

**CBMS Conference: Interface of Mathematical Biology and Linear Algebra**  
**List of Lectures**

*All lectures are held in Room 119, Business Administration 1 (BA1)*

**Lecture 1:** *Monday May 23, 9:00-10:30*

Stephen Kirkland Introduction to Some Topics in Linear Algebra

**Lecture 2:** *Monday May 23, 11:00-12:30*

Pauline van den Driessche Introduction to Mathematical Epidemiology: Basic Models

**Lecture 3:** *Monday May 23, 14:00-15:30*

Mark Lewis An Introduction to Discrete-Time Stage-Structured Population Models

**Lecture 4:** *Tuesday May 24, 9:00-10:30*

Pauline van den Driessche Computation of  $R_0$  and Sensitivity for Models of Infectious Diseases

**Lecture 5:** *Tuesday May 24, 14:00-15:30*

Stephen Kirkland Markov Chains and Applications to Population Models

**Lecture 6:** *Wednesday May 25, 9:00-10:30*

Mark Lewis Stage-Structured Integrodifference Population Models and Spreading Speeds

**Lecture 7:** *Wednesday May 25, 14:00-15:30*

Pauline van den Driessche Sign Pattern Matrices in Population Biology

**Lecture 8:** *Thursday May 26, 9:00-10:30*

Pauline van den Driessche Target Reproduction Numbers and Applications to Biological Models

**Lecture 9:** *Thursday May 26, 11:00-12:30*

Stephen Kirkland Group Inverse: Theory, Computation, and Applications in Mathematical Biology

**Lecture 10:** *Friday May 27, 9:00-10:30*

Mark Lewis Persistence Dynamics for Stage-Structured Integrodifference Models

**CBMS Conference**  
*Interface of Mathematical Biology and Linear Algebra\**  
Stephen Kirkland, Mark Lewis, and Pauline van den Driessche

Lecture 1: Introduction to some topics in linear algebra (SK)

Matrix theory is a mature area of mathematics that is applied across a wide range of disciplines in science and engineering. In this lecture we will look "under the hood" at some of the results and techniques in matrix theory that make it such a powerful tool in mathematical biology. In particular we will discuss the Jordan canonical form, the Perron-Frobenius theorem for nonnegative matrices, and M-matrices. Throughout we will emphasise connections with matrix models for stage-classified populations, and patch models for populations or epidemics.

Lecture 2: Introduction to mathematical epidemiology: Basic models (PvdD)

A general scheme for formulating and analyzing basic models of disease dynamics is analyzed. This is illustrated with a simple ordinary differential equation (ODE) Susceptible-Infectious-Recovered model that includes demographics. The model results are used to estimate the proportion of the population that need to be effectively vaccinated to give herd immunity. If the epidemic is short lived, for example, annual influenza, then demography may be ignored, and a final size equation and attack rate are derived. Discrete time disease models are formulated with different recruitment functions, and the resulting dynamics investigated.

Lecture 3: An introduction to discrete-time stage-structured population models (ML)

In this lecture I will introduce discrete-time stage-structured models in ecology. These models are primarily used to model persistence and extinction dynamics for species with complex life history dynamics. They can be applied to populations of weeds (such as scentless chamomile) and invaders (such as zebra mussels) as well as to a wide variety of endangered species. I will discuss the mathematical methods for analyzing asymptotic dynamics (stability of equilibria, eigenvalue sensitivity, net reproductive rate), with a view to showing how the methods can provide biological insight regarding the study populations and their management.

Lecture 4: Computation of  $R_0$  and sensitivity for models of infectious diseases (PvdD)

The basic reproduction number  $R_0$  plays an important role in the dynamics of infectious diseases, often determining if the disease eventually dies out or persists in the population. By considering a simple Susceptible-Infectious-Recovered model, this number is determined from both biological and mathematical aspects. A general method involving matrices for determining  $R_0$  in ODE disease models is then discussed, and illustrated with a model for West Nile virus (a vector-host disease). To determine best control methods, it is useful to know which model parameters have a high impact on  $R_0$ . This can be measured by sensitivity or elasticity indices. These are described, and computed for a vector disease of cattle using estimated parameter values.

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\* This NSF-CBMS conference will be held at the University of Central Florida, Orlando, FL during May 23-27, 2022.

### Lecture 5: Markov chains and applications to population models (SK)

Because of their well-developed theory and ease of formulation, Markov chains are a widely applied class of stochastic processes, appearing in economic models, web search, and wireless network design. In the ecological setting, Markov chains are used to model not only the life cycle, but also species succession. In this lecture we give a matrix-oriented introduction to Markov chains, including their convergence properties, stationary distributions and first passage times. Connections with applications in ecology will be highlighted.

### Lecture 6: Stage-structured integrodifference population models and spreading speeds (ML)

In this lecture I will build on the theory for discrete-time stage-structured population models and include spatial structure into the population model. The resulting stage-structured population models can be used to analyse the rate of population spread when individuals are introduced into new environments. I will introduce and develop the mathematical theory for travelling waves, spreading speeds, generational spreading speeds. If time permits I will discuss the internal spatial structure of waves using the approach of “inside dynamics”. Applications will be made to the spread of scentless chamomile.

### Lecture 7: Sign pattern matrices in population biology (PvdD)

In some models, the signs of parameters rather than their exact values may be known. For example, foxes eat rabbits, but how much benefit does a fox obtain by eating one rabbit? So rather than analyzing numerical matrices, sign pattern matrices need to be analyzed. This qualitative topic has a rich history for about the last 50 years, and relates to the theory of directed graphs. There are a few applications relevant to population biology, and possibly many more that need to be explored. Basic definitions and concepts for ODE models are introduced, focussing on sign stability and potential stability of sign patterns. These are illustrated with biological models, including the Goodwin model in cellular physiology, and an infectious disease model with several recovery stages.

### Lecture 8: Target reproduction numbers and applications to biological models (PvdD)

Target reproduction numbers are defined and shown to unify threshold parameters in population biology, including the net reproductive value used in ecology and the basic reproduction number used in epidemiology. Both algebraic (using matrices) and graphical (using weighted digraphs) approaches to computing target reproduction numbers are developed. Knowledge of these target reproduction numbers is demonstrated to aid in measuring the change of certain model parameters in order to protect endangered species, control invasive species, and to determine disease control strategies.

### Lecture 9: Group inverse: Theory, computation, and applications in mathematical biology (SK)

Eigenvalues and eigenvectors of matrices can carry information that has important implications for matrix-based models. (Indeed this is a key theme of this conference.) How do eigenvalues/eigenvectors behave when the entries in a matrix are perturbed? It turns out that a certain generalised inverse - the group inverse - is central tool for understanding this type of perturbation problem. In this lecture we give a brief introduction to the group inverse and discuss

its utility in spectral perturbation problems. The group inverse technique is especially useful in the settings of nonnegative matrices and M-matrices, and applications of that technique to matrix population models and patch models will be emphasised. We will also discuss some of the approaches to computing the group inverse numerically.

### Lecture 10: Persistence dynamics for stage-structured integrodifference models (ML)

In this lecture I will develop the general theory for population persistence and critical patch size problems with stage-structured integrodifference models. I will relate the critical patch size problem to the spreading speed analysis from Lecture 6 in the case of populations with unidirectional flow dynamics (e.g., rivers). Here, I will develop an analytical approach to model population persistence using a spatial version of the net reproductive rate (now arising from an infinite-dimensional next generation operator) and will also derive other related metrics for population persistence. Applications will be made to zebra mussel dynamics in rivers.

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