Module 11: Lesson 1 Lecture Notes

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Contents

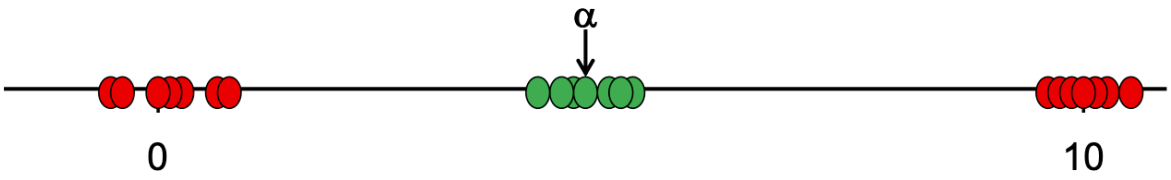
Simulation

Introducing simulation

- Suppose we have a stochastic epidemic model (e.g. SIR)
- Simulation = producing a realisation of the model (i.e. possible outcome)
  - Producing an outcome according to the correct distribution of all possible outcomes
- For the SIR model
  - producing a set of infection and removal times according to the correct distribution inherent in the model
- Why is it useful?
  - Helps us understand model behaviour
  - It is useful for testing our inference procedure (finding or estimating model parameters) e.g. validate our method against data from the simulation where we know the "truth"
- For example:
  - Perform N (=1000) simulations
  - Have model with parameter vector θ fixed at θ_T
  - For each simulation, estimate the model parameters to get $\theta_1, ..., \theta_N$
  - The average of the model estimates should be close to the true value of θ_T
- Also useful for model checking
  - Let's say we estimate model parameter α

  - For each value of α, we perform a large number of simulations and see whether the output of each is similar to the actual data

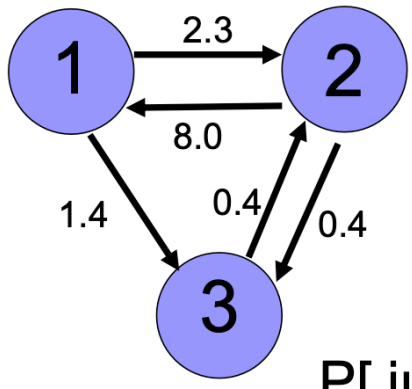
- Suppose we have a mixture model, e.g. looking at seroprevalence data where some people infected and others aren't, and x_k is the IgG value
  - $x_k \sim N(0,1)$ with probability 0.5, and $x_k \sim N(10,1)$, if we just fit a single parameter, we will be way off and we can check our predictions against the data to show that our model guess will never look like the data



- Simulations can be used for prediction
  - e.g. estimate epidemic model parameters up to time T and simulate forward using these estimates

Simulating Markov models

- Let the state space be denoted $S = \{1, 2, 3, ..., n\}$
  - S is the set of states the MC can visit and each state can be multidimensional
- We care about the tendency of the chain to move from $i \to j$
  - $\Pr(X(t+dt) = j | X(t) = i) = q_{ij}dt + o(dt)$
- The chain stays in state i for time T_i
  - $T_i \sim \text{Exp}(\sum_{j \neq i} q_{ij})$
  - $P(T_i > t) = \exp(-\sum_{j \neq i} q_{ij})$
- When it leaves state i, the chain jumps to state j with probability $q_{ij} / \sum_{j \neq i} q_{ij}$
- The time spent in state i and the choice of where to jump to **are independent**, and they are also independent of the same quantities in other states and at other times



Here $q_{12} = 2.3$, $q_{21} = 8.0$ etc

If chain enters state 1, time spent there is

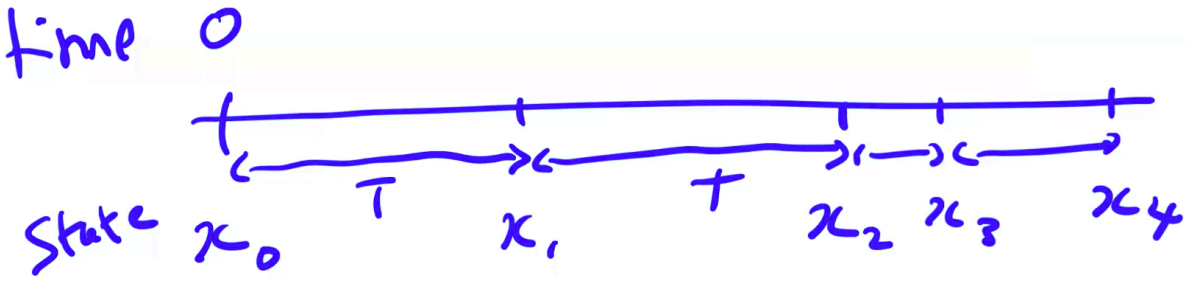
$T_1 \sim \text{Exp}(2.3+1.4) = \text{Exp}(3.7)$

$$P[\text{jump to state 2 next}] = \frac{2.3}{2.3+1.4}$$

Gillespie algorithm (next event simulation)

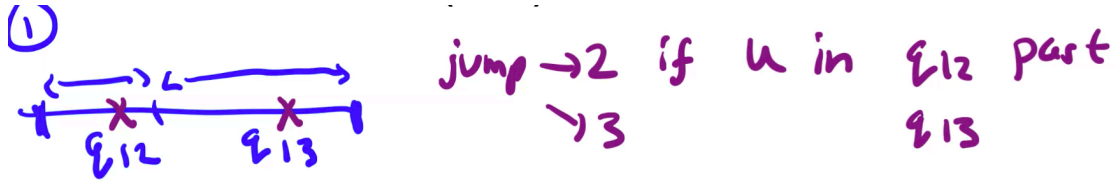
- All that is needed is to generate the time spent in a state, and the next state that is visited

