Master

Written exam Introduction Computational Science
23 October 2019, 13.00 - 16.00, OMHP D0.08

This exam has 3 assignments. Each assignment has equal weight in the final grade.

Assignment 1 [10 POINTS, every question is 2 points]

1 What is Uncertainty Quantification?
2 ~~1~~ What is a continuous time model?
3 ~~2~~ What is an endemic state?
4 ~~3~~ What is the Critical Community Size (CCS)?
5 ~~4~~ What is a Poisson process?

Assignment 2 [10 points]

Consider an SIR type model with four compartments: the Susceptible compartment with X individuals; the Recovered compartment with Z individuals; and two compartments of infected individuals, the travelling infected compartment with Y_T individuals and the non-travelling infected compartment with Y_{NT} individuals. Finally, N is the total number of individuals.

As susceptible individuals become infected, assume they always first become a travelling infected individual. Susceptible individuals can be infected both by travelling and non-travelling infected individuals. We assume frequency dependent transmission and write the force of infection as $\lambda = \beta_T X \frac{Y_T}{N} + \beta_{NT} X \frac{Y_{NT}}{N}$.

The rationale of travelling versus non-travelling infected individuals is that some persons feel so sick that they stay at home, while others are also infectious but still travel around in the community.

1 Is β_T larger than β_{NT} or vice-versa, and explain why. (1 point)

Travelling infected individuals can become non-travelling individuals at a rate α. And both travelling and non-travelling individuals can recover, with rates γ_T and γ_{NT} respectively, and move to the Recovered compartment.

We assume no demography.

2 Write the equations for this SIR model in terms of X, Y_T, Y_{NT}, Z (1 point)
3 Derive the fixed points for this model (2 points)
4 Does the model have an endemic state? Explain why? (1 point)

We will now apply this model to childhood diseases. First, we take into account vaccination, so susceptible individuals are vaccinated immediately after birth, before they become infected. Assume a birth rate μ, with births only in the Susceptible compartment, and assume deaths in all compartments, with equal death rates, which is the same as the birth rate, μ. Also assume that upon birth, a fraction p is vaccinated, so they are protected from the infection and are no longer susceptible.

5 Update your model from (2) taking into account demography and vaccination (1 point)

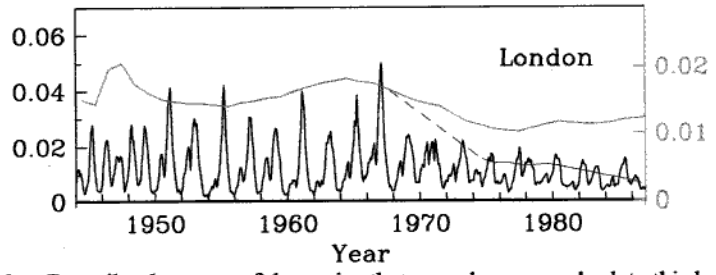
Your updated model has as a special case the standard SIR model with demography as was introduced and discussed at length during the lectures.

6 What special parameter settings are needed to find the standard SIR model with demography from your updated model from (5), and demonstrate this indeed produces the standard SIR model with demography. (1 point)

In order to produce yearly outbreaks (of childhood diseases) one ingredient is still missing in the updated model from (5).

7 Described what is missing to give yearly outbreaks in the model, and based on your knowledge of the standard SIR with demography model, what kind of dynamics could you expect? (2 points)

Finally, consider dynamic variability in childhood disease incidence in real data. The graph below is based on Figure 5.16 from Keeling and Rohani, Case reports for measles in London 1944 to 1988. The black line demonstrates weekly reported cases, with the gray line depicting the per capita birth rate. The dashed grey line demonstrates effective birth rate, correcting for vaccination, that started in 1968.



8 Describe the types of dynamics that you observe, and relate this back to what you know about SIR models with seasonal forcing. (1 point)

Assignment 3 [10 points]

Consider stochastic models for spreading of infectious diseases.

1 What are the five hallmarks of dynamics of such models? (1 point)
2 One of those hallmarks is stochastic extinction. What is it, and when is this most likely to happen? (2 points)
3 What is a metapopulation model in infectious disease modelling? (1 point)

Consider two subpopulations with a one-way coupling, meaning population 1 is coupled to population 2, but not vice-versa. Also assume that population 1 is large enough to be described as fully deterministic.

4 Assuming that population 2 is also deterministic, formulate the SIR equations with demography for these coupled populations. You may assume equal birth/death rates and recovery rates in both populations (1 point)

For these two coupled deterministic models, now assume that an infection is introduced in population 1, and that population 2 is fully susceptible. Also assume that this infection has a basic reproductive ratio that allows it to spread and cause an epidemic

5 Explain in words the dynamics in this coupled model. (1 point)

Finally assume that population 2 is too small to be considered fully deterministic. Replace the model population 2 now with a stochastic SIR model.

6 What do you observe now? Take the strength of coupling between population 1 and 2 into account in your discussion (2 points)

Finally consider a metapopulation model with two metapopulation, where both metapopulations are small and are modelled with a discrete event model. Within each of the subpopulations we assume the standard SIR with demography.

7 To implement the standard SIR with demography in a discrete event model would require 6 events. What are these events? No need to also mention the rates at which these events happen. (1 point)

The coupling between both subpopulations is via commuting.

8 What additional events are required to model commuting? Again, No need to also mention the rates at which these events happen. (1 point)