrete~~ vs **continuous** time
- **compartment-** vs ~~individual-~~based
- ~~deterministic~~ vs **stochastic** dynamics

$$
\begin{aligned}
dS/dt &= -\beta SI/N - \sqrt{\beta SI/N}dW_1 \\
dI/dt &= \beta SI/N - \gamma I + \sqrt{\beta SI/N}dW_1 - \sqrt{\gamma I}dW_2 \\
dR/dt &= \gamma I + \sqrt{\gamma I}dW_2
\end{aligned}
$$

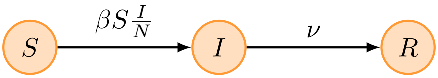
(not covered in this course)

Continuous-time discrete stochastic models

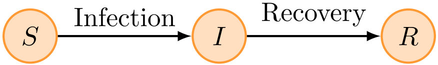
- ~~discrete~~ vs **continuous** time
- ~~compartment-~~ vs **individual-**based
- ~~deterministic~~ vs **stochastic** dynamics

We model these as a so-called **continuous-time Markov chains**.

Event-based view



Event-based view



- **infection**: $(S, I, R) \to (S-1, I+1, R)$ with rate $\beta SI/N$
- **recovery**: $(S, I, R) \to (S, I+1, R)$ with rate γI

Moving to continuous time

Discrete time

```
for (ts in 1:steps) {
  update all compartments
}
```

(see Session 8: Stochastic individual-based models)

Continuous time

```
while (time < finaltime) {
  advance time and record next event
}
```

(this session)

Gillespie algorithm

Repeat until end time:

1. Calculate rates of all possible events

```
rates <- c(
  infection =  beta * S * I / N,
  recovery =  gamma * I
)
```

2. Determine time of next event

```
rexp(n =  1, rate = sum(rates))
```

3. Determine which event happens

```
sample(x = length(rates), size = 1, prob = rates)
```

and update system state according to event.

Now, put it in R

Practical structure

- Part 1: Stochastic simulations using the Gillespie algorithm
- Part 2: A faster alternative: the `adaptivetau` package

Representing uncertainty

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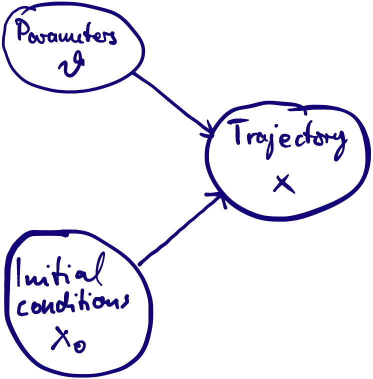
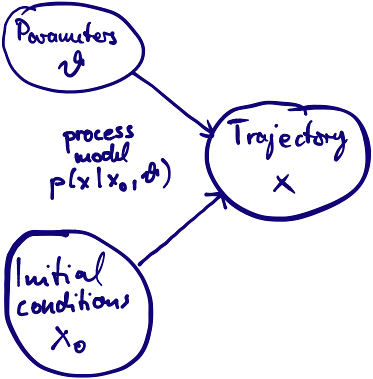
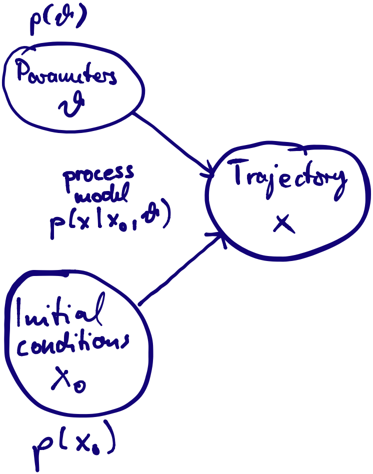
The deterministic view



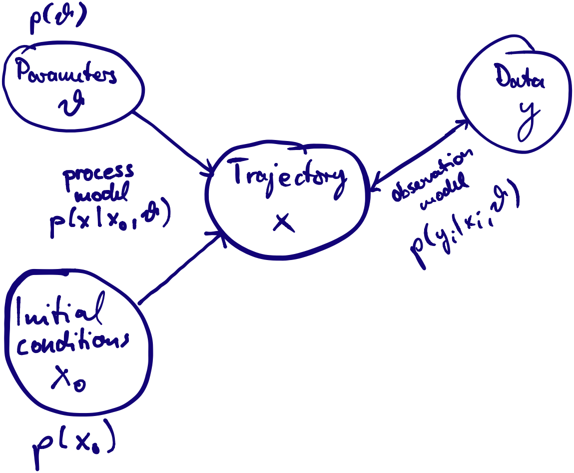
The stochastic view



Other types of uncertainty



Linking models to data



See LSHTM short course on Model Fitting and Inference for Infectious Disease Dynamics.

Further reading

- L.J.S. Allen (2017). A primer on stochastic epidemic models: Formulation, numerical simulation, and analysis. Infectious Disease Modelling, 2(2):128–142. https://doi.org/10.1016/j.idm.2017.03.001
- M.J. Keeling, P. Rohani (2017). Modeling Infectious Diseases in Humans and Animals. Princeton University Press.
- D.T. Gillespie (1976). A general method for numerically simulating the stochastic time evolution of coupled chemical reactions. J Comput Phys, 22(4):403–434, 1976. ISSN 0021-9991. https://doi.org/10.1016/0021-9991(76)90041-3
- Y. Cao, D.T. Gillespie, and L.R. Petzold (2007). Adaptive explicit-implicit tau-leaping method with automatic tau selection. J Chem Phys, 126(22):224101 URL https://doi.org/10.1063/1.2745299
- A.A. King, M. Domenech de Cellès, F.M.G. Magpantay and Pejman Rohani (2015). Avoidable errors in the modelling of outbreaks of emerging pathogens, with special reference to Ebola. Proc Roy Soc B 282(1806). https://doi.org/10.1098/rspb.2015.0347