Algorithm:



- Initialise (t=0, X(0) = x0)
- for state i:
  - Calculate L (sum of the jump rates out of state i)
    - $L = \sum_{j \neq i} q_{ij}$
  - Generate time spent in state i
    - $T_i \sim \text{Exp}(L)$
  - Sample from a uniform distribution ($u = \text{U}[0, 1]$)
  - If $u < \frac{\sum_{j \leq 1, j \neq i} q_{ij}}{L}$
    - $k = 1$
    - Divide by L to normalize so it's between 0 and 1
  - Else if $u < \frac{\sum_{j \leq 2, j \neq i} q_{ij}}{L}$
    - $k = 2$

- Continue until k determined



  - Update current time
  - Record t and k
    - Time of next event $= t + T_i$
    - State jumped to is k
- The algorithm outputs a sequence of times (t_k) and a corresponding sequence of states (x_k)

Example: general epidemic model (SIR)

- Due to the Poisson process infection mechanism and exponentially distributed infectious period
  - $\{[S(t), I(t)] : t \geq 0\}$
- If the chain is currently at (s, i), then it can jump to:
  - $(s-1, i+1)$ (infection) at rate $\beta si/N$
  - $(s, i-1)$ (removal) at rate γi
- Therefore, the time spent in (s, i)
  - $T_{(s,i)} \sim \text{Exp}([\beta si/N] + \gamma i)$
- Once the chain leaves (s, i)
  - Probability of infection $(s-1, i+1)$: $\frac{\beta s}{\beta s + N\gamma}$
  - Probability of recovery $(s, i-1)$: $\frac{N\gamma}{\beta s + N\gamma}$
  - Calculate probabilities by dividing rate of interest by sum of the rates
- Apply the algorithm iteratively
- Can sometimes be useful to keep track of the type of each event e.g. infection or recovery

Simulating non-Markov models

- Same idea as before
  - Generating time until next event
  - But independence properties of Markov chain are lost so we need to explicitly generate the times of future events as the algorithm evolves
- In the Markov SIR model:
  - Infections occur according to a Poisson process of rate $\beta S_t I_t/N$
  - Each infective remains so for a period of time $T_I \sim \text{Exp}(\gamma)$
- In the non-Markov SIR model
  - A common generalisation is to let the infectious period distribution T_I be non-exponential e.g. constant, Gamma

  - Infectious period T_I drawn from specified distribution with parameter vector θ
  - Now two model parameters β and θ
- To simulate the epidemic
  - Generate removal time of each individual as they become infected
    - The time of next removal is known, as is the identity of the removed individual
  - Generate possible time-to-next infection
    - $T \sim \text{Exp}(\beta si/N)$
    - If $T <$ time of next removal, next event is an infection
      - Otherwise, next removal occurs
      - If removal occurs first, then i in $T \sim \text{Exp}(\beta si/N)$ changes, so we no longer have the correct distribution for time to next infection and it needs to be updated

Example: non-Markov SIR model

- Lets assume we have a fixed infectious period
  - $T_I = c$
- We need $\vec{r}$ which contains the removal times of all the current infectives
- Initialize:
  - $S = N - 1$
  - $I = 1$
  - $t = 0$
  - $\vec{r} = (c)$
    - We only have one infective, so $\vec{r}$ only contains 1 removal time $(0 + c)$
- While $i > 0$:
  - $T \sim \text{Exp}(\beta SI/N)$
    - Draw from the time to next infection distribution
  - $R = \min(r)$
    - Time of the next removal
  - if $t + T < R$ (current time + potential time to next infection $<$ time of next removal)
    - $S = S - 1, I = I + 1$
    - Add new removal time $r \leftarrow (t + T + c)$
    - Update current time $t = t + T$
  - else:
    - $I = I - 1$
    - Remove minimal element of r, our vector of removal times
    - Update current time $t = R$ so that it equals the time of the next removal (i.e. the one that just happened)
- Non-constant infectious period

- Generate a random sample from the distribution T_I for the infectious period of an individual who has just become infected
- While $i > 0$:
  - $T \sim \text{Exp}(\beta SI/N)$
    - Draw from the time to next infection distribution
  - $R = \min(r)$
    - Time of the next removal
  - if $t + T < R$ (current time + potential time to next infection < time of next removal)
    - $S = S - 1, I = I + 1$
    - Generate $c \sim T_I$
    - Add new removal time $r \leftarrow (t + T + c)$
    - Update current time $t = t + T$
  - else:
    - $I = I - 1$
    - Remove minimal element of r, our vector of removal times
    - Update current time $t = R$ so that it equals the time of the next removal (i.e. the one that just happened)

Discussion

When infections and removals happen at the same time, do we consider to be Markov or non-Markov

Things are actually happening instantaneously, it's just that we make them discrete when we aggregate data.

In the non-Markov model example, the time to infection is exponential, so why is it not a Markov model

- The joint distribution of the number of susceptibles and infected at each time
  - Markov model is a markov chain
  - Not a markov chain in non-markov model as infectious period distribution is non-exponential
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