Dynamical systems theory – a main tool in mathematical modelling

In the course you are supposed to learn how to apply most known general methods in continuous dynamical systems to find out essential understanding of the reasons for spreading of most important diseases like malaria. The general methods you learn about dynamical systems and the way you apply them is useful in any other type of mathematical modelling. The application can be completely different but the mathematical analysis and way of interpretation is the same which is often confusing for some non-mathematician thinking that different application may need completely different math.

The importance of basics

Anyhow to have a good understanding about how to build and analyse different models used for examining malaria it is necessary to start with learning the basics of simple epidemical modelling. Most models are built on basic same ideas and understanding these basics gives you a background for understanding a lot of more complicated models and constructing variations of the models yourself.

Epidemics and types of transmission

We can differ between to general types of epidemic diseases, those which are transmitted directly from host to host and those which need a so called vector to transmit the disease. The vector is a living being where important stages in the spreading development of the disease takes place. The vector itself need not suffer much from the disease like in malaria where most mosquitos are not infected and the disease is not a reason for death.

The importance of simplicity, main elements of epidemic modelling

Anyhow to build models for vector diseases it is easier to start with understanding simple diseases like swine flu. To build a model the host population of the disease is divided into parts. Most important are the Suspective (not infected but may become infected), Latent (infected but not infectious), Infective, Recoverd but not for ever. Groups like dead ones, recovered for ever and vaccinated are central but do not affect the further spread of disease and may be excluded as variables. The size of these population groups are the variables. To build equations we use assumptions about transmission between these groups, for example, the rate of becoming infected should be an increasing function of the numbers of suspectible and infected. The rate of recovering should be an increasing function of the number of infectious usually taken as linear. Observe that the groups of hosts are divided into are not the same as those observed as sick with symptoms, the groups are the important ones for transmission. You can, of course, be infectious without being sick and sick without being infectious.

About more complicated models

In more complicated models we need more groups. In vector diseases we have groups for both hosts and vectors. Sometimes we may need different age groups, geographical groups of differ between females and males or other properties of the host or vector. Malaria is much more severe for those infected first time while malaria by some others is considered like we consider normal influenzas, thus here it is of interest to differ between these groups in the model. The dimension of the model might thus increase but not necessary increasing the dimension of the mathematically important part of the model. We here meet the problem of simplification without omitting essential factors.

Types of mathematical models

Mathematically models can be divided into different types. We differ between discrete and continuous models also taking into account existence of hybrid models. Among continuous models we differ between systems of ordinary differential equations and partial differential equations. Both discrete and continuous can have delay or stochastic terms. We here examine in detail only deterministic models of systems of differential equations, but we may be can compare the results by doing some experiments on models where stochastics and delay are included. We also note that even if the final model is written as a deterministic system without delay the derviation of the model and the interpretion of the parameters may include elements from this more complicated theory. It is also not excluded to compare with results we can get from discrete models using the math learnt in earlier parts of the course in dynamical systems.

First part of course

In the first part of the course we get familiar with the most common epidemical models and more detailed about different models in malaria modelling. Even if this part is considered as a motivation part for the essential mathematical theory introduced a little bit later we are heavily based on mathematical analysis, especially numerical experiments. Our analysis at the beginning will mainly be based on properties we can see from elementary analysis of the direction field.

Analysis for fixed parameters

We discover by experiments in which part of the space of the variables we expect essential special solutions like equilibria, periodic solutions and may be chaos. We also discover that these can be of three main types: attracting, repelling or saddle type. Theoretically important details and criteria to be given later. The special solutions attract a set of other so called transient solutions and these basins of attractions are estimated. Later you might learn how to get

important theoretical estimates using Lyapunov function technics.
For example, it is usual that the model have two types of equilibria,
a disease-free one and an endemic one. It is important then to
know which initial conditions are attracted to which equilibria
and by which strategy (for example, how to vaccinate) we can get into
desired part.

Bifurcation analysis

Of course, all models contain expect variables also parameters and our main analysis
is to find out how the general qualitative behaviour changes when
parameters are changed (called bifurcation analysis).
This is, of course, important for controlling the disease, but also for finding out
essential new factors in understanding of the development of the disease.
It is important to note that very rough models giving only rough estimates
and seemingly useless for the sizes of the variables
can give better understanding and results.
Parameters in big models can usually be fitted to give good correspondance
with data but the models cannot be used for predicting as they might be completely wrong
in essential factors anyhow.

Please do simple ASAP

We will start spending some time on two-dimensional systems.
The aim is that everybody should be able to do simple experiments and
understand how to differ between different behaviour for changes in
intial conditions and parameters. You will be given, we hope, easy exercises
on which we can check that you have understand the essential background
before we continue and it is important that you give priority in using your time for
those exercises asap. A lot of numerical experiments as background are supposed
to be done.

High dimension and visualization

After simple systems we consider what can be done in higher dimensional systems.
Before we give the mathematical problems below we spend some time on
the visualization problem. Models can easily grow in dimension but may
anyhow have essential things which can be seen in lower dimension.
It is usual with epidemical models of dimension five, six or higher.
If we try to plot solution curves for dimension six system and project it
to a two-dimensional space we have 15 possibilities choosing pairs of the
variables. If we think it is better with three dimensional we get even
20 possibilities. So we have to choose the most informative ones.
Sometimes it is more informative to have plots for some representative
expressions of the variables than the variables themselves.

Suggestions for laboration projects

In the first part of the course you are involved in formulating concrete problems where you later can use mathematical theory.

These problems are expected to be included:

finding equilibria and their types for concrete parameters

examining the change in the position of the equilibria and the conclusion for practical interpretation (formulas for equilibria depending on parameters)

examining changes in the type of equilibria and bifurcation analysis (diving the parameter space into parts with different behaviour of the system, finding tresholds for desired behaviours)

estimation of regions where the equilibria are if these cannot be solved for by exact formules (finding nice approximative formulas)

estimation of regions for the parameters giving different qualitative behaviour if these cannot be solved for by exact formules (finding nice approximative formulas)

estimation of basins of attractions of equilibria. Might mean where to have intial conditions to get desired behaviour. (simple geometric arguments or using Lyapunov function technics)

estimation of regions of existence of periodic or chaotic solutions, their types and basins of attraction
(we should observe that also saddle types with basins of attractions play an essential role forming boundaries between different stable behaviours)

the conncetion with discrete dynamics analysing the behaviour around periodic solutions using Poincare map

Malaria models that might be included.

Ross original two-dimensional model (must be) and it's different interpretations. Two-dimensional generalizations of Ross model.

Developing the Ross model by taking into account latent periods (especially important for mosquitoes)

Developing models taking into account immunity factors

Developing models giving special attention to severe cases

Developing models taking into account resistance developments to drugs

Models with seasonal variations

Immunological models

Models giving estimates for impacts of environmental factors.