# Short Course in Mathematical Modelling of Infectious Diseases

## 5 – 7 January 2006

## COURSE DESCRIPTION

## Seminar Sessions

### *Introduction: Anatomy of an infectious disease epidemic*

The spread of infectious diseases through human populations has been the subject of scientific investigation for hundreds of years. Concepts such as disease take-off, the epidemic curve, endemicity and fade-out are of use for analyzing most infectious diseases. The course will begin with a general introduction to mathematical models using these concepts.

### *A first model: SEIR (Part 1 & Part 2)*

Members of a population can be classified as either susceptible (S), infected but not yet infectious (E), infectious (I) or recovered and immune (R) with respect to any particular infectious pathogen. The SEIR model has been developed based on two assumptions: that individuals mix freely, and that the rate at which infections occur is influenced by the number of infectious individuals. This session will introduce concepts using arithmetic in Part 1 and then extended with a little more mathematics in Part 2.

### *A refresher in mathematics*

Some mathematics in modelling is unavoidable. In this session, key concepts that will be used later in the course, and some that are often referred to in non-specialist modelling articles, will be described.

### *Case study 1: Influenza in a boarding school*

Using the SEIR model and an excel spreadsheet, the group will see how a mathematical model can be used to investigate an outbreak of influenza in a boarding school.

### *Developing model structure*

The very basic SEIR model is already of considerable use for investigating many hypotheses. By making minor modifications to this simple structure, additional questions may be answered. In this session, a number of examples with key parameters for different diseases will be introduced to illustrate this versatility.

### *Estimating the basic reproductive number*

The basic reproductive number, $R_0$, of an infectious disease in a given population is defined as the average number of secondary cases generated by a single typically infectious individual in an otherwise susceptible population. This figure can be estimated using a number of different techniques, depending on the amount and quality of data available. This session will introduce the methods used to estimate $R_0$.

### *Vector-borne diseases*

Diseases like malaria, Japanese encephalitis and dengue are not spread directly by human-to-human contact but require an intermediate host. The number, distribution and behaviour of such hosts have a significant impact on the disease transmission dynamics, which in turn determine options available for control. Application of mathematical models to infectious conditions which require an intermediate host will be discussed.

### *The health economics of infectious disease*

Economic evaluation in health care compares the inputs (costs) and outcomes (benefits) of alternative programmes. Different types of models used in economic analyses will be briefly introduced, and examples will be used to illustrate their use and limitations in the economic analysis of vaccination programmes.

### *Case study 2: Age mixing patterns*

Compared to adults, children generally mingle with larger groups of people who are usually peers at school. In particular, younger children, have more skin-to-skin contacts than adults because of the nature of their play. Intensity of mixing is highly dependent on school terms. A single model which includes age-specific mixing and seasonal variation in mixing will be presented.

### *Case study 3: STI mixing patterns*

Heterogeneity in people's choice of partner has a substantial effect on the way that a sexually transmitted infection (STI) spreads through a population. This case study will involve construction of a simple matrix to reflect sexual mixing behavior within a modern, developed population. The effect of the parameters of mixing to model output and its sensitivity to changes in the parameters will be discussed.

### *Vaccination against childhood diseases*

This session demonstrates how models may be used to address major public health questions, such as whether a new vaccination programme should be introduced.

### *Anti-microbial resistance*

Resistance to antibacterial, antiviral, and antimalarial drugs is a growing problem worldwide. At a practical level, solutions are needed to retard and, ideally, reverse the spread of drug resistance in many pathogens. The major mechanisms by which resistance spreads, approaches to modelling resistant strains, and insights from models into the control of drug-resistant pathogens will be discussed.

### *Within-host HIV models*

Whilst the vast majority of disease models have focused on the spread of infection among people, compartmental models can also be useful in understanding pathogenesis within the host. HIV is probably the infection where such models have been most successfully applied. This session will introduce simple models of the within-host dynamics of HIV that explore the interaction between the immune system (CD4+ T-cells) and the virus.

## Outbreak Team Exercise

This exercise will simulate the outbreak of a new or re-emerging pathogen in the population of Hong Kong. Participants will work in teams and will be presented with simulated data, relevant papers and fictional news reports. A number of interventions may be deployed, each with an associated cost. Each team will be required to decide on a combination of available interventions, while remaining within a budget. Teams will need to make short presentations about their choices. The combination of interventions that results in fewest deaths will be considered the most successful.